Phylogenetic analysis demonstrating four new species in *Megasporoporia* sensu lato (Polyporales, Basidiomycota)

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Abstract

*Megasporoporia* sensu lato is a common polypore genus in tropics, the members of which are readily recognized in the field because of their resupinate, light-coloured basidiocarps with big pores. The species of the genus usually grow on fresh fallen trunks and branches. The genus was recognized as polyphyletic by molecular analyses and divided into three genera: *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella*. In the present study, phylogenies based on the combined 2-gene (ITS + nLSU) and 4-gene (ITS + nLSU + mtSSU + TEF) sequences datasets of *Megasporoporia* sensu lato are analysed, and 21 lineages nested in three clades (the *Megasporia* clade, the *Megasporoporia* sensu stricto clade and the *Megasporoporiella* clade) are formed. Based on morphological examination, four new species, *Megasporia bambusae*, *Megasporia fusiformis*, *Megasporoporia inflata* and *Megasporoporiella australiae*, are described based on materials from Australia, China and Malaysia, and a new combination, *Megasporoporiella hubeiensis* comb. nov., is proposed. *Megasporoporiella pseudocavernulosa* is selected as the type species of *Megasporoporiella* because the previous type species *Megasporoporiella cavernulosa* was misidentified. *Polyporus megasporoporus* is the revised name for *Megasporoporiella lacerata*. In addition, a comparison of main characteristics and an identification key of *Megasporoporia* sensu lato are provided.

Keywords – morphology – phylogeny – polymerase – Polyporaceae – taxonomy

Introduction

Ryvarden et al. (1982) established *Megasporoporia* Ryvarden & J.E. Wright in 1982, and four species were addressed in the genus. Species of the genus are easily recognized in the field because of their light coloured, resupinate basidiocarps with big pores. Microscopically, the genus is characterized by a dimitic hyphal structure with generative hyphae bearing clamp connections, skeletal hyphae usually branched and dextrinoid, presence of cystidioles and dendrophydidia in most species, and hyaline, thin-walled, big basidiospores (Ryvarden et al. 1982, Dai et al. 2004, Li & Cui 2013a, Yuan et al. 2017, Cui et al. 2019). Ecologically, the major members of the genus have a distribution in tropics, and usually grow on fallen trunks, branches and twigs which are not...
much decayed. The species diversity was for long underestimated, and 14 species were described recently (Dai & Li 2002, Dai & Wu 2004, Cui & Dai 2007, Zhou & Dai 2008, Du & Cui 2009, Li & Cui 2013a, Yuan et al. 2017). In addition, the molecular phylogeny demonstrated that the genus is polyphyletic, and two genera – *Megasporia* B.K. Cui et al. and *Megasporoporiella* B.K. Cui et al. were derived from *Megasporoporia* (Li & Cui 2013a). So, the definition of *Megasporoporia* by Ryvarden et al. (1982) is in sensu lato, including three genera: *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* (Li & Cui 2013a). These three genera are distinctly different in phylogeny, but it is very difficult to distinguish them morphologically because their major characteristics are overlapped.

Based on more samples of *Megasporoporia* sensu lato from Australia, China and Malaysia, and using combined 2-gene (ITS + nLSU) and 4-gene (ITS + nLSU + mtSSU + TEF) sequences datasets, further phylogenetic analyses on the genus are carried out. Four new species belonging to *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* are detected, and their illustrated descriptions are provided. *Dichomitus hubeiensis* Hai J. Li & B.K. Cui is nested in the *Megasporoporiella* clade, and its morphology fits well *Megasporoporiella*, so the combination of *Megasporoporiella hubeiensis* is proposed.

**Materials & Methods**

**Morphological studies**

The studied specimens are deposited in the herbaria of the Institute of Microbiology, Beijing Forestry University (BJFC), the Institute of Applied Ecology, Chinese Academy of Sciences (IFP), Universidade Federal de Pernambuco (URM), and the private herbarium of Josef Vlasák (JV). Morphological descriptions are based on field notes and herbarium specimens. Microscopic analyses follow Li & Cui (2013a). In the description: CB = Cotton Blue, CB+ = cyanophilous in Cotton Blue, CB− = acyanophilous in Cotton Blue, IKI = Melzer’s reagent, IKI− = neither amyloid nor dextrinoid, KOH = 2% potassium hydroxide, L = arithmetic average of all spore length, W = arithmetic average of all spore width, Q = L/W ratios, and n = number of spores/measured from given number of specimens (Yuan et al. 2017). Color terms are cited from Anonymous (1969) and Petersen (1996).

**DNA extraction, PCR amplification and sequencing**

The total genomic DNA was extracted from the dried specimens using CTAB rapid plant genome extraction kit (Aidlab Biotechnologies Co., Ltd, Beijing), according to the manufacturer’s instructions with some modifications (Chen et al. 2016, Shen et al. 2019). The PCR primers for all genes are listed in Table 1. The PCR protocol for ITS, nLSU, mtSSU, and TEF were followed by Rehner & Buckley (2005) and Li & Cui (2013a), and some adjustments were made to suit different species of *Megasporoporia* sensu lato. The PCR products were purified and sequenced in Beijing Genomics Institute (China) with the same primers. All newly generated sequences were deposited at GenBank (http://www.ncbi.nlm.nih.gov/) and listed in Table 2.

| Gene | Primer | Primer sequences (5’-3’)* | Reference |
|------|--------|---------------------------|-----------|
| ITS  | ITS5   | GGA AGT AAA AGT CGT AAC AAG G | White et al. 1990 |
|      | ITS4   | TCC TCC GCT TAT TGA TAT GC | White et al. 1990 |
| nLSU | LR0R   | ACC CGC TGA ACT TAA GC     | Vilgalys & Hester 1990 |
|      | LR7    | TAC TAC CAC CAA GAT CT     | Vilgalys & Hester 1990 |
| mtSSU | MS1   | CAG CAG TCA AGA ATA TTA GTC AAT G | White et al. 1990 |
|      | MS2    | GCG GAT TAT CGA ATT AAA TAA C | White et al. 1990 |
| TEF  | 983F   | GCY CCY GGH CAY CGT GAY TTY AT | Rehner & Buckley 2005 |
|      | 1567R  | ACH GTR CCR ATA CCA CCR ATC TT | Rehner & Buckley 2005 |
Degeneracy codes: S = G or C, W = A or T, R = A or G, Y = C or T, N = A or T or C or G, D = G or A or T, M = A or C.

Table 2 Information on samples of *Megasporoporia sensu lato* used in this study

| Species                  | Sample no. | Geographic origin | GenBank accessions | References |
|--------------------------|------------|-------------------|--------------------|------------|
|                          |            |                   | ITS     | nLSU | mtSSU | TEF     |               |
| *Cerioporus squamosus*   | Cui10394  | China             | KX8516  | 35   | KX8517| KX8517  | Cui et al. 2019 |
|                          |            |                   | KX8516  | 88   | 14    | 89    | Zhou et al. 2016 |
| *C. squamosus*           | Cui10595  | China             | KU1897  | 78   | KU1899| KU1899  | Cui et al. 2019 |
|                          |            |                   | KU1898  | 09   | 60    | 25    | Cui et al. 2019 |
| *Crassisporus macroporus*| Cui14468  | China             | MK1164  | 86   | MK1164| MK1165  | Cui et al. 2019 |
| *C. macroporus*          | Cui14465  | China             | MK1164  | 85   | MK1164| MK1165  | Cui et al. 2019 |
| *C. imbricatus*          | Dai 10788 | China             | KC8673  | 50   | KC8674| KX8383  | Cui et al. 2019 |
| *C. imbricatus*          | Cui6556   | China             | KC8673  | 26   | KC8674| –      | Cui et al. 2019 |
| *Daedaleopsis confragosa*| Cui6892   | China             | KU8924  | 28   | KU8924| KX8383  | Cui et al. 2019 |
| *D. confragosa*          | Cui9756   | China             | KU8924  | 38   | KU8924| –      | Cui et al. 2019 |
| *D. hainanensis*         | Dai9268   | China             | KU8924  | 34   | KU8924| KX8384  | Li et al. 2016 |
| *D. hainanensis*         | Cui5178   | China             | KU8924  | 35   | KU8924| KX8384  | Li et al. 2016 |
| *D. purpurea*            | Dai8060   | Japan             | KU8924  | 42   | KU8924| KX8384  | Li et al. 2016 |
| *D. purpurea*            | Dai13583a | China             | KX8320  | 54   | KX8320| KX8384  | Li et al. 2016 |
| *D. subtropicus*         | Dai12883  | China             | KX8320  | 5     | KX8320| KX8384  | Li et al. 2014 |
| *D. subtropica*          | Dai12885  | China             | KX8320  | 84   | KX8320| KX8384  | Li et al. 2014 |
| *Datronia mollis*        | Dai11456  | China             | JX55925 | 3    | JX55925| KX8384  | Li et al. 2014 |
| *D. mollis*              | Dai11253  | China             | JX55925 | 3    | JX55925| KX8384  | Li et al. 2014 |
| *D. subtropicus*         | Dai12883  | China             | KC4151  | 84   | KC4151| KX8384  | Li et al. 2014 |
| *D. subtropica*          | Dai12885  | China             | KC4151  | 85   | KC4151| KX8384  | Li et al. 2014 |
| *Dichomitus amazonicus*  | URM87859  | Brazil            | MW989   | 394  | MW965 | –      | Present study |
| *D. cylindrosporus*      | Ryvarden4518 | Belize        | –       | –    | –    | –      | – |
| *D. squalens*            | Cui9639    | China             | JQ78040 | 6    | JQ78040| KX8384  | Li & Cui 2013a |
| *D. squalens*            | Cui9725    | China             | JQ78040 | 8    | JQ78040| KX8384  | Li & Cui 2013a |
| *Echinochaete russiceps* | Dai13868   | China             | KX8320  | 51   | KX8320| KX8384  | Cui et al. 2019 |
| *E. russiceps*           | Dai13866   | China             | KX8320  | 50   | KX8320| KX8384  | Cui et al. 2019 |
| *Favolus acervatus*      | Cui11053   | China             | KU1897  | 74   | KU1897| KU1899  | Zhou & Cui 2017 |
| *F. acervatus*           | Dai10749b  | China             | KU1897  | 74   | KU1897| KU1899  | Zhou & Cui 2017 |
| *F. niveus*              | Cui11129   | China             | KU1897  | 53   | KU1897| KU1899  | Zhou & Cui 2017 |
| *F. niveus*              | Dai13276   | China             | KU1897  | 55   | KU1897| KU1899  | Zhou & Cui 2017 |
Table 2 Continued.

| Species | Sample no. | Geographic origin | GenBank accessions | References |
|---------|------------|-------------------|-------------------|-----------|
| M. rimosa | Cui11079 | China | KX5489 | Zhau & Cui 2017 |
| M. rimosa | Cui13757 | China | KX5489 | Zhau & Cui 2017 |
| H. glabra | Dai12993 | China | KX9006 | Cui et al. 2019 |
| H. glabra | Cui11367 | China | KX9006 | Cui et al. 2019 |
| Horndonemoporus latissimus | Cui6625 | China | HQ8766 | Zhao & Cui 2012 |
| H. latissimus | Dai12054 | China | KX9006 | Cui et al. 2019 |
| Megasporia bambusae | Dai22106 | China | MW694 | Present study |
| M. bambusae | Dai20064 | China | MW694 | Present study |
| M. cystidiolophora | Cui2642 | China | JQ78039 | Li & Cui 2013a |
| M. cystidiolophora | Cui2688 | China | JQ78038 | Li & Cui 2013a |
| M. ellipsoidae | Dai19743 | China | MW694 | Present study |
| M. ellipsoidae | Cui5222 | China | JQ31436 | Li & Cui 2013a |
| M. fusiformis | Dai18596 | Malaysia | MW694 | Present study |
| M. fusiformis | Dai18578 | Malaysia | MW694 | Present study |
| M. guangdongensis | Cui9130 | China | JQ31437 | Li & Cui 2013a |
| M. guangdongensis | Cui13986 | China | MG8472 | Cui et al. 2019 |
| M. hengduanensis | Cui8076 | China | JQ78039 | Li & Cui 2013a |
| M. hengduanensis | Cui8176 | China | JQ31437 | Li & Cui 2013a |
| M. hexagonoides | Cui6592 | China | JQ78040 | Li & Cui 2013a |
| M. hexagonoides | Cui13853 | China | MW694 | Present study |
| M. major | Cui10253 | China | JQ31436 | Li & Cui 2013a |
| M. major | Yuan1183 | China | JQ31436 | Li & Cui 2013a |
| M. rimosa | Dai15357 | China | KY4494 | Yuan et al. 2017 |
| M. rimosa | Dai21997 | China | MW422 | Present study |
| M. tropica | Cui13740 | China | KY4494 | Yuan et al. 2017 |
| M. tropica | Cui13660 | China | KY4494 | Yuan et al. 2017 |
| M. violacea | Cui6570 | China | JQ78039 | Li & Cui 2013a |

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| Species                  | Sample no.       | Geographic origin | GenBank accessions       | References       |
|-------------------------|------------------|-------------------|--------------------------|------------------|
|                         |                  |                   | ITS   | nLSU | mtSSU  | TEF   |                     |
| M. violacea             | Cui13845         | China             | MG8472 |     | MG8472 | MG8472 | MG8677              | Cui et al. 2019 |
|                         |                  |                   | 11     | 20   | 32     | 03    |                      |                  |
| M. violacea             | Cui13838         | China             | MG8472 |     | MG8472 | MG8472 | MG8677              | Cui et al. 2019 |
|                         |                  |                   | 10     | 19   | 31     | 02    |                      |                  |
| M. yunnanensis          | Cui12614A        | China             | KY4494 |     | KY4494 | WK694  | MZ6186              | Yuan et al. 2017 |
|                         |                  |                   | 42     | 53   | 922    | 28    |                      |                  |
| M. yunnanensis          | Dai13870         | China             | KY4494 |     | KY4494 | WK694  | –                   | Yuan et al. 2017 |
|                         | (Holotype)       |                   | 43     | 54   | 907    | –     |                      |                  |
| Megasporoporia bannaensis | Dai12306        | China             | JQ31436 |     | JQ31437 | –     | –                   | Li & Cui 2013a  |
|                         | (Holotype)       |                   | 2      | 9    | –      | –     |                      |                  |
| M. bannaensis           | Dai13596         | China             | KX9006 |     | KX9007 | KX9007 | KX9008              | Cui et al. 2019 |
|                         |                  |                   | 53     | 02   | 54     | 38    |                      |                  |
| M. cavernulosa          | JV0904/52J       | USA               | JF89410 |     | –      | –     | –                   | Present study   |
|                         |                  |                   | 7      | –    | –      | –     |                      |                  |
| M. cavernulosa          | JV0904/50J       | USA               | JF89410 |     | –      | –     | –                   | Present study   |
|                         |                  |                   | 5      | –    | –      | –     |                      |                  |
| M. cavernulosa          | JV0904/81        | USA               | MW989  |     | –      | –     | –                   | Present study   |
|                         |                  |                   | 395    | –    | –      | –     |                      |                  |
| M. inflata              | Dai17882         | Malaysia          | MW694  |     | MW694  | MW694  | –                   | Present study   |
|                         |                  |                   | 886    | 929  | 914    | –     |                      |                  |
| M. inflata              | Dai17478         | Malaysia          | MW694  |     | MW694  | MW694  | MZ6186              | Present study   |
|                         | (Holotype)       |                   | 887    | 930  | 915    | 33    |                      |                  |
| M. mexicana             | JV1806/4J        | Honduras          | MW989  |     | –      | –     | –                   | Present study   |
|                         |                  |                   | 396    | –    | –      | –     |                      |                  |
| M. minor                | Dai18322         | Vietnam           | MW694  |     | MW694  | MW694  | MZ6186              | Li & Cui 2013a  |
|                         |                  |                   | 881    | 925  | 901    | 24    |                      |                  |
| M. minor                | Dai12170         | China             | JQ31436 |     | JQ31438 | MW694  | MF4949              | Present study   |
|                         | (Holotype)       |                   | 3      | 0    | 902    | 80    |                      |                  |
| M. minuta               | Zhou120          | China             | JX16305 |     | JX16305 | MW694  | –                   | Present study   |
|                         |                  |                   | 5      | 6    | 36     | –     |                      |                  |
| M. minuta               | Cui13945         | China             | MW989  |     | MW965  | –      | –                   | Present study   |
|                         |                  |                   | 397    | 596  | –      | –     |                      |                  |
| M. setulosa             | JV1008_51J       | USA               | JF89410 |     | –      | –     | –                   | Present study   |
|                         |                  |                   | 9      | –    | –      | –     |                      |                  |
| M. setulosa             | JV1008_102J      | USA               | JF89411 |     | –      | –     | –                   | Present study   |
|                         |                  |                   | 0      | –    | –      | –     |                      |                  |
| Megasporoporiella australiae | Dai18657       | Australia        | MW694  |     | MW694  | MW694  | MZ6186              | Present study   |
|                         | (Holotype)       |                   | 888    | 931  | 916    | 34    |                      |                  |
| M. australiae           | Dai18658         | Australia        | MW694  |     | MW694  | MW694  | MZ6186              | Present study   |
|                         |                  |                   | 889    | 932  | 917    | 35    |                      |                  |
| M. hubeiensis           | Dai18102         | China             | MW694  |     | MW694  | MW694  | MZ6186              | Present study   |
|                         |                  |                   | 890    | 933  | 918    | 36    |                      |                  |
| M. hubeiensis           | Dai18103         | China             | MW694  |     | MW694  | MW694  | –                   | Present study   |
|                         |                  |                   | 891    | 934  | 919    | –     |                      |                  |
| M. hubeiensis           | Wei2045          | China             | JQ78038 |     | JQ78042 | KX8383 | –                   | Present study   |
|                         | (Holotype)       |                   | 7      | 1    | 96     | –     |                      |                  |
| M. pseudocavernulosa    | Yuan1270         | China             | JQ31436 |     | JQ31439 | KX8383 | –                   | Present study   |
|                         | (Holotype)       |                   | 0      | 4    | –      | –     |                      |                  |
| M. pseudocavernulosa    | Dai19379         | China             | MW694  |     | MW694  | MW694  | MZ6186              | Present study   |
|                         |                  |                   | 882    | 904  | 904    | 26    |                      |                  |
| M. rhododendri          | Dai4226          | China             | JQ31435 |     | JQ31439 | MW694  | –                   | Present study   |
|                         | (Holotype)       |                   | 6      | 2    | 905    | –     |                      |                  |
| M. rhododendri          | Cui12432         | China             | MW694  |     | MW694  | MW694  | MZ6186              | Present study   |
|                         |                  |                   | 883    | 927  | 906    | 27    |                      |                  |
| Species                        | Sample no. | Geographic origin | GenBank accessions | References       |
|-------------------------------|------------|-------------------|--------------------|------------------|
|                               |            |                   | ITS nLSU mtSSU TEF |                  |
| *M. subcavernulosa*           | Cui9252    | China             | JQ78037 6 35 06   | Li & Cui 2013a   |
|                               |            |                   | JQ78041 22 34 05   |                  |
|                               | Cui14247   | China             | MG8472 6 22 34     | Li et al. 2014   |
|                               |            |                   | MG8472 35 36 46    |                  |
|                               | Cui8055    | China             | JX55926 9 6 36     | Li et al. 2014   |
| *Neodatronia gaoligongensis*  | Cui8186    | China             | JX55926 8 5 37     | Li et al. 2014   |
|                               |            |                   | MG8472 5 37         |                  |
|                               |            |                   | MG8677 05          |                  |
| *Perenniporia martia*         | Cui4055    | China             | KX9006 41 8 37     | Cui et al. 2019  |
|                               |            |                   | KX9006 88          |                  |
|                               |            |                   | KX9007 38          |                  |
|                               |            |                   | MG8472 36 22        |                  |
|                               |            |                   | KX9007 5 34         |                  |
|                               |            |                   | MG8677 05          |                  |
|                               | Cui7992    | China             | HQ8766 03 14 41    | Zhao & Cui 2012  |
|                               |            |                   | HQ6541 14 41        |                  |
|                               |            |                   | KF0510 35          |                  |
|                               |            |                   | KF1811 112         |                  |
| *Polyporus arcularius*        | Cui10998   | China             | KX5489 73 95 29    | Zhou & Cui 2017  |
|                               |            |                   | KX5489 95           |                  |
|                               |            |                   | KX5490 59          |                  |
|                               |            |                   | KX5490 29          |                  |
|                               |            |                   | KX5490 152         |                  |
|                               | Cui11398   | China             | KU1897 66 97 47    | Zhou et al. 2016 |
|                               |            |                   | KU1897 97          |                  |
|                               |            |                   | KU1899 11           |                  |
|                               |            |                   | KU1899 59          |                  |
|                               |            |                   | KU1899 97          |                  |
|                               |            |                   | KU1899 9703        |                  |
|                               |            |                   | KU1899 9703        |                  |
| *P. megasporoporus*           | Yuan3880   | China             | JQ31437 7 5        | Li & Cui 2013a  |
| (Megasporoporiella lacerata)  |            |                   | JQ31439 – 37       |                  |
|                               |            |                   | MW694 926          |                  |
|                                 |            |                   | MW694 903          |                  |
| *P. megasporoporus*           | Yuan3874   | China             | –                  | Present study    |
| (Megasporoporiella lacerata)  |            |                   | –                  |                  |
| *P. tuberaster*               | Dai12462   | China             | KU5075 80 84 90    | Zhou et al. 2016 |
|                               |            |                   | KU5075 84 90        |                  |
|                               |            |                   | KU5075 90           |                  |
|                               |            |                   | KU5075 483         |                  |
|                               | Dai11271   | China             | KU1897 69 00 50    | Zhou et al. 2016 |
|                               |            |                   | KU1897 97          |                  |
|                               |            |                   | KU1899 462         |                  |
|                               |            |                   | KU1899 97          |                  |
|                               |            |                   | KU1899 9703        |                  |
|                               | Dai12249   | China             | KU5075 81 83 85    | Zhou et al. 2016 |
|                               |            |                   | KU5075 85 91        |                  |
|                               |            |                   | KU5075 91           |                  |
|                               |            |                   | KU5075 9103        |                  |
| *P. varius*                   | Dai13874   | China             | KU1897 77 08 58    | Zhou et al. 2016 |
|                               |            |                   | KU1897 58          |                  |
|                               |            |                   | KU1899 23           |                  |
|                               |            |                   | KU1899 23           |                  |
|                               |            |                   | KU1899 23           |                  |
|                               |            |                   | KU1899 23           |                  |
|                               |            |                   | KU1899 23           |                  |
| *Trametes hirsuta*            | RLG5133T   | USA               | JN16494 1 1        | Li & Cui 2013a   |
|                               |            |                   | JN16494 1 1        |                  |
|                               |            |                   | JN16489 1 1        |                  |
|                               |            |                   | JN16489 4           |                  |
| *T. ochracea*                 | HHB13445sp | USA               | JN16495 4 2        | Li & Cui 2013a   |
|                               |            |                   | JN16495 2 4        |                  |
|                               |            |                   | JN16490 4           |                  |
|                               |            |                   | JN16490 4           |                  |

New species and sequences are shown in **bold**

**Phylogenetic analysis**

Sequences generated in this study were aligned with additional sequences downloaded from GenBank (Table 2) using Clustal X (Thompson et al. 1997) and BioEdit (Hall 1999). The data matrices were edited in Mesquite v3.04 software (Maddison & Maddison 2009). Sequence alignment was deposited at TreeBase (submission ID 28606 and 28610). Previous to phylogenetic analysis, ambiguous sequences at the start and the end were deleted and gaps were manually adjusted to optimize the alignment using BioEdit (Hall 1999). Two combined matrices were reconstructed for phylogenetic analyses as a 2-gene dataset (ITS + nLSU) and a 4-gene dataset (ITS + nLSU + mtSSU + TEF). The phylogenetic analyses used in this study followed the approach of Zhu et al. (2019) and Sun et al. (2020). Maximum parsimony (MP), Maximum likelihood (ML) and Bayesian inference (BI) were employed to perform phylogenetic analysis.

Sequences of *Trametes hirsuta* (Wulfen) Lloyd and *T. ochracea* (Pers.) Gilb. & Ryvarden were used as outgroups to root trees. All characters were equally weighted and gaps were treated as missing data. Trees were inferred using heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max-trees were set to 5,000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL),
consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated (Farris 1989, Farris et al. 1994, Swofford 2002, Yuan et al. 2017).

Maximum likelihood (ML) research was conducted with RAxML-HPC v. 8.2.3 (Stamatakis 2014) involved 1000 ML searches under the GTRGAMMA model, and only the maximum likelihood best tree from all searches was kept. In addition, 1000 rapid bootstrap replicates were run with the GTRCAT model to assess ML bootstrap values (ML) of the nodes.

MrMODELTEST 2.3 (Posada & Crandall 1998, Nylander 2004) also was used to determine the best-fit evolution model for the combined dataset of ITS + nLSU and ITS + nLSU + mtSSU + TEF sequences for estimating Bayesian inference (BI). Bayesian inference was calculated with MrBayes 3.2 (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 2 million generations until the split deviation frequency value < 0.01, and sampled every 100 generations. The first one-fourth sampled three were discarded as burn-in, while the remaining ones were used to calculate Bayesian posterior probabilities (BPP) of the clades.

Branches that received bootstrap support for Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian posterior probabilities (BPP) more than or equal to 50% (MP and ML) and 0.90 (BPP) were considered as significantly supported. (Figs 1-2). Phylogenetic trees were visualized with the program FigTree v. 1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/).

Results

Phylogenetic analyses

The consequence of phylogeny includes the combined dataset of ITS and nLSU sequences from 96 fungal collections representing 49 species. The dataset has an aligned length of 2074 characters, of which 1148 characters are constant, and 591 are parsimony-informative. MP analysis yields a tree (TL = 2588, CI = 0.388, RI = 0.795, RC = 0.309, HI = 0.612). The best-fit evolutionary model is selected by maximum parsimony (MP) from the combined dataset of ITS + nLSU sequences. The MP and ML values (≥ 50%) and BPP (≥ 0.90) are shown at the nodes. So, the topology from the MP tree is presented along with statistical values from the MP/ML/BPP algorithms (Fig. 1).

The consequence of phylogeny includes the combined dataset of ITS, nLSU, mtSSU, and TEF sequences from 94 fungal collections representing 48 species. The dataset has an aligned length of 3363 characters, of which 2177 characters are constant, and 1093 are parsimony-informative. MP analysis yields a tree (TL = 4864, CI = 0.409, RI = 0.772, RC = 0.316, HI = 0.591). The best-fit evolutionary model is selected by maximum parsimony (MP) from the combined dataset of ITS + nLSU sequences. The MP and ML values (≥ 50%) and BPP (≥ 0.90) are shown at the nodes. So, the topology from the MP tree is presented along with statistical values from the MP/ML/BPP algorithms (Fig. 2).

Our phylogenies support previous conclusions (Li & Cui 2013a, Yuan et al. 2017), three clades are formed in the topology (Fig. 1): Megasporia (79% MP, 99% ML, 1.00 BPP), Megasporoporia sensu stricto (91% MP, 99% ML, 1.00 BPP) and Megasporoporiella (95% MP, 100% ML, 1.00 BPP).

The Megasporia clade includes twelve species: M. bambusae sp. nov., M. cystidiolophora B.K. Cui & Hai J. Li, M. ellipsodea B.K. Cui & Hai J. Li, M. fusiformis sp. nov., M. guangdongensis B.K. Cui & Hai J. Li, M. hengduanensis B.K. Cui & Hai J. Li, M. hexagonoides B.K. Cui et al., M. major B.K. Cui & Hai J. Li, M. rimosa Y. Yuan et al., M. tropica Y. Yuan et al., M. violacea B.K. Cui et al. and M. yunnanensis Y. Yuan et al.

The Megasporoporia sensu stricto clade includes four species: M. bannaensis B.K. Cui & Hai J. Li, M. inflata sp. nov., M. minor B.K. Cui & Hai J. Li, and M. setulosa Rajchenb.

The Megasporoporiella clade includes five species: M. australiae sp. nov., M. hubeiensis comb. nov., M. pseudocavernulosa B.K. Cui & Hai J. Li, M. rhododendri B.K. Cui & Hai J. Li, and M. subcavernulosa B.K. Cui & Hai J. Li.
In addition, another clade (the unnamed clade of *Megasporoporia* sensu lato, Figs 1–2) includes three species: *Dichomitus amazonicus* Gomes-Silva et al., *Megasporoporia cavernulosa* (Berk.) Ryvarden and *M. mexicana* Ryvarden.

Four new species, *Megasporia bambusae*, *Megasporia fusiformis*, *Megasporoporia inflata*, *Megasporoporiella australiae*, and a new combination, *Megasporoporiella hubeiensis*, formed well-supported phylogenetic lineages (100% ML, 100% ML, 1.00 BPP) distinct from other known lineages (species) of *Megasporoporia* sensu lato (Fig. 2).

Figure 1 – Phylogeny of *Megasporoporia* sensu lato and related species generated by Maximum Parsimony based on combined ITS + nLSU sequences. Bootstrap supports for Maximum parsimony (MP), Maximum Likelihood (ML) and Bayesian posterior probabilities (BPP) were not lower than: 50% (MP and ML) and 0.90 (BPP) on the branches. The new species and combination were in bold.
Figure 2 – Phylogeny of *Megasporoporia* sensu lato and related species generated by Maximum Parsimony based on combined ITS + nLSU + mtSSU + TEF sequences. Bootstrap supports for MP, ML and BPP were not lower than: 50 % (MP and ML) and 0.90 (BPP) on the branches. The new species and combination were in bold.

**Taxonomy**

*Megasporia bambusae* Y.C. Dai, Yuan Yuan & Ya. R. Wang sp. nov.

Index Fungorum number: IF558811; Facesoffungi number: FoF10470

**Etymology** – *bambusae* (Lat.): referring to the species growing on bamboo.

*Basidiocarps* annual, resupinate, corky, without odor or taste when fresh, becoming hard corky upon drying, up to 2.7 cm long, 2.2 cm wide, and 0.2 mm thick at center; sterile margin distinct, white, up to 1 mm wide. Pore surface white to cream when fresh, cream to buff when dry; pores angular, 4–5 per mm; dissepiments thick, entire; subiculum pale buff, corky, up to 0.05 mm thick; tubes cream, paler than subiculum, corky, up to 0.15 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae weakly dextrinoid, CB+; tissues unchanged in KOH (not dissolved). *Subicular* generative hyphae hyaline, thin-walled, occasionally branched, 1.5–1.8 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to wide...
lumen, frequently branched, mostly flexuous, interwoven, 2.5–3 µm in diam. *Tramal* generative hyphae hyaline, thin-walled, occasionally branched, 1.5–1.8 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, frequently branched, mostly flexuous, interwoven, 1.5–2 µm in diam. *Dendrohyphidia* present. *Hyphal pegs* absent. *Cystidia* absent; *cystidioles* present, subulate or ventricose, thin-walled, smooth, 14–41 × 4.8–14.8 µm. *Basidia* clavate to pear-shaped, usually constricted in middle, with four sterigmata and a basal clamp connection, 20–35.2 × 10–14.8 µm; *basidioles* in shape similar to basidia, but distinctly smaller. Small tetrahedric or polyhedral crystals frequently present among hymenium. *Basidiospores* ellipsoid, hyaline, fairly thick-walled, smooth, IKI–, CB–, (10.5–)11.8–14(–14.8) × (5.5–)5.8–6.8(–7.5) µm, L = 12.67 µm, W = 6.53 µm, Q = 1.91–1.96 (n = 90/3).

**Known distribution** – widespread in tropical and subtropical regions.

**Materials examined** – China, Hainan Prov., Haikou, Jinniuling Park, on dead bamboo, 18 Nov 2020, Y.C. Dai 22106 (BJFC035998, holotype), Y.C. Dai 22113 (BJFC036005); Guangxi Auto. Reg., Yulin, Guishan Forest Park, on dead bamboo, 3 Jul 2019, Y.C. Dai 20064 (BJFC031738).

**Notes** – *Megasporia bambusae* is found from the tropical zone of China. It is readily distinguished from other species in *Megasporoporia* sensu lato by its fairly thick-walled basidiospores and growing on bamboo, all other members of *Megasporoporia* sensu lato have thin-walled basidiospores and growing on dicotyledon. *Megasporia bambusae* resembles *Megasporia cystidiolophora*, *Megasporia guangdongensis* and *Megasporoporiella rhododendri* by the overlapped distribution and almost the same size of pore (3–5 per mm), but the latter three species have thin-walled basidiospores and lacks dendrohyphidia. Phylogenetically, *Megasporia bambusae* is related to *Megasporia elipsoidea*, *M. yunnanensis*, *M. major*, *M. hexagonoides*, *M. fusiformis* and *M. rimosa* (Figs 1–2), but the latter six species have thin-walled basidiospores and growing on another angiosperm rather than bamboo (Ryvarden et al. 1982, Yuan et al. 2017).

**Figure 3** – Basidiocarps of *Megasporia bambusae* (the holotype, Dai 22106).
Figure 4 – Microscopic structures of *Megasporia bambusae* (drawn from the holotype, Dai 22106). A Basidiospores. B Basidia. C Basidioles. D Cystidioles. E Dendrohyphidia. E Hyphae from subiculum. G Hyphae from tubes.

*Megasporia fusiformis* Y.C. Dai, Yuan Yuan & Ya.R. Wang, sp. nov.

Index Fungorum number: IF558812; Facesoffungi number: FoF10471

Etymology – *fusiform* (Lat.): referring to the species producing fusiform basidiospores.
Basidiocarps annual, resupinate, corky, without odor or taste when fresh, becoming hard corky when dry, up to 11.6 cm long, 2.2 cm wide, and 0.4 mm thick at center; sterile margin distinct, white, up to 1 mm wide. Pore surface cream when fresh, cream to buff-yellow when dry; pores angular, 3.5–4 per mm; dissepiments thick, entire; subiculum cream, corky, up to 0.2 mm thick; tubes cream, paler than subiculum, corky, up to 0.2 mm long. Hyphal system dimitic; generative hyphae bearing clamp connections; skeletal hyphae sometime simple septate, IKI–, CB+; tissues unchanged in KOH (not dissolved). Subicular generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 2–2.5 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to wide lumen, frequently branched, occasionally simple septate, mostly flexuous, interwoven, 2.8–3 µm in diam. Tramal generative thin-walled, occasionally branched, 2–3 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, frequently branched, mostly flexuous, interwoven, 2–3.5 µm in diam. Dendrohyphidia present. Hyphal pegs absent. Cystidia absent; cystidioles present, ventricose, thin-walled, smooth, 23.2–28.5 × 5.2–9.5 µm. Basidia clavate, usually constricted in middle, with four sterigmata and a basal clamp connection, 25.2–38.2 × 8.2–11.5 µm; basidioles in shape similar to basidia, but distinctly smaller. Small tetrahedric or polyhedral crystals frequently present among hymenium. Basidiospores fusiform, hyaline, thin-walled, smooth, sometimes with one or two guttules, IKI–, CB–, (14.1–)15–19.8–(20.2) × (4–)4.2–6.8–(7) µm, L = 17.59 µm, W = 5.12 µm, Q = 3.24–3.68 (n = 60/2).

Known distribution – widespread in subtropical regions.

Materials examined – Malaysia. Selangor, Kota Damansara, Community Forest Reserve, on rotten angiosperm wood, 16 April 2018, Y.C. Dai 18596 (BJFC026884, holotype), Y.C. Dai 18578 (BJFC026866).

Figure 5 – Basidiocarps of Megasporia fusiformis (the holotype, Dai 18596).

Notes – Morphologically, Megasporia rimosa is similar to M. fusiformis by white to cream pore surface and extremely thin basidiocarp (less than 0.5 mm thick), but M. rimosa is different from M. fusiformis by its dextrinoid skeletal hyphae, cylindrical basidiospores and skeletal hyphae
without any septa (Yuan et al. 2017). Phylogenetically *M. fusiformis* is closer to *M. hexagonoides* and *M. rimosa* (Figs 1–2), but *M. hexagonoides* differs from *M. fusiformis* by the bigger pores (0.5–1 per mm vs. 3.5–4 per mm), the absence of dendrohyphidia, and skeletal hyphae without any septa (Dai & Cui 2008).

**Figure 6** – Microscopic structures of *Megasporia fusiformis* (drawn from the holotype, Dai 18596). A Basidiospores. B Basidia and basidioles. C Cystidioles. D Dendrohyphidia. E Hyphae from subiculum. F Hyphae from tubes.

*Megasporoporia inflata* Y.C. Dai, Yuan Yuan & Ya.R. Wang, sp. nov.  
Index Fungorum number: IF558813; Facesoffungi number: FoF10472
Etymology – *inflata* (Lat.): referring to the skeletal hyphae of the species become swollen in KOH.

*Basidiocarps* annual, resupinate, cushion-shaped, corky, without odor or taste when fresh, becoming hard corky upon drying, up to 9.5 cm long, 2 cm wide, and 3.5 mm thick at center; sterile margin thinning out, cream to clay buff, up to 1 mm wide. Pore surface cream to buff when fresh, buff when dry; pores round to angular, 2.5–3 per mm; dissepiments thick, entire; subiculum buff, corky, up to 1 mm thick; tubes pale buff, corky, up to 2.5 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae strongly dextrinoid, CB+; tissues more or less dissolved and skeletal hyphae become strongly swollen in KOH. *Subicular* generative hyphae infrequent, hyaline, thin-walled, moderately branched, mostly flexuous, 2–2.5 μm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, moderately branched, mostly flexuous, interwoven, 2–3.5 μm in diam. *Tramal* generative hyaline, thin-walled, moderately branched, 2–2.5 μm in diam; skeletal hyphae dominant, thick-walled with a narrow lumen to subsolid, moderately branched, mostly flexuous, interwoven, 2.5–3 μm in diam. *Dendrohyphidia* absent. *Hyphal pegs* absent. *Cystidia* and *cystidioles* absent. *Basidia* broadly barrel-shaped to pyriform, with four sterigmata and a basal clamp connection, 14.2–22.5 × 7–8.9 μm; *basidioles* dominant in hymenium, in shape similar to basidia, but smaller. Big rhomboid or polyhedric crystals frequently present among hymenium. *Basidiospores* cylindrical, hyaline, thin-walled, smooth, with one big guttule, IKI−, CB−, (9.8–)10–11.8(–12) × 3.5–4.2 μm, L = 10.38 μm, W = 3.86 μm, Q = 2.69–2.98 (n = 60/2).

Known distribution – widespread in tropical and subtropical regions.

Materials examined – Malaysia. Selangor, Kota Damansara Community Forest Reserve, on fallen angiosperm twig, 19 June 2017, Y.C. Dai 17478 (BJFC025011, holotype). Singapore. Bukit Timah Natural Reserve, on fallen angiosperm branch, 20 July 2017, Y.C. Dai 17882 (BJFC025414).

![Figure 7 – Basidiocarps of *Megasporoporia inflata* (the holotype, Dai 17478).](image-url)
Figure 8 – Microscopic structures of *Megasporoporia inflata* (drawn from the holotype, Dai 17478). A Basidiospores. B Basidia. C Basidioles. D Hyphae from subiculum. E Hyphae from tubes.

Notes – The skeletal hyphae of *Megasporoporia inflata* strongly swell in KOH, and this feature is unique in *Megasporoporia* sensu lato. In addition, *Megasporoporia inflata* lacks hyphal pegs, cystidioles and dendrohyphidia. So, the above characteristics stand out the new species from other members of *Megasporoporia* sensu lato. *Megaspora tropica* is similar to *Megasporoporia inflata* by occurring in tropical China, almost the same size of pores, strongly dextrinoid skeletal hyphae, the absence of hyphal pegs and dendrohyphidia, but the former has cystidioles and bigger basidiospores (14.7–18.8 × 5–6.5 μm vs. 10–11.8 × 3.5–4.2 μm), and its skeletal hyphae are unchanged in KOH (Yuan et al. 2017). Phylogenetically, *M. inflata* is closely related to
M. bannaensis (Figs 1–2), but the latter species has bigger pores (1–2 per mm) and their skeletal hyphae unchanged in KOH (Li & Cui 2013a).

**Megasporoporiella australiae** Y.C. Dai, Yuan Yuan & Ya.R. Wang, sp. nov. Figs 9–10

Index Fungorum number: IF558814; Facesoffungi number: FoF10473

Etymology – *australie* (Lat.): referring to the species found from Australia.

**Basidiocarps** annual, resupinate, corky, without odor or taste when fresh, becoming hard corky and cracked upon drying, up to 5.4 cm long, 2 cm wide, and 0.4 mm thick at center; sterile margin distinct, white to cream, cottony, up to 3 mm wide. Pore surface white to cream when fresh, vinaceous buff to fulvous when dry; pores round to angular, 3–4 per mm; dissepiments thick, entire; subiculum pale buff, corky, up to 0.2 mm thick; tubes cream, paler than subiculum, corky, up to 0.2 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae IKI−, CB+; tissues unchanged in KOH (not dissolved). *Subicular* generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 2–3 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, frequently branched, strongly flexuous, strongly interwoven, 2–3.5 µm in diam. *Tramal* generative hyphae hyaline, thin-walled, occasionally branched, 2–2.5 µm in diam; skeletal hyphae dominant, thick-walled with a narrow lumen, moderately branched, strongly flexuous, strongly interwoven, 2–3 µm in diam. *Dendrohyphidia* absent. *Hyphal pegs* absent. *Cystidia* absent; *cystidioles* present, tubular to fusoid, thin-walled, smooth, 29–41 × 2.5–11.5 µm. *Basidia* pear-shaped, with four sterigmata and a basal clamp connection, 35–38 × 9.5–12 µm; *Basidioles* in shape similar to basidia, but smaller, some with a few guttules. All the hymenial cells (cystidioles, basidia and basidioles) with abundant oily substance. Small tetrahedric or polyhedric crystals frequently present among hymenium. *Basidiospores* cylindrical, hyaline, thin-walled, smooth, sometimes with one big guttule, IKI−, CB−, (11.5–)11.8–15(–16.5) × (3.5–)4–6(–6.5) µm, L = 13.4 µm, W = 4.98 µm, Q = 2.52–2.64 (n = 60/2).

Known distribution – widespread in temperate region.

Figure 9 – Basidiocarp of *Megasporoporiella australiae* (the paratype, Dai 18658).
Figure 10 – Microscopic structures of *Megasporoporiella australiae* (drawn from the holotype, Dai 18658). A Basidiospores. B Basidia. C Basidioles. D Cystidioles. E Hyphae from subiculum. F Hyphae from tubes.

Materials examined – Australia. Melbourne. Dandenong Ranges Botanic Garden, on dead tree of *Rhododendron*, 12 May 2018, Y.C. Dai 18657 (BJFC27125, holotype), Y.C. Dai 18658 (BJFC27126).
Notes – Morphologically, *Megasporoporiella australiae* resembles *Megasporia cystidiocephora*, *Megasporia hengduanensis* and *Megasporoporia cavernulosa* by sharing almost the same size of pores and basidiospores, but the latter three species can be readily distinguished from *Megasporoporiella australiae* by their dextrinoid skeletal hyphae (Ryvarden et al. 1982, Cui & Dai 2007, Li & Cui 2013a). Phylogenetically, *M. australiae* is closely related to *M. rhododendri* (Figs 1, 2), but *M. rhododendri* can be distinguished from *M. australiae* by dextrinoid skeletal hyphae and ellipsoid basidiospores measuring as 11–14 × 6.5–8 μm (Dai et al. 2004).

*Megasporoporiella hubeiensis* (Hai J. Li & B.K. Cui) Y.C. Dai, Yuan Yuan & Ya. R. Wang, comb. nov.

Index Fungorum number: IF558815; Facesoffungi number: FoF10468

*Basidiocarps* biennial, resupinate, cushion-shaped, corky, without odor or taste when fresh, becoming hard corky upon drying, up to 2.4 cm long, 12 cm wide, and 2.4 mm thick at center; sterile margin thinning out, very narrow to almost lacking. Pore surface white to cream when fresh, vinaceous buff to fulvous when dry; pores round to angular, 1–2 per mm; dissepiments thick, entire; subiculum pale buff, corky, up to 0.6 mm thick; tubes concolorous with the pore surface, corky, up to 1.8 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae IKI–, CB+; tissues unchanged in KOH. (not dissolved). *Subicular* generative hyphae hyaline, thin-walled, occasionally branched, 2.5–2.8 μm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, frequently branched, mostly flexuous, interwoven, 2.8–3 μm in diam. *Tramal* generative hyphae hyaline, thin-walled, occasionally branched, 1.8–2.5 μm in diam; skeletal hyphae dominant, thick-walled with a narrow lumen, frequently branched, mostly flexuous, interwoven, 2.5–3 μm in diam. *Dendrohyphidia* present. *Hyphal pegs* absent. *Cystidia* absent; *cystidioles* present, subulate or ventricose, thin-walled, smooth. 18.2–37.2 × 6.3–10.5 μm. *Basidia* clavate, with four sterigmata and a basal clamp connection, 26.8–34.2 × 7.8–11.2 μm; *basidioles* in shape similar to basidia, but smaller. Small tetrahedric or polyhedral crystals frequently present among hymenium. *Basidiospores* cylindrical, hyaline, thin-walled, smooth, usually with one big guttule, IKI–, CB–, (11–)12–14.3(–14.8) × (4–)4.5–5.7(–6.5) μm, L = 13.26 μm, W = 5.12 μm, Q = 2.37–2.55 (n = 60/2).

**Figure 11** – Basidiocarps of *Megasporoporiella hubeiensis* (Dai 18102).
Figure 12 – Microscopic structures of *Megasporoporiella hubeiensis* (drawn from Dai 18103). A Basidiospores. B Basidia. C Basidioles. D Cystidioles. E Hyphae from subiculum. F Hyphae from tube.

≡ *Dichomitus hubeiensis* Hai J. Li & B.K. Cui, Nordic Journal Botany 31: 118 (2013).

Known distribution – widespread in temperate and subtropical regions.

Materials examined – China, Hebei, Zhuolu County, Xiaowutai Natural Reserve, Shanjiankou, on dead branch of *Salix*, 10 September 2017, Y.C. Dai 18102 (BJFC025632), Y.C.
Dai 18103 (BJFC025633); Hubei, Fang County, Shennongjia Natural Reserve, on fallen angiosperm branch, 22 September 2004, Wei 2045 (BJFC012314, holotype).

Notes – *Megasporoporiella hubeiensis* was originally described as *Dichomitus hubeiensis* Hai J. Li & B.K. Cui from subtropical China (Li & Cui 2013b). But our phylogenies (Figs 1–2) show the species nested in *Megasporoporiella* clade with a robust support (100% MP, 100% ML, 1.00 BPP). So, the above combination is proposed.

In addition, Li & Cui (2013a) defined *Megasporoporiella cavernulosa* as type species of the genus (Li & Cui 2013a), and they used the specimen Wu 9508-328 (AY333800) for phylogeny, however, the specimen represents *Megasporoporia subcavernulosa* rather than *Megasporoporia cavernulosa* (Dai & Wu 2004). *Megasporoporia cavernulosa* was originally described from America, specimens JV0904/50J, JV0904/52J and JV0904/81 collected from America are analyzed, and they are distantly related to *Megasporoporiella* (Fig. 1). In the present study we select *Megasporoporiella pseudocavernulosa* as the type species of *Megasporoporiella*.

For conveniences for the readers, a comparison of main characteristics (Table 3) and an identification key of *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* are provided as following.

**Table 3** The main characteristics of species of *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella*

| Species             | Pores (per mm) | Dextrinoid of skeletals | KOH reaction of skeletals | Cystidioles | Gloeocystidioles | Basidia (μm) | Shape of basidiospores | Basidiospores (μm) | Dendrohyphidia | Hyphal pegs | References               |
|---------------------|----------------|-------------------------|----------------------------|-------------|------------------|--------------|--------------------------|---------------------|----------------|-------------|--------------------------|
| *Megasporia bambusae* | 4–5            | [ + ]                   | [ − ]                      | +           | –                | 20–35 × 10–15 | ellipsoid               | 11.8–14 × 5.8–6.8   | +              | –           | Present study            |
| M. cystidiolophora  | 3–5            | [ ++ ]                  | [ − ]                      | +           | –                | 18–25 × 7–10  | cylindrical             | 11.7–14.9 × 4.1–5.6 | –              | –           | Cui & Dai (2007)         |
| M. ellipsoidea      | 1–1.5          | [ + ]                   | [ − ]                      | +           | +                | 23–40 × 9–15  | ellipsoid               | 12–15 × 6–8.2       | +              | +           | Du & Cui (2009)          |
| M. fusiformis       | 3.5–4          | [ − ]                   | [ − ]                      | +           | –                | 25–38 × 8–12  | fusiform                | 15–19.8 × 4.2–6.8   | –              | –           | Present study            |
| M. guangdongensis   | 4–5            | [ +++ ]                 | [ − ]                      | +           | –                | 20–28 × 5–8   | cylindrical             | 11–14.9 × 3.4–4.5   | –              | –           | Li & Cui (2013a)         |
| M. hengduanensis    | 2–3            | [ ++ ]                  | [ − ]                      | +           | –                | 30–37 × 9–12  | cylindrical             | 11–15 × 4.2–5.2     | –              | –           | Li & Cui (2013a)         |
| M. hexagonoides     | 0.5–1          | [ + ]                   | [ − ]                      | +           | –                | 38–40 × 8–12  | allantoid               | 17–21 × 5–6         | –              | –           | Dai & Cui (2008)         |
| M. major            | 1–1.5          | [ +++ ]                 | [ + ]                      | +           | –                | 24–38 × 12–16 | cylindrical             | 15.2–20 × 5.5–7.1   | +              | +           | Dai & Li (2002)          |
| M. rimosa           | 3–4            | [ + ]                   | [ − ]                      | +           | –                | 20–28 × 5–8   | cylindrical             | 16.8–20.2 × 4.3–5.5 | +              | –           | Yuan et al. (2017)       |
| M. tropica          | 2–3            | [ +++ ]                 | [ − ]                      | +           | –                | 20–25 × 7–10  | cylindrical             | 14.7–18.8 × 5–6.5   | –              | –           | Yuan et al. (2017)       |
| Species                      | Pores (per mm) | Dextrinoid of skeletals | KOH reaction of skeletals | Cystidioles | Gloecystidioles | Basidia (μm) | Shape of basidiospores | Basidiospores (μm) | Dendrohyphidia | Hyphal pegs | References                  |
|------------------------------|----------------|-------------------------|---------------------------|-------------|-----------------|--------------|-------------------------|-------------------|----------------|-------------|--------------------------------|
| M. violacea                  | 5–7            | [ +++ ]                 | [ – ]                     | +           | –               | 13–19 × 5–10 | cylindrical            | 11–14.9 × 3.2–5  | +              | –           | Du & Cui (2009)               |
| M. yunnanensis               | 2–3            | [ + ]                   | [ – ]                     | +           | –               | 30–35 × 9–11 | cylindrical            | 15–20.8 × 5.5–7.1| +              | –           | Yuan et al. (2017)            |
| Megasporoporia bannaensis    | 1–2            | [ +++ ]                 | [ – ]                     | +           | –               | 20–32 × 8–10 | cylindrical            | 10–14 × 3.9–4.6 | –              | +           | Li & Cui (2013a)              |
| M. inflata                   | 2.5–3          | [ +++ ]                 | [ +++ ]                   | –           | –               | 14–23 × 7–9  | cylindrical            | 10–11.8 × 3.5–4.2| –              | –           | Present study                |
| M. minor                     | 6–7            | [ +++ ]                 | [ – ]                     | +           | –               | 18–26 × 6–8  | ellipsoid             | 6–7.8 × 2.6–4   | –              | +           | Li & Cui (2013a)              |
| M. setulosa                  | 1–2            | [ +++ ]                 | [ – ]                     | –           | –               | 18–29 × 7–10 | cylindrical            | 10–14 × 4.2–5.7 | –              | +           | Present study, Ryvarden et al. (1982) |
| Megasporoporiella australiae | 3–4            | [ – ]                   | [ – ]                     | +           | +               | 35–38 × 10–12| cylindrical            | 11.8–15 × 4–6   | –              | –           | Present study, Li & Cui (2013a) |
| M. hubeiensis                | 1–2            | [ – ]                   | [ – ]                     | +           | –               | 27–34 × 8–11 | cylindrical            | 12–14.3 × 4.5–7 | +              | –           | Present study, Li & Cui (2013a), Present study |
| M. pseudocavernulosa         | 1.5–2.5        | [ ++ ]                  | [ – ]                     | +           | –               | 34–52 × 10–12| allantoid             | 10.8–14 × 5.3–6.5| –              | +           | Li & Cui (2013a)              |
| M. rhododendri               | 4–5            | [ ++ ]                  | [ – ]                     | +           | –               | 23–40 × 9–14 | ellipsoid             | 11–14 × 6.5–8   | –              | –           | Dai et al. (2004)             |
| M. subcavernulosa            | 2–4            | [ + ]                   | [ – ]                     | –           | –               | 18–24 × 8–11 | cylindrical            | 9–12.1 × 4.2–5.2| +              | +           | Dai & Wu (2004)               |

Abbreviations: [+] = weakly dextrinoid / slightly swollen; [++] = moderately dextrinoid; [+++] = strongly dextrinoid / distinctly swollen; [–] = indextrinoid/not swollen; + = present; – = absent.

Key to known species of *Megaspora*, *Megasporoporia* sensu stricto and *Megasporoporiella*

1. Pores < 1 per mm .................................................. *Megasporia hexagonoides* 2
2. Pores > 1 per mm .................................................. *Megasporia violacea* 3
3. Pores 5–7 per mm .................................................. *Megasporoporia minor* 4
4. Pore surface violet to greyish violet ......................................... *Megasporia violacea* 3
5. Pore surface cream to buff ................................................. *Megasporoporia minor* 5
4. Basidiospores cylindrical, allantoid or fusiform ..............................Megasporia ellipsoidea
5. Pores 1–2 per mm ..........................................................Megasporia bambusae
6. Dendrohyphidia present; on bamboo .............................................Megasporoporiella rhododendri
7. Basidiospores fusiform .........................................................Megasporia fusiformis
8. Hyphal pegs present .....................................................................Megasporoporia bannaensis
9. Skeletal hyphae weakly to moderately dextrinoid ............................Megasporia guangdongensis
10. Basidiospores > 15 µm long ......................................................Megasporia major
11. Cystidioles present; Asian species ..............................................Megasporoporia inflata
12. Dendrohyphidia present, cystidioles absent .................................Megasporoporiella pseu
docavernulosa
13. Skeletal hyphae strongly dextrinoid .............................................Megasporia yunnanensis
14. Dendrohyphidia present, cystidioles absent .................................Megasporoporiella aust
draliae
15. Dendrohyphidia absent .............................................................Megasporia hubeiensis
16. Basidiospores < 15 µm long ......................................................Megasporoporia hubeiensis
17. Dendrohyphidia absent .............................................................Megasporoporia rimosa
18. Basidiocarps cracked when dry .................................................Megasporia yunnanensis
19. Gloeocystidioles present, skeletal hyphae indextrinoid ..................Megasporoporia hubeiensis
20. Pore surface cream to buff, pores 2–3 per mm ............................Megasporia cystidiolophora

Discussion

Dichomitus D.A. Reid resembles Megasporoporia sensu lato by light colored and resupinate basidiocarps, a dimitic hyphal system with generative hyphae bearing clamp connections, cyanophilous skeletal hyphae, and hyaline, thin-walled basidiospores; that is why Masuka & Ryvarden (1999), Robledo & Rajchenberg (2007) merged them, but without molecular analysis. Type species of Dichomitus, D. squalens, is included in our phylogeny and it is distantly related to Megasporia, Megasporoporia sensu stricto, Megasporoporiella, and the unnamed clade of Megasporoporia sensu lato. (Figs 1–2). Morphologically, Dichomitus lacks hyphal pegs and dendrohyphidia, its skeletal hyphae are indextrinoid and dendritically branched in which they are very similar to Polyporus sensu stricto; while the most species of Megasporia, Megasporoporia sensu stricto and Megasporoporiella have hyphal pegs and dendrohyphidia, and their skeletal hyphae are dextrinoid in most species. So, we treat Dichomitus, Megasporia, Megasporoporia sensu stricto and Megasporoporiella as independent genera.

As mentioned in the introduction, Megasporia, Megasporoporia sensu stricto and Megasporoporiella are distinct in phylogeny, but it is impossible to separate each other by morphology. So, we treat our new species and the combination in Megasporia, Megasporoporia sensu stricto and Megasporoporiella, but for the discussion of their similar species, all the members of Megasporoporia sensu lato are included. In our phylogeny (Figs 1, 2), Dichomitus amazonicus,
Megasporoporia cavernulosa and M. mexicana are nested in three lineages and formed a clade. Dichomitus amazonicus was described from neotropics (Gomes-Silva et al. 2012), corresponding specimen URM 87859 is examined, and the specimen has strongly dextrinoid skeletal hyphae and hyphal pegs (not mentioned in the original description). Megasporoporia cavernulosa was originally described from Brazil (Ryvarden 1984), and it has dendorphydia and dextrinoid skeletal hyphae. Megasporoporia mexicana was originally described from Mexico (Ryvarden et al. 1982), and it was combined in Dichomitus without DNA data (Ryvarden 2007). A specimen of Megasporoporia mexicana from Honduras (JV1806/4J, sequenced) is studied, and it has hyphal pegs and dextrinoid skeletal hyphae which are different from D. squalens (the type species of Dichomitus). Phylogenetically, these three species are distantly related to Dichomitus, Megasporia, Megasporoporia sensu stricto and Megasporoporiella. A new genus might be set up to accommodate them, for the time being, we treat them as present names because more materials need to be examined and phylogenetically analyzed.

Megasporoporia minuta Y.C. Dai & X.S. Zhou was described from China without phylogenetic analysis (Zhou & Dai 2008), but our phylogenies show its type is distantly related to Megasporoporia sensu lato (Figs 1–2). Its type (Zhou 120) and another specimen Cui 13945 are studied, they have perennial basidiocarps, small pores (6–8 per mm), indextrinoid skeletal hyphae, narrowly ovoid basidiospores, lack hyphal pegs, dendorphydia and tetrahedric or polyhedric crystals. These characteristics do not fit the definition of Megasporoporia sensu lato. So, the species is excluded from Megasporia, Megasporoporia sensu stricto and Megasporoporiella. Moreover, Megasporoporiella lacerata B.K. Cui & Hai J. Li was described from China based on morphology and a single gene phylogeny (Li & Cui 2013a). Although its morphological characteristics are similar to that of Megasporoporia sensu lato. However, our phylogenies based on 2-gene and 4-gene sequences datasets show that M. lacerata is closer to Polyporus tuberaster (type species of Polyporus sensu stricto, Figs 1, 2). So, the species should be combined into Polyporus. However, Polyporus laceratus Berk. (Ann. nat. Hist., Mag. Zool. Bot. Geol. 3: 392, 1839) is existed, and the species is re-named as following.

**Polyporus megasporoporus** Y.C. Dai, Yuan Yuan & Ya.R. Wang, nomen. nov.

Index Fungorum number: IF558816; Facesoffungi number: FoF10469

Etymology – megasporopus (Lat.): referring to the species similar with Megasporoporia.

As given by Li and Cui 2013: 377.

= Megasporoporiella lacerata B.K. Cui & Hai J. Li, Mycologia 105(2): 377 (2013).

Material examined – China. Yunnan Province. Baoshan County, Gaoligong Mountains, Biahuailing Nature Reserve, on fallen angiosperm branch, 09 Sep 2007, Yuan 3880 (holotype in IFP, isotype in BJFC).

Besides the species in our phylogeny and the above discussion, the taxa Dichomitus affixus (Corner) T. Hatt. (Hattori 2002), D. africanus Ryvarden (Ryvarden 2019), D. amygaldinus (Berk & Ravnel) Ryvarden (Ryvarden 1977), D. anoectoporus (Berk & M.A. Curtis) Ryvarden (Ryvarden 1984), D. cameroonensis Ryvarden (Ryvarden 2018), D. citricremeus Masuka & Ryvarden (Masuka & Ryvarden 1999), D. costaricensis Ryvarden (Ryvarden 2012), D. cylindrosporus Ryvarden (Ryvarden 2007), D. delicatulus (Henn.) Masuka & Ryvarden (Masuka & Ryvarden 1999), D. densiporus Ryvarden (Ryvarden 2019), D. deviatus Ipulet & Ryvarden (Ipulet & Ryvarden 2005), D. ecuadorensis Ryvarden (Laessoe & Ryvarden 2010), D. efibulatus A.M. Ainsw. & Ryvarden (Ainsworth & Ryvarden 2008), D. epitephrus (Berk.) Ryvarden (Cunningham 1965), D. grandisporus Aime & Ryvarden (Aime et al. 2007), D. leucoplacus (Berk.) Ryvarden (Ryvarden 1977), D. newhookii P.K. Buchanan & Ryvarden (Buchanan & Ryvarden 2000), D. papuanus Quant (Quanten 1996), D. perennis Ryvarden (Ryvarden 2007) & D. sinuolatus H.S. Yuan (Yuan 2013) are recorded in Dichomitus, but most of these taxa lack DNA data, and we did not yet exam their vouchers, and for the time being they are not included in Megasporoporia.
sensu lato. By comparing the original descriptions of these species, the new species we have recently described are different from them.

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