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Stephen Joshua Taerum*

Ophiostomatatoid fungi (*Ascomycota*) associated with *Ips acuminatus* (Coleoptera) in eastern Poland

Supplementary Material

Fig. S1. Phylogram from Maximum Likelihood (ML) analyses of ITS data for *Graphilbum* spp. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Sporothrix cracoviensis* represents the outgroup

/ ⌐ **Graphilbum acuminatum 99116IA MN548951**
          G. acuminatum 68816IA MN548950
83/98 ⌐ **G. acuminatum 72016IA OQ352133**
          G. acuminatum 100816IA MN548952
100/100   100/100 ⌐ *G. translucens* SNM101 MZ019544
                   └ *G. translucens* SNM144 MZ019546
                    G. puerense CMW41942 OK165563
                G. carpaticum CBS145835 MN548956
*/100   *G. sparsum* CBS405.77 MN548977
                        G. gorcense CMW34153 MN548972
              G. curvidentis CBS145832 KY568502
              97/100 ⌐ *G. niveum* SNM145 MZ019548
        /   └ *G. crescericum* CMW43659 KY568504
      96/*   *G. sexdentatum* CBS145814 MN548968
    96/93   *G. furuicola* CBS145813 MN548961
                  G. interstitiale CBS145816 MN548963
100/100   100/100 ⌐ *G. ipis-grandicollis* VPRI43762 MW066405
97/82   └ *G. ipis-grandicollis* VPRI43759 MW066402
╶╫╴   100/100 ⌐ *G. fragrans* CMW44159 KY568497
Î 10   └ **G. fragrans 27018IA MW540783**
100/100
╶╫╴ *Sporothrix cracoviensis* KFL2514bRJTD MH283503
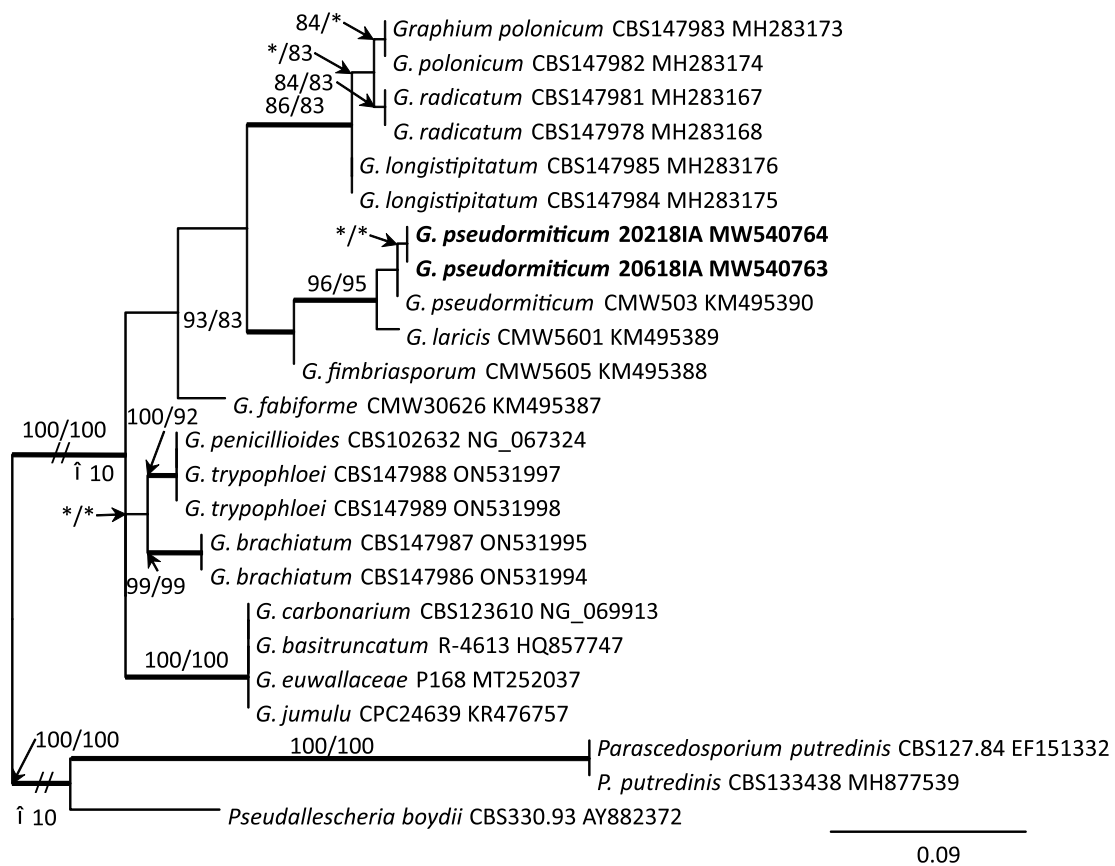Î 10 *S. cracoviensis* KFL714RJTD MH283500

0.2

Fig. S2. Phylogram from Maximum Likelihood (ML) analyses of *TEF1* data for *Graphilbum* spp. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Sporothrix cracoviensis* represents the outgroup
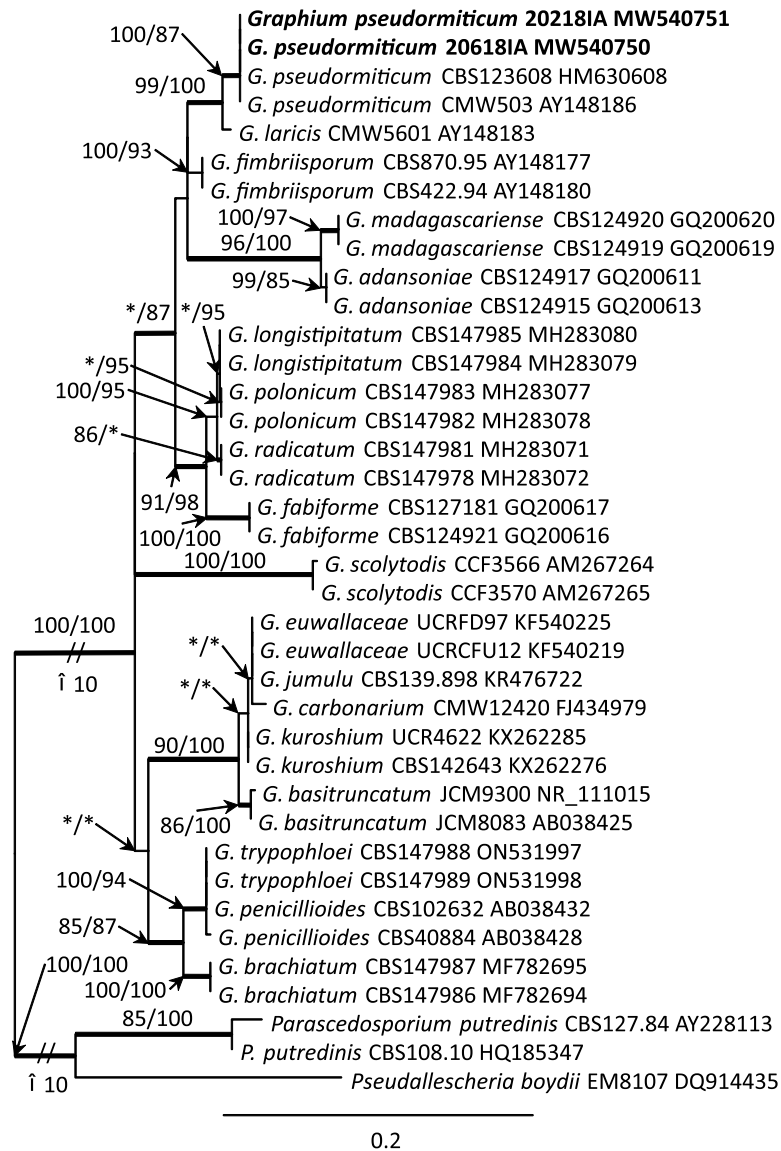
Fig. S3. Phylogram from Maximum Likelihood (ML) analyses of ITS data for *Graphium* spp. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Parascedosporium putredinis* and *Pseudallescheria boydii* represent the outgroup
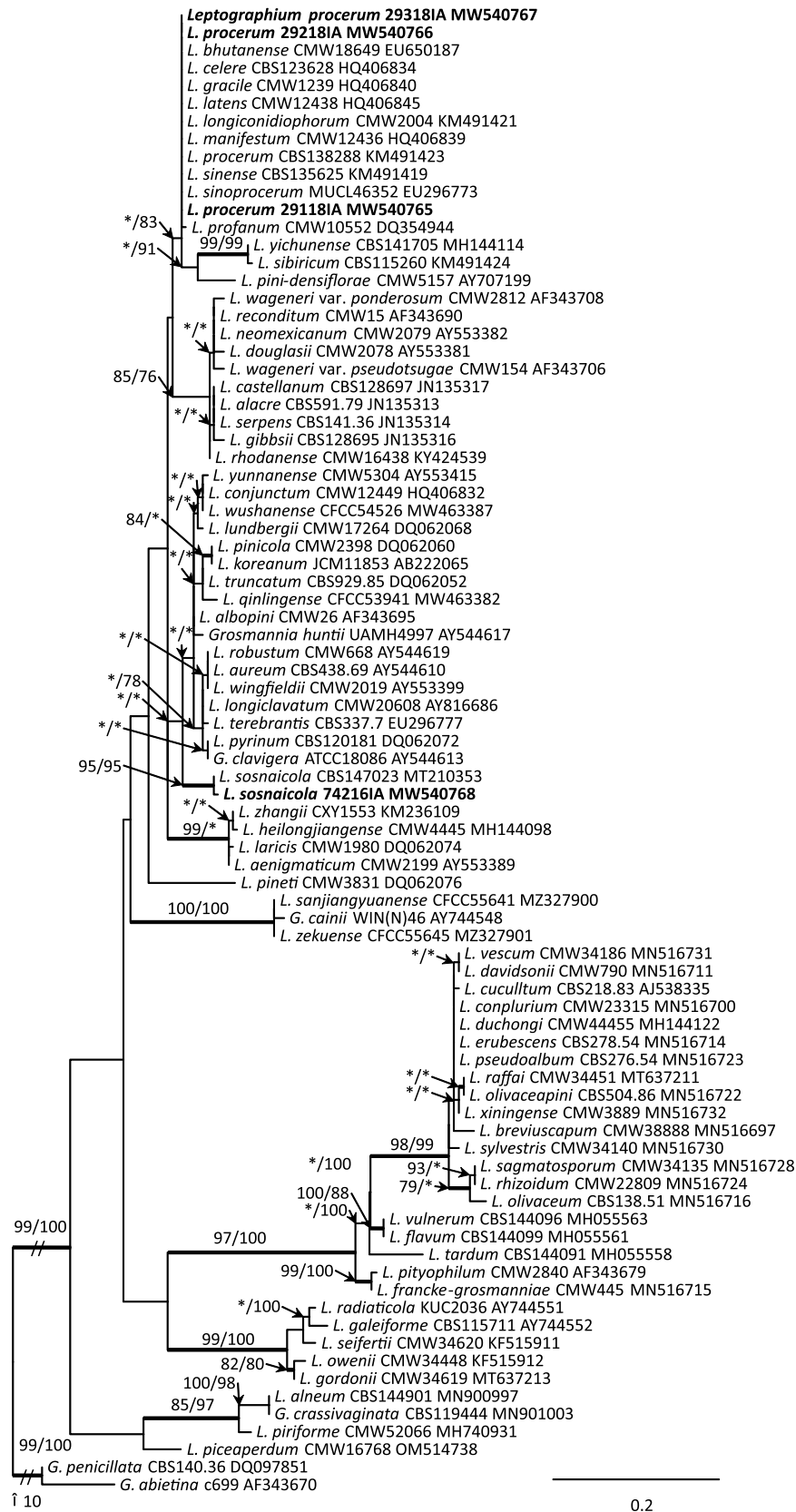
Fig. S4. Phylogram from Maximum Likelihood (ML) analyses of LSU data for *Graphium* spp. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Parascedosporium putredinis* and *Pseudallescheria boydii* represent the outgroup
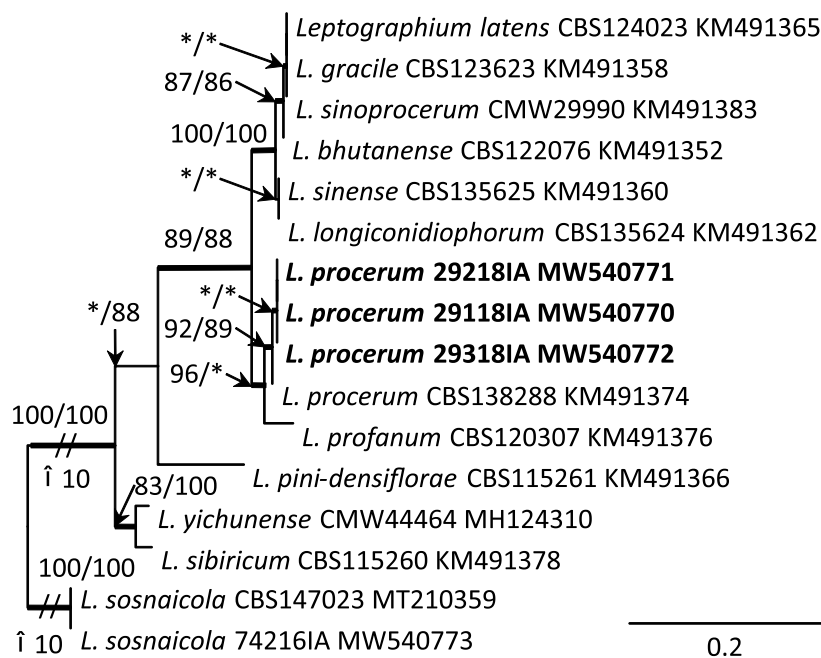
Fig. S5. Phylogram from Maximum Likelihood (ML) analyses of LSU data for *Leptographium* spp. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Grosmannia penicillata* and *G. abietina* represent the outgroup

/
87/86
100/100
/
89/88
*/88
/
92/89
96/*
100/100
Î 10
83/100
100/100
Î 10

Leptographium latens CBS124023 KM491365
L. gracile CBS123623 KM491358
L. sinoprocerum CMW29990 KM491383
L. bhutanense CBS122076 KM491352
L. sinense CBS135625 KM491360
L. longiconidiophorum CBS135624 KM491362
L. procerum 29218IA MW540771
L. procerum 29118IA MW540770
L. procerum 29318IA MW540772
L. procerum CBS138288 KM491374
L. profanum CBS120307 KM491376
L. pini-densiflorae CBS115261 KM491366
L. yichunense CMW44464 MH124310
L. sibiricum CBS115260 KM491378
L. sosnaicola CBS147023 MT210359
L. sosnaicola 74216IA MW540773

0.2

Fig. S6. Phylogram from Maximum Likelihood (ML) analyses of *TUB2* data for *Leptographium procerum* species complex. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Leptographium sosnaicola* represents the outgroup
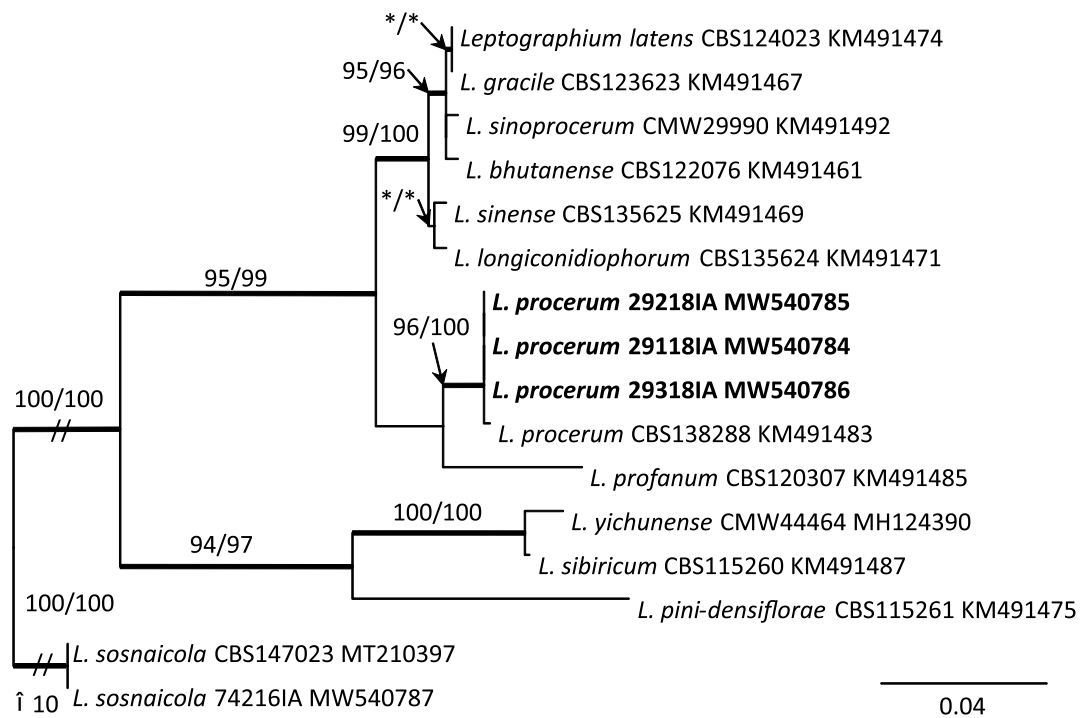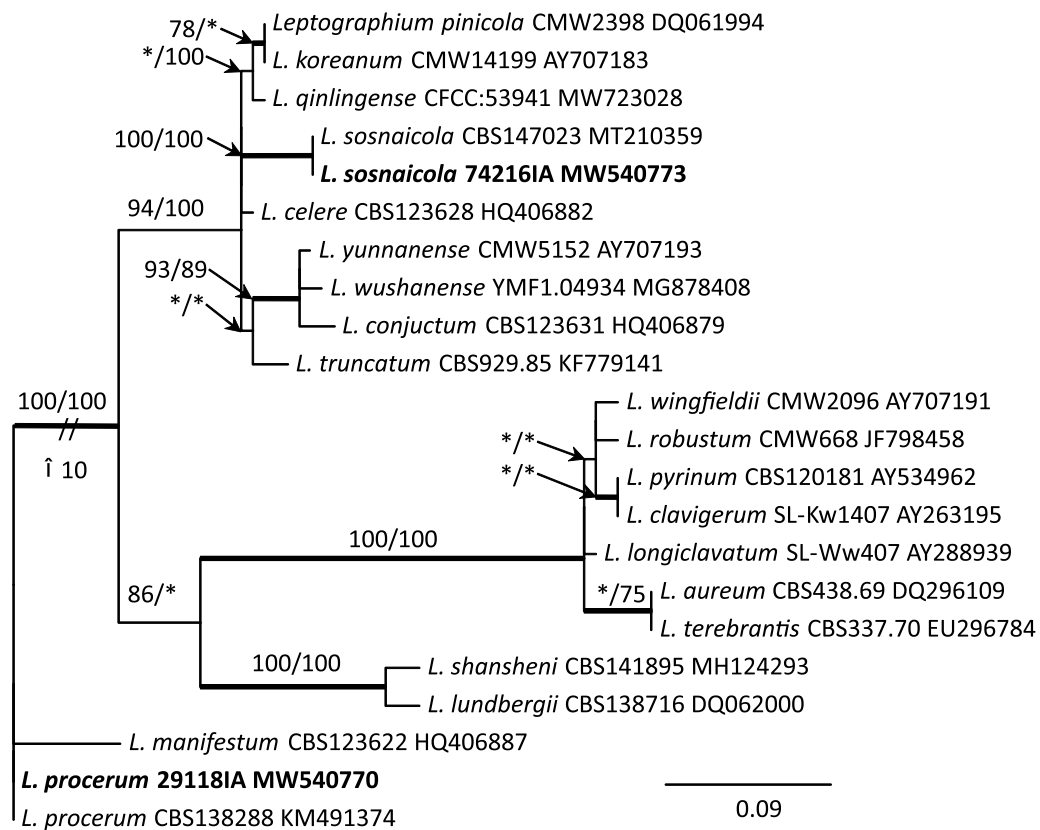
Fig. S7. Phylogram from Maximum Likelihood (ML) analyses of *TEF1* data for *Leptographium procerum* species complex. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Leptographium sosnaicola* represents the outgroup

Fig. S8. Phylogram from Maximum Likelihood (ML) analyses of *TUB2* data for *Leptographium lundbergii* species complex. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Leptographium procerum* representss the outgroup
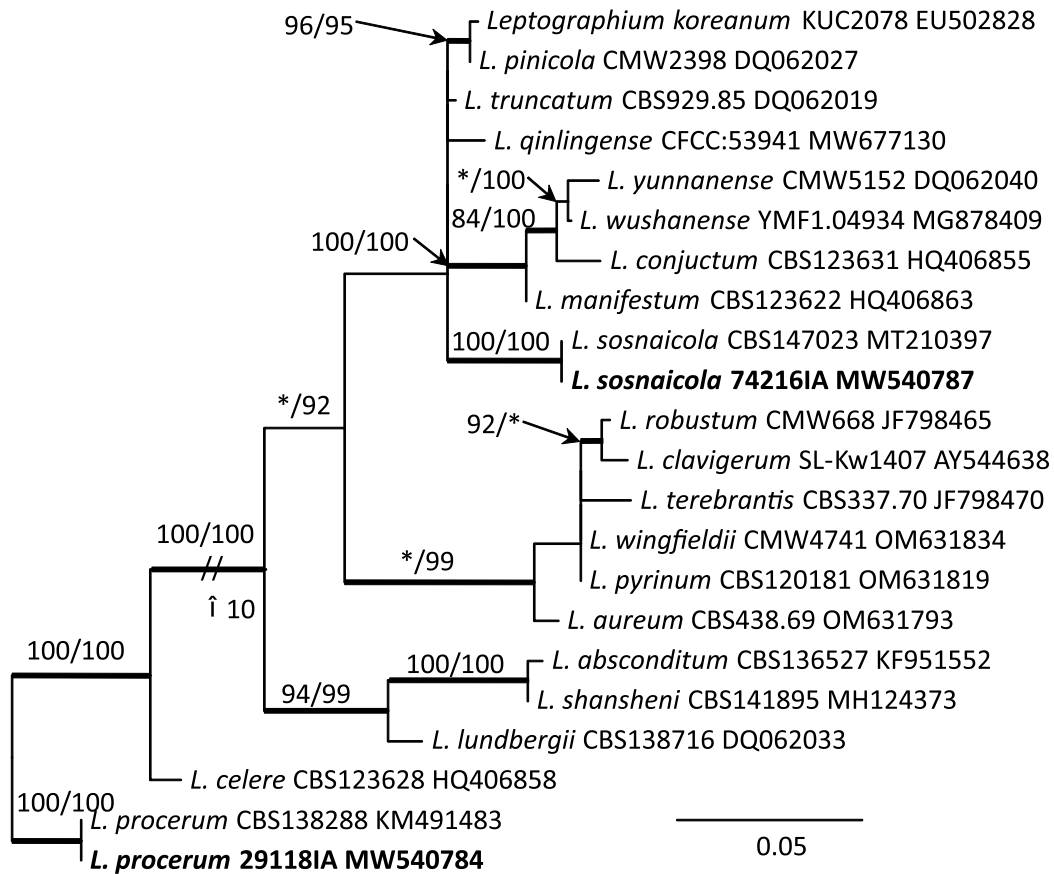
Fig. S9. Phylogram from Maximum Likelihood (ML) analyses of *TEF1* data for *Leptographium lundbergii* species complex. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Leptographium procerum* representss the outgroup
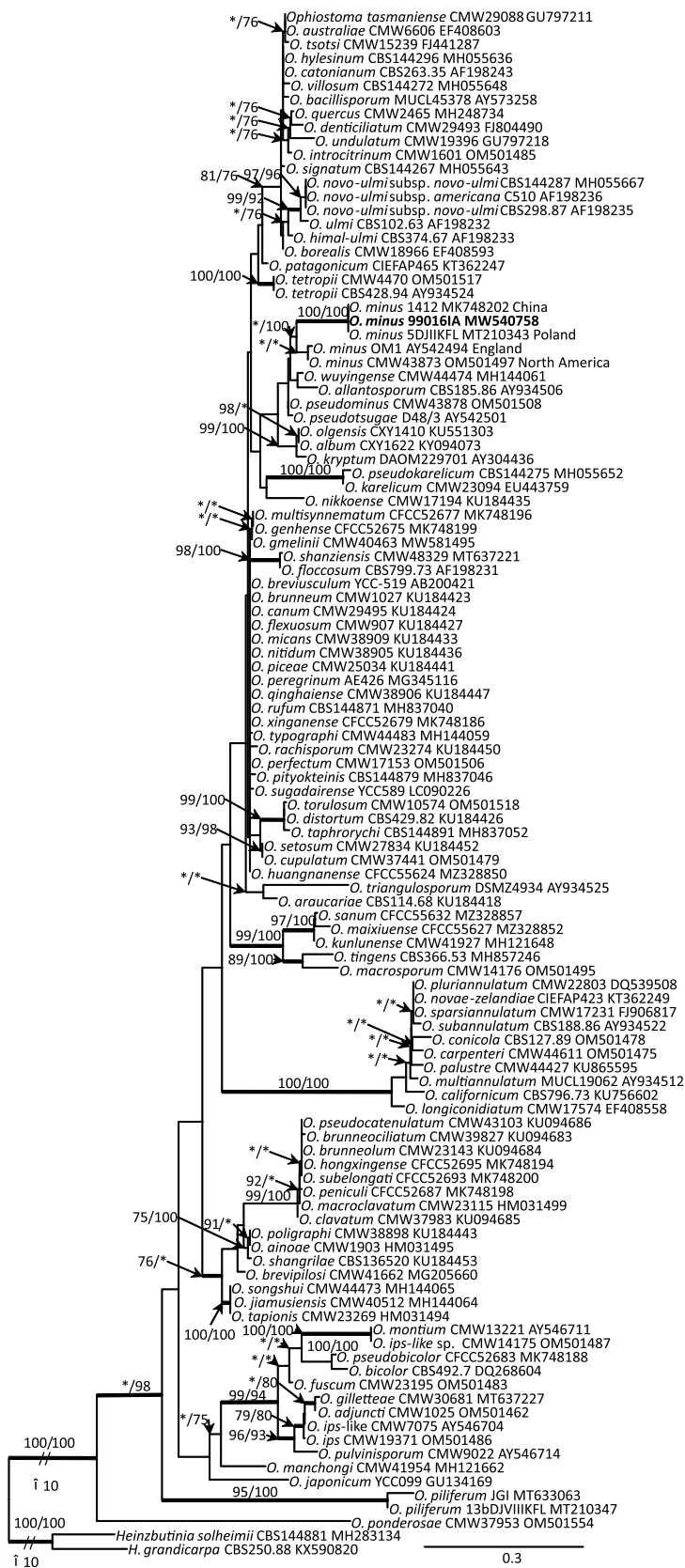
Fig. S10. Phylogram from Maximum Likelihood (ML) analyses of ITS data for *Ophiostoma* spp. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Heinzbutinia solheimii* and *H. grandicarpa* represent the outgroup

/ ⌐ *Ophiostoma minus* 1160RJP JX444618 Poland
└ *O. minus* CFCC52697 MN896044 China
*/95 ⌐ *O. minus* OM1 AY542505 England
⌐ *O. minus* 88-3685 AY542506 Sweden
└ *O. minus* 109aPRJ KU319095 Poland
93/90
97/100 ⌐ *O. minus* 5DJIIKFL MT210377 Poland
└ **O. minus 99016IA MW540774**
*/100
100/100 ⌐ *O. minus* MY28EW1 AY672913 Canada
└ *O. minus* OM6 AY542509 North America
*/100
100/99 ⌐ *O. piliferum* CMW7879 DQ296097
└ *O. piliferum* CBS129.32 AF221628
/
87/94 ⌐ *O. wuyingense* CMW44474 MH124255
└ *O. pseudotsugae* D48/3 AY542511
99/100 ⌐ *O. olgensis* CXY1410 KU882942
└ *O. kryptum* DAOM229701 AY305685
Î 10
─── *O. album* CXY1622 MH360979
// ─── *Heinzbutinia grandicarpa* CBS250.88 KX590762

0.2

Î 10

Fig. S11. Phylogram from Maximum Likelihood (ML) analyses of *TUB2* data for *Ophiostoma minus* species complex. Sequences obtained in this study are in bold. Bootstrap values ≥ 75% for ML and Maximum Parsimony (MP) analyses are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities values ≥ 0.95 obtained from Bayesian Inference (BI) analyses. *Bootstrap values <75%. The tree is drawn to scale (see bar) with branch lengths measured in the number of substitutions per site. *Heinzbutinia grandicarpa* represents the outgroup