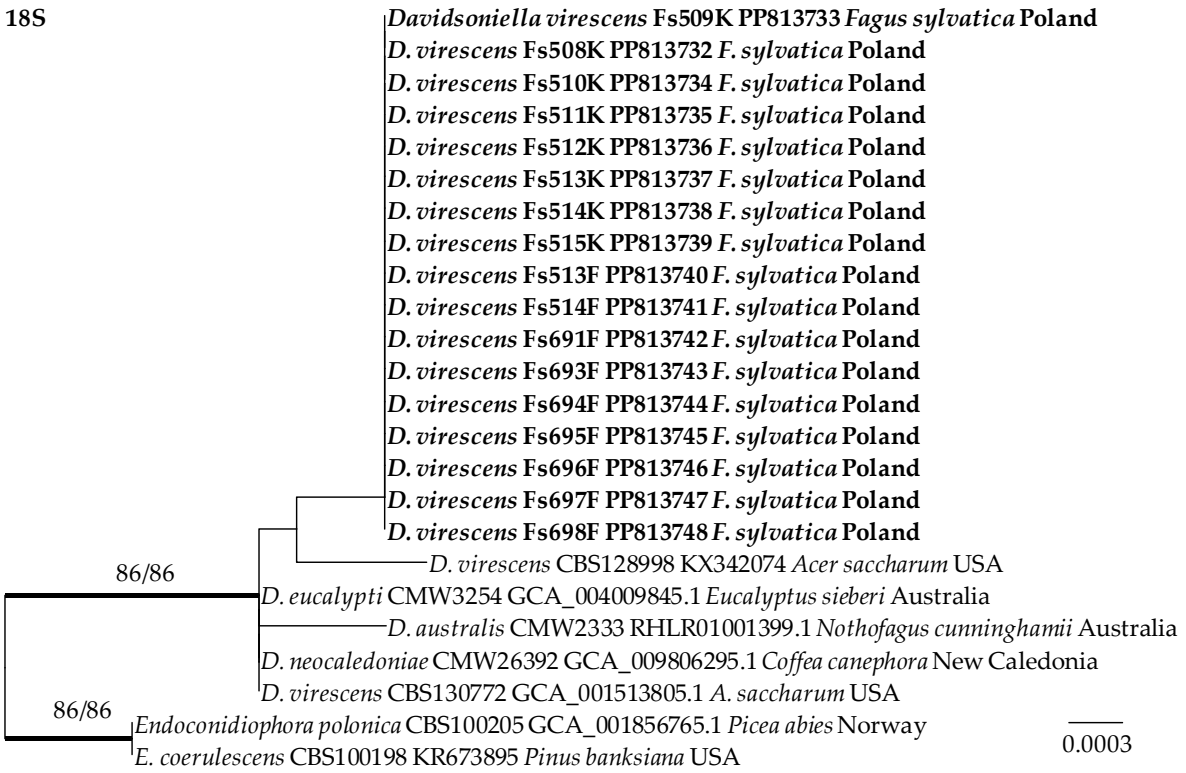



**Figure S1.** Phylogram obtained from analyses of small subunit (SSU) ribosomal DNA (18S) data for the genus *Davidsoniella*. Sequences obtained during this study are presented in bold type. The presented phylogram was obtained from Maximum Likelihood (ML) analyses. The bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probability values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. * Bootstrap values <75%. The tree is drawn to scale (see bar) with branch length measured in the number of substitutions per site. *Endoconidiophora coerulescens* and *E. polonica* represent the outgroup.

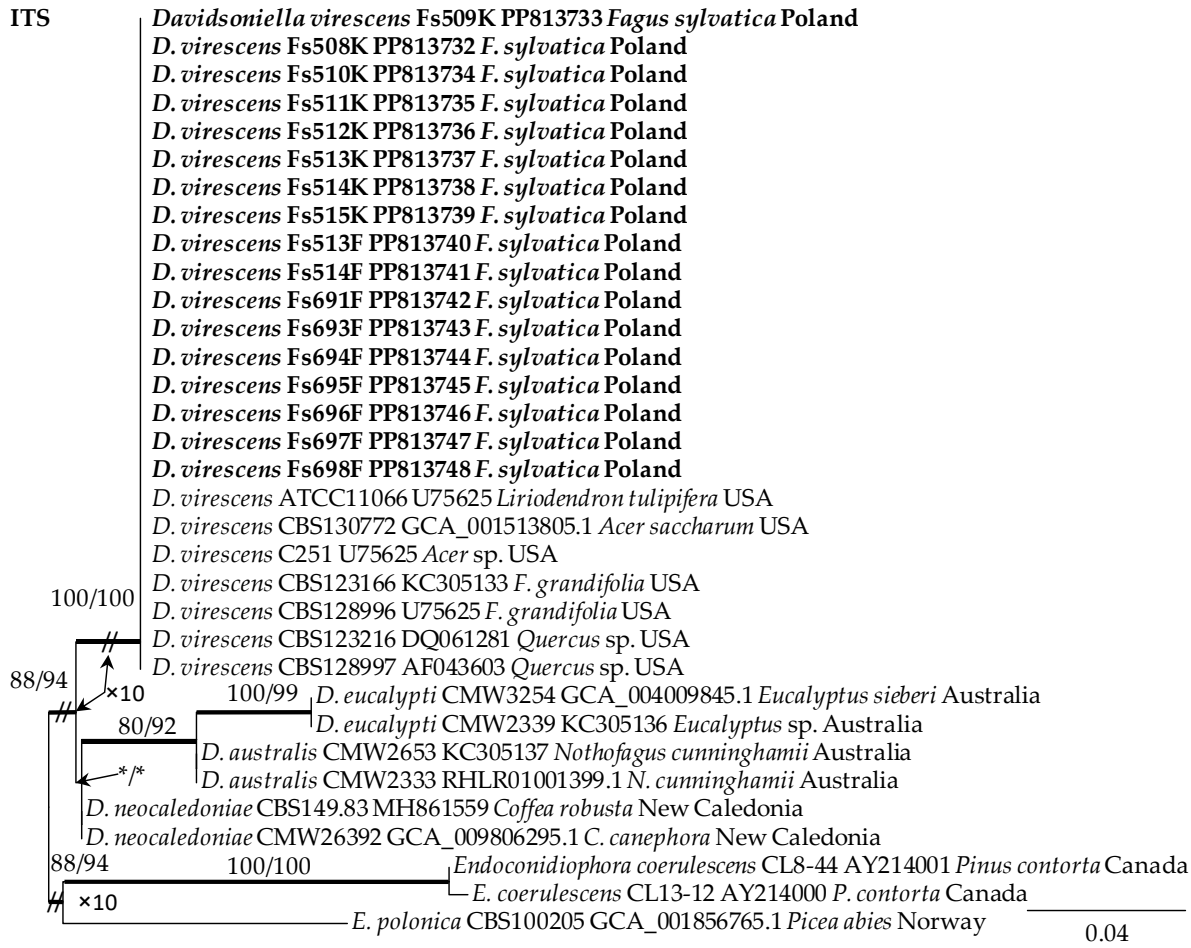



**Figure S2.** Phylogram obtained from analyses of internal transcribed spacer (ITS) data for the genus *Davidsoniella*. Sequences obtained during this study are presented in bold type. The presented phylogram was obtained from Maximum Likelihood (ML) analyses. The bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probability values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. * Bootstrap values <75%. The tree is drawn to scale (see bar) with branch length measured in the number of substitutions per site. *Endoconidiophora coerulescens* and *E. polonica* represent the outgroup.




**Figure S3.** Phylogram obtained from analyses of large subunit (LSU) ribosomal DNA (28S) data for the genus *Davidsoniella*. Sequences obtained during this study are presented in bold type. The presented phylogram was obtained from Maximum Likelihood (ML) analyses. The bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probability values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. * Bootstrap values <75%. The tree is drawn to scale (see bar) with branch length measured in the number of substitutions per site. *Endoconidiophora coerulescens* and *E. polonica* represent the outgroup.

**Table S1.** Primers used in this study to amplify and sequence barcode regions in molecular identification.

| Gene | Primer | Sequence | References |
|---|---|---|---|
| β-tubulin 2 (TUB2) | T10PBCer | 5′-TCTATAGGTCCACCTCCAGAC-3′ | This study |
| | Bt2b | 5′-ACCCTCAGTGTAGTGACCCTTGGC-3′ | Glass and Donaldson [38] |
| The small subunit (18S) of the nuclear rDNA (SSU) | SSJ | 5′-CTGGTTGATCCTGCCAGTAG-3′ | Hausner et al. [39] |
| | SST | 5′-ACGGAGACCTTGTTACGACT-3′ | Hausner et al. [39] |
| Internal transcribed spacer (ITS) | ITS5 | 5′-GGAAGTAAAAGTCGTAACAAGG-3′ | White et al. [40] |
| | ITS4 | 5′-TCCTCCGCTTATTGATATGC-3′ | White et al. [40] |
| The large subunit (28S) of the nuclear rDNA (LSU) | LR0R | 5′-ACCCGCTGAACTTAAGC-3′ | Rehner and Samuels [41] |
| | LR6 | 5′-CGCCAGTTCTGCTTACC-3′ | Vilgalys and Hester [42] |
| Translation elongation factor 1-α (TEF1) | EFCF1 | 5′-AGTGCGGTGGTATCGACAAG-3′ | Oliveira et al. [43] |
| | EFCF2 | 5′-TGCTCACGGGTCTGGCCAT-3′ | Oliveira et al. [43] |
| | EFCF3 | 5′-ATGGCCAGACCCGTGAGCA-3′ | Oliveira et al. [43] |
| | EFCF6PB [1] | 5′-CATRTCACGGACGGCGAARC-3′ | This study |

[1] Degenerate primer.

**Table S2**. Isolates and GenBank accession numbers for reference sequences used in the phylogenetic analyses.

| Species | Strains | Host | Collector | Origin | GenBank Accession Numbers | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | 18S | ITS | 28S | TUB2 | TEF1 |
| *Davidsoniella australis* | CMW 2333 | *Nothofagus cunninghamii* | M. Hall | Australia | RHLR01001399 | RHLR01001399 | RHLR01001399 | RHLR01001399 | RHLR01001399 |
| | CMW 2653 | *Nothofagus cunninghamii* | ? | Australia | – | KC305137 | – | – | – |
| | C 631 | *Nothofagus cunninghamii* | Glen A. Kile | Australia | – | | – | – | HM569648 |
| | CMW 2339 | *Eucalyptus* sp. | ? | Australia | – | KC305136 | – | KC336012 | – |
| | CMW 3254[E] | *Eucalyptus sieberi* | Mark J. Dudzinski | Australia | GCA_004009845 | GCA_004009845 | GCA_004009845 | GCA_004009845 | HM569647 |
| | CMW 26392 | *Coffea canephora* | ? | New Caledonia | GCA_009806295 | GCA_009806295 | GCA_009806295 | GCA_009806295 | GCA_009806295 |
| | CBS 149.83[T] | *Coffea robusta* | Roger Dadant | New Caledonia | – | MH861559 | MH873294 | – | HM569649 |
| | ATCC11066[T] | *Liriodendron tulipifera* | George Henry Hepting | USA | – | U75625 | – | – | – |
| | CBS 130772 | *Acer saccharum* | David Houston | USA | GCA_001513805 | GCA_001513805 | GCA_001513805 | GCA_001513805 | GCA_001513805 |
| | C 251 | *Acer* sp. | David Houston | USA | – | U75625 | – | – | – |
| | CBS 128998 | *Acer saccharum* | David Houston | USA | KX342074 | – | MH878037 | – | HM569645 |
| | CBS 123166 | *Fagus grandifolia* | David Houston | USA | – | KC305133 | | KC336011 | EF070413 |
| | CBS 128996 | *Fagus grandifolia* | David Houston | USA | – | U75625 | U47824 | – | HM569646 |
| | CBS 123216 | *Quercus* sp. | Thomas Hinds | USA | – | DQ061281 | – | – | AY529011 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| *Endoconidiophora coerulescens* | CBS 128997 | *Quercus* sp. | Thomas Hinds | USA | – | AF043603 | AF043603 | – | – |
| | CBS 100198 | *Pinus banksiana* | Thomas Harrington | USA | KR673895 | – | – | – | HM569653 |
| | CL8-44 | *Pinus contorta* | Peter Arne Loppnau | Canada | – | AY214001 | AY214001 | – | – |
| | CL13-12 | *Pinus contorta* | Peter Arne Loppnau | Canada | – | AY214000 | AY214000 | – | – |
| *Endoconidiophora polonica* | CBS 137.34 | Moist timber | Kneteman | Netherlands | – | – | MH866946 | – | – |
| | CBS 140.37 | *Picea abies* | T. Rohde | Germany | – | – | KM495329 | – | – |
| | CBS 100205[N] | *Picea abies* | Halvor Solheim | Norway | GCA_001856765 | GCA_001856765 | MH874300 | GCA_001856765 | HM569656 |
| | CBS 133.38 | *Picea abies* | Wincenty Siemaszko | Poland | – | – | NG_070434 | – | – |
| | CBS 228.83 | *Picea abies* | Halvor Solheim | Norway | – | – | MH873307 | – | – |

[T] Type, [E] Ex-holotype, [N] Ex-neotype.