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New geographical records of *Neopestalotiopsis* and *Pestalotiopsis* species in Guangdong Province, China

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Abstract

A study of monocotyledon inhabiting fungi in Guangdong Province, China resulted in the collection of several pestaloid taxa. Evidence from multi-locus phylogenies using ITS, BT and tef 1–α, together with morphology revealed *Neopestalotiopsis alpapicalis*, *Pestalotiopsis diploclisiae* and *P. parva* from living leaves of *Phoenix roebelenii*. *Pestalotiopsis parva* was also found on a dead petiole of *Phoenix* sp. and *P. diploclisiae* on dead leaves of *Butia* sp. *Pestalotiopsis foedans*, *P. lawsoniae*, *P. macadamia* and *P. virgatula* have been reported in Guangdong Province, and *Pestalotiopsis parva* and *P. diploclisiae* reported for the first time. This *Neopestalotiopsis alpapicalis* collection is the first species of the genus collected from this province. We provide descriptions and illustrations for these three isolates. Additionally, we provide a list of *Pestalotiopsis* and *Neopestalotiopsis* species recorded from China.

Key words – Appendage bearing conidia – Coelomycetes – Monocotyledons – Saprobes – Sporocadaceae

Introduction

Pestalotiopsis Steyaert was introduced to accommodate pestaloid species with 5-celled conidia (Steyaert 1949). Maharachchikumbura et al. (2014) re-examined *Pestalotiopsis* at the morphological and molecular levels and introduced two new genera, *Neopestalotiopsis* and *Pseudopestalotiopsis*. Currently, these three genera placed in Sporocadaceae (Amphisphaeriales) (Wijayawardene et al. 2018, Hyde et al. 2020). *Neopestalotiopsis* typified by *N. protearum* (Crous & L. Swart) Maharachch., K.D. Hyde & Crous, is morphologically distinguished from other pestaloid genera by its varicolored median cells and indistinct conidiophores which are often reduced to conidiogenous cells. *Pestalotiopsis* typified by *P. guepinii* (Desm.) Steyaert and is easily

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distinguished from other pestaloid genera as its conidia have concolourous median cells (Maharachchikumbura et al. 2014).

Species in both *Pestalotiopsis* and *Neopestalotiopsis* commonly occur as endophytes in leaves (Hu et al. 2007, Liu et al. 2010, Maharachchikumbura et al. 2012a, Debbab et al. 2013, Chen et al. 2018, Norphanphoun et al. 2019), saprobes on dead leaves (Ariyawansa & Hyde 2018, Tsai et al. 2018), bark and twigs (Ellis & Ellis 1997) or human and animal pathogens (Monden et al. 2013). Some species found from soil, fabrics, wools and some are in the extreme environments (Guba 1961, Strobel et al. 1996, Tejesvi et al. 2007). Some *Pestalotiopsis* species can degrade plastics (Russell et al. 2011). Pestaloid endophytes produce chemical compounds, which use in therapeutic applications and agriculture (Aly et al. 2010, Xu et al. 2010, 2014). Therefore, investigation of novel pestaloid taxa and their chemical properties are of importance.

In this study, we collected three pestaloid taxa from Shenzhen, Guangdong Province, China, and their identifications, and phylogenetic relationships are investigated based on morphology and DNA sequence data of the internal transcribed spacer (ITS), β-tubulin (BT) and partial translation elongation factor 1-α gene (tef 1–α). Additionally, a list of *Pestalotiopsis* and *Neopestalotiopsis* species recorded from China is provided.

Materials & Methods

Sample collection and fungal isolation

Samples were collected in a survey of monocotyledon inhabiting fungi during 2018–2019 in Guangdong Province, China. The samples were brought to the laboratory in paper bags. They were examined and photographed using a Carl Zeiss Discovery V8 stereomicroscope fitted with Axiocam. The morphological characters were photographed using a Nikon Eclipse 80i compound microscope fitted with a Canon 450D digital camera. All microscopic measurements were made with Tarosoft image framework (v. 0.9.0.7). Colony characters were recorded from cultures grown on potato dextrose agar (PDA).

Single conidia isolation was carried out following the method described by Senanayake et al. (2018). Germinated conidia were aseptically transferred into fresh PDA plates, and incubated at 16°C to obtain pure cultures. Cultures were later transferred to PDA slants and stored at 4°C for further studies. All the voucher specimens are deposited in the fungaria of Mae Fah Luang University (MFLU), and living cultures are deposited at the Culture Collection of Kunming Institute of Botany (KUMCC).

DNA extraction, PCR amplification and DNA sequencing

Fungal mycelium grown on PDA for two weeks at 16°C in the dark and fruit bodies directly picked from the specimens were used for DNA extraction using M5 fungal Genomic DNA extraction kit. PCR reactions were carried out using ITS1/ITS4 for internal transcribed spacer nrDNA (ITS) (White et al. 1990), BT2a/BT2b for β-tubulin (BT) (Glass & Donaldson 1995), and EF1-728F/EF2 for translation elongation factor 1-α (tef 1–α) (Rehner 2001, Liu et al. 2017) genes according to the same protocol of Maharachchikumbura et al. (2014).

The amplification reactions were carried out with the following protocol: 25 μL reaction volume containing 1 μL of DNA template, 1 μL of each forward and reverse primers, 12.5 μL of 2×PCR Master Mix and 9.5 μL of double-distilled sterilized water (ddH_2O). The PCR products were observed on 1% agarose electrophoresis gel stained with ethidium bromide. Purification and sequencing of PCR products were carried out at the Sunbiotech Company, Beijing, China. Sequence quality was checked and sequences were concatenated with DNASTAR Lasergene v.7.1. Sequences derived in this study were deposited in the GenBank, and accession numbers were obtained (Table 1).

Sequence alignment and phylogenetic analyses

BLASTn searches were made using the newly generated sequences to assist taxon sampling for phylogenetic analyses. All sequences obtained from GenBank and used by Maharachchikumbura et al. (2014, 2016), Liu et al. (2017), Nozawa et al. (2017), Ariyawansa & Hyde (2018), Chen et al. (2018), Tibpromma et al. (2018), Tsai et al. (2018), Watanabe et al. (2018), Norphanphoun et al. (2019), are listed in Table 1. DNA sequence data of the ITS, BT and tef 1–α sequence alignments were done using default settings of MAFFT v.7 (Katoh et al. 2017) and manually adjusted using BioEdit 7.1.3 (Hall 1999) to allow maximum alignment and minimum gaps. The evolutionary models for phylogenetic analyses were determined by MrModeltest v. 2.3 under the Akaike Information Criterion (AIC) was implemented in PAUP v. 4.0b10 (Nylander 2004).

Maximum likelihood analysis was performed by RAxML (Stamatakis & Alachiotis 2010) implemented in raxmlGUIv.1.3 (Silvestro & Michalak 2012). The search strategy was set to rapid bootstrapping, and the analysis carried out using the GTRGAMMAI model of nucleotide substitution with 1,000 replicates.

For the Bayesian inference (BI) analyses of the individual loci and concatenated ITS, BT and tef 1–α alignment, the above-mentioned model test was used to determine the best fitting nucleotide substitution model settings for MrBayes v. 3.0b4. Dirichlet base frequencies and the GTR+I+G model with inverse gamma-distributed rate were predicted by the MrModeltest analysis for all three data partitions and used in the Bayesian analysis.

The Markov Chain Monte Carlo sampling (MCMC) resulted in MrBayes v. 3.0b4 (Huelsenbeck et al. 2003) was used to calculate Posterior probability values (Zhaxybayeva & Gogarten 2002). Four simultaneous Markov chains were initially run for 10,000,000 generations, and every 500th generation was sampled. The distribution of log-likelihood scores was observed to check whether sampling is in stationary phase or not and Tracer v1.5 was used to check if further runs were required to reach convergence or not (Rambaut & Drummond 2007).

The Bayesian analysis lasted 10,000,000 generations (average standard deviation of split frequencies value = 0.0098), and the consensus tree and posterior probabilities were calculated after discarding the first 20% of sampled trees as burn-in. The remaining trees were used for calculating posterior probabilities in the majority rule consensus tree. The bootstrap values equal to or greater than 0.9 are given below or above each node (Figs 1, 2). The phylogram was visualized in FigTree v. 1.2.2 (Rambaut & Drummond 2008).

Table 1 Details of the isolates used in the phylogenetic tree. Newly generated sequences are bold.

Taxon	**Culture accession number**	**Genbank number**		
		ITS	**β-tubulin**	**tef 1–α**
Neopestalotiopsis acrostichi	MFLUCC 17-1754	MK764272	MK764338	MK764316
Neopestalotiopsis alpapicalis	MFLUCC 17-2544	MK357772	MK463545	MK463547
Neopestalotiopsis alpapicalis	**KUMCC 20-0036**	**MT222276**	**MT135199**	**MT175375**
Neopestalotiopsis alpapicalis	**KUMCC 20-0037**	**MT222277**	**MT135200**	**MT175376**
Neopestalotiopsis aotearoa	CBS 367.54	KM199369	KM199454	KM199526
Neopestalotiopsis asiatica	MFLUCC 12-0286	JX398983	JX399018	JX399049
Neopestalotiopsis australis	CBS 114159	KM199348	KM199432	KM199537
Neopestalotiopsis brachiata	MFLUCC 17-1555	MK764274	MK764340	MK764340
Neopestalotiopsis brasiliensis	PA10	N/A	MK286948	MK253112
Neopestalotiopsis chiangmaiensis	MFLUCC 18-0113	N/A	MH412725	MH388404
Neopestalotiopsis chrysea	MFLUCC 12-0261	JX398986	JX399021	JX399052
Neopestalotiopsis clavispora	MFLUCC 12-0281	MN121843	MN121844	MN121845
Neopestalotiopsis cocoes	MFLU 15-0220	NR-156312	N/A	N/A
Neopestalotiopsis coffea-arabicae	HGUP 4015	KF412647	KF412641	KF412644
Neopestalotiopsis cubana	CBS 600.96	KM199347	KM199438	KM199521
Neopestalotiopsis egyptiaca	PEST1	KP943747	KP943746	KP943748
Neopestalotiopsis ellipsospora	MFLUCC 12-0283	JX398981	JX399015	JX399046
Neopestalotiopsis eucalypticola	CBS 264.37	KM199376	KM199431	KM199551
Neopestalotiopsis foedans	CGMCC 3.9123	JX398987	JX399022	JX399053
Neopestalotiopsis formicarum	CBS 362.72	KM199358	KM199455	KM199517

Table 1 Continued.

Taxon	Culture accession number	Genbank number		
		ITS	**β-tubulin**	**tef 1–α**
Neopestalotiopsis honoluluana	CBS 111535	N/A	KM199461	KM199546
Neopestalotiopsis honoluluana	CBS 114495	KM199364	KM199457	KM199548
Neopestalotiopsis iraniensis	P815	N/A	N/A	N/A
Neopestalotiopsis javaensis	CBS 257.31	KM199357	KM199457	KM199548
Neopestalotiopsis keteleeria	MFLUCC 13-0915	KJ503820	KJ503821	KJ503822
Neopestalotiopsis macadamiae	BRIP 63737c	NR-161002	KX186654	KX186627
Neopestalotiopsis magna	MFLUCC 12-0055	KF582795	KF582793	KF582791
Neopestalotiopsis mesopotamica	CBS 464.69	KM199353	KM199436	N/A
Neopestalotiopsis musae	MFLUCC 15-0776	NR-156311	KX789686	KX789685
Neopestalotiopsis natalensis	CBS 138.41	NR-156288	KM199466	KM199552
Neopestalotiopsis pandanicola	KUMCC 17-0175	N/A	MH412720	MH388389
Neopestalotiopsis pernambucana	RV01	KJ792466	N/A	N/A
Neopestalotiopsis petila	MFLUCC 17-1737	MK764276	MK764342	MK764320
Neopestalotiopsis phangngaensis	MFLUCC 18-0119	MH388354	MH412721	MH388390
Neopestalotiopsis piceana	CBS 225.30	KM199371	KM199451	KM199535
Neopestalotiopsis piceana	CBS 394.48	KM199368	KM199453	KM199527
Neopestalotiopsis protearum	CBS 114178	JN712498	KM199463	KM199542
Neopestalotiopsis rhizophorae	MFLUCC 17-1550	MK764277	MK764343	MK764321
Neopestalotiopsis rosae	CBS 124745	KM199360	KM199430	KM199524
Neopestalotiopsis rosicola	CFCC 51992	KY885239	KY885245	KY885243
Neopestalotiopsis samarangensis	CBS 115451	KM199365	KM199447	KM199556
Neopestalotiopsis saprophytica	CBS 115452	KM199345	KM199433	KM199538
Neopestalotiopsis saprophytica	MFLUCC 12-0282	JX398982	JX399017	JX399048
Neopestalotiopsis sonneratae	MFLUCC 17-1744	MK764280	MK764346	MK764324
Neopestalotiopsis sp.	CBS 266.37	KM199349	KM199459	KM199547
Neopestalotiopsis sp.	CBS 323.76	KM199350	KM199458	KM199550
Neopestalotiopsis sp.	FMB 0127	N/A	MH460876	MH523647
Neopestalotiopsis sp.	FMB 0128	N/A	MH460875	MH523646
Neopestalotiopsis sp.	CBS 119.75	KM199356	KM199439	KM199531
Neopestalotiopsis sp.	LC3318	KX894964	KX895296	KX895181
Neopestalotiopsis sp.	LC6285	KX895013	KX895346	KX895232
Neopestalotiopsis sp.	LC6471	KX895019	KX895352	KX895238
Neopestalotiopsis sp.	LPS61	MF379331	N/A	N/A
Neopestalotiopsis sp.	SC2A3	KU252210	KU252477	KU252390
Neopestalotiopsis sp.	SC2A4	KX146639	KX146757	KX146698
Neopestalotiopsis sp.	SC3A3	KU252211	KU252478	KU252391
Neopestalotiopsis sp.	SC5A9	KU252212	KU252479	KU252392
Neopestalotiopsis sp.	YN1A5	KU252216	KU252483	KU252396
Neopestalotiopsis sp.	ZJ1A2	KU252215	KU252482	KU252395
Neopestalotiopsis sp.	CBS 274.29	KM199375	KM199448	KM199534
Neopestalotiopsis sp.	CBS 322.76	KM199366	KM199446	KM199536
Neopestalotiopsis sp.	CBS 360.61	KM199346	KM199440	KM199522
Neopestalotiopsis sp.	CBS 110.20	KM199342	KM199442	KM199540
Neopestalotiopsis sp.	CBS 164.42	KM199367	KM199434	KM199520
Neopestalotiopsis sp.	URM7148	N/A	N/A	KU306740
Neopestalotiopsis steyaertii	IMI 192475	KF582796	KF582794	KF582792
Neopestalotiopsis surinamensis	CBS 111494	N/A	KM199462	KM199530
Neopestalotiopsis surinamensis	CBS 450.74	KM199351	KM199465	KM199518
Neopestalotiopsis thailandica	MFLUCC 17-1730	MK764281	MK764347	MK764325
Neopestalotiopsis umbrinospora	MFLUCC 12-0285	JX398984	JX399019	JX399050
Neopestalotiopsis vitis	JZB340018	KU140694	KU140685	KU140676
Neopestalotiopsis zimbabwana	CBS 111495	JX556231	KM199456	KM199545
Pestalotiopsis adusta	ICMP 6088	JX399006	JX399037	JX399070
Pestalotiopsis adusta	MFLUCC 10-0146	JX399007	JX399038	JX399071
Pestalotiopsis aggestorum	LC6301	KX895015	KX895348	KX895234

Table 1 Continued.

Taxon	Culture accession number	Genbank number		
		ITS	β-tubulin	tef 1–α
Pestalotiopsis aggestorum	LC8186	KY464140	KY464160	KY464150
Pestalotiopsis anacardiacearum	IFRDCC 2397	KC247154	KC247155	KC247156
Pestalotiopsis arceuthobii	CBS 434.65	KM199341	KM199427	KM199516
Pestalotiopsis arengae	CBS 331.92	KM199340	KM199426	KM199515
Pestalotiopsis australasiae	CBS 114126	KM199297	KM199409	KM199499
Pestalotiopsis australasiae	CBS 114141	KM199298	KM199410	KM199501
Pestalotiopsis australis	CBS 114193	KM199334	KM199385	KM199477
Pestalotiopsis australis	CBS 119350	KM199333	KM199384	KM199476
Pestalotiopsis biciliata	CBS 124463	KM199308	KM199399	KM199505
Pestalotiopsis biciliata	CBS 790.68	MH859228	KM199400	KM199507
Pestalotiopsis brachiata	LC2988	KX894933	KX895265	KX895150
Pestalotiopsis brachiata	LC8188	KY464142	KY464162	KY464152
Pestalotiopsis brassicae	CBS 170.26	KM199379	N/A	KM199558
Pestalotiopsis camelliae	CBS 443.62	KM199336	KM199424	KM199512
Pestalotiopsis camelliae	MFLUCC 12-0277	KY319138	KY363542	KY342366
Pestalotiopsis chamaeropis	CBS 113604	KM199323	KM199389	KM199471
Pestalotiopsis chamaeropis	CBS 186.71	KM199325	KM199390	KM199472
Pestalotiopsis chinensis	LC3013	KX894939	KX895271	KX895156
Pestalotiopsis clavata	MFLUCC 12-0268	JX398990	JX399025	JX399056
Pestalotiopsis colombiensis	CBS 118553	KM199307	KM199421	KM199488
Pestalotiopsis digitalis	ICMP 5434	KP781879	KP781883	N/A
Pestalotiopsis diploclisiae	CBS 115587	KM199314	KM199416	KM199485
Pestalotiopsis diploclisiae	**KUMCC 20–0035**	**MT222272**	**N/A**	**MT175371**
Pestalotiopsis distincta	LC3232	KX894961	KX895293	KX895178
Pestalotiopsis diversiseta	MFLUCC 12-0287	NR_120187	JX399040	JX399073
Pestalotiopsis dracontomelon	MFLUCC 10-0149	KP781877	N/A	KP781880
Pestalotiopsis ericacearum	OP023	KC537807	KC537821	KC537814
Pestalotiopsis formosana	NTUCC 17-0010	MH809382	MH809386	MH809390
Pestalotiopsis formosana	NTUCC 17-0009	MH809381	MH809385	MH809389
Pestalotiopsis funerea	ML4DY	EF055197	EF055234	N/A
Pestalotiopsis furcata	MFLUCC 12-0054	JQ683724	JQ683708	JQ683740
Pestalotiopsis gaultheria	IFRD 411-014	KC537805	KC537819	KC537812
Pestalotiopsis gibbosa	Pes6	LC311589	LC311590	LC311591
Pestalotiopsis grevilleae	CBS 114127	KM199300	KM199407	KM199504
Pestalotiopsis hawaiiensis	CBS 114491	KM199339	KM199428	KM199514
Pestalotiopsis hollandica	CBS 265.33	KM199328	KM199388	KM199481
Pestalotiopsis humus	CBS 115450	KM199319	KM199418	KM199487
Pestalotiopsis humus	CBS 336.97	KM199317	KM199420	KM199484
Pestalotiopsis inflexa	MFLUCC 12-0270	JX399008	JX399039	JX399072
Pestalotiopsis intermedia	MFLUCC 12-0259	JX398993	JX399028	JX399059
Pestalotiopsis italiana	MFLUCC 12-0657	KP781878	KP781882	KP781881
Pestalotiopsis jesteri	CBS 109350	KM199380	KM199468	KM199554
Pestalotiopsis jiangxiensis	LC4399	KX895009	KX895341	KX895227
Pestalotiopsis jinchanghensis	LC6636	KX895028	KX895361	KX895247
Pestalotiopsis jinchanghensis	LC8190	KY464144	KY464164	KY464154
Pestalotiopsis kenyana	CBS 442.67	KM199302	KM199395	KM199502
Pestalotiopsis kenyana	CBS 911.96	KM199303	KM199396	KM199503
Pestalotiopsis knightiae	CBS 111963	KM199311	KM199406	KM199495
Pestalotiopsis knightiae	CBS 114138	KM199310	KM199408	KM199497
Pestalotiopsis licualacola	HGUP 4057	KC492509	KC481683	KC481684
Pestalotiopsis linearis	MFLUCC 12-0271	JX398992	JX399027	JX399058
Pestalotiopsis longiappendiculata	LC3013	KX894939	KX895271	KX895156
Pestalotiopsis lushanensis	LC4344	KX895005	KX895337	KX895223
Pestalotiopsis lushanensis	LC8182	KY464136	KY464156	KY464146
Pestalotiopsis macadamiae	BRIP 63738b	KX186588	KX186680	KX186621

Table 1 Continued.

Taxon	Culture accession number	Genbank number		
		ITS	β-tubulin	tef 1–α
Pestalotiopsis malayana	CBS 102220	KM199306	KM199411	KM199482
Pestalotiopsis microspora	UMAS P15	KT337388	N/A	N/A
Pestalotiopsis monochaeta	CBS 144.97	KM199327	KM199386	KM199479
Pestalotiopsis monochaeta	CBS 440.83	KM199329	KM199387	KM199480
Pestalotiopsis montellica	MFLUCC 12-0279	JX399012	JX399043	JX399076
Pestalotiopsis neglecta	1100	AB482220	LC311599	LC311600
Pestalotiopsis neolitseae	NTUCC 17-011	MH809383	MH809387	MH809391
Pestalotiopsis novae-hollandiae	CBS 130973	KM199337	KM199425	KM199511
Pestalotiopsis oryzae	CBS 111522	KM199294	KM199394	KM199493
Pestalotiopsis oryzae	CBS 171.26	MH854881	KM199397	KM199494
Pestalotiopsis paeoniicola	TR40	N/A	KY930634	N/A
Pestalotiopsis paeoniicola	TR41	N/A	KY930635	N/A
Pestalotiopsis pallidotheae	110	N/A	LC311584	LC311585
Pestalotiopsis papuana	CBS 331.96	KM199321	KM199413	KM199491
Pestalotiopsis papuana	CBS 887.96	KM199318	KM199415	KM199492
Pestalotiopsis parva	**KUMCC 20-0038**	**MT222274**	**MT135197**	**MT175373**
Pestalotiopsis parva	**MFLU 20-0060**	**MT222275**	**MT135198**	**MT175374**
Pestalotiopsis parva	CBS 265.37	KM199312	KM199404	KM199508
Pestalotiopsis parva	CBS 278.35	KM199313	KM199405	KM199509
Pestalotiopsis portugalica	CBS 393.48	KM199335	KM199422	KM199510
Pestalotiopsis rhizophorae	MFLUCC 17-0417	MK764284	MK764350	MK764328
Pestalotiopsis rhododendri	CBS 144024	MH554109	MH554782	MH554543
Pestalotiopsis rhododendri	OP086	KC537804	KC537818	KC537811
Pestalotiopsis rosea	MFLUCC 12-0258	JX399005	JX399036	JX399069
Pestalotiopsis scoparia	CBS 176.25	KM199330	KM199393	KM199478
Pestalotiopsis shorea	MFLUCC 12-0314	KJ503811	KJ503814	KJ503817
Pestalotiopsis sp.	UMAS 1705	KT337373	N/A	N/A
Pestalotiopsis sp.	CBS 263.33	KM199316	KM199414	KM199489
Pestalotiopsis sp.	CBS 264.33	KM199322	KM199412	KM199490
Pestalotiopsis sp.	HGUP 4057	KC492509	KC481683	KC481684
Pestalotiopsis spathulata	CBS 356.86	KM199338	KM199423	KM199513
Pestalotiopsis telopeae	CBS 113606	KM199295	KM199402	KM199498
Pestalotiopsis telopeae	CBS 114161	KM199301	KM199469	KM199559
Pestalotiopsis thailandica	MFLUCC 17-1616	MK764285	MK764351	MK764329
Pestalotiopsis theae	CMU-ELA1	JX205216	N/A	N/A
Pestalotiopsis theae	CPO Pe	JQ619652	N/A	N/A
Pestalotiopsis trachicarpicola	CBS 111507	MH553960	MH554619	MH554378
Pestalotiopsis trachicarpicola	HN 56.2	N/A	MK360941	MK512494
Pestalotiopsis unicolor	MFLUCC 12-0275	JX398998	JX399029	MK512494
Pestalotiopsis unicolor	MFLUCC 12-0276	JX398999	JX399030	N/A
Pestalotiopsis verruculosa	MFLUCC 12-0274	JX398996	N/A	JX399061
Pestalotiopsis yanglingensis	LC3067	KX894949	KX895281	KX895166
Pestalotiopsis yanglingensis	LC4553	KX895012	KX895345	KX895231

Abbreviations: BRIP: The Plant Pathology Herbarium, Queensland, Australia; CBS: Culture collection of the Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, The Netherlands; CFCC: Chinese Forestry Culture Collection Center, Chinese Academy of Sciences, Beijing, China; CGMCC: China General Microbiological Culture Collection Center, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China; HGUP: The Plant Pathology Herbarium of Guizhou University, China; ICMP: International Collection of Microorganisms from Plants, Auckland, New Zealand; IFRDCC: International Fungal Research & Development Centre Culture Collection, China; IMI: Culture collection of CABI Europe UK Centre, Egham, UK; KUMCC: Culture Collection of Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China; MFLU: Mae Fah Luang University Herbarium, Chiang Rai; Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; NTUCC: National Taiwan University culture collection, Taiwan; UMAS: Department of Plant Science and Environmental Ecology, Faculty of Resource Science and Technology, University Malaysia Sarawak

Results

Phylogenetic inferences

The first combined BT, ITS and tef 1–α sequence dataset comprised 102 strains of *Pestalotiopsis*, and *Neopestalotiopsis* sp. (CBS 119.75) was the outgroup taxon. The second combined BT, ITS and tef 1–α sequence data set comprised 72 sequences of *Neopestalotiopsis* with *Pestalotiopsis parva* (CBS 265.37) as the outgroup taxon. Both concatenated data matrixes comprised 1527 characters (ITS: 566, BT: 469 and tef 1–α: 490). All individual trees generated under different criteria. Single-gene datasets were essentially similar in topology and not significantly different from the tree generated from the concatenated dataset (not discussed herein).

Maximum likelihood analysis for *Pestalotiopsis* with 1,000 bootstrap replicates yielded a tree with the likelihood value of ln: –13138.225580 and the following model parameters: alpha: 0.550988; Π(A): 0.239550, Π(C): 0.287070, Π(G): 0.215467 and Π(T): 0.257914. Maximum likelihood analysis for *Neopestalotiopsis* with 1,000 bootstrap replicates yielded a tree with the likelihood value of ln –6466.001103 and the following model parameters: alpha: 0.731256; Π(A): 0.234344, Π(C): 0.266539, Π(G): 0.216132 and Π(T): 0.282985. The ML analyses also resulted in similar tree topologies to those obtained in the Bayesian analyses. The best scoring RAxML trees derived from the analyses of the concatenated datasets for *Pestalotiopsis (*ingroup*)* and *Neopestalotiopsis (*ingroup*)* are shown in Figs 1, 2, respectively. Maximum likelihood bootstrap values ≥50% and Bayesian inference (BI) ≥0.9 are given at each node.

In our concatenated ML analyses, one *Pestalotiopsis* isolate (KUMCC 20–0035) form a distinct subclade with *P. diploclisiae* (CBS 115449) with high statistical support (Fig. 1). In addition, the other two isolates of *Pestalotiopsis (*KUMCC 20–0038 and MFLU 20–0060*)* form a separate, high statistical supported lineage with *Pestalotiopsis parva* (CBS 278.35 and CBS 265.37). Hence, *Pestalotiopsis* strains of KUMCC 20–0038/MFLU 20–0060 is confirmed as *Pestalotiopsis parva* (Fig. 1). In the second dataset, two strains of *Neopestalotiopsis* form a distinct subclade with *Neopestalotiopsis alpapicalis* and *N. rhizophorae* with high statistical support. Hence, this collection is proposed here as *Neopestalotiopsis alpapicalis* (Fig. 2).

Taxonomy

Pestalotiopsis diploclisiae Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 160 (2014) Fig. 3

Facesoffungi number: FoF 06982

Saprobic, associated with dead leaves of *Butia* sp. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 500–900 μm diam., pycnidial, globose, blackish brown, immersed on substrate, semi-immersed in PDA, releasing conidia as a black, slimy, globose, glistening mass on culture media. *Conidiophores* indistinct or reduced to conidiogenous cells. *Conidiogenous cells* 5–20 × 2–3 μm ($\bar{x}$ = 11 × 2.8 μm, n = 20), discrete, lageniform, hyaline, smooth-walled, annellidic, proliferating 2–3 times percurrently, collarette present, may not appears as flared. *Conidia* 18–25 × 5–7 μm ($\bar{x}$ = 23 × 6 μm, n = 20), fusiform to clavate, straight to slightly curved, wall of one side curved than other side, 4-euseptate; basal cell obconic with a truncate base, hyaline or sometimes greenish brown, thick-and smooth-walled, 2–3.5 μm long ($\bar{x}$ = 2.9 μm, n = 20); three median cells ± equal, each 4–5 μm long ($\bar{x}$ = 4 μm), doliiform or trapezoid, concolorous, pale brown, septa and periclinal walls darker than rest of the cell, wall smooth; apical cell 3–5 μm long ($\bar{x}$ = 3.9 μm, n = 20), hyaline, conic to acute with truncate base; apical appendages 8–13 ×0.5–1 μm ($\bar{x}$ = 11.5 × 0.5 μm, n = 40), 3–4 (mostly 3), tubular, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, rough; single basal appendage, tubular, unbranched, centric, 3–6 μm long ($\bar{x}$ = 4.9 μm, n = 20).

Culture characteristics – Colonies on PDA reaching 2 cm diam., after 1 week at 18°C, under dark, colonies circular, medium dense, aerial mycelium on surface raised, white from above and reverse; fruiting bodies appears as black slimy bubbles.

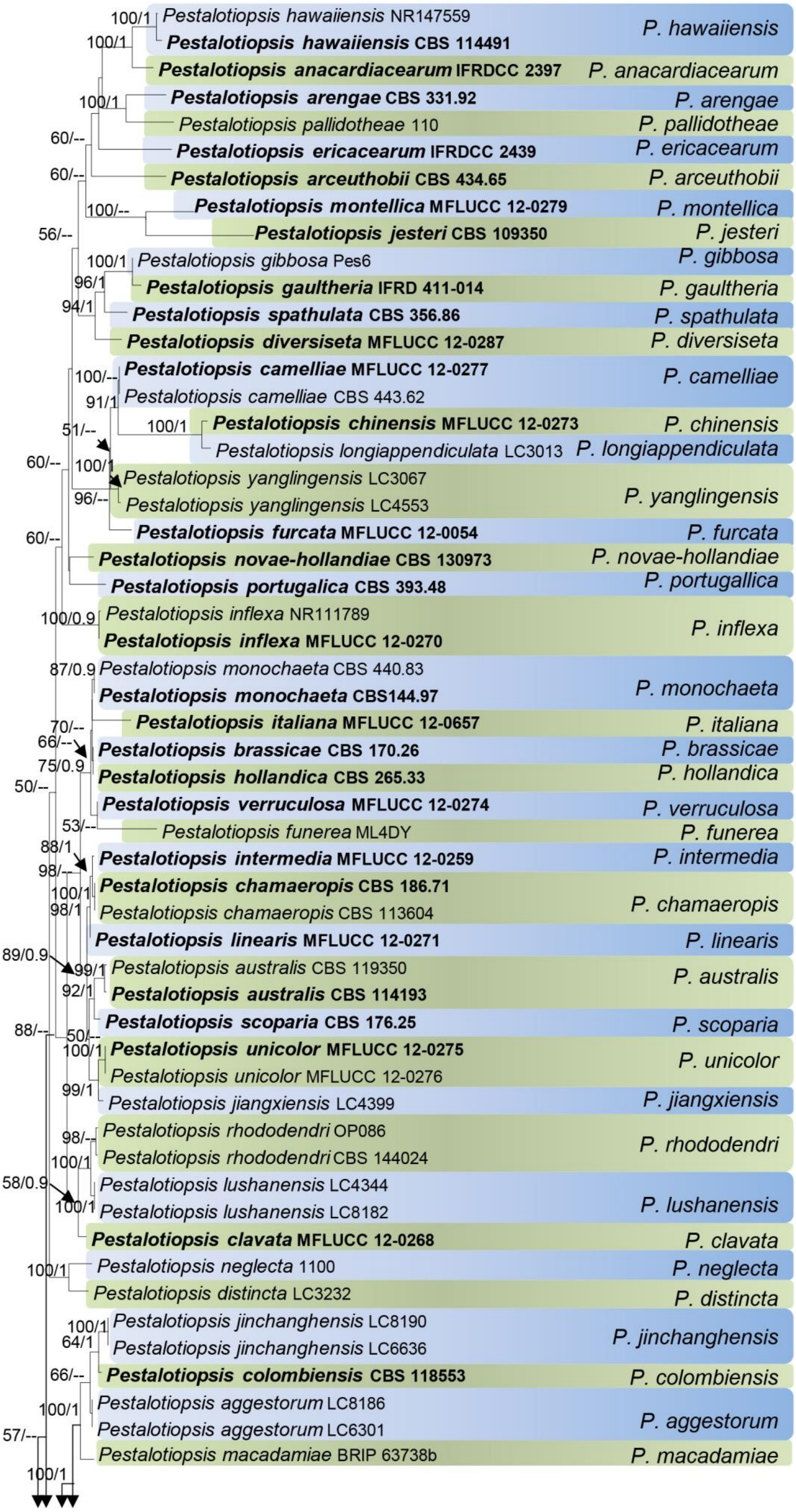

Fig. 1 – Phylogram generated from maximum likelihood analysis based on combined ITS, BT and tef 1–α sequence data. Bootstrap support values for ML greater than 50% and Bayesian posterior

probabilities greater than 0.9 are given near nodes respectively. The tree is rooted with *Neopestalotiopsis* sp (CBS 119.75). Ex-type strains are in black bold and the newly generated sequences are indicated in blue bold.

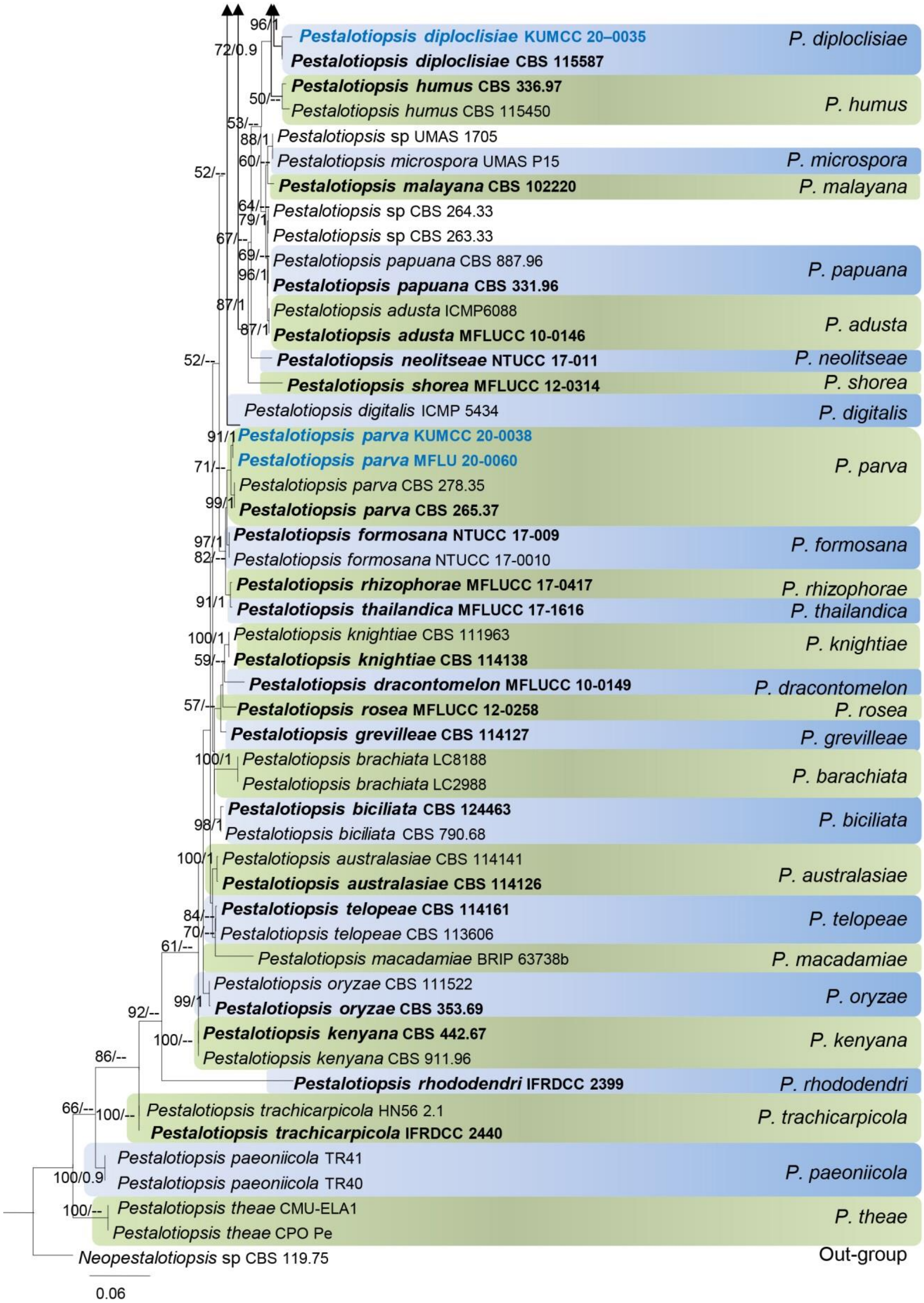

Fig. 1 – Continued.

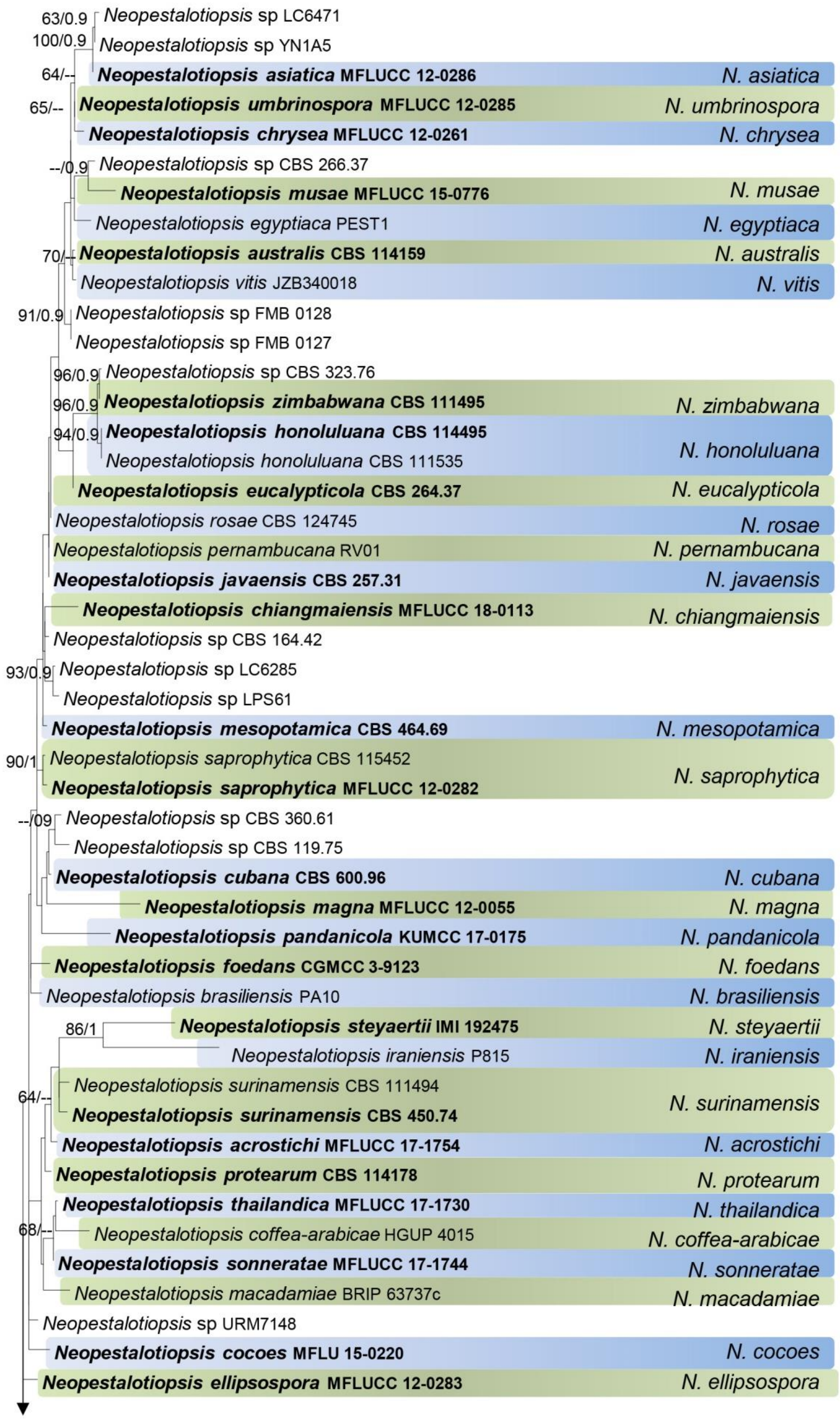

Fig. 1 – Continued.

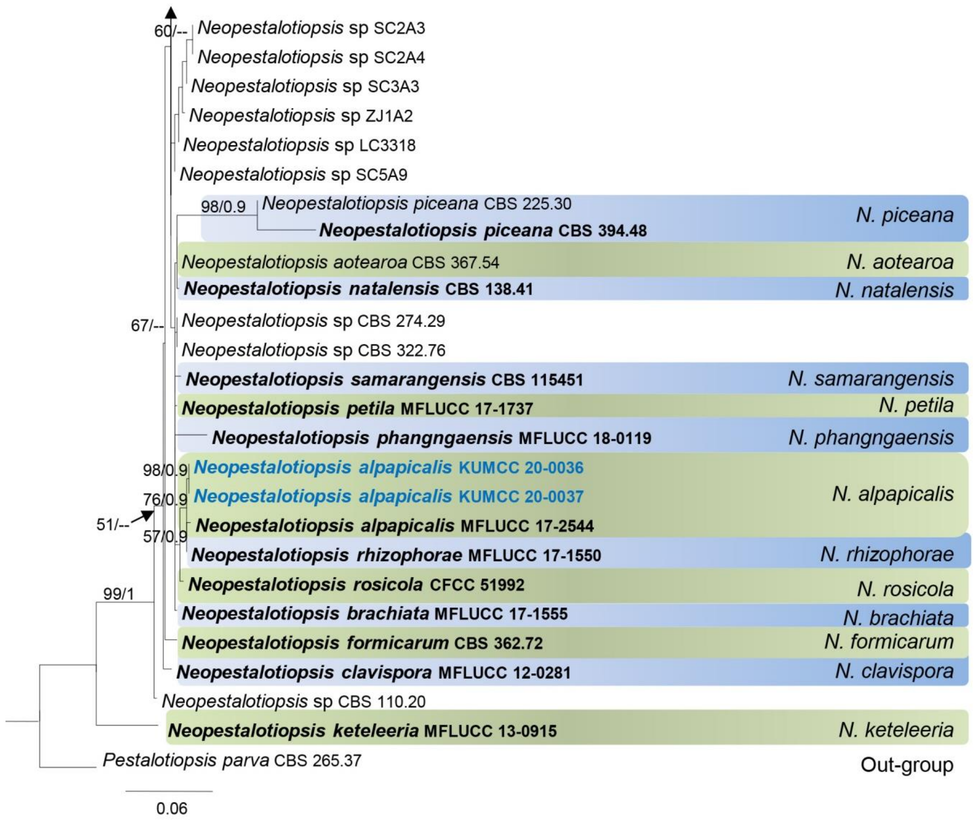

Fig. 2 – Phylogram generated from maximum likelihood analysis based on combined ITS, BT and tef 1–α sequence data. Bootstrap support values for ML greater than 50% and Bayesian posterior probabilities greater than 0.9 are given near nodes respectively. The tree is rooted with *Pestalotiopsis parva* (CBS 265.37). Ex-type strains are in black bold and the newly generated sequences are indicated in blue bold.

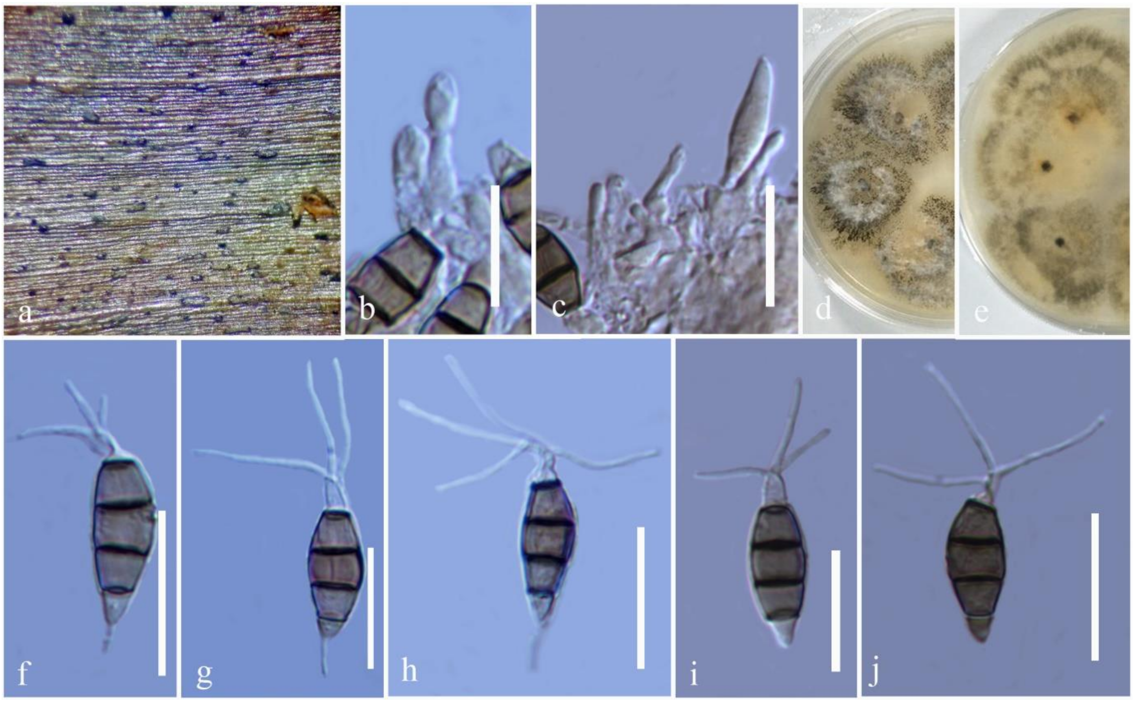

Fig. 3 – *Pestalotiopsis diploclisiae* (MFLU 20–0059). a Conidiomata on substrate. b-c Conidiogenous cells attached to conidia. d Upper surface of culture on PDA. e Lower surface of culture on PDA. f-j Conidia. Scale bars: b-c = 50 µm, f-j = 15 µm.

Material examined – CHINA, Guangdong Province, Shenzhen, Nanshan District, Mountain Yangtai Forest Park, 22º39′21.26″N 113º57′18.53″E, dead leaves of *Butia* sp. (Arecaceae), 5 September 2018, I. C. Senanayake, SI 66, (MFLU 20–0059; living culture KUMCC 20–0035).

Notes – Phylogenetically, our *Pestalotiopsis diploclisiae* collection (KUMCC 20–0035) is closely related to *P. diploclisiae* (CBS 115449) with high bootstrap support. Type strains of *Pestalotiopsis diploclisiae* were collected from fruits of *Diploclisia glaucescens* and *Psychotria tutcheri* in Hong Kong, while our *P. diploclisiae* strain (KUMCC 20–0035) collected from a dead leaf of *Butia* sp. in Shenzhen (China) closer to Hong Kong. The prologue provided by Maharachchikumbura et al. (2014) for *Pestalotiopsis diploclisiae* was based on the morphology derived from cultures. However, our description and illustration are based on the morphology derived from the specimen. Our strain produces smaller (5–11 × 2–3 μm), discrete, lageniform conidiogenous cells and smaller (17–24 × 6–7 μm), fusiform to clavate conidia with conic to acute apical cell and 3–4 apical appendages. Except for the size variation in conidia and conidiogenous cells, our collection of *Pestalotiopsis diploclisiae* (KUMCC 20–0035) is morphologically identical to its holotype. Comparison of the ITS regions DNA sequence of *Pestalotiopsis diploclisiae* (KUMCC 20–0035) with *P. diploclisiae* (CBS 115449) gives 0.94% base pair differences and therefore, our strain assigned as *Pestalotiopsis diploclisiae.*

Pestalotiopsis parva Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 175 (2014) Fig. 4

Facesoffungi number: FoF 07749

Saprobic, associated with dead petiole of *Phoenix* sp. Appears as black spots coming out from plant epidermis surface. Sexual morph: Undetermined. Asexual morph: *Conidiomata* pycnidial, globose, immersed in substrate, semi-immersed on PDA, brown, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–10 × 2–3 ($\bar{x}$ = 8.9 × 2.4 μm, n = 20), discrete, subcylindrical to lageniform, hyaline, smooth, thin-walled, annellidic, proliferating once percurrently. *Conidia* 17–21 × 6–7 μm, ($\bar{x}$ = 18.9 × 6.8 μm, n = 20), fusiform to mostly globose, straight, 4-septate; basal cell conic to acute with a truncate base, hyaline or sometimes pale brown, thin and smooth-walled, 2.5–4 μm long ($\bar{x}$ = 3 μm, n = 20); three median cells ± equal, each 3–5 μm long ($\bar{x}$ = 4 μm, n = 20), doliiform, pale brown, septa darker than rest of the cell, concolorous, wall rugose; apical cell 3–4.5 μm long ($\bar{x}$ = 3.5 μm, n = 20), hyaline, subcylindrical to obconic, with 2–3 tubular appendages on apical cell, arising from the apical crest, unbranched, flexuous, 9–18 × 0.6–0.9 μm ($\bar{x}$ = 13 × 1 μm, n = 20); basal appendage single, tubular, unbranched, centric, 3–4.5 μm long, ($\bar{x}$ = 3.6 μm).

Culture characters – Colonies on PDA reaching 2.5 cm diam**.**, within 1 week at 20ºC, under dark, circular with several layers, medium dense, aerial mycelium clots concentrated along the colony margin, flat, filiform margin, white from above and reverse; fruiting bodies did not appear on cultures.

Material examined – CHINA, Guangdong Province, Shenzhen, Nanshan, Nanhai Avenue, Shenzhen University, dead petiole of *Phoenix* sp. (Arecaceae), 28 August 2018, I.C. Senanayake, SI 9, (MFLU 20–0060, living culture KUMCC 20–0038).

Notes – One of our *Pestalotiopsis* strain (KUMCC 20–0038) clusters with the type species of *P. parva* (CBS 265.37) with moderate bootstrap support in the phylogenetic analysis. *Pestalotiopsis parva* was introduced based on only two strains as CBS 265.37 and CBS 278.35 (Maharachchikumbura et al. 2014). However, the collected localities of those strains are unknown. Maharachchikumbura et al. (2014) described *Pestalotiopsis parva* based on the morphology derived from cultures. However, we obtained morphological characters of our *Pestalotiopsis* strain directly from the specimen, not from culture. Comparison of the ITS sequence of *Pestalotiopsis parva* KUMCC 20–0038 with *P. parva* CBS 265.37 and CBS 278.35 revealed that the base pair differences between them are less than 1% (0.88% and 0.88% respectively) which propose our strain as an existing species (Jeewon & Hyde 2016).

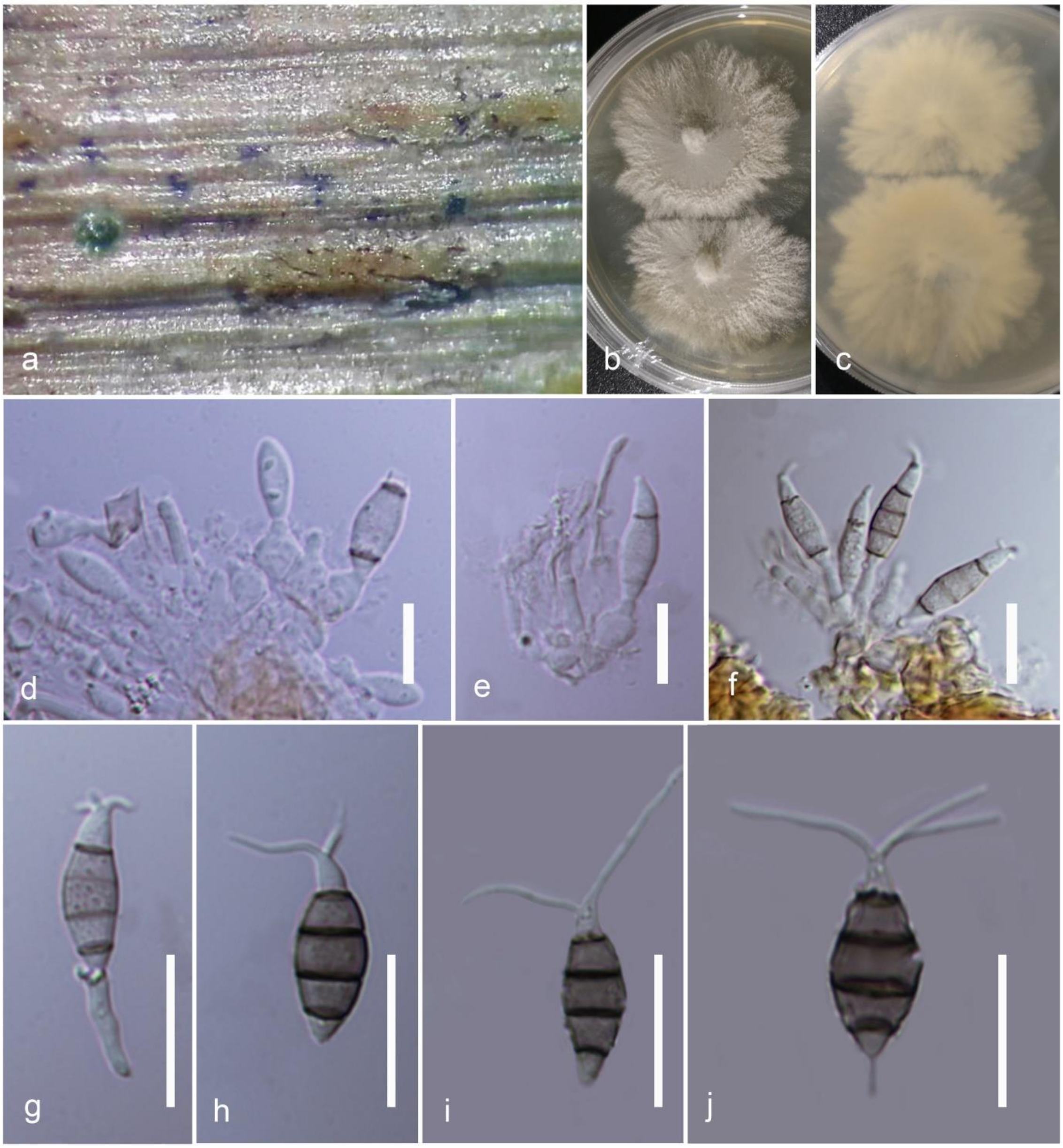

Fig. 4 – *Pestalotiopsis parva* (MFLU 20–0060). a Conidiomata on substrate. b Upper surface of culture on PDA. c Lower surface of culture on PDA. d-f Conidiogenous cells attached to conidia. g-j Conidia. Scale bars: d-j = 20 μm.

Neopestalotiopsis alpapicalis Vin. Kumar, Gentekaki & K.D. Hyde, in Kumar, Cheewangkoon, Gentekaki, Maharachchikumbura, Brahmange & Hyde, Phytotaxa 393(3): 253 (2019) Fig. 5

Facesoffungi number: FoF 05753

Saprobic or *pathogenic*, associated with living leaves of *Phoenix roebelenii*. Sexual morph: Undetermined. Asexual morph: Appears as swollen areas with split barks. *Conidiomata* 25–80 μm diam., pycnidial, globose, black, immersed in substrate, superficial in PDA, releasing conidia as a black, slimy, globose, mass on culture media. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–6 × 3–4 μm ($\bar{x}$ = 5 × 4 μm, n = 20), discrete, annellidic, globose to umbonate, short, hyaline, smooth-walled, simple, wide at the base. *Conidia* 24–28 × 9–11 μm ($\bar{x}$ = 26 × 10 μm, n = 20), ellipsoid, straight to slightly curved, 4–(6)-septate; basal cell conic to obconic with a truncate base, hyaline, thin-and smooth-walled, 3–4 μm long ($\bar{x}$ = 3.8 μm, n = 20); 3–(5) median cells, each 4.5–7 μm long ($\bar{x}$ = 5.5 μm, n = 20), 4–7 μm long ($\bar{x}$ = 5.6 μm, n = 20), 4–6 μm long ($\bar{x}$ = 4.6 μm, n = 20), doliiform, concolorous, pale brown, septa and periclinal walls darker than rest of the cell, wall rugose; apical cell 3–6 μm long ($\bar{x}$ = 4.6 μm, n = 20), long, hyaline, conic to obtuse with truncate base; apical appendages 7–12 µm long (x̅ = 10 µm, n = 20), short, 1–4, more tubular, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous; single basal appendage, tubular, unbranched, rarely branched, centric, 4–6 µm long (x̅ = 4.7 µm, n = 20).

Culture characteristics – Colonies on PDA reaching 2 cm diam**.**, within 10 days at 18°C, under dark, circular, medium dense, aerial mycelium clots scattered on PDA, flat, filiform margin, white from above and reverse; black, globose, sporulate on cultures after 4 weeks incubate at 20°C in dark.

Material examined – CHINA, Guangdong Province, Shenzhen, Luohu District, Fairy-lake botanical garden, 22º34′43.10″N 114°09′55.98″E, living leaves of *Phoenix roebelenii* O'Brien (Arecaceae), 26 July 2018, I.C. Senanayake, SI 100, (MFLU 20–0061, living culture KUMCC 20–0037); CHINA, Guangdong, Shenzhen, Luohu District, Fairy-lake botanical garden, 22°34′43.10″N 114°09′55.98″E, living leaves of *Musa* sp. (Musaceae), 26 July 2018, I.C. Senanayake, SI 103, (MFLU 20–0058, living culture KUMCC 20–0036).

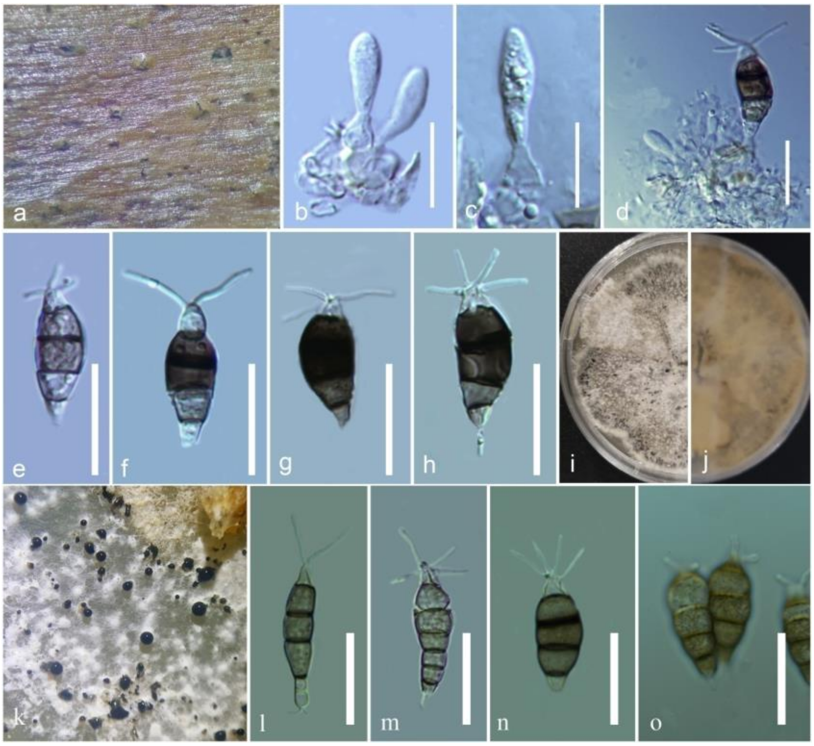

Fig. 5 – *Neopestalotiopsis alpapicalis* (MFLU 20–0058). a Conidiomata on substrate. b-d Conidiogenous cells attached to conidia. e-h Conidia from fruit bodies in substrate. i upper surface of culture on PDA. j Lower surface of culture on PDA. k Conidioma on PDA. l-o Conidia derived from culture (l; unusual basal cell, m; conidia with six cells, o; wall ornamentations). Scale bars: b-h, l-o = 25 µm.

Notes – In the phylogenetic analysis (Fig. 2), our *Neopestalotiopsis* strain forms a distinct subclade basal to *N. alpapicalis* (MFLUCC 17–2544), and *N. rhizophorae* (MFLUCC 17–1550) with moderate bootstrap support. There are 1.27%, 1.07% and 1.02% base pair differences of the ITS (566bp), BT (469bp) and tef 1–α (490bp) sequences of our *Neopestalotiopsis* strains with *N. alpapicalis* (MFLUCC 17–2544), and these values are 1.59%, 0.85%, and 1.02% for *N. rhizophorae* (MFLUCC 17–1550). However, multi-locus gene regions use in this study may not enough to separate *Neopestalotiopsis* species well and there are no more gene regions available in GenBank. Therefore, determination of taxonomy of *Neopestalotiopsis* strains is challenging.

However, morphologically our *Neopestalotiopsis* collection is similar to *N. alpapicalis* more than *N. rhizophorae* in having highly pigmented, conidia with shorter, tubular, apical appendages which are attached to the tip of apical cell. It is difficult to clarify and compare the morphological characters of fungi grown in different media and different growth conditions. Our *Neopestalotiopsis* strain is a saprobe collected from a terrestrial, monocotyledon plant in China, while *Neopestalotiopsis alpapicalis* collected with leaf spots of mangrove plants in Thailand. Therefore, based on available molecular data, morphology and ecological data we named this species as *N. alpapicalis.*

Discussion

Pestalotiopsis parva and *Neopestalotiopsis alpapicalis* collected from *Phoenix* are mostly dominant in northern and central Africa, Southeastern Europe, Southern Asia and east to Southern China (Chase et al. 2000). Fruits of some *Phoenix* species are edible and used as raw materials in the sugar industry. *Phoenix roebelenii* is widely grown for its ornamental value and its fruit used as food for livestock and poultry (Riffle & Craft 2003). *Phoenix* species have some resistant to pests and tolerance to soil variation and drought. Therefore, *Phoenix* species used for reforestation in swamps, deserts and mangrove coasts. *Pestalotiopsis diploclisiae* collected from dead leaves of *Butia*, which is an ornamental genus (Faria et al. 2011) and fruits of *Butia* species are used as foods, such as juices, liquor, marmalades and ice cream, while seeds are used to extract oil. *Musa* species are also important as a food source.

Even though fungal diversity associated with these plants have been studied, the micro-fungi inhabiting them are poorly known in Guangdong Province (Chobba et al. 2013, Shen et al. 2014, Wei et al. 2007, Zakaria & Aziz 2018). In this study, we collected several pestaloid taxa on Butia, Phoenix and Musa species and identified them through morpho-phylogenetic studies. Here, we provide taxonomic details for them.

Colonies of *Pestalotiopsis parva* grew faster on PDA than *Neopestalotiopsis alpapicalis* and *Pestalotiopsis diploclisiae* and did not sporulate in culture. *Pestalotiopsis diploclisiae* and *Neopestalotiopsis alpapicalis* sporulate in culture after four weeks of incubation at 20°C in the dark. Both *Pestalotiopsis diploclisiae* and *Neopestalotiopsis alpapicalis* initially formed copious aerial mycelia clots and those clots disappear with the formation of conidiomata on the PDA.

A checklist of *Neopestalotiopsis* and *Pestalotiopsis* fungi in China is given in Table 2. This includes seven species of *Neopestalotiopsis* and 69 species of *Pestalotiopsis*. Pestaloid fungi are common phytopathogens that cause a variety of diseases, including canker lesions, shoot dieback, leaf spots, needle blight, tip blight, grey blight, scabby canker, severe chlorosis, fruit rots and various post-harvest diseases (Crous et al. 2011, Zhang et al. 2013, Maharachchikumbura et al. 2014). *Pestalotiopsis clavispora* and *P. anacardiacearum* have been reported to cause grey leaf spots and associated with the mango tip borer by *Penicillaria jocosatrix*, respectively in China. *Pestalotiopsis camelliae* was associated with grey leaf blight of *Camellia japonica* and *Pestalotiopsis ericacearum* with leaf spots of *Rhododendron delavayi.*

Table 2 Checklist of *Neopestalotiopsis* and *Pestalotiopsis* fungi in China

Taxon	Host/substrate	Province	References
Neopestalotiopsis asiatica	leaves of tree	Hunan	Maharachchikumbura et al. (2014)
N. chrysea	dead leaves	Guangxi	Maharachchikumbura et al. (2014)
N. clavispora	dead leaves of *Magnolia* sp.	Guangxi	Maharachchikumbura et al. (2014)
N. ellipsospora	dead plant material	Yunnan	Maharachchikumbura et al. (2014)
N. foedans	mangrove plant leaves	Hainan	Maharachchikumbura et al. (2014)
N. saprophytica	leaves of *Magnolia*	Yunnan	Maharachchikumbura et al. (2014)
N. umbrinospora	dead leaves	Guangxi	Maharachchikumbura et al. (2014)
Pestalotiopsis adusta	leaves of *Podocarpus macrophyllus*	Guangxi	Wei et al. (2007)
P. affinis	unknown	Yunnan	Chen et al. (2002)

Table 2 Continued.

Taxon	Host/substrate	Province	References
P. aggestorum	leaves of *Camellia sinensis*	Yunnan	Liu et al. (2017)
P. alpiniae	leaves of *Alpinia galanga*	Guangxi	Chen et al. (2002)
P. anacardiacearum	living leaf of *Mangifera indica*	Yunnan	Maharachchikumbura et al. (2013)
P. antiaris	leaves of *Antiaris toxicaria*	Guangxi	Chen et al. (2002)
P. apiculata	trunk and leaves of *Cunninghamia lanceolata*	Fujian	Huang (1983)
P. brideliae	living leaves of *Bridelia morcica*	China	Chen & Wei (1997)
P. briosiana	twigs of *Camellia sasanqua*	Yunnan	Wei et al. (2007)
P. camelliae	leaves of *Camellia japonica*	Yunnan	Zhang et al. (2012a)
P. canarii	living leaves of *Canarium album*	Guangxi	Chen et al. (2003)
P. chinensis	leaves of *Taxus*	Yunnan	Maharachchikumbura et al. (2012b)
P. clavata	leaf of *Buxus*	Yunnan	Maharachchikumbura et al. (2014)
P. coffeae-arabicae	living leaves of *Coffea arabica*	Hainan	Song et al. (2013)
P. crassiuscula	leaves of *Podocarpus macrophyllus*	Zhejiang	Wei et al. (2007)
P. dilleniae	leaves of *Dillenia turbinata*	Guangxi	Chen et al. (2002)
P. dilucida	leaves of *Camellia sinensis*	Jiangxi	Liu et al. (2017)
P. *diospyri*	leaves of *Podocarpus macrophyllus*		Wei et al. (2007)
P. disseminata	leaves of *Podocarpus macrophyllus*		Wei et al. (2007)
P. diversiseta	leaves of *Rhododendron*		Maharachchikumbura et al. (2014)
P. dracaenae	leaves of *Dracaena fragrans*		Ariyawansa et al. (2015)
P. ericacearum	leaves of *Rhododendron delaveyi*		Zhang et al. (2013)
P. *foedans*	twigs of *Podocarpus massoniana*	Guangdong	Wei et al. (2007)
P. gaultheriae	on *Gaultheria*	Yunnan	Maharachchikumbura et al. (2014)
P. hainanensis	stem of *Podocarpus macrophyllus*	Hainan	Liu et al. (2007)
P. heterocornis	fruit and bark of *Podocarpus macrophyllus*	Zhejiang	Wei et al. (2007)
P. inflexa	leaf of tree	Hunan	Maharachchikumbura et al. (2014)
P. intermedia	dead leaf of tree	Hubei	Maharachchikumbura et al. (2014)
P. jiangxiensis	on *Camellia*	Jiangxi	Liu et al. (2017)
P. jinchanghensis	on leaves of *Camellia sinensis*	Yunnan	Liu et al. (2017)
P. keteleeriae	on leaves of *Keteleeria pubescens*	Guizhou	Song et al. (2014)
P. kunmingensis	leaves of *Podocarpus macrophyllus*	Yunnan	Wei & Xu (2004)

Table 2 Continued.

Taxon	Host/substrate	Province	References
P. kwangsiensis	leaves of *Sinopimelodendron kuwangsiensis*	Guangxi	Chen et al. (2002)
P. lawsoniae	leaves of *Pinus massoniana*; twigs of *Podocarpus massoniana*	Guangxi Guangdong	Wei et al. (2007)
P. licualicola	living leaves of *Licuala grandis*	Hainan	Geng et al. (2013)
P. lijiangensis	unknown	Yunnan	Zhou et al. (2008)
P. linearis	leaves of *Trachelospermum*	Yunnan	Maharachchikumbura et al. (2014)
P. longiappendiculata	*Camellia sinensis*	Fujian	Liu et al. (2017)
P. lushanensis	*Camellia* sp	Jiangxi	Liu et al. (2017)
P. macadamii	living leaves of *Macadamia integrifolia*	Guangdong	Akinsanmi et al. (2017)
P. *menezesiana*	leaves of *Podocarpus macrophyllus*	Guangxi	Wei et al. (2007)
P. microspora	twigs of *Podocarpus macrophyllus*	Guangxi	Wei et al. (2007)
P. nattrassioides	unknown	Yunnan	Zhao & Zhao (2012)
P. neglecta	twigs of *Podocarpus nagi*	Guangxi	Wei et al. (2007)
P. nelumbonis	leaves of *Nelumbo nucifera*	Guangxi	Chen et al. (2002)
P. olivacea	leaves of *Podocarpus nagi*	Yunnan	Wei et al. (2007)
P. *oxyanthi*	leaves of *Podocarpus macrophyllus*	Zhejiang	Wei et al. (2007)
P. pachirae	living leaves of *Pachira macrocarpa*	Yunnan	Chen et al. (2003)
P. phaii	living leaves of *Phaius tankervilleae*	Yunnan	Chen et al. (2003)
P. *photiniae*	twigs of *Camellia japonica*, *Camellia sasanqua*, Leaves of *Podocarpus massoniana*	Guangxi Zhejiang, Yunnan	Wei et al. (2007)
P. photiniicola	leaves of *Photinia serrulata*	Guizhou	Chen et al. (2017)
P. pleurocrinita	unknown	Yunnan	Zhao & Zhao (2012)
P. rhododendri	dead parts of leaves of *Rhododendron sinogrande*	Yunnan	Maharachchikumbura et al. (2014)
P. rhodomyrtus	living leaves of *Rhodomyrtus tomentosa*	Guangxi	Zhang et al. (2013)
P. rosea	isolated from leaves of *Pinus*	Yunnan	Maharachchikumbura et al. (2014)
P. schimae	leaves of *Schima superba*	Guangxi	Chen et al. (2002)
P. subshorea	leaves of *Michelia hedyosperma*	Guangxi	Ariyawansa et al. (2015)
P. synsepali	leaves of *Synsepalum dulcificum*	Hainan	Chen et al. (2002)

Table 2 Continued.

Taxon	Host/substrate	Province	References
P. theae	leaves of *Camellia sinensis*, *Camellia reticulata* and *Camellia nitidissima*, twigs of *Podocarpus macrophyllus*	Zhejiang, Guangxi Yunnan Zhejiang	Wei et al. (2007)
P. trachycarpicola	leaves of *Trachycarpus fortune*, *Podocarpus macrophyllus*	Yunnan	Zhang et al. (2012b)
P. unicolor	leaf of *Rhododendron*	Hunan	Maharachchikumbura et al. (2012b)
P. verruculosa	leaf of *Rhododendron*	Yunnan	Maharachchikumbura et al. (2012b)
P. virgatula	leaves of *Podocarpus macrophyllus*, twigs of *Podocarpus massoniana*	Zhejiang Guangdong	Wei et al. (2007)
P. vismiae	unknown	Guangxi, Yunnan	Zhang et al. (2003)
P. yanglingensis	on *Camellia sinensis*	Jiangxi	Liu et al. (2017)
P. yunnanensis	twigs of *Podocarpus macrophyllus* and grown on leaf segments of *Dianthus caryophyllus*	Yunnan	Wei et al. (2013)
P. zonata	fruits of *Podocarpus macrophyllus*	Zhejiang	Wei et al. (2007)

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