New species and records of Diaporthe from Jiangxi Province, China

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Abstract

Diaporthe species have often been reported as important plant pathogens, saprobes and endophytes on a wide range of plant hosts. Although several Diaporthe species have been recorded, little is known about species able to infect forest trees in Jiangxi Province. Hence, extensive surveys were recently conducted in Jiangxi Province, China. A total of 24 isolates were identified and analysed using comparisons of DNA sequence data for the nuclear ribosomal internal transcribed spacer (ITS), calmodulin (cal), histone H3 (his3), partial translation elongation factor-1α (tef1) and β-tubulin (tub2) gene regions, as well as their morphological features. Results revealed five novel taxa, D. bauhiniae, D. ganzhouensis, D. schimae, D. verniciicola, D. xunwuensis spp. nov. and three known species, D. apiculatum, D. citri and D. multiguttulata.

Keywords

DNA phylogeny, five new taxa, forest trees, systematics, taxonomy

Introduction

The genus Diaporthe Nitschke (Sordariomycetes, Diaporthales) represents a cosmopolitan group of fungi occupying diverse ecological behaviour as plant pathogens, endophytes and saprobes (Muralli et al. 2006; Rossman et al. 2007; Udayanga et al. 2014,
2015; Fan et al. 2015, 2018; Guarnaccia and Crous 2017; Guarnaccia et al. 2018; Yang et al. 2018, 2020; Manawasinghe et al. 2019; Marin-Felix et al. 2019). Diaporthe species are responsible for diseases on a wide range of plant hosts, including agricultural crops, forest trees and ornamentals, some of which are economically important. Several symptoms, such as root and fruit rots, dieback, stem cankers, leaf spots, leaf and pod blights and seed decay are caused by Diaporthe spp. (Uecker 1988; Rehner and Uecker 1994; Mostert et al. 2001; Santos et al. 2011; Thompson et al. 2011; Udayanga et al. 2011).

Diaporthe was historically considered as monophyletic, based on its typical sexual morph and Phomopsis asexual morph (Gomes et al. 2013). However, Gao et al. (2017) recently revealed its paraphyletic nature, showing that Mazzantia (Wehmeyer 1926), Ophiodiaporthe (Fu et al. 2013), Pustulomyces (Dai et al. 2014), Phaeocytostroma and Stenocarpella (Lamprecht et al. 2011) are embedded in Diaporthe s. lat. Furthermore, Senanayake et al. (2017) recently included additional two genera in Diaporthe s. lat., namely Paradiaporthe and Chiangraiomycetes.

Species identification criteria in Diaporthe were originally based on host association, morphology and culture characteristics (Mostert et al. 2001; Santos and Phillips 2009; Udayanga et al. 2011), which led to the description of over 200 species (Hyde et al. 2020). Some species of Diaporthe were reported to colonise a single host plant, while other species were found to be associated with different host plants (Santos and Phillips 2009; Diogo et al. 2010; Santos et al. 2011; Gomes et al. 2013). In addition, considerable variability of the phenotypic characters was found to be present within a species (Rehner and Uecker 1994; Mostert et al. 2001; Santos et al. 2010; Udayanga et al. 2011). During the past decade, a polyphasic approach, based on multi-locus DNA data, morphology and ecology, has been employed for species boundaries in the genus Diaporthe (Crous et al. 2012; Huang et al. 2015; Guarnaccia and Crous 2017; Guarnaccia et al. 2018; Yang et al. 2018, 2020). The classification of Diaporthe has been progressing and the basis for the species identification is a combination of morphological, cultural, phytopathological and phylogenetical analyses (Gomes et al. 2013; Udayanga et al. 2014, 2015; Fan et al. 2015; Huang et al. 2015; Gao et al. 2016, 2017; Guarnaccia and Crous 2017; Guarnaccia et al. 2018; Yang et al. 2018, 2020; Manawasinghe et al. 2019).

In Jiangxi Province, China, some forest trees were observed to be infected with fungal pathogens that cause dieback and leaf spots. Cankered branches and leaves with typical Diaporthe fruiting bodies were also found in the area. However, we found that only limited research had been undertaken regarding the fungal pathogens isolated from forest trees in Jiangxi Province. Hence, the present study was conducted to identify Diaporthe species that cause dieback and leaf spots disease in the forest trees in Jiangxi Province through morphological and multi-locus phylogenetic analyses, based on modern taxonomic concepts.
Materials and methods

Isolates

Fresh specimens of *Diaporthe* were isolated from the collected branches and leaves of six host plants during the collection trips conducted in Jiangxi Province (Table 1). A total of 24 isolates were established by removing a mucoid conidia mass from conidiomata, spreading the suspension on the surface of 1.8% potato dextrose agar (PDA) and incubating at 25 °C for up to 24 h. A single germinating conidium was plated on to fresh PDA plates. Specimens were deposited at the Museum of the Beijing Forestry University (BJFC). Axenic cultures were maintained at the China Forestry Culture Collection Centre (CFCC).

Morphological observation

Agar plugs (6 mm diam.) were taken from the edge of actively-growing cultures on PDA and transferred on to the centre of 9 cm diam. Petri dishes containing 2% tap water agar, supplemented with sterile pine needles (PNA; Smith et al. 1996) and potato dextrose agar (PDA) and incubated at 25 °C under a 12 h near-ultraviolet light/12 h dark cycle to induce sporulation, as described in recent studies (Gomes et al. 2013; Lombard et al. 2014). Colony characters and pigment production on PNA and PDA were noted in the 10-day culture. Colony features were rated according to the colour charts of Rayner (1970). Cultures were examined periodically for the development of conidiomata. The microscopic examination was based on the morphological features of conidiomata obtained from the fungal growth, mounted in clear lactic acid. At least 30 conidia were measured to calculate the mean size/length. Micro-morphological observations were done at 1000× magnification using a Leica compound microscope (DM 2500) with interference contrast (DIC) optics. Descriptions, nomenclature and illustrations of taxonomic novelties were deposited at MycoBank (www.MycoBank.org).

DNA extraction, PCR amplification and sequencing

Genomic DNA was extracted from colonies grown on cellophane-covered PDA, using a CTAB (cetyltrimethylammonium bromide) method (Doyle and Doyle 1990). DNA was estimated by electrophoresis in 1% agarose gel and the yield was measured using the NanoDrop 2000 (Thermo Scientific, Waltham, MA, USA), following the user manual (Desjardins et al. 2009). The PCR amplifications were performed in the DNA Engine Peltier Thermal Cycler (PTC-200; Bio-Rad Laboratories, Hercules, CA, USA). The primer set ITS1/ITS4 (White et al. 1990) was used to amplify the ITS region. The primer pair CAL228F/CAL737R (Carbone and Kohn 1999) was used to amplify the calmodulin gene (*cal*) and the primer pair CYLH4F (Crous et al. 2004) and H3-1b (Glass and Donaldson 1995) were used to amplify part of the histone H3 (*his3*) gene.
Table 1. Reference sequences included in molecular phylogenetic analyses of *Diaporthe*.

| Species | Isolate | Host | Location | GenBank accession numbers |
|---------|---------|------|----------|--------------------------|
| *D. acercola* | MFLUCC 17-0956 | *Acer negundo* | Italy | KJ964224 KJ964137 NA KJ964180 KJ964074 |
| *D. acerigna* | CFCC 52554 | *Acer tataricum* | China | MH121489 MH121413 MH121449 MH121531 NA |
| *D. acutipontis* | CGMCC 3.18285 | *Coffea* sp. | China | KX986764 KX999274 NA KX999155 KX999195 |
| *D. alangi* | CFCC 52556 | *Aulagium kurzii* | China | MH121491 MH121415 MH121451 MH121533 MH121573 |
| *D. alina* | CBS 146.46 | *Alnus sp.* | Netherlands | KC343008 KC343250 KC343592 KC343743 KC343976 |
| *D. ampelina* | STEU 2660 | *Vitis vinifera* | France | AF230751 AF745026 NA AF745056 JX275452 |
| *D. amygdali* | CBS 126.079 | *Praus dulcis* | Portugal | KC343022 KC343264 KC343566 KY343748 KC343990 |
| *D. anglica* | CBS 111.592 | *Hiraculum ghyphodendrum* | Austria | KC343027 KC343569 KC343511 KC343753 KC343995 |
| *D. apiculatum* | | | | |
| *D. arecae* | CFCC 52527 | *Areca catechu* | India | KC343032 KC343274 KC343516 KC343758 KC344000 |
| *D. artemisi* | CBS 114.979 | *Artemisia camphorata* | Hong Kong | KC343034 KC343276 KC343518 KC343670 KC344002 |
| *D. asaeana* | MFLUCC 12-0299a | Unknown dead leaf | Thailand | KT459414 KT459464 NA KT459448 KT459432 |
| *D. baubiniiae* | CGMCC 3.17533 | *Camellia sinensis* | China | KP267986 NA NA KP267970 KP293476 |
| *D. beilharzii* | | | | |
| *D. biglobata* | CGMCC 3.17252 | *Citrus grandis* | China | JX109378 JX109389 JX109359 JX109376 JX108591 |
| *D. biglobata* | CGMCC 3.17248 | *Citrus limon* | China | JX109382 NA JX109354 NA JX109661 JX109403 |
| *D. biglobata* | CFCC 52584 | *Juglandus regia* | China | MH121159 MH121437 MH121477 MH121561 MH121598 |
| *D. bohmeriae* | CPC 28222 | *Vitis vinifera* | Czech | MG281017 MG281710 MG281363 MG281536 MG281188 |
| *D. brasiliensis* | CBS 133.183 | *Aspidochlamys tonomatana* | Brazil | KC343042 KC343284 KC343526 KC343768 KC344010 |
| *D. caatingae* | CBS 141542 | *Tecoma inamona* | Brazil | KY089272 NA NA KY115603 KY115600 |
| *D. caryae* | CFCC 52563 | *Carya illinoensis* | China | MH121498 MH121422 MH121458 MH121540 MH121580 |
| *D. celeniae* | CPC 28262 | *Vitis vinifera* | Czech | MG281017 MG281712 MG281363 MG281538 MG281190 |
| *D. clastrotina* | CBS 139.27 | *Celastrus sp.* | USA | KC343947 KC343289 KC343531 KC343773 KC344015 |
| *D. creicida* | CFCC 52565 | *Cercis chinensis* | China | MH121500 MH121424 MH121460 MH121542 MH121582 |
| *D. charleworthii* | BRIP 54884m | *Rhaponticum rugosum* | Australia | KJ197288 NA NA KJ197250 KJ197268 |
| *D. cinnamonii* | CFCC 52569 | *Cinnamomum sp.* | China | MH121504 NA MH121464 MH121546 MH121586 |
| *D. citri* | AR 3405 | *Citrus sp.* | USA | KC843311 KC843157 NA KC843071 KC843187 |
| *D. citrus* | CFCC 53079 | *Citrus sinensis* | China | MK573940 MK574579 MK574595 MK574615 MK574635 |
| *D. citri* | CFCC 53080 | *Citrus sinensis* | China | MK573941 MK574580 MK574596 MK574616 MK574636 |
| *D. citri* | CFCC 53081 | *Citrus sinensis* | China | MK573942 MK574581 MK574597 MK574617 MK574637 |
| *D. citri* | CFCC 53082 | *Citrus sinensis* | China | MK573943 MK574582 MK574598 MK574618 MK574638 |
| *D. citri* | CGMCC 3.15224 | *Citrullus lanatus* | China | JQ954645 KC574579 JQ90515 JQ954663 KC357459 |
| *D. citri* | CGMCC 3.15225 | *Citrus sinensis* | China | JQ954648 KC574579 NA JQ954666 NA |
| *D. collaria* | MFLU 17-2770 | *Magnolia champaca* | Thailand | MG800115 MG873042 NA MG873040 MG873041 |
| *D. conica* | CFCC 52571 | *Alangium chinense* | China | MH121506 MH121428 MH121466 MH121548 MH121588 |
| *D. curvicornis* | CBS 136.25 | *Aegaeolobus linearis* | Unknown | KC343031 KC343273 KC343515 KC343757 KC343999 |
| *D. cuprea* | CBS 117.499 | *Aegaeolobus linearis* | South Africa | KC343057 KC343299 KC343541 KC343783 KC344025 |
| *D. davidi* | ZJUD89 | *Citrullus lanatus* | China | JQ90624 NA JQ90566 JQ90503 JQ90445 |
| *D. endophylica* | CBS 133.811 | *Schinus terebinthifolius* | Brazil | KC343065 KC343307 KC343549 KC343791 KC343965 |
| *D. ert* | AR5193 | *Ulmus sp.* | Germany | KJ210529 KJ349999 KJ420850 KJ210550 KJ420799 |
| Species                  | Isolate    | Host                                      | Location       | GenBank accession numbers          |
|-------------------------|------------|-------------------------------------------|----------------|-----------------------------------|
| Diaporthe fraxini-      | BRIP 54781 | Fraxinus angustifolia                     | Australia      | JX862528 NA NA JX862534 KF170920  |
| angustifoliae            |            |                                           |                |                                   |
| Diaporthe fraxincola     | CFCC 52582 | Fraxinus chinensis                        | China          | MH121517 MH121435 NA MH121559 NA  |
| Diaporthe fructicola     | MAFF 246408| Pseudalia edulis \* D. edulis f. flavicornis | Japan          | LC342734 LC342738 LC342737 LC342735 LC342736 |
| Diaporthe fukubunii      | MAFF 625034| Pyrus pyrifolia                           | Japan          | JQ807469 NA NA JQ807418 NA       |
| Diaporthe fuscola        | CGMCC 3.17087| Lithocarpus glabra                       | China          | KF576281 KF576233 NA KF576256 KF576305 |
| Diaporthe genae          | CBS 180.91 | Cannabis sativa                           | USA            | KC343112 KC343354 KC343596 KC343838 KC344080 |
| Diaporthe gonzosensis    | CFCC 5087   | Unknown dead wood                        | China          | MK432665 MK442985 MK443010 MK578139 MK578065 |
| Diaporthe garethjonesii  | MFLUCC 12-0542a| Unknown dead leaf                     | Thailand       | KT459423 KT459470 NA KT459457 KT459441 |
| Diaporthe guangziemii    | JZB320094  | Vitis vinifera                            | China          | MK357577 MK376277 NA MK523566 MK500168 |
| Diaporthe gulae          | BRIP 54025  | Helianthus annuus                         | Australia      | JF431299 NA NA KJ197271 JN645803 |
| Diaporthe helicis        | AR5211     | Hedera helix                              | France         | KJ210538 KJ345043 KJ240875 KJ210559 KJ420828 |
| Diaporthe heterophyllae  | CBS 143769 | Acasia heterophylla                       | France         | MG600222 MG600218 MG600220 MG600224 MG600226 |
| Diaporthe hispaniae      | CPC 30321  | Vitis vinifera                            | Spain          | MG281112 MG281820 MG281471 MG281644 MG281296 |
| Diaporthe iberae         | JZB320123  | Vitis vinifera                            | China          | MK353809 MK500235 NA MK523570 MK500148 |
| Diaporthe incompleta     | CGMCC 3.18288| Camellia sinensis                        | China          | KY986794 KY999289 KY999265 KY999186 KY999226 |
| Diaporthe infersa        | CBS 133812 | Schinus terebinthifolius                  | Brazil         | KC343126 KC343368 KC343610 KC343852 KC344094 |
| Diaporthe juglandicola   | CFCC 51134 | Juglon mandshurica                        | China          | KU985101 KX024616 KX024622 KX024628 KX024634 |
| Diaporthe kadurae        | CFCC 52586 | Kadowia longipetulata                     | China          | MH121521 MH121439 MH121479 MH121563 MH121600 |
| Diaporthe kochmanii      | BRIP 54033  | Helianthus annuus                         | Australia      | JF431295 NA NA JN645809 NA       |
| Diaporthe kongii         | BRIP 54031  | Portalaca grandiflora                     | Australia      | JF431301 NA NA JN645797 KJ197272 |
| Diaporthe litchicola     | BRIP 54030  | Litchi chinensis                          | China          | JX862533 NA NA JX862539 KF170925 |
| Diaporthe littorcarpus   | CGMCC 3.15175| Lithocarpus glabra                        | China          | KC353104 KF576235 KC153095 KF576311 |
| Diaporthe lonicenae      | MFLUCC 17-0963| Lonicera sp.                              | Italy          | KY964190 KY964116 NA KY964146 KY964073 |
| Diaporthe lusitanicae    | CBS 12312  | Forsnicolum vulgare                       | Portugal       | KC343136 KC343578 KC343620 KC343862 KC344104 |
| Diaporthe macrolecii     | BRIP 57892a| Helianthus annuus                         | Australia      | KJ197277 NA NA KJ197239 KJ197257 |
| Diaporthe middletonii    | BRIP 54884e| Raphisap rustam undulatum                 | Australia      | KJ197286 NA NA KJ197248 KJ197266 |
| Diaporthe miricica       | BRIP 54736j| Raphisap rustam undulatum                 | Australia      | KJ197282 NA NA KJ197244 KJ197262 |
| Diaporthe musigena       | MFLUCC 16-0113| Prunus persica                            | China          | KU557563 KU557611 NA KU557631 KU557585 |
| Diaporthe multiguttulata | ZJUD98     | Citrus grandis                            | China          | KJ409633 NA KJ409755 KJ409512 KJ409454 |
| Diaporthe neilliae       | BRIP 54000  | Citrus maxima                             | China          | MK432645 MK442967 MK442992 MK578121 MK578084 |
| Diaporthe novae          | CGMCC 3.17093| Citrus maxima                             | China          | MK432646 MK442968 MK442993 MK578122 MK578049 |
| Diaporthe novoccini      | CGMCC 3.17531| Citrus maxima                             | China          | MK432647 MK442969 MK442994 MK578123 MK578050 |
| Diaporthe ochracea       | CBS 129519 | Musa sp.                                  | Australia      | KC343143 KC343385 KC343627 KC343869 KC344111 |
| Diaporthe oeillae        | CBS 144.27 | Spinacea sp.                              | USA            | KC343144 KC343386 KC343628 KC343870 KC344112 |
| Diaporthe penetireum     | CBS 109490 | Ambrosia trifida                          | USA            | KC343145 KC343387 KC343629 KC343871 KC344113 |
| Diaporthe pascoei        | BRIP 54847  | Persia americana                          | Australia      | JX862532 NA NA JX862538 KF170924 |
| Diaporthe passiflorica   | CBS 141329 | Passiflora floridica                      | Malaysia       | KX222892 NA KX228367 NA KX228387 |
| Diaporthe penetireum     | CGMCC 3.17532| Camellia sinensis                        | China          | KP714505 NA KP714493 KP714517 KP714529 |
| Diaporthe perjuncta      | CBS 109745 | Ulmus glabra                              | China          | KC343172 KC343414 KC343656 KC343898 KC344140 |
| Species              | Isolate            | Host                                | Location               | GenBank accession numbers           |
|----------------------|--------------------|-------------------------------------|------------------------|-------------------------------------|
|                      |                    |                                     |                        |ITS cal bns3 tefl mh2               |
| D. perseae           | CBS 151.73         | Persea gratissima                   | Netherlands            | KC343173 KC343415 KC343657 KC343899 KC344141 |
| D. pescicola         | MFLUCC 16-0105     | Prunus persica macrophylla          | China                  | KU557555 KU557603 NA KU557623 KU557579 |
| D. podocarpis-     | CGMCC 3.18281      | Podocarpus macrophylla              | China                  | XX986774 XX999278 XX999246 XX999167 XX999207 |
|                      |                    |                                     |                        |                                     |
| D. pseudomangiferae | CBS 101339         | Mangifera indica                    | Dominican Republic     | KC343181 KC345423 KC345665 KC345907 KC344149 |
| D. pseudophoenix-   | CBS 462.69         | Phoenix dactylifera                 | Spain                  | KC343184 KC345426 KC345668 KC345910 KC344152 |
|                      |                    |                                     |                        |                                     |
| D. porulai-pinnatae | MFLUCC 136413      | Prunus pinnata macrophylla          | South Africa           | KF777159 NA NA NA KF777252          |
| D. pterocarpica     | MFLUCC 10-0580a    | Pterocarpus indicus                 | Thailand               | JQ619887 JX197433 NA JX275403 JX275441 |
|                      |                    |                                     |                        |                                     |
| D. pulla             | CBS 338.89         | Hedera helix                        | Yugoslavia             | KC343152 KC343394 KC343636 KC343878 KC344120 |
| D. pyracanthae      | CAA 4683           | Pyracantha coccinea                 | Portugal               | KY435635 KY435656 KY435645 KY435625 KY435666 |
|                      |                    |                                     |                        |                                     |
| D. racemae          | CBS 143770         | Eucaula racemosa                    | South Africa           | MG600223 MG600219 MG600221 MG600225 MG600227 |
| D. rutetata          | CFCC 50062         | Juglandus mandshurica               | China                  | KP208847 KP208849 KP208851 KP208853 KP208855 |
|                      |                    |                                     |                        |                                     |
| D. sacchari          | BRIP 54609b        | Helianthus annuus                   | Australia              | KJ197287 NA NA KJ197249 KJ197267 |
| D. sarcophagus       | CFCC 51986         | Sambucus williamii                 | China                  | KY852495 KY852499 KY852503 KY852507 KY852511 |
|                      |                    |                                     |                        |                                     |
| D. schima           | CFCC 51013         | Schima superba                      | China                  | MK432640 MK442962 MK442987 MK578116 MK578043 |
| D. schisandrae      | CFCC 51988         | Schisandra chinensis               | China                  | KY852497 KY852501 KY852505 KY852509 KY852513 |
| D. scotti           | MFLU 15-1279       | Schisandra chinensis               | Italy                  | KY964226 KY964139 NA KY964182 KY964109 |
| D. senae            | CFCC 51636         | Senna bicapularis                  | China                  | KY203724 KY228875 NA KY228885 KY228891 |
| D. serpentina       | BRIP 55665a        | Helianthus annuus                   | Australia              | KJ197274 NA NA KJ197236 KJ197254 |
| D. sienensis        | MFLUCC 10-573a     | Dasypachys lanceolata               | Thailand               | JQ619879 NA NA JX275393 JX275429 |
| D. sojae            | FAU 6935           | Glycine max                         | sp                     | USA KJ90719 KJ612116 KJ652908 KJ590762 KJ610875 |
| D. stenospora       | CBS 139099         | Vaccinium corymbosum               | Italy                  | KJ160579 KJ160548 MF183550 KJ160611 KJ160528 |
| D. tabescens        | ICMP 20663         | Citrus sp                           | China                  | KJ90587 NA KJ90529 KJ90466 KJ90408 |
| D. tabellipicola    | MFLU 17-1197       | Dead wood                           | China                  | MG746632 NA NA MG746633 MG746634 |
| D. subordinaria     | CBS 464.90         | Plantago lanceolata                 | New Zealand            | KC343214 KC343456 KC343698 KC343940 KC344182 |
| D. tanicola         | MFLUCC 16-0117     | Prunus persica                      | China                  | KU557567 NA NA KU557635 KU557591 |
| D. tectae           | MFLUCC 12-0777     | Tectona grandis                     | China                  | KU712430 KU749345 NA KU749359 KU749377 |
| D. tectonendophytica| MFLUCC 13-0471     | Tectona grandis                     | China                  | KU712439 KU749354 NA KU749367 KU749354 |
| D. tectonigera      | MFLUCC 12-0767     | Tectona grandis                     | China                  | KU712429 KU749358 NA KU749371 KU749376 |
| D. terebinthifoliid | CBS 133180         | Schinus terebinthifolius            | Brazil                 | KC343216 KC343458 KC343700 KC343942 KC344184 |
| D. teratum           | CFCC 3.15183       | Teratumena gymnastisbenna           | China                  | KC153098 NA NA KC153089 NA |
| D. thunbergii       | MFLUCC 10-576a     | Thunbergia laurifolia              | Thailand               | JQ619893 JX197440 NA JX275409 JX275449 |
| D. tiensinensis     | CFCC 51999         | Inglandia regia                    | China                  | MF279843 MF279888 MF279828 MF279858 MF279873 |
| D. tiliobasis       | BRIP 62248a        | Theobroma cacao                    | Australia              | KR936130 NA NA KR936133 KR936132 |
| D. ukurundiensis    | CFCC 52592         | Acker ukurundien                    | China                  | MH121527 MH121445 MH121485 MH121569 NA |
| D. uslobiensi       | CFCC 3.17569       | Citrus sp                           | China                  | KJ90587 NA KJ90529 KJ90466 KJ90408 |
| D. undulata         | CFCC 52594         | Carica ilicifolia                  | China                  | MH121529 MH121447 MH121487 MH121606 |
| D. variegata        | CGMCC 3.18293      | Leaf of unknown host                | China-Laos border      | KX98798 NA KX999269 KX999190 KX999230 |
| D. variegata        | BRIP 57887a        | Podium gajtosa                      | Australia              | KR936126 NA NA KR936129 KR936128 |

Species: D. perseae, D. pescicola, D. podocarpis-macrophylli, D. pseudomangiferae, D. pseudophoenix-nicola, D. porulai-pinnatae, D. pterocarpica, D. pulla, D. pyracanthae, D. racemosae, D. rostrata, D. sackstonii, D. sambucusii, D. sojae, D. sterilis, D. streptocarpica, D. subclavata, D. subellipicola, D. subordinaria, D. taoicola, D. tectonae, D. tectonendophytica, D. tectonigena, D. terebinthifoliid, D. tibetensis, D. tiliobasis, D. ukurundiensis, D. uslobiensi, D. undulata, D. variegata.
**Diaporthe** species from cankered branches and leaves

| Species                 | Isolate     | Host                | Location | GenBank accession numbers |
|-------------------------|-------------|---------------------|----------|---------------------------|
|                         |             |                     |          | **ITS** | **cal** | **his3** | **tef1** | **tub2** |
| *D. verniciicola*       | CFCC 53109  | Vernicia montana    | China    | MK573944 | MK574583 | MK574599 | MK574619 | MK574639 |
| *D. verniciicola*       | CFCC 53110  | Vernicia montana    | China    | MK573945 | MK574584 | MK574600 | MK574620 | MK574640 |
| *D. verniciicola*       | CFCC 53111  | Vernicia montana    | China    | MK573946 | MK574585 | MK574601 | MK574621 | MK574641 |
| *D. verniciicola*       | CFCC 53112  | Vernicia montana    | China    | MK573947 | MK574586 | MK574602 | MK574622 | MK574642 |
|                         |             |                     |          | MK573944 | MK574583 | MK574599 | MK574619 | MK574639 |
| *D. viniferae*          | JZB20071    | Vitis vinifera      | China    | MK341551 | MK500107 | MK500119 | MK500012 |
| *D. virgiliae*          | CMW40748    | Virgilia arboidea   | South Africa | KP247566 | NA    | NA    | NA    | KP247575 |
| *D. xishuangbanica*     | CGMCC 3.18282 | Camellia sinensis    | China    | KX986783 | NA    | KX999255 | KX999175 | KX999216 |
| *D. xishuangbanica*     | CFCC 53085  | Unknown dead wood   | China    | MK432663 | MK442983 | MK443008 | MK578137 | MK578065 |
| *D. xishuangbanica*     | CFCC 53086  | Unknown dead wood   | China    | MK432664 | MK442984 | MK443009 | MK578138 | MK578064 |
| *D. yunnanensis*        | CGMCC 3.18289 | Coffea sp.          | China    | KX986796 | KX999290 | KX999267 | KX999188 | KX999228 |
| **Diaporthella corylina** | CBS 121124  | Corylus sp.         | China    | KC343004 | KC343246 | KC343488 | KC343730 | KC343972 |

Newly sequenced material is indicated in bold type. NA, not applicable.

The primer pair EF1-728F/EF1-986R (Carbone and Kohn 1999) was used to amplify a partial fragment of the translation elongation factor 1α gene (**tef1**). The primer sets T1 (O’Donnell and Cigelnik 1997) and Bt2b (Glass and Donaldson 1995) were used to amplify the beta-tubulin gene (**tub2**); the additional combination of Bt2a/Bt2b (Glass and Donaldson 1995) was used in case of amplification failure of the T1/Bt2b primer pair. The PCR amplifications of the genomic DNA with the phylogenetic markers were done using the same primer pairs and conditions as in Yang et al. (2018). The PCR products were assayed via electrophoresis in 2% agarose gels, while the DNA sequencing was performed using an ABI PRISM 3730XL DNA Analyser with a BigDye Terminator Kit v.3.1 (Invitrogen, USA) at the Shanghai Invitrogen Biological Technology Company Limited (Beijing, China).

**Phylogenetic analyses**

The quality of the amplified nucleotide sequences was checked and combined using SeqMan v.7.1.0 and reference sequences were retrieved from the National Center for Biotechnology Information (NCBI), based on recent publications on the genus *Diaporthe* (Guarnaccia et al. 2018; Yang et al. 2018, 2020). Sequences were aligned using MAFFT v. 6 (Katoh and Toh 2010) and corrected manually using Bioedit 7.0.9.0 (Hall 1999). The best-fit nucleotide substitution models for each gene were selected using jModelTest v. 2.1.7 (Darriba et al. 2012) under the Akaike Information Criterion.

The phylogenetic analyses of the combined gene regions were performed using Maximum Likelihood (ML) and Bayesian Inference (BI) methods. ML was conducted using PhyML v. 3.0 (Guindon et al. 2010), with 1000 bootstrap replicates while BI was performed using a Markov Chain Monte Carlo (MCMC) algorithm in MrBayes v. 3.0 (Ronquist et al. 2003). Two MCMC chains, started from random trees for 1,000,000 generations and trees, were sampled every 100th generation, resulting in a
total of 10,000 trees. The first 25% of trees were discarded as burn-in of each analysis. Branches with significant Bayesian Posterior Probabilities (BPP) were estimated in the remaining 7500 trees. Phylogenetic trees were viewed with FigTree v.1.3.1 (Rambaut and Drummond 2010) and processed by Adobe Illustrator CS5. Sequence alignment and phylogenetic trees were deposited in TreeBASE (submission ID: S25213). The nucleotide sequence data of the new taxa were deposited in GenBank (Table 1).

**Results**

The phylogenetic position of the 24 isolates of *Diaporthe* was determined by the phylogenetic analysis of the combined ITS, *cal*, *his3*, *tef1* and *tub2* sequences data. Reference sequences of the representative species used in the analysis were selected from Yang et al. (2018) and supplemented with sequences from GenBank. The ITS, *cal*, *his3*, *tef1*, *tub2* and combined data matrices contained 522, 541, 529, 520, 535 and 2659 characters with gaps, respectively. The alignment comprised of 142 strains together with *Diaporthella corylina* (culture CBS 121124) which was selected as the outgroup. The best nucleotide substitution model used for the analysis of ITS, *his3* and *tub2* was TrN+I+G, while HKY+I+G was used for *cal* and *tef1*. The topologies resulting from ML and BI analyses of the concatenated dataset were congruent (Fig. 1) and the sequences from the 24 *Diaporthe* isolates formed eight distinct clades as shown in Fig. 1, representing five undescribed species and three known species.

**Taxonomy**

*Diaporthe apiculatum* Y.H. Gao & L. Cai, in Gao, Liu & Cai, Syst. Biodiv. 14: 106. 2016.

Figure 2

**Description.** Conidiomata pycnidial, discoid, immersed in bark, scattered, slightly erumpent through bark surface, with a solitary undivided locule. Ectostromatic disc yellowish to grey, one ostiole per disc, (300–)305–357(–368) μm diam. Ostiole medium black, up to level of disc. Locule undivided, (338–)357–450(–464) μm diam. Conidiophores reduced to conidiogenous cells. Conidiogenous cells cylindrical, hyaline, densely aggregated, phialidic, unbranched, straight or slightly curved. Beta conidia hyaline, aseptate, filiform, hamate, eguttulate, base subtruncate, tapering towards one apex, (26.5–)30–39.5(–43) × 1.5–2 μm. Alpha conidia not observed.

**Culture characters.** Colony originally flat with white fluffy aerial mycelium, becoming yellowish to pale green mycelium with age, marginal area irregular, conidiomata absent.

**Specimens examined.** China. Jiangxi Province: Ganzhou City, Fengshan Forest Park, on branches of *Rhus chinensis*, 25°45’12”N, 115°00’41”E, 23 Jul 2018, Q. Yang, Y. Liu, Y.M. Liang & C.M. Tian (BJFC-S1680; living culture: CFCC 53068, CFCC 53069 and CFCC 53070).
**Figure 1.** Phylogram of *Diaporthe* from a Maximum Likelihood analysis based on combined ITS, *cal*, *his3*, *tef1* and *tub2*. Values above the branches indicate Maximum Likelihood bootstrap (left, ML BP ≥ 50%) and Bayesian probabilities (right, BI PP ≥ 0.90). The tree is rooted with *Diaporthella corylina*. Strains in current study are in blue font and the ex-type cultures are in bold font.
**Figure 1.** Continued.

**Figure 2.** *Diaporthe apiculatum* on *Rhus chinensis* (BJFC-S1680) **a**, **b** habit of conidiomata in wood **c** transverse section of conidiomata **d** longitudinal section through conidiomata **e** conidiogenous cells attached with beta conidia **f** the colony on PDA. Scale bars: 200 μm (**b–d**); 10 μm (**e**).
**Notes.** *Diaporthe apiculatum* was originally described as an endophyte from healthy leaves of *Camellia sinensis* in Jiangxi Province, China (Gao et al. 2015). In the present study, three isolates (CFCC 53068, CFCC 53069 and CFCC 53070) from symptomatic branches of *Rhus chinensis* were found congruent with *D. apiculatum*, based on DNA sequence and morphological data (Fig. 1). The clade was, therefore, confirmed to be *D. apiculatum* and was found to be both an endophyte and a pathogen.

**Diaporthe bauhiniae** C.M. Tian & Q. Yang, sp. nov.

MycoBank No: 829519

**Figure 3**

**Diagnosis.** Distinguished from the phylogenetically closely-related species *D. psoraleae-pinnatae* in alpha and beta conidia.

**Etymology.** Named after *Bauhinia*, the host genus where the fungus was isolated.

**Description.** Conidiomata pycnidial, immersed in bark, scattered, slightly erumpent through bark surface, nearly flat, discoid, with a solitary undivided locule. Ectostromatic disc grey to brown, one ostiole per disc. Locule circular, undivided, (180–)200–290(–300) μm diam. Conidiophores reduced to conidiogenous cells. Conidiogenous cells hyaline, cylindrical, unbranched, straight, tapering towards the apex. Alpha conidia hyaline, aseptate, ellipsoidal to fusiform, biguttulate to multi-guttulate, (7.5–)9–13(–14) × (1.5–)2–2.5(–3) μm. Beta conidia hyaline, aseptate, filiform, straight to sinuous, eguttulate, (25–)28.5–40(–43) × 1 μm.

**Culture characters.** Colony at first white, becoming wine-red in the centre with age. Aerial mycelium white, dense, fluffy, conidiomata absent.

**Specimens examined.** China. Jiangxi Province: Ganzhou City, on branches of *Bauhinia purpurea*, 25°52'21"N, 114°56'44"E, 11 May 2018, Q. Yang, Y. Liu & Y.M. Liang (holotype BJFC-S1621; ex-type living culture: CFCC 53071; living culture: CFCC 53072 and CFCC 53073).

**Notes.** Three isolates representing *D. bauhiniae* cluster in a well-supported clade and appear most closely related to *D. psoraleae-pinnatae*. *Diaporthe bauhiniae* can be distinguished from *D. psoraleae-pinnatae*, based on ITS and *tub2* (38/458 in ITS and 11/418 in *tub2*). Morphologically, *D. bauhiniae* differs from *D. psoraleae-pinnatae* in having narrower alpha conidia (2–2.5 vs. 2.5–3 μm) and the beta conidia of *D. psoraleae-pinnatae* were not observed (Crous et al. 2013).

**Diaporthe citri** (H.S. Fawc.) F.A. Wolf, J. Agric. Res., Washington 33(7): 625, 1926.  

**Figure 4**

**Description.** Leaf spots subcircular to irregular, pale brown, with dark brown at margin. Pycnidia solitary, scattered on the leaf surface. Pycnidial conidiomata in culture, globose, erumpent, single or clustered in groups of 3–5 pycnidia, coated with hyphae, cream to yellowish translucent conidial droplets exuded from ostioles. Conidiophores
Figure 3. *Diaporthe bauhiniae* on *Bauhinia purpurea* (BJFC-S1621) **a** habit of conidiomata in wood **b** transverse section of conidiomata **c** longitudinal section through conidiomata **d** the colony on PDA **e** conidiogenous cells attached with alpha conidia **f** Alpha conidia **g** Beta conidia. Scale bars: 100 μm (**b, c**); 10 μm (**e–h**).

Figure 4. *Diaporthe citri* on *Citrus sinensis* (BJFC-S1658) **a, b** symptoms on leaves of host plant **c** culture on PDA (30d) **d** conidiomata **e** alpha conidia **f** conidiophores and alpha conidia. Scale bars: 10 μm (**e, f**).

Reduced to conidiogenous cells. Conidiogenous cells hyaline, unbranched, septate, straight, slightly tapering towards the apex, 14.5–25 × 2–3 μm. Alpha conidia hyaline, aseptate, rounded at one end, apex at the other end, usually with two large guttulate, (9.5–)10.5–12 × 3.5–4.5 μm. Beta conidia not observed.

**Culture characters.** Colony originally flat with white fluffy aerial mycelium, becoming greyish mycelium with age, with yellowish-cream conidial drops exuding from the ostioles.

**Specimens examined.** China. Jiangxi Province: Ganzhou City, on leaves of *Citrus sinensis*, 24°59′44″N, 115°31′01″E, 13 May 2018, Q. Yang, Y. Liu & Y.M.
Diaporthe species from cankered branches and leaves

Liang (BJFC-S1658; living culture: CFCC 53079 and CFCC 53080); 24°59’45”N, 115°31’02”E, 13 May 2018, Q. Yang, Y. Liu & Y.M. Liang (BJFC-S1659; living culture: CFCC 53081 and CFCC 53082).

Notes. *Diaporthe citri* is a widely distributed species in citrus-growing regions. In the present study, four isolates (CFCC 53079, CFCC 53080, CFCC 53081 and CFCC 53082) from symptomatic leaves of *Citrus sinensis* were congruent with *D. citri*, based on DNA sequence and morphological data (Fig. 1). The clade was, therefore, confirmed to be *D. citri*.

**Diaporthe ganzhouensis** C.M. Tian & Q. Yang, sp. nov.

MycoBank No: 829522

Figure 5

**Diagnosis.** Distinguished from the phylogenetically closely-related species *D. vawdreyi* in having longer conidiophores and wider alpha conidia.

**Etymology.** Named after Ganzhou City where the species was first collected.

**Description.** On PDA: Conidiomata pycnidial, subglobose, solitary, deeply embedded in the medium, erumpent, dark brown to black. Pale yellow conidial drops exuding from ostioles. Conidiophores (12–)15.5–21 × 1.5–2 μm, cylindrical, hyaline, phialidic, branched, straight or slightly curved. Alpha conidia 6.5–8.5(–9) × 2–2.5(–3) μm, aseptate, hyaline, ellipsoidal to fusiform, rounded at one end, slightly apex at the other end, biguttulate. Beta conidia hyaline, aseptate, filiform, sinuous at one end, eguttulate, (21.5–)25.5–31(–33) × 1 μm.

**Culture characters.** Colony at first white, becoming yellowish with age. Aerial mycelium white, dense, fluffy, with visible solitary conidiomata at maturity.

**Specimens examined.** China. Jiangxi Province: Ganzhou City, unknown dead wood, 25°45’17”N, 115°00’41”E, 23 Jul 2018, Q. Yang, Y. Liu, Y.M. Liang & C.M. Tian (holotype BJFC-C004; ex-type culture: CFCC 53087; living culture: CFCC 53088).

Notes. *Diaporthe ganzhouensis* comprises the isolates CFCC 53087 and CFCC 53088, revealed to be closely related to *D. vawdreyi* in the combined phylogenetic tree (Fig. 1). *Diaporthe ganzhouensis* can be distinguished, based on ITS, *tef1*-α and *tub2* loci from *D. vawdreyi* (6/456 in ITS, 63/357 in *tef1*-α and 40/469 in *tub2*). *Diaporthe ganzhouensis* differs morphologically from *D. vawdreyi* in having longer conidiophores (15.5–21 vs. 6–15 μm) and wider alpha conidia (2–2.5 vs. 1.5–2 μm) (Crous et al. 2015).

**Diaporthe multiguttulata** F. Huang, K.D. Hyde & Hong Y. Li, in Huang et al., *Fungal Biology* 119(5): 343. 2015.

Figure 6

**Description.** Conidiomata pycnidial, 692–750(–800) μm diam., solitary and with single necks erumpent through host bark. Tissue around neck is cylindrical. Locule circular, undivided, 450–565(–600) μm diam. Conidiophores reduced to conidiogenous cells. Con-
idiogenous cells unbranched, straight or slightly curved, apical or base sometimes swelling, (8.5–)9–10.5(–11) × 1.5–2 μm. Alpha conidia hyaline, aseptate, ellipsoidal, biguttulate or with one large guttulate, rounded at one end, slightly apex at the other end, occasionally submedian constriction, (7.5–)8–9(–10.5) × 4–5(–5.5) μm. Beta conidia not observed.
Cultured characters. Colony originally flat with white felty aerial mycelium, becoming pale green mycelium with age, margin area irregularly, with visible solitary conidiomata at maturity.

Specimens examined. China. Jiangxi Province: Ganzhou City, on branches of *Citrus maxima*, 25°51′28″N, 114°55′19″E, 11 May 2018, Q. Yang, Y. Liu & Y.M. Liang (BJFC-S1614; living culture: CFCC 53095, CFCC 53096 and CFCC 53097).

Notes. *Diaporthe multiguttulata* was originally described as an endophyte from a healthy branch of *Citrus grandis* in Fujian Province, China (Huang et al. 2015). In the present study, three isolates (CFCC 53095, CFCC 53096 and CFCC 53097) from symptomatic branches of *Citrus maxima* were congruent with *D. multiguttulata*, based on DNA sequence data and confirmed from the morphological analysis (Fig. 1). The clade, therefore, was verified as *D. multiguttulata* which could exist both as an endophyte and a pathogen.

### Diaporthe schimae C.M. Tian & Q. Yang, sp. nov.

Mycobank No: 829526

Figure 7

Diagnosis. Distinguished from the phylogenetically closely-related species *D. sennae* in having larger alpha conidia and longer beta conidia.

Etymology. Named after the host genus *Schima* on which the fungus was isolated.

Description. Leaf spots subcircular to irregular, pale brown, with dark brown at margin. Pycnidia solitary, scattered on the leaf surface. Pycnidial conidiomata in culture, globose, (150–)173–357(–373) μm in its widest diam., erumpent, single or clustered in groups of 3–5 pycnidia, coated with hyphae, cream to yellowish translucent conidial droplets exuded from ostioles. Conidiophores reduced to conidiogenous cells. Conidiogenous cells hyaline, unbranched, septate, straight, slightly tapering towards the apex. Alpha conidia scarce, hyaline, aseptate, ellipsoidal to spindle-shaped, four small guttulate, (7.5–)8–8.5(–9) × 2.5–3 μm. Beta conidia abundant, hyaline, aseptate, filiform, straight to sinuous at one end, eguttulate, (25–)27.5–38.5(–40.5) × 1–1.5 μm.

Culture characters. Colony entirely white, with fluffy aerial mycelium, concentric zonation, margin fimbricate, reverse slightly yellowish.

Specimens examined. China. Jiangxi Province: Ganzhou City, Fengshan Forest Park, on leaves of *Schima superba*, 25°44′22″N, 114°59′40″E, 15 May 2018, Q. Yang, Y. Liu & Y.M. Liang (holotype BJFC-S1661; ex-type culture: CFCC 53103); 24°40′51″N, 115°34′36″E, 15 May 2018, Q. Yang, Y. Liu & Y.M. Liang (BJFC-S1662; living culture: CFCC 53104); 24°40′52″N, 115°34′54″E, 15 May 2018, Q. Yang, Y. Liu & Y.M. Liang (BJFC-S1663; living culture: CFCC 53105).

Notes. *Diaporthe schimae* occurs in an independent clade (Fig. 1) and was revealed to be phylogenetically distinct from *D. sennae*. *Diaporthe schimae* can be distinguished with *D. sennae* by 41 nucleotides in concatenated alignment, in which three were
distinct in the ITS region, 20 in the *tef1-a* region and 18 in the *tub2* region. *Diaporthe schimae* differs morphologically from *D. sennae* in having larger alpha conidia and longer beta conidia (8–8.5 × 2.5–3 vs. 5.5–6.3 × 1.5–1.7 μm in alpha conidia; 27.5–38.5 vs. 18.4–20 μm in beta conidia) (Yang et al. 2017a).

*Diaporthe verniciicola* C.M. Tian & Q. Yang, sp. nov.
MycoBank No: 832921
Figure 8

**Diagnosis.** Distinguished from the phylogenetically closely-related species *D. rostrata* in having smaller alpha conidia; and from *D. juglandicola* in having wider alpha conidia.

**Etymology.** Named after the host genus *Vernicia* on which the fungus was isolated.

**Description.** Conidiomata pycnidial, 825–1050 × 445–500 μm diam., solitary and with single necks erumpent through host bark. Tissue around neck is conical. Locule circular, undivided, 400–665 μm diam. Conidiophores reduced to conidiogenous cells. Conidiogenous cells unbranched, straight or sinuous, 14.5–21.5 × 1–1.5 μm. Alpha conidia hyaline, aseptate, ellipsoidal to fusiform, with 1–2-guttulate, 7–8.5 × 3–3.5 μm. Beta conidia not observed.

**Culture characters.** Colony white to yellowish, with dense and felted mycelium in the centre, lacking aerial mycelium, conidiomata absent.
Specimens examined. China, Jiangxi Province: Ganzhou City, on branches of Vernicia montana, 24°40′51″N, 115°34′52″E, 12 May 2018, Q. Yang, Y. Liu & Y.M. Liang (holotype BJFC-S1622; ex-type culture: CFCC 53109); 24°40′52″N, 115°34′50″E, 12 May 2018, Q. Yang, Y. Liu & Y.M. Liang (BJFC-S1623; living culture: CFCC 53110); 24°45′14″N, 115°34′00″E, 12 May 2018, Q. Yang, Y. Liu & Y.M. Liang (BJFC-S1624; living culture: CFCC 53111); 25°44′15″N, 114°59′32″E, 15 May 2018, Q. Yang, Y. Liu & Y.M. Liang (BJFC-S1624; living culture: CFCC 53112).

Notes. Two isolates of *D. verniciicola* clustered in a well-supported clade (ML/BI = 100/1) and appeared closely related to *D. rostrata* and *D. juglandicola* (Fig. 1). Morphologically, *D. verniciicola* is similar to *D. rostrata* characterised by conidiomata with single necks erumpent through the host bark. However, the new taxon can be distinguished from *D. rostrata* in having smaller alpha conidia (7–8.5 × 3–3.5 vs. 8.5–11.5 × 4–5 μm) (Fan et al. 2015) and *D. verniciicola* differs from *D. juglandicola* in having wider alpha conidia (3–3.5 vs. 2.5–3 μm) (Yang et al. 2017b). This is the first discovery of a *Diaporthe* species isolated from infected branches or twigs on *Vernicia montana* and was confirmed as a new species, based on phylogeny and morphology.

*Diaporthe xunwuensis* C.M. Tian & Q. Yang, sp. nov.
MycoBank No: 829521
Figure 9

Diagnosis. Distinguished from the phylogenetically closely-related species *D. oraccinii* in having longer conidiophores and larger alpha conidia.
Etymology. Named after the county (Xunwu) where the species was first collected.

Description. On PDA: Conidiomata pycnidial, globose, solitary or aggregated, deeply embedded in the medium, erumpent, dark brown to black. Hyaline conidial drops exuding from ostioles. Conidiophores (18.5–)21.5–30(–32.5) × 1–1.5(–2) μm, cylindrical, hyaline, phialidic, unbranched, straight to sinuous. Alpha conidia (6.5–)7–8.5 × 2–3 μm, aseptate, hyaline, ellipsoidal to fusiform, rounded at one end, slightly apex at the other end, usually with 2-guttulate. Beta conidia not observed.

Culture characters. Colony at first white, becoming dark brown in the centre with age. Aerial mycelium white, dense, fluffy, with black conidial drops exuding from the ostioles.

Specimens examined. China. Jiangxi Province: Ganzhou City, unknown dead wood, 25°45’17”N, 115°00’41”E, 23 Jul 2018, Q. Yang, Y. Liu, Y.M. Liang & C.M. Tian (holotype BJFC-C003; ex-type culture: CFCC 53085; living culture: CFCC 53086).

Notes. Two isolates representing Diaporthe xunwuensis clustered in a well-supported clade and appear most closely related to D. oraccinii. Diaporthe xunwuensis can be distinguished from D. oraccinii, based on ITS, his3 and tef1-α loci (5/471 in ITS, 5/432 in his3 and 5/325 in tef1-α). Morphologically, D. xunwuensis differs from D. oraccinii in having longer conidiopores (21.5–30 vs. 10.5–22.5 μm) and larger alpha conidia (7–8.5 × 2–3 vs. 5.5–7.5 × 0.5–2 μm) (Gao et al. 2016).

Discussion

The current study described eight Diaporthe species from 24 strains, based on a large set of freshly-collected specimens. It includes five new species and three known species, which were sampled from six host genera distributed in Jiangxi Province of China (Table 1). In this study, 142 reference sequences (including outgroup) were selected, based on BLAST searches of NCBI’s GenBank nucleotide database and included in the phylogenetic analyses (Table 1). Phylogenetic analyses, based on five combined loci (ITS, cal, his3, tef1 and rub2), as well as morphological characters, revealed the diversity of Diaporthe species in Jiangxi Province, mainly focusing on diebacks from major ecological or economic forest trees.
The identification and characterisation of novel taxa and new host records indicate the high potential of *Diaporthe* to evolve rapidly. In the present study, five species were first reported in China as pathogens. Amongst these species, *D. baubiniae* was characterised by having longer alpha conidia (9–13 × 2–2.5 μm). *Diaporthe ganzhouensis* and *D. xunwuensis* were isolated from unknown dead wood, but *D. ganzhouensis* can be distinguished from *D. xunwuensis* in having beta conidia and was supported by analysis of the sequence data. *Diaporthe schimae* was identified as the most widespread species from isolates collected in Jiangxi Province. *Diaporthe verniciicola* have conidiomata with single necks erumpent through the host bark. Furthermore, two new host records were described, *D. apiculatum* from *Rhus chinensis* and *D. multiguttulata* from *Citrus maxima*.

Recent plant pathological studies have revealed that several *Diaporthe* species cause disease, particularly to important plant hosts on a wide range of economically-significant agricultural crops, such as blueberries, citrus, grapes, oaks, sunflowers, soybeans, tea plants, tropical fruits, vegetables and various trees (van Rensburg et al. 2006; Santos and Phillips 2009; Santos et al. 2011; Thompson et al. 2011; Grasso et al. 2012; Lombard et al. 2014; Huang et al. 2015; Udayanga et al. 2015; Gao et al. 2016; Guarnaccia et al. 2018; Yang et al. 2020). For example, research conducted by Huang et al. (2015) revealed seven endophytic *Diaporthe* species on *Citrus*; Gao et al. (2016) demonstrated that *Diaporthe* isolates associated with *Camellia* spp. could be assigned to seven species and two species complexes; Guarnaccia et al. (2018) explored the occurrence, diversity and pathogenicity of *Diaporthe* species associated with *Vitis vinifera* and revealed four new *Diaporthe* species; Yang et al. (2018) provided the first molecular phylogenetic framework of *Diaporthe* diversity associated with dieback diseases in China. Following the adoption of DNA sequence-based methods, *Diaporthe* taxonomy is actively changing, with numerous species being described each year.

The present study is the first evaluation of *Diaporthe* species, associated with dieback diseases in Jiangxi Province using the combined morphology and molecular data and provided useful information for evaluating the pathogenicity of various species. Multiple strains from different locations should also be subjected to multi-locus phylogenetic analysis to determine intraspecific variation and redefine species boundaries. The descriptions and molecular data of *Diaporthe* species, provided in this study, represent a resource for plant pathologists, plant quarantine officials and taxonomists for identification of *Diaporthe*.

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