Three new *Diaporthe* species from Shaanxi Province, China

Qin Yang¹,², Ning Jiang², Cheng-Ming Tian²

¹ Key Laboratory for Non-Wood Forest Cultivation and Conservation of the Ministry of Education, Central South University of Forestry and Technology, Changsha 410004, China ² The Key Laboratory for Silviculture and Conservation of the Ministry of Education, Beijing Forestry University, Beijing 100083, China

Corresponding author: Cheng-Ming Tian (chengmt@bjfu.edu.cn)

Academic editor: D. Haelewaters | Received 17 December 2019 | Accepted 5 April 2020 | Published 4 May 2020

Citation: Yang Q, Jiang N, Tian C-M (2020) Three new *Diaporthe* species from Shaanxi Province, China. MycoKeys 67: 1–18. https://doi.org/10.3897/mycokeys.67.49483

Abstract

*Diaporthe* species (Sordariomycetes, Diaporthales) are often reported as important plant pathogens, saprobes and endophytes on a wide range of plant hosts. In this study, *Diaporthe* specimens were collected from symptomatic twigs and branches at the Huoditang Forest Farm in Shaanxi Province, China. Identification was done using a combination of morphology and comparison of DNA sequence data of the nuclear ribosomal internal transcribed spacer (ITS), calmodulin (*cal*), histone H3 (*his3*), partial translation elongation factor-1α (*tef1*) and β-tubulin (*tub2*) gene regions. Three new *Diaporthe* species are proposed: *D. albosinensis*, *D. coryli* and *D. shaanxiensis*. All species are illustrated and their morphology and phylogenetic relationships with other *Diaporthe* species are discussed.

Keywords

Diaporthaceae, Dieback, DNA phylogeny, Systematics, Taxonomy

Introduction

*Diaporthe* species (Sordariomycetes, Diaporthales) are associated with a wide range of plant hosts as pathogens, endophytes or saprobes of crops, ornamentals and forest trees (Murali et al. 2006, Rossman et al. 2007, García-Reyne et al. 2011, Gomes et al. 2013, Udayanga et al. 2015, Dissanayake et al. 2017, Guarnaccia and Crous 2017, 2018,
Wijayawardene et al. 2017, Yang et al. 2017a, b, 2018, Fan et al. 2018, Guarnaccia et al. 2018). The sexual morph of *Diaporthe* is characterised by immersed ascomata and an erumpent pseudostroma with elongated perithecial necks. Asci are unitunicate, clavate to cylindrical. Ascospores are fusoid, ellipsoid to cylindrical, hyaline, biseriate to uniseriate in the ascus, sometimes with appendages (Udayanga et al. 2011). The asexual morph is characterised by ostiolate conidiomata, with cylindrical phialides producing three types of hyaline, aseptate conidia (Udayanga et al. 2011, Gomes et al. 2013).

Species identification in *Diaporthe* has traditionally been based on host association, morphology and culture characteristics (Mostert et al. 2001, Santos and Phillips 2009, Udayanga et al. 2011), resulting in the description of over 200 species (Hyde et al. 2020). Multiple species of *Diaporthe* can colonise a single host and one species can be associated with different hosts (Santos and Phillips 2009, Diogo et al. 2010, Santos et al. 2011, Gomes et al. 2013). In addition, considerable within-species variability of phenotypic characters has been reported (Rehner and Uecker 1994, Mostert et al. 2001, Udayanga et al. 2011). Thus, a polyphasic taxonomic approach, based on multilocus DNA data, morphology and ecology, has been increasingly employed for species boundaries in the genus *Diaporthe* (Gomes et al. 2013, Huang et al. 2013, 2015, Udayanga et al. 2014a, b, 2015, Fan et al. 2015, Du et al. 2016, Gao et al. 2016, 2017, Guarnaccia and Crous 2017, Guarnaccia et al. 2018, Long et al. 2019).

Huoditang is located in the middle part of the southern slope of the Qinling Mountains at 33°18'~33°28'N, 108°21'~108°29'E. It belongs to the transitional zone of the northern subtropical and warm temperate zone in China. The terrain is complex and the climate is changeable (Zhang and Cao 2007). The plant communities are complex and, as a result, species diversity of fungi in the forest area is high (Zhang and Cao 2007). During trips to collect forest pathogens causing dieback in Shaanxi Province, cankered branches with typical *Diaporthe* fruiting bodies were investigated and sampled. The aim of the present study was to identify these fungi, based on modern polyphasic taxonomic concepts.

**Materials and methods**

**Isolates**

Fresh specimens of *Diaporthe* were collected from symptomatic twigs or branches in Shaanxi Province (Table 1). Isolates were obtained by removing a mucoid spore mass from conidiomata and spreading the suspension on the surface of 1.8% potato dextrose agar (PDA) in a 9 cm diam. Petri dish. Petri dishes were incubated at 25 °C until spores germinated. Single germinating conidia were transferred on to new PDA plates, which were kept at 25 °C in the dark. Specimens are deposited in the Museum of the Beijing Forestry University (BJFC). Axenic cultures are maintained in the China Forestry Culture Collection Centre (CFCC).
**Table 1.** Isolates and GenBank accession numbers used in the phylogenetic analyses of *Diaporthe*.

| Species          | Isolate          | Host                   | Location    | GenBank accession numbers |
|------------------|------------------|------------------------|-------------|---------------------------|
|                  |                  |                        |             |                           |
| *D. acercola*    | MFLUCC 17-0956   | Acer negundo           | Italy       | KY964224 KY964135 NA KY964180 KY964074 |
| *D. acerigena*   | CFCC 52554       | Acer tataricum         | China       | MH121489 MH121413 MH121449 MH121531 NA |
| *D. alboinensis* | CFCC 53066       | Betula alboinensis     | China       | MK432659 MK442979 MK443004 MK578133 MK578059 |
|                  | CFCC 53067       | Betula alboinensis     | China       | MK432660 MK442980 MK443005 MK578134 MK578060 |
| *D. aloeae*      | CBS 146.46       | Aloe sp.               | Netherlands | KC343008 KC343259 KC343492 KC343734 KC343976 |
| *D. ambigua*     | CBS 114015       | Pyrus communis         | South Africa | KC343010 KC343252 KC343494 KC343736 KC343978 |
| *D. anacardi*    | CBS 720.97       | Anacardium occidentale | East Africa | KC343024 KC343266 KC343508 KC343750 KC343992 |
| *D. angelesae*   | CBS 111592       | Heracleum sphondylium  | Austria     | KC343027 KC343269 KC343511 KC343753 KC343995 |
| *D. apiculatum*  | CGMCC 3.17533    | Camellia sinensis      | China       | KP267896 NA NA KP267970 KP293476 |
| *D. aquatica*    | IFRDCC 3051      | Aquatic habitat        | China       | JQ797437 NA NA NA NA NA |
| *D. arctii*      | CBS 139280       | Arctium lappa         | Austria     | KJ590736 KJ612133 KJ659218 KJ590776 KJ610891 |
| *D. aseana*      | MFLUCC 12-0299a  | Unknown dead leaf      | Thailand    | KT459414 KT459464 NA KT459448 KT459432 |
| *D. asheicola*   | CBS 134067       | Vaccinium ashei        | Chile       | KJ160562 KJ160542 NA KJ160594 KJ160518 |
| *D. betulae*     | CBS 136972       | Vaccinium corymbium    | Italy       | KJ160565 NA MF418264 KJ160597 NA |
| *D. beilharziae* | BRI 54792        | Indigofera australis   | Australia   | JX862529 NA NA JX862535 KF170921 |
| *D. benedicti*   | BPI 893190       | Saffix sp.             | USA         | KM669929 KM69862 NA KM609785 NA |
| *D. betulina*    | CFCC 50649       | Betula platyphylla    | China       | KT732950 KT732997 KT733001 KT733020 |
| *D. betulina*    | CFCC 52560       | Betula alboinensis     | China       | MH121495 MH121419 MH121455 MH121537 MH121577 |
| *D. biccinta*    | CBS 121004       | Juglini sp.            | USA         | KC343134 KC343576 KC343618 KC343860 KC344102 |
| *D. cariae*      | CFCC 52563       | Carya illinoinensis    | China       | MH121498 MH121422 MH121458 MH121540 MH121580 |
| *D. casinse*     | CPC 21916        | Cassine peregrina      | South Africa | KF777155 NA NA KF777244 NA |
| *D. celata*      | CPC 28262        | Vitis vinifera         | Czech Republic | MG281017 MG281712 MG281363 MG281538 MG281690 |
| *D. cebidus*     | CFCC 52565       | Cercis chinensis       | China       | MH121500 MH121424 MH121460 MH121542 MH121582 |
| *D. chamaeropis* | CBS 454.81       | Chamaeropis balantii   | Greece      | KC343048 KC343290 KC343552 KC343774 KC344016 |
| *D. charlesworthii* | BRI 54884m      | Rapistrum rugosirum    | Australia   | KJ197288 NA NA KJ197250 KJ197268 |
| *D. chesnici*    | CFCC 52567       | Akeci chesnici         | China       | MH121502 MH121426 MH121462 MH121544 MH121584 |
| *D. ciborii*     | MFLUCC 17-1023   | Cichorium ixythys      | Italy       | KY964220 KY964133 NA KY964176 KY964104 |
| *D. cinamomoni*  | CFCC 52569       | Cinnamomum sp.         | China       | MH121504 NA MH121464 MH121546 MH121586 |
| *D. citriana*    | CGMCC 3.15224    | Citrus unshiu          | China       | JQ954645 KC357491 KJ490515 JQ95466 JQ357459 |
| *D. citrichinensis* | CGMCC 3.15252  | Citrus sp.             | China       | JQ954645 KC357494 NA JQ95466 NA |
| *D. compactum*   | CGMCC 3.17536    | Camellia sinensis      | China       | KP267854 NA KP293508 KP267928 KP293434 |
| *D. conica*      | CFCC 52571       | Ailanthum chinensis    | China       | MH121506 MH121428 MH121466 MH121548 MH121588 |
| *D. crysii*      | CFCC 53083       | Corylus mandshurica    | China       | MK432661 MK442981 MK443006 MK578135 MK578061 |
|                  | CFCC 53084       | Corylus mandshurica    | China       | MK432662 MK442982 MK443007 MK578136 MK578062 |
| *D. cucurbitae*  | CBS 136.25       | Arctium sp.            | Unknown     | KC343031 KC343273 KC343515 KC343757 KC343999 |
| *D. cuppatea*    | CBS 117499       | Aquapalbus lonaris     | South Africa | KC343057 KC343299 KC343541 KC343783 KC344025 |
| Species                  | Isolate         | Host                | Location        | GenBank accession numbers |
|-------------------------|-----------------|---------------------|-----------------|---------------------------|
|                         |                 |                     |                 | **ITS** | **cal** | **his** | **tef** | **tub** |
| *D. cynaroidis*         | CBS 122676      | *Protea cynaroides* | South Africa    | KC343058 | KC343300 | KC343542 | KC343784 | KC344026 |
| *D. cytophora*          | FAU461          | *Citrus limon*      | Italy           | KC343307 | KC343314 | NA        | KC343116 | KC343221 |
| *D. discoidiopsis*      | ZJUD89          | *Citrus unshiu*     | China           | KJ490624 | NA        | KJ490566 | KJ490503 | KJ490445 |
| *D. dorycnii*           | MFLUCC 17-1015  | *Dorycnium hirsutum*| Italy           | KY964215 | NA        | KJ964171 | KY964099 |           |
| *D. elaegni-glabrata*   | CGMCC 3.18287   | *Elaeagnus glabra*  | China           | KX096779 | KX0999281 | KX0999251 | KX099971 | KX0999212 |
| *D. endophytica*        | CBS 133811      | *Schinus terebinthifolius* | Brazil | KC343065 | KC343307 | KC343549 | KC343791 | KC343065 |
| *D. eres*               | AR5193          | *Ulmus sp.*         | Germany         | KJ210529 | KJ420850 | KJ210550 | KJ420799 |           |
| *D. eucalyptorum*       | CBS 132525      | *Eucalyptus sp.*    | Australia       | NR120157 | NA        | NA        | NA        | NA        |
| *D. foeniculacea*       | CBS 125208      | *Foeniculum vulgare*| Portugal        | KC343104 | KC343346 | KC343588 | KC343830 | KC344072 |
| *D. fraxini-(angustifoliae* | BRIP 54781     | *Fraxinus chinensis*| Italy           | JX862528 | NA        | NA        | JX862534 | KF170920 |
| *D. fraxincola*         | CFCC 52582      | *Glebionis sp.*     | Brazil          | KJ490574 | KJ490566 | KJ490503 | KJ490445 |           |
| *D. fructicola*         | MAFF 246408     | *Parthenocissus tricuspidata* | Japan | LC342734 | LC342738 | LC342737 | LC342735 | LC342736 |
| *D. fuscolivella*       | CGMCC 3.17087   | *Listerocarpus globus* | China | KF576281 | KF576233 | NA        | KF576256 | KF576305 |
| *D. garethjonnetii*     | MFLUCC 12-0542a| *Unkown dead leaf* | Thailand        | KT459423 | KT459470 | NA        | KT459457 | KT459441 |
| *D. guangxieni*         | JZB320094       | *Vitis vinifera*    | China           | KJ490574 | KJ490566 | KJ490503 | KJ490445 |           |
| *D. helicis*            | AR5211          | *Helianthus annuus* | France          | KJ210538 | KJ435043 | KJ420875 | KJ210559 | KJ420828 |
| *D. heterophyllae*      | CBS 143769      | *Acatia heterophylla*| France         | MG600222 | MG600218 | MG600220 | MG600224 | MG600226 |
| *D. hubeiensis*         | JZB320123       | *Vitis vinifera*    | China           | KJ490574 | KJ490566 | KJ490503 | KJ490445 |           |
| *D. incompleta*         | CGMCC 3.18288   | *Camellia sinensis* | China           | KX096794 | KX0999289 | KX0999265 | KX0999186 | KX0999226 |
| *D. inopinata*          | CBS 133813      | *Myrtus ilicifolia* | Brazil          | KC343125 | KC343365 | KC343607 | KC343849 | KC344091 |
| *D. infecunda*          | CBS 133812      | *Schinus terebinthifolius* | Brazil | KC343126 | KC343368 | KC343610 | KC343852 | KC344094 |
| *D. juglandiscola*      | CFCC 51134      | *Juglans mandshurica*| China         | KJ985101 | KX024616 | KX024622 | KX024628 | KX024634 |
| *D. kadsureae*          | CFCC 52586      | *Kadsura longipediculata* | China | MH121521 | MH121439 | MH121479 | MH121563 | MH121600 |
| *D. litchicola*         | BRIP 54900      | *Litchi chinensis*  | Australia       | JX862533 | NA        | NA        | JX862539 | KF170925 |
| *D. laustianicae*       | CBS 123212      | *Foeniculum vulgare*| Portugal        | KC343136 | KC343378 | KC343620 | KC343862 | KC344104 |
| *D. mastrevicii*        | BRIP 57892a     | *Helanthus annuus*  | Australia       | KJ197277 | NA        | NA        | KJ197239 | KJ197257 |
| *D. miltioides*         | BRIP 54884e     | *Rhaponticum rugosum* | Australia       | KJ197286 | NA        | NA        | KJ197248 | KJ197266 |
| *D. millettiae*         | GUCC9167        | *Milletia reticulata* | China         | MK398674 | MK502086 | NA        | MK480609 | MK502089 |
| *D. mirifica*           | BRIP 54736j     | *Helanthus annuus*  | Australia       | KJ197282 | NA        | NA        | KJ197244 | KJ197262 |
| *D. miyajige*           | CBS 129519      | *Musa sp.*          | Australia       | KC343143 | KC343385 | KC343627 | KC343869 | KC344111 |
| *D. neiliiae*           | CBS 144.27      | *Spinacea sp.*     | USA             | KC343144 | KC343386 | KC343628 | KC343870 | KC344112 |
| *D. neoarctii*          | CBS 109490      | *Ambrosia trifida*  | USA             | KC343145 | KC343387 | KC343629 | KC343871 | KC344113 |
| *D. nolofaghi*          | BRIP 54801      | *Nolofaghi cunninghamii* | Australia   | JX862530 | NA        | NA        | JX862536 | KF170922 |
| *D. novem*              | CBS 127270      | *Glycine max*       | Croatia         | KC343155 | KC343397 | KC343640 | KC343881 | KC344123 |
| *D. oracini*            | CGMCC 3.17531   | *Camellia sinensis* | China           | KP267863 | NA        | KP295517 | KP267957 | KP295443 |
| *D. ovalispora*         | KCFM208659      | *Citrus limon*      | China           | KJ490628 | NA        | KJ490570 | KJ490507 | KJ490449 |
| *D. ovicicola*          | CGMCC 3.17093   | *Citrus sp.*        | China           | KF576265 | KF576223 | NA        | KF576240 | KF576289 |
| Species              | Isolate       | Host                          | Location          | GenBank accession numbers                |
|----------------------|---------------|-------------------------------|-------------------|-----------------------------------------|
|                      |               |                               |                   | **ITS**  | **cal** | **his3** | **tef1** | **tub2** |
| D. osmanthi          | GUCC9165      | Osmanthus fragrans            | China             | MK398675 | MK302087 | NA       | MK480610 | MK502090 |
| D. padina            | CFCC 52590    | Padus racemosa                | China             | MH121525 | MH121443 | MH121483 | MH121567 | MH121604 |
| D. pandanicola       | MFLU 18-0006  | Pandanus sp.                  | Thailand          | MG646974 | NA       | NA       | NA       | MG646930 |
| D. pascoei           | BRIP 54847    | Peraea americana              | Australia         | JX862532 | NA       | NA       | JX862538 | KF170924 |
| D. pasifloricola     | CBS 141529    | Passiflora fjielada           | Malaysia          | KX228292 | NA       | KX228367 | NA       | KX228387 |
| D. peraeae           | CBS 151.73    | Peraea gratusisima            | Netherlands       | KC343173 | KC343415 | KC343657 | KC343899 | KC344141 |
| D. peciciola         | MFLUCC 16-0105| Prunus persica                | China             | KU557555 | KU557603 | NA       | KU557623 | KU557579 |
| D. phaeolorum        | AR4203        | Prunus vulgaris               | USA               | KJ590738 | NA       | KJ659220 | NA       | KF004507 |
| D. podocarpi-        | CGMCC 3.18281 | Podocarpus macrophyllus       | China             | KX986774 | KX992787 | KX992467 | KX991675 | KX992077 |
| macropodiphilus      | CBS 101339    | Mangifera indica              | Dominican Republic| KC343181 | KC343423 | KC343665 | KC343907 | KC344149 |
| D. pseudopseudoncicola| MFLUCC 462.69 | Phoenix dacylifera            | South Africa      | KC343184 | KC343426 | KC343668 | KC343910 | KC344152 |
| D. pornelea-         | CBS 136413    | Pseudox pinata               | South Africa      | KF777195 | NA       | NA       | NA       | KF777252 |
| pinnaeae              |               |                               |                   |           |          |          |          |          |
| D. palla             | CBS 338.89    | Hedera helix                  | Yugoslavia        | KC343152 | KC343394 | KC343636 | KC343878 | KC344120 |
| D. racemose          | CBS 143770    | Euclenia racemose            | South Africa      | MG600223 | MG600219 | MG600221 | MG600225 | MG600227 |
| D. ravennica         | MFLUCC 15-0479| Tamarix sp.                   | Italy             | KU900335 | NA       | NA       | KX365197 | KX432254 |
| D. rhuticola         | CBS 129528    | Rubus pendulina              | South Africa      | JF951146 | KC843124 | NA       | KC843100 | KC843205 |
| D. roae              | MFLU 15-1550  | Rosa sp.                      | Thailand          | MG828894 | NA       | NA       | MG843878 |
| D. rosicola          | MFLU 17-0646  | Rosa sp.                      | UK                | MG828895 | NA       | NA       | MG829270 | MG843877 |
| D. rudis             | AR3422        | Laburnum anagyroides          | Austria           | KC843331 | KC843146 | NA       | KC843090 | KC843177 |
| D. sackstonii        | BRIP 54669b   | Helianthus annuus             | Australia         | KJ197287 | NA       | NA       | KJ197249 | KJ197267 |
| D. salicicola        | BRIP 54825    | Salix purpurea                | Australia         | JX862531 | NA       | NA       | JX862537 | JX862531 |
| D. sambucinii        | CFCC 51986    | Sambucus williamsii          | China             | KY852495 | KY852499 | KY852503 | KY852507 | KY852511 |
| D. schini            | CBS 133181    | Schinus terebintifolius       | Brazil            | KC343191 | KC343433 | KC343675 | KC343917 | KC344159 |
| D. schoeni           | MFLU 15-1279  | Sceous nigricans              | Italy             | KY964226 | KY964139 | NA       | KY964182 | KY964109 |
| D. sericola          | CFCC 51634    | Senna bicapsularis           | China             | KY203722 | KY228873 | KY228879 | KY228883 | KY228889 |
| D. serafiniae        | BRIP 55665a   | Helianthus annuus             | Australia         | KJ197274 | NA       | NA       | KJ197236 | KJ197254 |
| D. shaanxiensis      | CFCC 53106    | on branches of liana          | China             | MK432654 | MK442976 | MK443001 | MK578130 | NA       |
|                      | CFCC 53107    | on branches of liana on liana| China             | MK432655 | MK442977 | MK443002 | MK578131 | NA       |
| Species                  | Isolate     | Host                      | Location      | GenBank accession numbers |
|--------------------------|-------------|---------------------------|---------------|---------------------------|
|                          |             |                           |               | ITS          | his3 | tef1 | tub2 |
| *D. subordinaria*        | CBS 464.90  | *Plantago lanceolata*     | New Zealand  | KC343214    | KC343456 | KC343608 | KC343940 | KC344182 |
| *D. texonemophytica*     | MFLUCC 13-0471 | *Tectona grandis*      | China         | KU712439    | KU749354   | NA   | KU749367 | KU749354 |
| *D. texonigena*          | MFLUCC 12-0767 | *Tectona grandis*       | China         | KU712429    | KU749358   | NA   | KU749371 | KU749397 |
| *D. teretisphiala*       | CBS 133180  | *Schizomax teretisphiala* | Brazil        | KC343216    | KC343458   | KC343700 | KC343942 | KC344184 |
| *D. terrae*              | MFLUCC 13.15183 | *Tetraena gymnanthera*   | China         | KC153098    | NA   | NA   | KC153089 | NA          |
| *D. thunbergii*          | MFLUCC 10-576a | *Thuernbergia laurifolia* | Thailand      | JX619893    | JX197440   | NA   | JX275409 | JX275449 |
| *D. tibetensis*          | CFCC 51999  | *Iuglandis rega*         | China         | MF279843    | MF279888   | MF279828 | MF279858 | MF279873 |
| *D. uckermani*           | FAL656      | *Cucumis melo*           | USA           | KJ590726    | KJ612122   | KJ659215 | KJ590747 | KJ610881 |
| *D. ukurunduensis*       | CFCC 52592  | *Acer ukurunduense*      | China         | MH121527    | MH121445   | MH121485 | MH121569 | NA          |
| *D. unispori*            | CFCC 52594  | *Carya illinensis*       | China         | MH121529    | MH121447   | MH121487 | MH121571 | MH121606 |
| *D. unicolor*            | CBS 160.32  | *Oxyconus macrocarpos*   | USA           | KC343228    | KC343470   | KC343712 | KC343954 | KC344196 |
| *D. velutina*            | CGMCC 3.18286 | *Neolitsea sp.*        | China         | KX986790    | NA   | KX999261 | KX999182 | KX999223 |
| *D. vinifera*            | JZB320071   | *Vitis vinifera*         | China         | MK341551    | MK500107   | NA   | MK500119 | MK500112 |
| *D. xishuangbanica*      | CGMCC 3.18282 | *Camellia sinensis*     | China         | KX986783    | NA   | KX999255 | KX999175 | KX999216 |
| *D. yunnanensis*         | CGMCC 3.18289 | *Coffee sp.*            | China         | KX986796    | KX999290   | KX999267 | KX999188 | KX999228 |
| *D. xiphoftella corinna*  | CBS 121124  | *Corylus sp.*            | China         | KC343004    | KC343246   | KC345488 | KC343730 | KC343972 |

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

**Morphological analysis**

Morphological observations of the asexual morph in the natural environment were based on features of the fruiting bodies produced on infected plant tissues and micro-morphology, supplemented by cultural characteristics. Conidiomata from tree barks were sectioned by hand, using a double-edged blade and structures were observed under a dissecting microscope. The gross morphology of fruiting bodies was recorded using a Leica stereomicroscope (M205 FA). Fungal structures were mounted in clear lactic acid and micromorphological characteristics were examined at 1000× magnification using a Leica compound microscope (DM 2500) with differential interference contrast (DIC) optics. Thirty measurements of each structure were determined for each collection. Colony characters and pigment production on PDA were noted after 10 d. Colony colours were described according to Rayner (1970).

**DNA extraction, PCR amplification and sequencing**

Genomic DNA was extracted from colonies grown on cellophane-covered PDA, using the CTAB [cetyltrimethylammonium bromide] method (Doyle and Doyle 1990). PCR amplifications of phylogenetic markers were done using the same primer pairs.
and conditions as in Yang et al. (2018). PCR products were assayed via electrophoresis in 2% agarose gels. DNA sequencing was performed using an ABI PRISM 3730XL DNA Analyzer 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 our amplified nucleotide sequences was checked and combined by 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, Long et al. 2019). Sequences were aligned using MAFFT v. 7.310 (http://mafft.cbrc.jp/alignment/server/index.html) (Katoh and Standley 2016) and manually corrected 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.

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. BI was performed using a Markov Chain Monte Carlo (MCMC) algorithm in MrBayes v. 3.0b4 (Ronquist and Huelsenbeck 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. Alignment and trees were deposited in TreeBASE (submission ID: S25522). The nucleotide sequence data of the new taxa have been deposited in GenBank (Table 1).

Results

Phylogenetic analyses

The five-gene sequence dataset (ITS, cal, his3, tef1 and tub2) was analysed to infer the interspecific relationships within Diaporthe. The dataset consisted of 124 sequences including the outgroup, Diaporthea corylina (culture CBS 121124). A total of 2555 characters including gaps (505 for ITS, 513 for cal, 528 for his3, 475 for tef1 and 522 for tub2) were included in the phylogenetic analysis. The best nucleotide substitution model for ITS, his3 and tub2 was TrN+I+G, while HKY+I+G was selected for both cal and tef1. The topologies resulting from ML and BI analyses of the concatenated dataset were congruent (Fig. 1). Isolates from Shaanxi Province formed three individual clades representing three undescribed species.
Figure 1. Phylogram of *Diaporthe* resulting from a maximum likelihood analysis based on combined ITS, *cal, his3, tef1* and *tub2*. Numbers above the branches indicate ML bootstraps (left, ML BS ≥ 50%) and Bayesian Posterior Probabilities (right, BPP ≥ 0.90). The tree is rooted with *Diaporthella corylina*. Isolates in current study are in blue. “-” indicates ML BS < 50% or BI PP < 0.90.
**Diaporthe albosinensis** C.M. Tian & Q. Yang, sp. nov.

MycoBank No: 829518

Fig. 2

**Diagnosis.** Distinguished from *D. fraxinicola* in having shorter conidiophores and longer beta conidia.

**Etymology.** Named after the host plant, *Betula albosinensis*, from which the holotype was collected.

**Description.** Conidiomata pycnidial, conical, immersed in bark, solitary to aggregated, erumpent through the bark surface, with a solitary undivided locule. Ectostromatic disc yellowish to brown, one ostiole per disc. Ostiole medium black,
up to the level of disc. *Locule* undivided, (280–)290–375(–380) μm diam. *Conidiophores* (6–)8.5–13(–14.5) × (1.5–)2–2.5 μm, hyaline, cylindrical, smooth, phialidic, unbranched, straight or slightly curved. *Alpha conidia* hyaline, aseptate, fusiform, 0–1-guttulate, (7–)8–10(–11) × 2.5–3 μm. *Beta conidia* hyaline, aseptate, filiform,
straight or slightly curved, eguttulate, base subtruncate, tapering towards one apex, (24–)25.5–30(–32) × 1–1.5 μm.

**Culture characters.** Cultures incubated on PDA at 25 °C in the dark. Colony originally flat with white felted aerial mycelium, becoming light brown due to pigment formation, conidiomata irregularly distributed over agar surface, with yellowish conidial drops exuding from the ostioles.

**Specimens examined.** China. Shaanxi Province: Ningshan County, Huoditang Forest Farm, 33°28’25"N, 108°29’39"E, on branches of *Betula albosinensis*, 10 July 2018, N. Jiang (holotype BJFC-S1670; ex-type living culture: CFCC 53066; living culture: CFCC 53067).

**Notes.** Two isolates, representing *D. albosinensis*, are retrieved in a well-supported clade (ML BS/BPP=100/1) and appear most closely related to *D. fraxinicola* (Fig. 1). *Diaporthe albosinensis* can be distinguished from *D. fraxinicola*, based on *tef1* and *tub2* loci (3/335 in *tef1* and 19/429 in *tub2*). Morphologically, *D. albosinensis* differs from *D. fraxinicola* in having shorter conidiophores (8.5–13 vs. 10.5–17.5 μm) and longer beta conidia (25.5–30 vs. 19–29.5 μm) (Yang et al. 2018).

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

_MycoBank No: 829520_

Fig. 3

**Diagnosis.** Distinguished from *D. ukurunduensis* and *D. citrichinensis* in having larger alpha conidia.

**Etymology.** Named after the genus of the host plant from which the holotype was collected, *Corylus*.

**Description.** _Conidiomata_ pycnidial, conical to spherical, immersed in the host bark, erumpent from surface of host branches, scattered, 950–1200 × 420–650 μm diam., covered by orange discharged conidial masses at maturity, usually conspicuous. _Ectostromatic disc_ inconspicuous. _Central column_ beneath the disc more or less conical, bright yellow. _Conidiophores_ reduced to conidiogenous cells. _Conidiogenous cells_ cylindrical, hyaline, smooth, unbranched, tapering towards the apex, (8.5–)10–12(–13) × (2–)2.5–3 μm. _Alpha conidia_ hyaline, aseptate, fusiform, multiguttulate, rarely 2-guttulate, (10.5–)11.5–13(–13.5) × 3–3.5 μm. _Beta conidia_ not observed.

**Culture characters.** Cultures incubated on PDA at 25 °C in the dark. Colony flat, felty with thick texture at the marginal area, with thin texture in the centre, producing beige pigment after 7–10 d. Aerial mycelium white, dense, conidiomata distributed in the centre, with translucent conidial drops exuding from the ostioles.

**Specimens examined.** CHINA. Shaanxi Province: Ningshan County, Huoditang Forest Farm, 33°28’26"N, 108°29’40"E, on branches of *Corylus mandshurica*, 10 July 2018, N. Jiang (holotype BJFC-S1671; ex-type living culture: CFCC 53083); 33°28’26"N, 108°29’38"E, on branches of *Corylus mandshurica*, 10 July 2018, N. Jiang (paratype BJFC-S1672; living culture: CFCC 53084).
Notes. We generated sequences for two isolates of *D. coryli*, CFCC 53083 and CFCC 53084. This new species is phylogenetically most closely related to *D. ukurunduensis* and *D. citrichinensis* (Fig. 1). *Diaporthe coryli* can be distinguished from *D. ukurunduensis*, based on ITS, *his3* and *tef1* loci (8/467 in ITS, 1/460 in *his3* and 1/336 in *tef1*); and from *D. citrichinensis* based on *tef1* and *tub2* loci (4/335 in *tef1* and 25/428 in *tub2*). Morphologically, *D. coryli* can be distinguished from both *D. ukurunduensis* (11.5–13 × 3–3.5 vs. 5–6 × 2–3 μm) and *D. citrichinensis* (11.5–13 × 3–3.5 vs. 5.5–9 × 1.5–2.5 μm) in having larger alpha conidia (Huang et al. 2013, Gao et al. 2016).

Figure 3. *Diaporthe coryli* on *Corylus mandshurica* (BJFC-S1671). A, B Habit of conidiomata in wood C transverse section of conidiomata D longitudinal section through conidiomata E conidiogenous cells attached with alpha conidia F alpha conidia. Scale bars: 500 μm (B–D); 10 μm (E); 20 μm (F).
**Diaporthe shaanxiensis** C.M. Tian & Q. Yang, sp. nov.
MycoBank No: 829527

**Fig. 4**

**Diagnosis.** Distinguished from *D. aquatica* and *D. incompleta* in having longer beta conidia.

**Etymology.** Named after Province Shaanxi, where the holotype was collected.

**Description.** *Conidiomata* pycnidial, immersed in bark, scattered, erumpent through the bark surface, discoid, with a solitary undivided locule. *Ectostromatic disc* yellowish to pale brown, one ostiole per disc, usually conspicuous, (485–)500–687(–

**Figure 4.** *Diaporthe shaanxiensis* on liana (BJFC-S1674). **A, B** Habit of conidiomata on twig **C** transverse section through conidiomata **D** longitudinal section through conidiomata **E** conidiogenous cells attached with beta conidia **F** beta conidia. Scale bars: 200 μm (**B–D**); 10 μm (**E, F**).
695) μm diam. **Locule** circular, undivided, (500–)526–765(–792) μm diam. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** hyaline, cylindrical, unbranched, slightly curved, tapering towards the apex, (12.5–)14.5–17(–18) × 1–1.5(–2) μm. **Alpha conidia** not observed. **Beta conidia** hyaline, aseptate, filiform, straight to curved, eguttulate, (35.5–)37–47.5(–50) × 1 μm.

**Culture characters.** Cultures incubated on PDA at 25 °C in the dark. Colony originally flat with white fluffy aerial mycelium, becoming pale brown with pigment, with visible solitary conidiomata at maturity.

**Specimens examined.** CHINA. Shaanxi Province: Ningshan County, Huoditang Forest Farm, 33°28′25″N, 108°29′39″E, on branch of liana, 10 July 2018, N. Jiang (holotype BJFC-S1674; ex-type living culture: CFCC 53106); 33°28′24″N, 108°29′38″E, on branch of liana, 10 July 2018, N. Jiang (Paratype BJFC-S1675; living culture: CFCC 53107).

**Notes.** In the combined tree, *D. shaanxiensis* is a distinct clade with maximum support and it appears to be most closely related to *D. aquatica* and *D. incompleta* (Fig. 1). *Diaporthe shaanxiensis* can be distinguished from *D. aquatica* by a 17 nt difference in the ITS region. For *D. aquatica*, only ITS sequences are available in NCBI GenBank (Hu et al. 2012). The new species can be distinguished from *D. incompleta*, based on ITS, cal, his3 and tef1 (24/454 in ITS, 14/443 in cal, 66/468 in his3 and 24/311 in tef1). Morphologically, *D. shaanxiensis* differs from both *D. aquatica* (37–47.5 vs. 9–12.5 μm) and *D. incompleta* (37–47.5 vs. 19–44 μm) in having longer beta conidia (Gao et al. 2016, 2017).

**Discussion**

In this study, an investigation of forest pathogens from Huoditang in Shaanxi Province was carried out and Diaporthe canker was observed as a common disease. Identification of our collections was conducted, based on isolates from fruiting bodies using five combined loci (ITS, cal, his3, tef1 and tub2), as well as morphological characters. Three new *Diaporthe* species were described. These are *D. albosinensis* sp. nov., *D. coryli* sp. nov. and *D. shaanxiensis* sp. nov.

*Diaporthe albosinensis* is associated with *Betula albosinensis*. Thus far, six *Diaporthe* species have been reported from *Betula*. These are *D. alleghaniensis*, *D. betulae*, *D. betulicola*, *D. betulina*, *D. eres* and *D. melanocarpa* (Kobayashi 1970, Gomes et al. 2013, Du et al. 2016, Yang et al. 2018). Morphologically, *D. albosinensis* differs from *D. betulae* (600–1250 μm), *D. betulicola* (700–1300 μm) and *D. betulina* (670–905 μm) in having smaller locules (Du et al. 2016, Yang et al. 2018); and from *D. alleghaniensis* (5–8 × 1.5–2 μm) and *D. eres* (6.5–8.5 × 3–4 μm) in having larger alpha conidia (Arnold 1967, Anagnostakis 2007, Gomes et al. 2013). In addition, our phylogenetic reconstruction of a five-locus dataset adds support for the new species, although no sequence data are currently available for *D. alleghaniensis*, *D. betulicola* and *D. melanocarpa* (Fig. 1). Interestingly, *D. melanocarpa* is found on different plant hosts; it was described from
Pyrus melanocarpa in London and then recorded from Amelanchier, Betula and Cornus (Dearness 1926, Wehmeyer 1933, Kobayashi 1970). Diaporthe coryli is characterised by the ostiole with orange discharged conidial masses and a yellow central column (Fig. 3). Diaporthe shaanxiensis was found on branches of liana with an obvious ostiole per disc and characterised by hyaline, filiform beta conidia. Alpha conidia were found neither in the natural environment nor in culture for this species.

Species delimitation of Diaporthe has improved considerably by using a combination of morphological, cultural, phytopathological and molecular phylogenetic analyses (Udayanga et al. 2014a, b, 2015, Fan et al. 2015, Gao et al. 2017, Guarnaccia and Crous 2017, Hyde et al. 2017, 2020, Guarnaccia et al. 2018, Yang et al. 2018, Long et al. 2019). As a result, many Diaporthe canker diseases and new species have been discovered and reported from all over the world and also in China. The descriptions and molecular data of Diaporthe species represent an important resource for plant pathologists, plant quarantine officials and taxonomists.

Acknowledgements
This study is financed by the Research Foundation of Education Bureau of Hunan Province, China (Project No.: 19B608) and the introduction of talent research start-up fund project of CSUFT (Project No.: 2019YJ025). We are grateful to Chungen Piao, Minwei Guo (China Forestry Culture Collection Center, Chinese Academy of Forestry, Beijing) and reviewers Lu Quan and Jadson Bezerra.

References
Crous PW, Gams W, Stalpers JA, Robert V, Stegehuis G (2004) MycoBank: an online initiative to launch mycology into the 21st century. Studies in Mycology 50: 19–22.
Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: more models, new heuristics and parallel computing. Nature Methods 9: 772. https://doi.org/10.1038/nmeth.2109
Dearness J (1926) New and noteworthy fungi. Mycologia 18: 236–255. https://doi.org/10.1080/00275514.1926.12020515
Diogo E, Santos JM, Phillips AJ (2010) Phylogeny, morphology and pathogenicity of Diaporthe and Phomopsis species on almond in Portugal. Fungal Diversity 44: 107–115. https://doi.org/10.1007/s13225-010-0057-x
Dissanayake AJ, Phillips AJL, Hyde KD, Yan JY, Li XH (2017) The current status of species in Diaporthe. Mycosphere 8: 1106–1156. https://doi.org/10.5943/mycosphere/8/5/5
Doyle JJ, Doyle JL (1990) Isolation of plant DNA from fresh tissue. Focus 12: 13–15. https://doi.org/10.2307/2419362
Du Z, Fan XL, Hyde KD, Yang Q, Liang YM, Tian CM (2016) Phylogeny and morphology reveal two new species of Diaporthe from Betula spp. in China. Phytotaxa 269: 90–102. https://doi.org/10.11646/phytotaxa.269.2.2
Fan XL, Hyde KD, Udayanga D, Wu XY, Tian CM (2015) Diaporthe rostrata, a novel ascomycete from Juglans mandshurica associated with walnut dieback. Mycological Progress 14: 1–8. https://doi.org/10.1007/s11557-015-1104-5

Fan XL, Yang Q, Bezerra JDP, Alvarez LV, Tian CM (2018) Diaporthe from walnut tree (Juglans regia) in China, with insight of Diaporthe eres complex. Mycological Progress 1–13. https://doi.org/10.1007/s11557-018-1395-4

Gao YH, Liu F, Cai L (2016) Unravelling Diaporthe species associated with Camellia. Systematics and Biodiversity 14: 102–117. https://doi.org/10.1080/14772000.2015.1101027

Gao YH, Liu F, Duan W, Crous PW, Cai L (2017) Diaporthe is paraphyletic. IMA Fungus 8: 153–187. https://doi.org/10.5598/imafungus.2017.08.01.11

Garcia-Reyne A, López-Medrano F, Morales JM, Esteban CG, Martín I, Eraña I, Meije Y, Lalucea A, Alastruey-Izquierdo A, Rodríguez-Tudela JL, Aguado JM (2011) Cutaneous infection by Phomopsis longicolla in a renal transplant recipient from Guinea: first report of human infection by this fungus. Transplant Infectious Disease 13: 204–207. https://doi.org/10.1111/j.1399-3062.2010.00570.x

Gomes RR, Glienke C, Videira SIR, Lombard L, Groenewald JZ, Crous PW (2013) Diaporthe: a genus of endophytic, saprobic and plant pathogenic fungi. Persoonia 31: 1. https://doi.org/10.3767/003158513X666844

Guarnaccia V, Crous PW (2017) Emerging citrus diseases in Europe caused by species of Diaporthe. IMA Fungus 8: 317–334. https://doi.org/10.5598/imafungus.2017.08.02.07

Guarnaccia V, Crous PW (2018) Species of Diaporthe on Camellia and Citrus in the Azores Islands. Phytopathologia Mediterranea 57(2).

Guarnaccia V, Groenewald JZ, Woodhall J, Armengol J, Cinelli T, Eichmeier A, Ezra D, Fontaine F, Gramaje D, Gutierrez-Aguirregabiria A, Kalitera J, Kiss L, Larignon P, Luque J, Mognai L, Naor V, Raposo R, Sándor E, Váczy KZ, Crous PW (2018) Diaporthe diversity and pathogenicity revealed from a broad survey of grapevine diseases in Europe. Persoonia 40: 135–153. https://doi.org/10.3767/persoonia.2018.40.06

Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Systematic Biology 59: 307–321. https://doi.org/10.1093/sysbio/syq010

Hall T (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98.

Hu DM, Cai L, Hyde KD (2012) Three new ascomycetes from freshwater in China. Mycologia 104: 1478–1489. https://doi.org/10.3852/11-430

Huang F, Hou X, Dewdney MM, Fu Y, Chen G, Hyde KD, Li HY (2013) Diaporthe species occurring on Citrus in China. Fungal Diversity 61: 237–250. https://doi.org/10.1007/s13225-013-0245-6

Huang F, Udayanga D, Wang X, Hou X, Mei X, Fu Y, Hyde KD, Li HY (2015) Endophytic Diaporthe associated with Citrus: A phylogenetic reassessment with seven new species from China. Fungal Biology 119: 331–347. https://doi.org/10.1016/j.funbio.2015.02.006

Hyde KD, Dong Y, Phookamsak R, Jeewon R, Bhat DJ, Jones EBG, Liu NG, Abeywickrama PD, Mapook A, Wei DP, Perera RH, Manawasinghe IS, Pem D, Bundhun D, Karunarathna A, Ekanayaka AH, Bao DF, Li JF, Samarakoon MC, Chaiwan N, Lin CG, Phutthacha-
Taxonomy of Diaporthe

roen K, Zhang SN, Senanayake IC, Goonasekara ID, Thambugala KM, Phukhamsakda C, Tennakoon DS, Jiang HB, Yang J, Zeng M, Huanraluek N, Liu JK, Wijesinghe SN, Tian Q, Tibpromma S, Brahmanage RS, Boonmee S, Huang SK, Thiyagaraja V, Lu YZ, Jayawardena RS, Dong W, Yang EF, Singh SK, Singh SM, Rana S, Lad SS, Anand G, Devadatha B, Niranjan M, Sarma VV, Liimatainen K, Aguirre-Hudson B, Niskanen T, Overall A, Lúcio R, Alvarenga M, Gibertoni TB, Pfiegler WP, Horváth E, Imre A, Alves AL, da Silva Santos AC, Tiago PV, Bulgakov TS, Wanasinghe DN, Bahkali AH, Doilom M, Elgorban AM, Maharachchikumbura SSN, Rajeshkumar KC, Haelwaters D, Mortimer PE, Zhao Q, Lumyong S, Xu JC, Sheng J (2020) Fungal diversity notes 115–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 100: 5–277. https://doi.org/10.1007/s13225-020-00439-5

Katoh K, Toh H (2010) Parallelization of the MAFFT multiple sequence alignment program. Bioinformatics 26: 1899–1900. https://doi.org/10.1093/bioinformatics/btq224

Kobayashi T (1970) Taxonomic studies of Japanese Diaporthaceae with special reference to their life-histories. Bulletin of the Government Forest Experiment Station 226: 1–242.

Long H, Zhang Q, Hao YY, Shao XQ, Wei XX, Hyde KD, Wang Y, Zhao DG (2019) Diaporthe species in south-western China. MycoKeys 57: 113. https://doi.org/10.3897/mycokeys.57.35448

Mostert L, Crous PW, Kang JC, Phillips AJ (2001) Species of Phomopsis and a Libertella sp. occurring on grapevines with specific reference to South Africa: morphological, cultural, molecular and pathological characterization. Mycologia 93: 146–167. https://doi.org/10.1080/00275514.2001.12061286

Murali TS, Suryanarayanan TS, Geeta R (2006) Endophytic Phomopsis species: host range and implications for diversity estimates. Canadian Journal of Microbiology 52: 673–680. https://doi.org/10.1139/w06-020

Rambaut A, Drummond A (2010) FigTree v.1.3.1. Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, UK.

Rayner RW (1970) A mycological colour chart. Commonwealth Mycological Institute, Kew, UK.

Rehner SA, Uecker FA (1994) Nuclear ribosomal internal transcribed spacer phylogeny and host diversity in the coelomycete Phomopsis. Canadian Journal of Botany 72: 1666–1674. https://doi.org/10.1139/b94-204

Ronquist F, Huelsenbeck JP (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572–1574. https://doi.org/10.1093/bioinformatics/btg180

Rossman AY, Farr DF, Castlebury LA (2007) A review of the phylogeny and biology of the Diaporthales. Mycoscience 48: 135–144. https://doi.org/10.1007/S10267-007-0347-7

Santos JM, Phillips AJL (2009) Resolving the complex of Diaporthe (Phomopsis) species occurring on Foeniculum vulgare in Portugal. Fungal Diversity 34: 111–125.

Santos JM, Vrandečić K, Ćosić J, Duvnjak T, Phillips AJL (2011) Resolving the Diaporthe species occurring on soybean in Croatia. Persoonia 27: 9–19. https://doi.org/10.3767/003158511X603719

Udayanga D, Castlebury LA, Rossman AY, Chukeatirote E, Hyde KD (2014b) Insights into the genus Diaporthe: phylogenetic species delimitation in the D. eres species complex. Fungal Diversity 67: 203–229. https://doi.org/10.1007/s13225-014-0297-2
Udayanga D, Castlebury LA, Rossman AY, Hyde KD (2015) The *Diaporthe* *sojae* species complex: Phylogenetic re-assessment of pathogens associated with soybean, cucurbits and other field crops. Fungal Biology 119: 383–407. https://doi.org/10.1016/j.funbio.2014.10.009

Udayanga D, Castlebury LA, Rossman AY, Hyde KD (2014a) Species limits in *Diaporthe*: molecular re-assessment of *D. citri*, *D. cytopsorella*, *D. foeniculina* and *D. rudis*. Persoonia 32: 83–101. https://doi.org/10.3767/003158514X679984

Udayanga D, Liu X, McKenzie EH, Chukeatirote E, Bahkali AH, Hyde KD (2011) The genus *Phomopsis*: biology, applications, species concepts and names of common phytopathogens. Fungal Diversity 50: 189–225. https://doi.org/10.1007/s13225-011-0126-9

Wijayawardene NN, Hyde KD, Rajeshkumar KC, Hawksworth DL, Madrid H, Kirk PM, Braun U, Singh RV, Crous PW, Kukwa M, Lücking R, Kurtzman CP, Yurkov A, Haelewaters D, Aptroot A, Lumbsch HT, Timdal E, Ertz D, Etayo J, Phillips AJL, Groenewald JZ, Papizadeh M, Selbmann L, Dayarathne MC, Weerakoon G, Jones EBG, Suëtrong S, Tian Q, Castanéda-Ruiz RF, Bahkali AH, Pang KL, Tanaka K, Dai DQ, Sakayaroj J, Hujslová M, Lombard L, Shenoy BD, Suija A, Maharachchikumbura SSN, Thambugala KM, Wansinghe DN, Sharma BO, Gaikwad S, Pandit G, Zucconi L, Onofri S, Egidi E, Raja HA, Kodsiueb R, Cáceres MES, Pérez-Ortega S, Fiuza PO, Monteiro JS, Vasilyeva LN, Shivas RG, Prieto M, Wedin M, Olariaga I, Lateef AA, Agrawal Y, Fazeli SAS, Amoozegar MA, Zhao GZ, Pfliegler WP, Sharma G, Oset M, Abdel MA, Takamatsu S, Bensch K, Silva NI, De Kesel A, Karunarathna A, Boonmee S, Pfister DH, Lu YZ, Luo ZL, Boonyuen N, Daranagama DA, Senanayake IC, Jayasiri SC, Samarakoon MC, Zeng XY, Doilom M, Quijada L, Rampadarath S, Heredia G, Disanayake AJ, Jayawardana RS, Perera PH, Tang LZ, Phukhamsakda C, Hernández-Restrepo M, Ma XY, Tibpromma S, Gusmao LFP, Weerahewa D, Karunarathna SC (2017) Notes for genera: Ascomycota. Fungal Diversity 86: 1–594. https://doi.org/10.1007/s13225-017-0386-0

Yang Q, Fan XL, Du Z, Tian CM (2017a) *Diaporthe* species occurring on *Senna bicapsularis* in southern China, with descriptions of two new species. Phytotaxa 302: 145–155. https://doi.org/10.11646/phytotaxa.302.2.4

Yang Q, Fan XL, Du Z, Tian CM (2017b) *Diaporthe juglandicola* sp. nov. (Diaporthales, Ascomycetes), evidenced by morphological characters and phylogenetic analysis. Mycosphere 8: 817–826. https://doi.org/10.5943/mycosphere/8/5/3

Yang Q, Fan XL, Guarnaccia V, Tian CM (2018) High diversity of *Diaporthe* species associated with dieback diseases in China, with twelve new species described. MycoKeys 39: 97–149. https://doi.org/10.3897/mycokeys.39.26914

Zhang CX, Cao ZM (2007) Primary analysis of macrofungi flora of Huoditang Mts. Journal of Yunnan Agricultural University 22: 345–348.