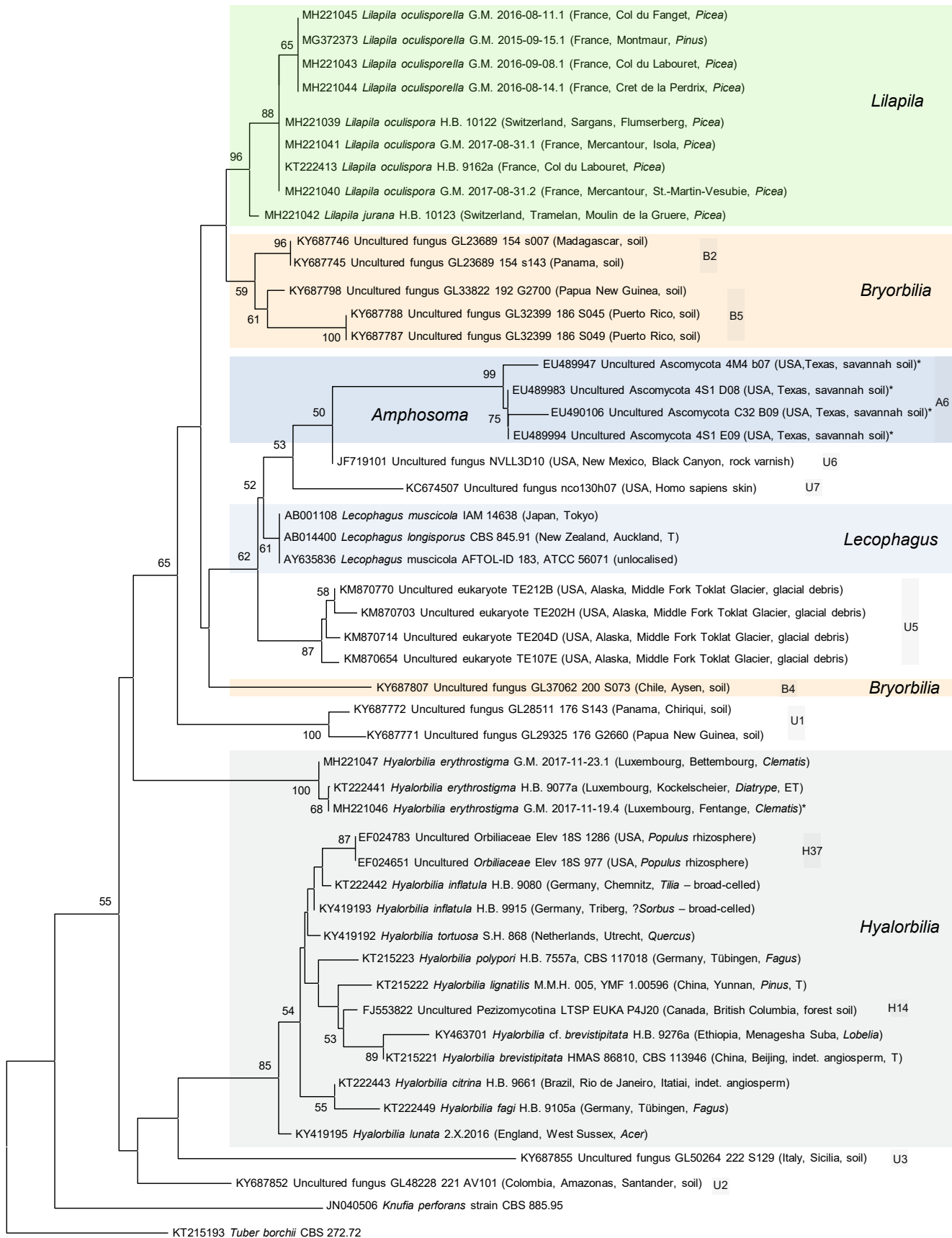
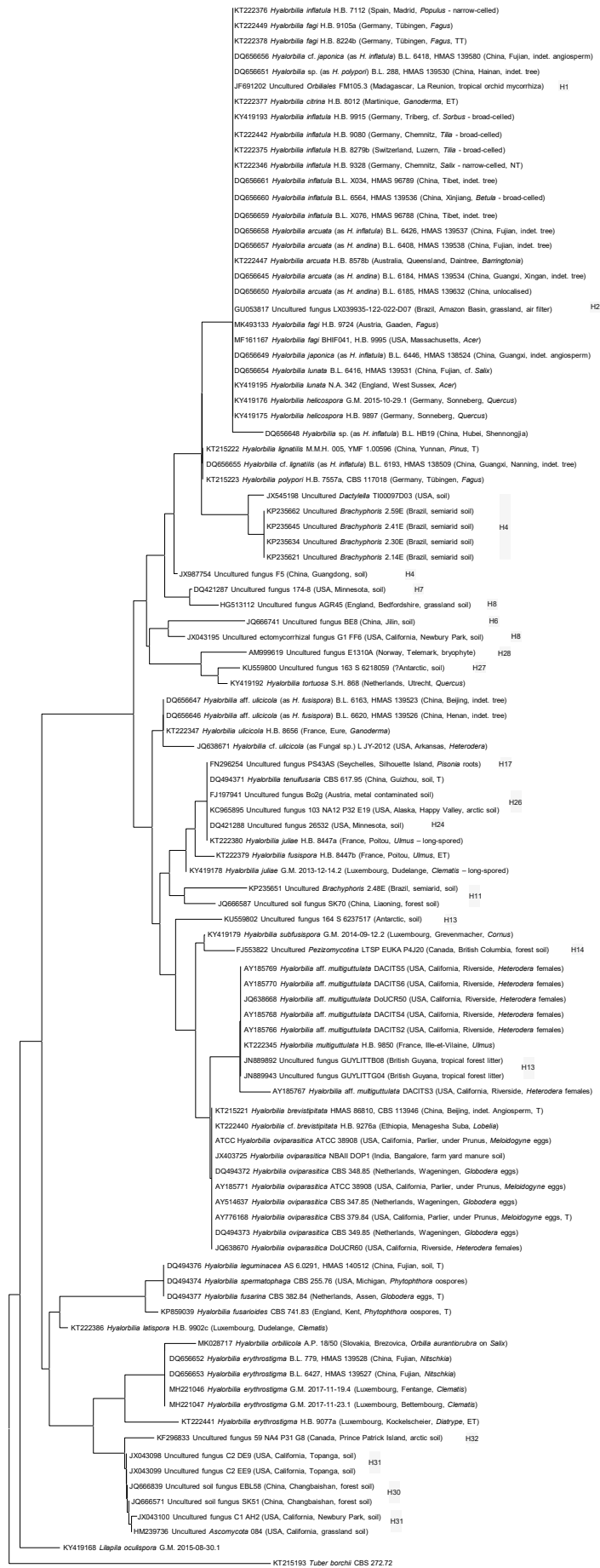


Phylogenetic analysis S1: NJ analysis of *Orbiliomycetes* based on SSU (V1–V5) rDNA dataset (59 sequences, 1089 positions, aligned with MUSCLE) using MEGA6 (500 replicates). The tree is rooted with *Saccharomyces cerevisiae* and *Neolecta irregularis*. T = type, ET = epitype, * = without SSU (V1–V2).

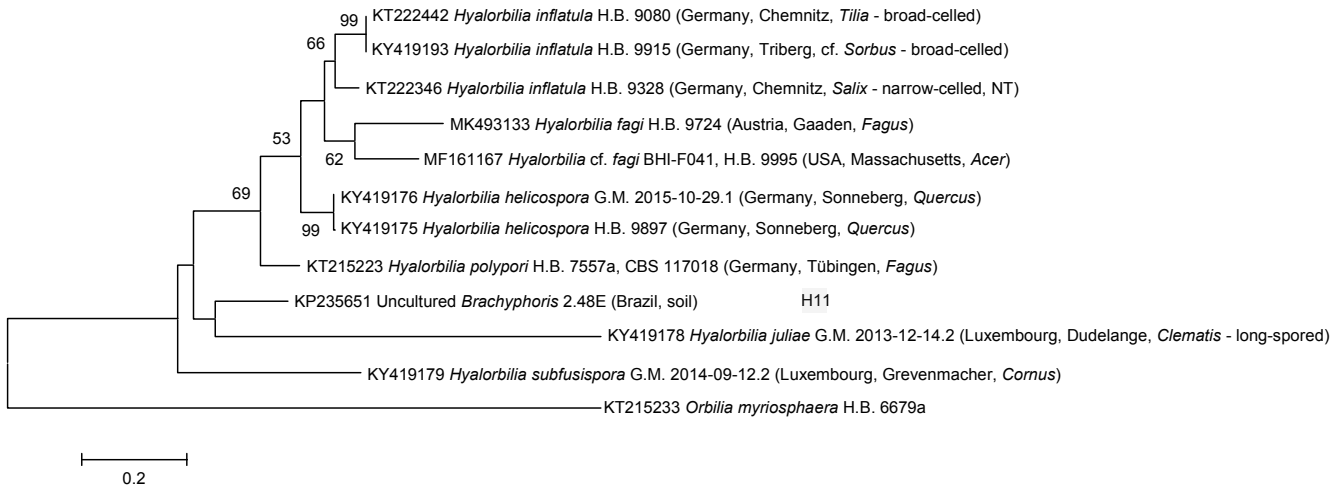


0.005

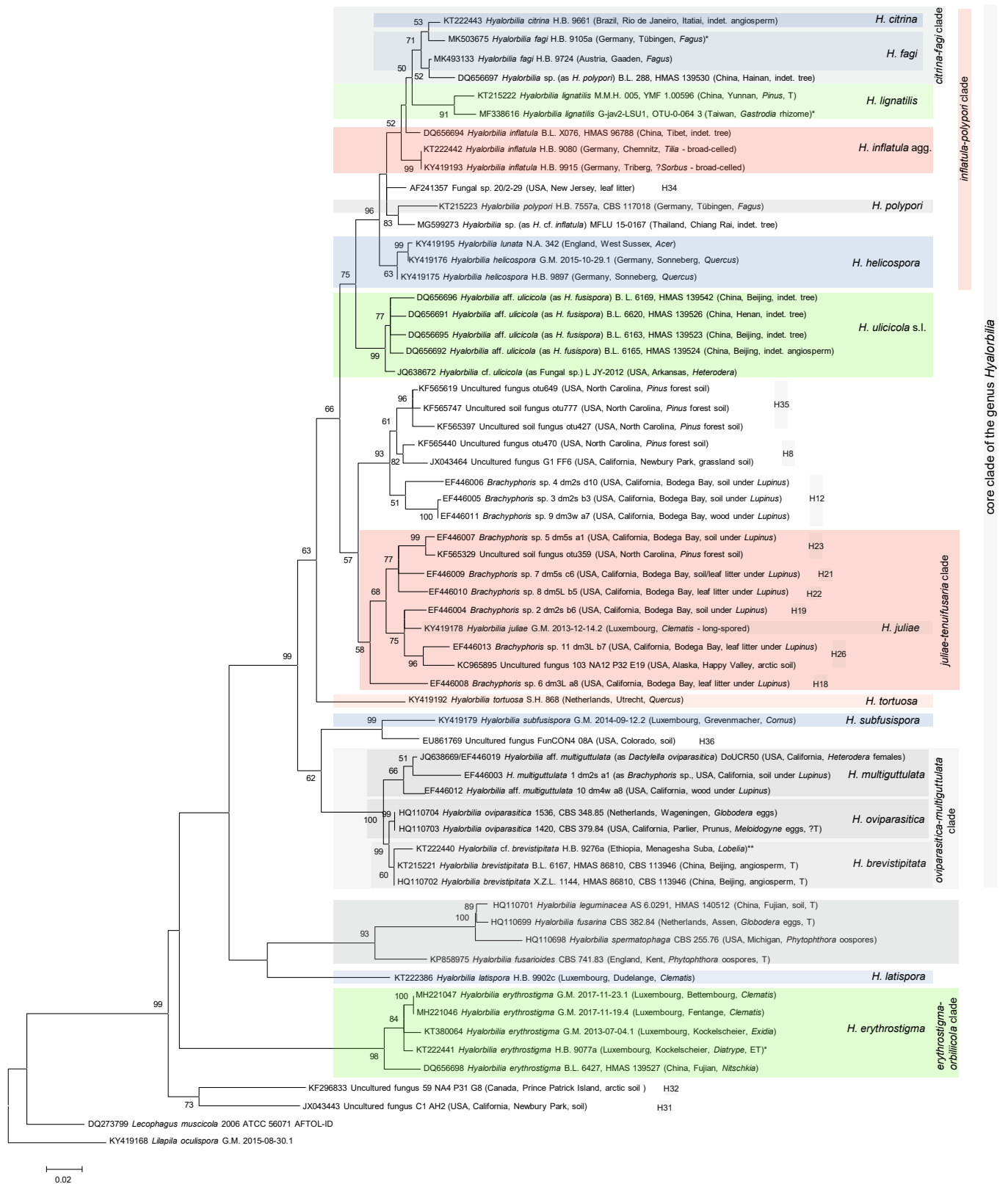
Phylogenetic analysis S2: NJ analysis of the *Lecophagus-Amphosoma* clade and the *Hyalorbilia* clade based on SSU (V8–V9) rDNA dataset (50 sequences, 366 positions, aligned with MUSCLE) using MEGA6 (500 replicates). The tree is rooted with *Tuber borchii* and *Knufia perforans*. T = type, ET = epitype, * = without SSU (V8).



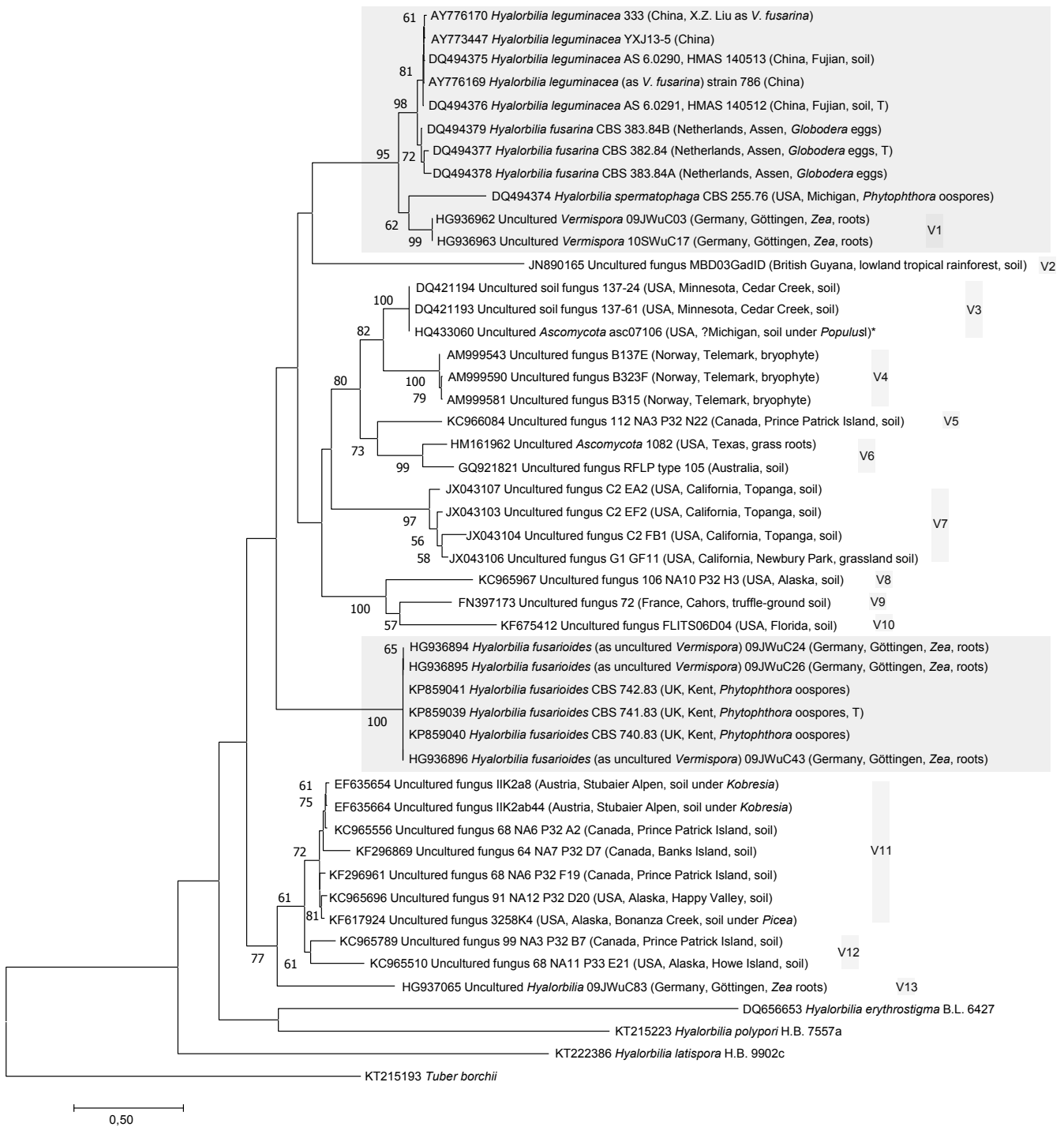
Phylogenetic analysis S3: NJ analysis of the genus *Hyalorbilia* based on 5.8S rDNA dataset (100 sequences, 155 positions) using MEGA6 (500 replicates). The tree is rooted with *Tuber borchii* and *Lilapila oculispora*. T = type, ET = epitype, NT = neotype, TT = topotype.



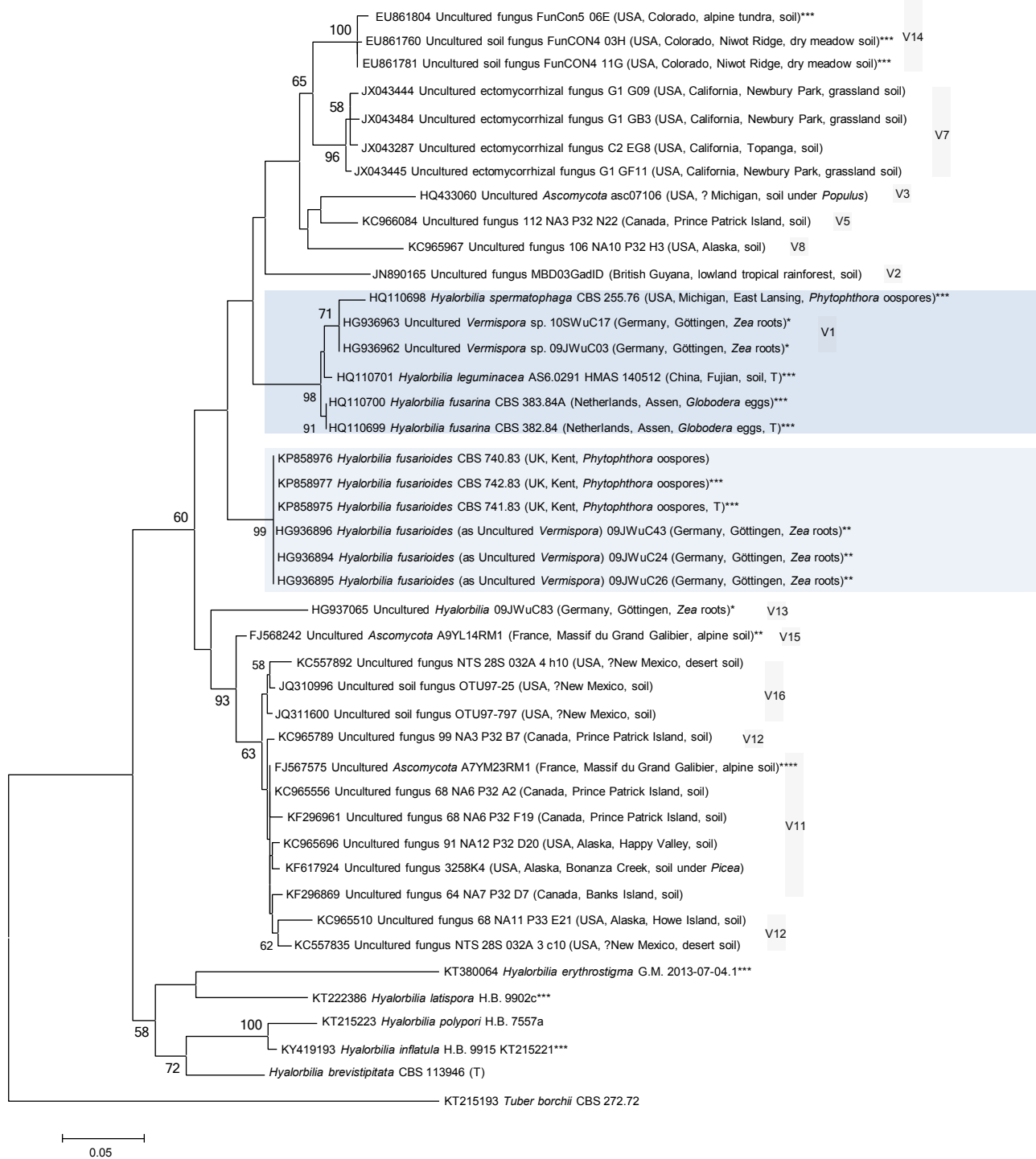
Phylogenetic analysis S4: Phylogram of the genus *Hyalorbilia* inferred from ML analysis of S1506 intron rDNA dataset (12 sequences, 479 positions, aligned with MUSCLE) using the T3+G model in MEGA6 (500 replicates). The tree is rooted with *Orbilia myriosphaera*. ET = epitype, NT = neotype.



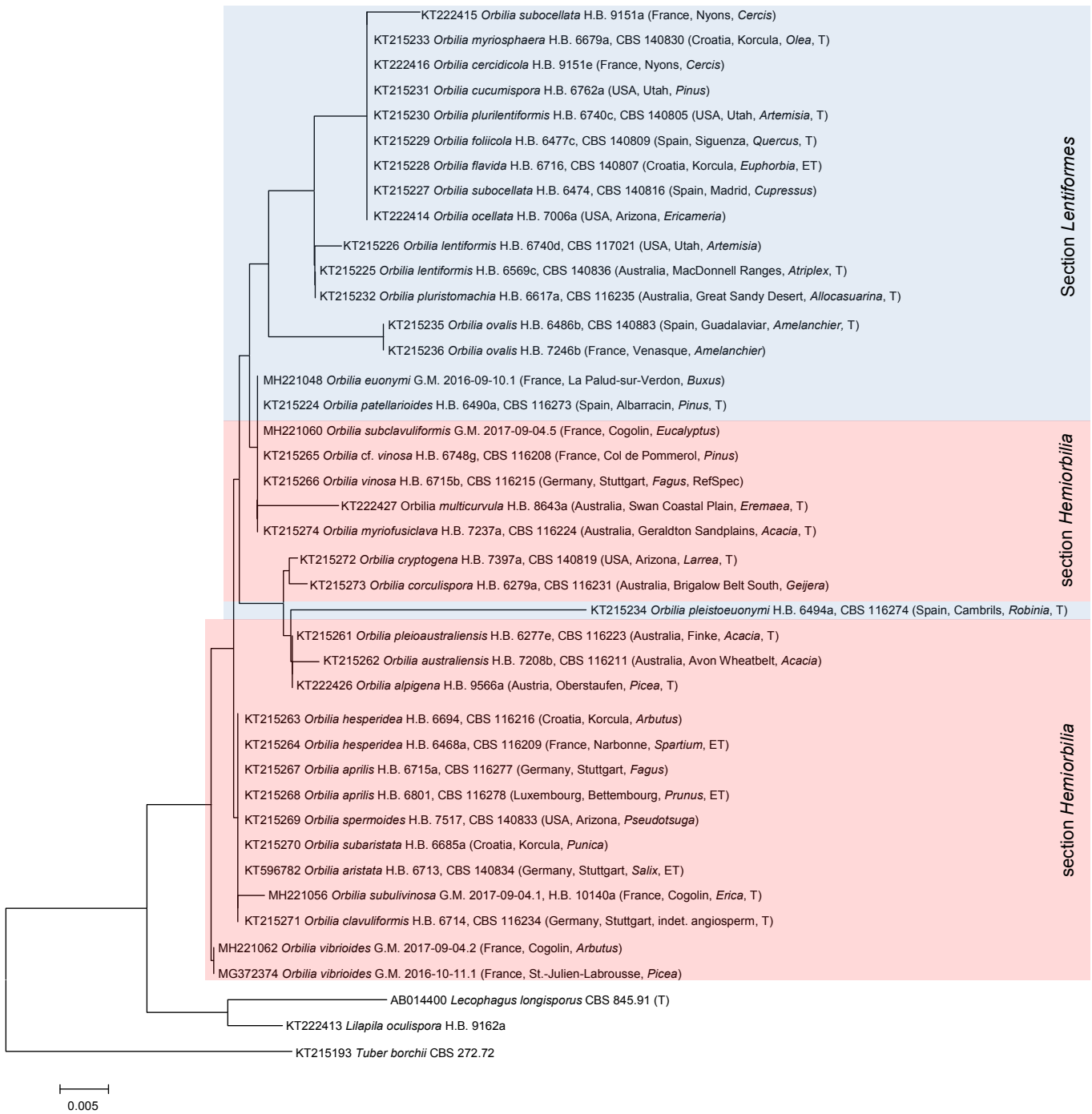
Phylogenetic analysis S5: Phylogram of the genus *Hyalorbilia* inferred from ML analysis of LSU (D1–D3) rDNA dataset (62 sequences, 962 positions, aligned with MUSCLE) using the GTR+G+I model in MEGA6 (500 replicates). The tree is rooted with *Lilapila oculispora* and *Lecophagus muscicola*. T = type, ET = epi-type, * = without LSU (D2–D3), ** = without LSU (D3).



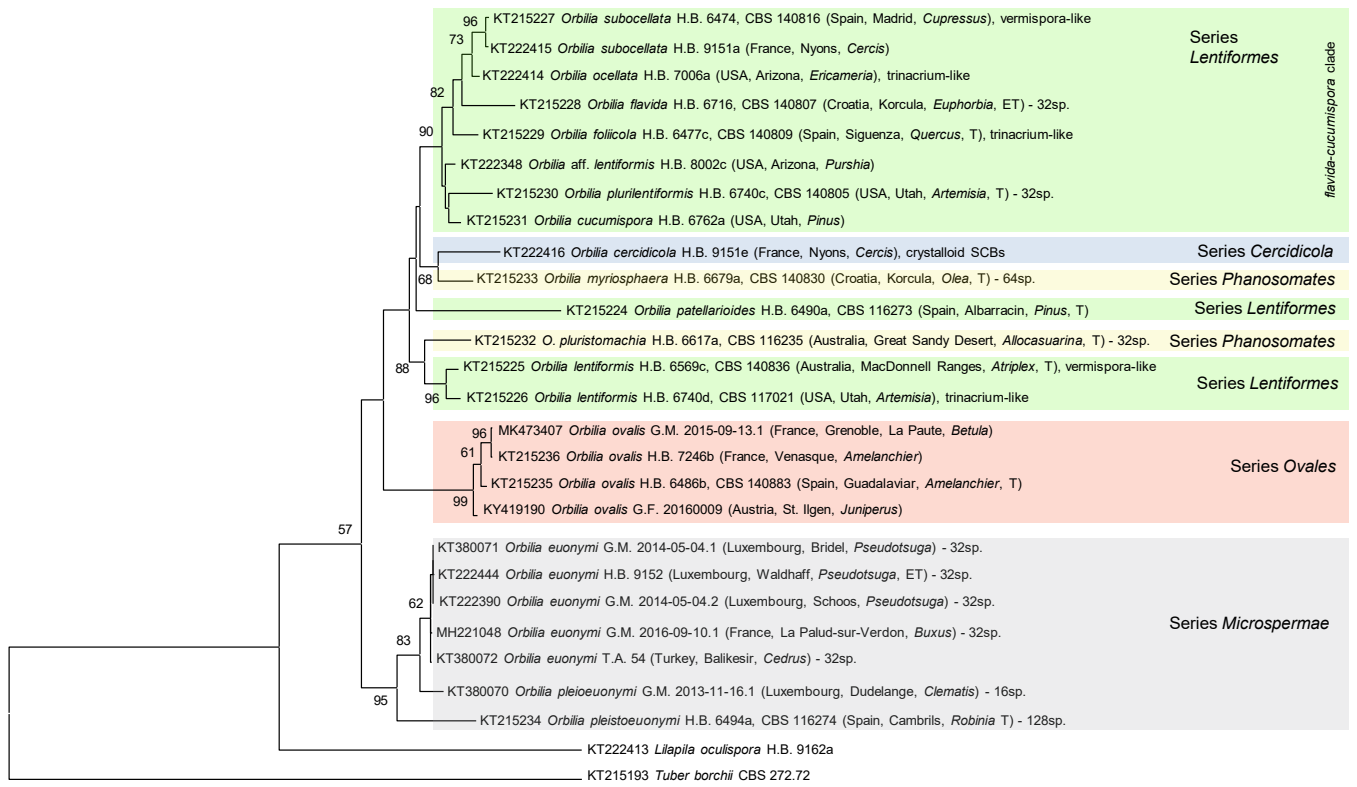
Phylogenetic analysis S6: Phylogram of the *Vermispora* clade of the genus *Hyalorbilia* inferred from ML analysis of ITS1-5.8S-ITS2 rDNA dataset (48 sequences, 947 positions, aligned with MUSCLE) using the GTR+G model in MEGA7. The tree is rooted with *Tuber borchii* and includes three members of *Hyalorbilia*. T = type, * = without ITS1.



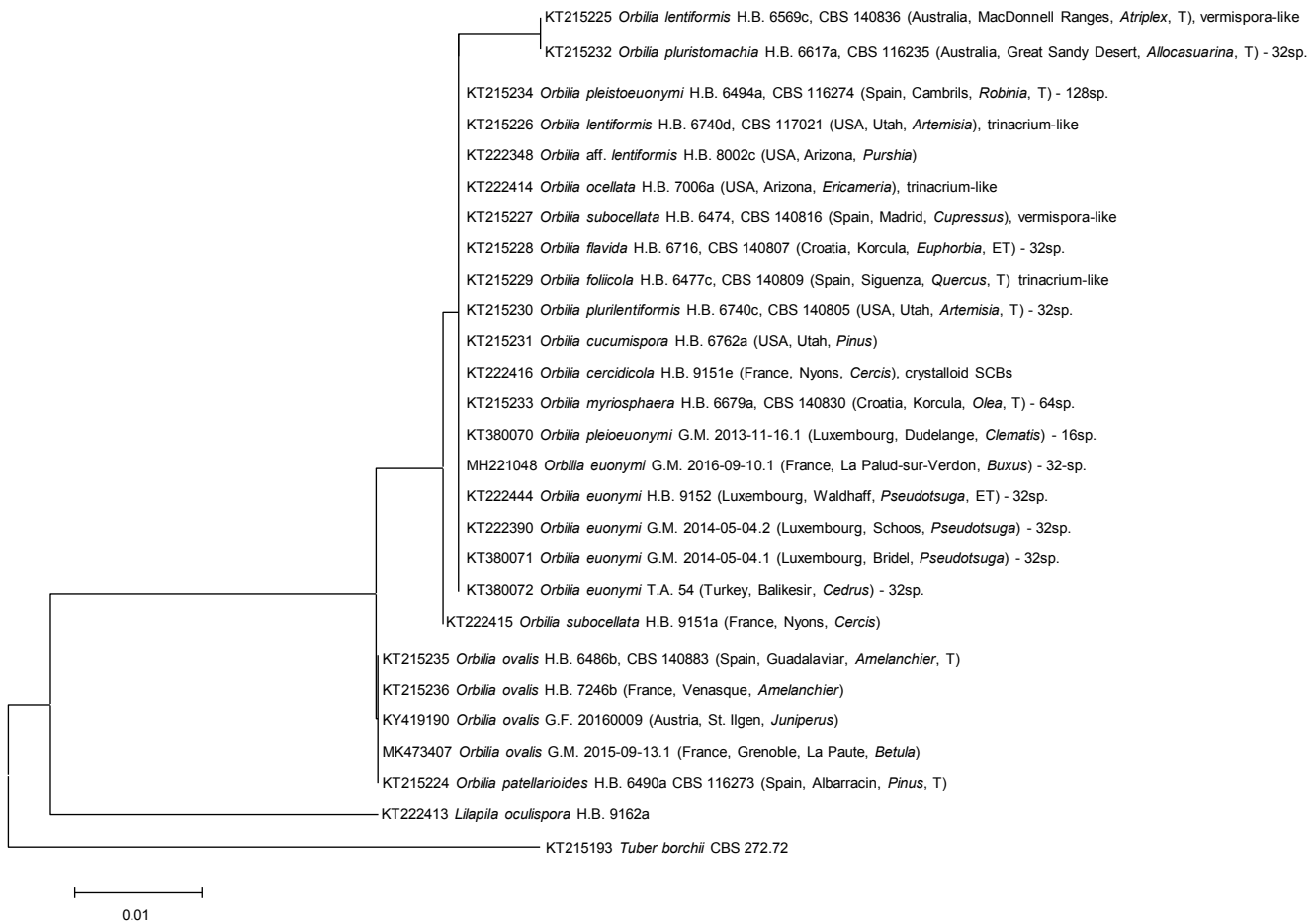
Phylogenetic analysis S7: Phylogram of the *Vermispora* clade of the genus *Hyalorbilia* inferred from ML analysis of LSU (D1–D3) rDNA dataset (43 sequences, 932 positions, aligned with MUSCLE) using the K2+G model in MEGA6 (500 replicates). The tree is rooted with *Tuber borchii* and includes five members of *Hyalorbilia*. T = type, * = with LSU (D1), ** = with LSU (D2–D3), *** = with LSU (D1–D3).



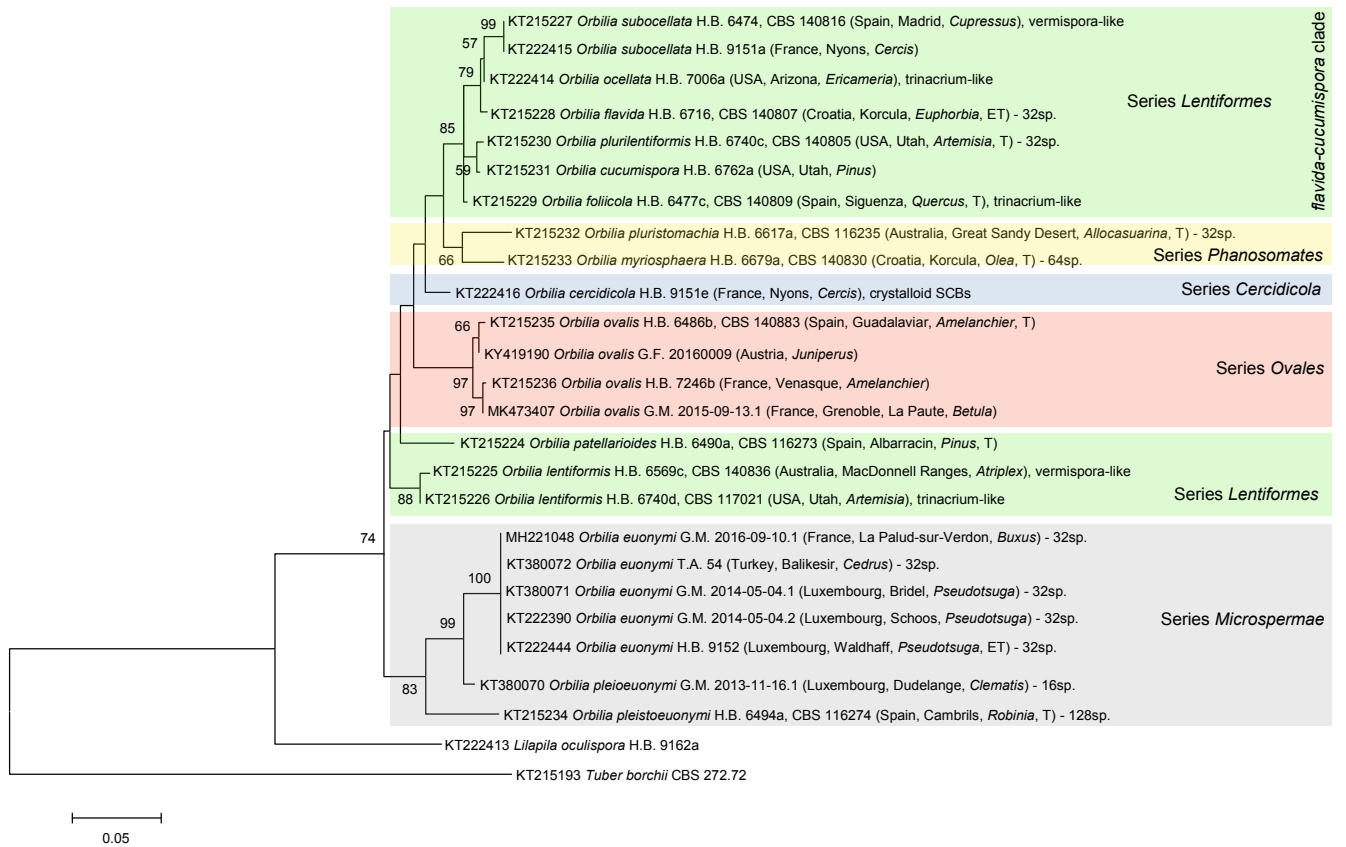
Phylogenetic analysis S8: NJ analysis of sections *Lentiformes* and *Hemiorbilia* based on SSU (V8–V9) rDNA dataset (41 sequences, 363 positions, aligned with MUSCLE) using MEGA6 (500 replicates). Note affinity of three members of section *Lentiformes* with members of section *Hemiorbilia*. The tree is rooted with *Tuber borchii*, *Lilapila oculispora*, and *Lecophagus longisporus*. Asci 8-spored except when otherwise stated; RefSpec = reference specimen, T = type, ET = epitype.



Phylogenetic analysis S9: Phylogram of section *Lentiformes* inferred from ML analysis of ITS1-5.8S-ITS2 rDNA dataset (27 sequences, 731 positions, aligned with MUSCLE) using the TN+G model in MEGA6 (500 replicates). The tree is rooted with *Tuber borchii* and *Lilapila oculispora*. Asci 8-spored except when otherwise stated; T = type, ET = epitype.



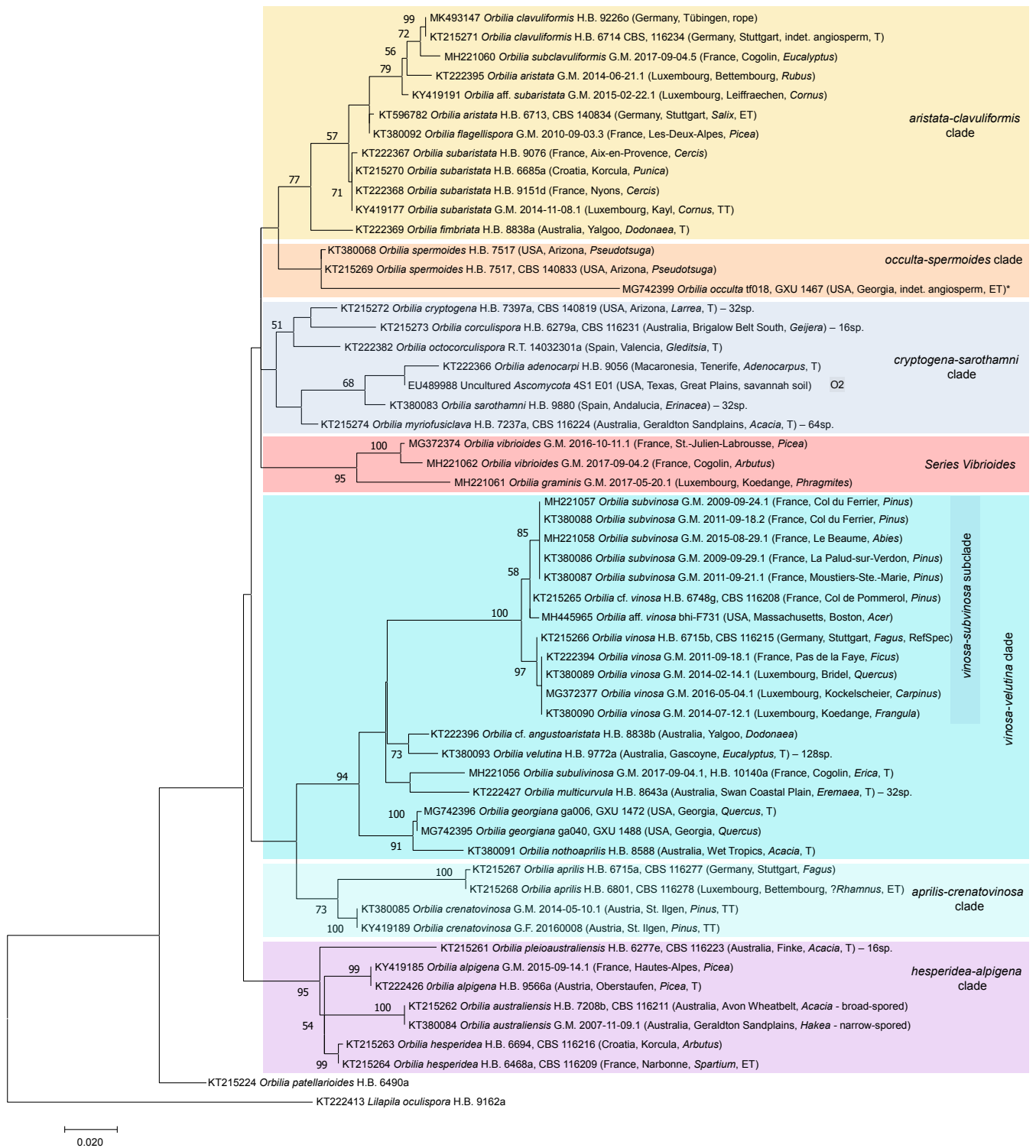
Phylogenetic analysis S10: NJ analysis of section *Lentiformes* based on 5.8S rDNA dataset (27 sequences, 155 positions) using MEGA6 (500 replicates). The tree is rooted with *Tuber borchii* and *Lilapila oculispora*. Asci 8-spored except when otherwise stated; T = type, ET = epitype.



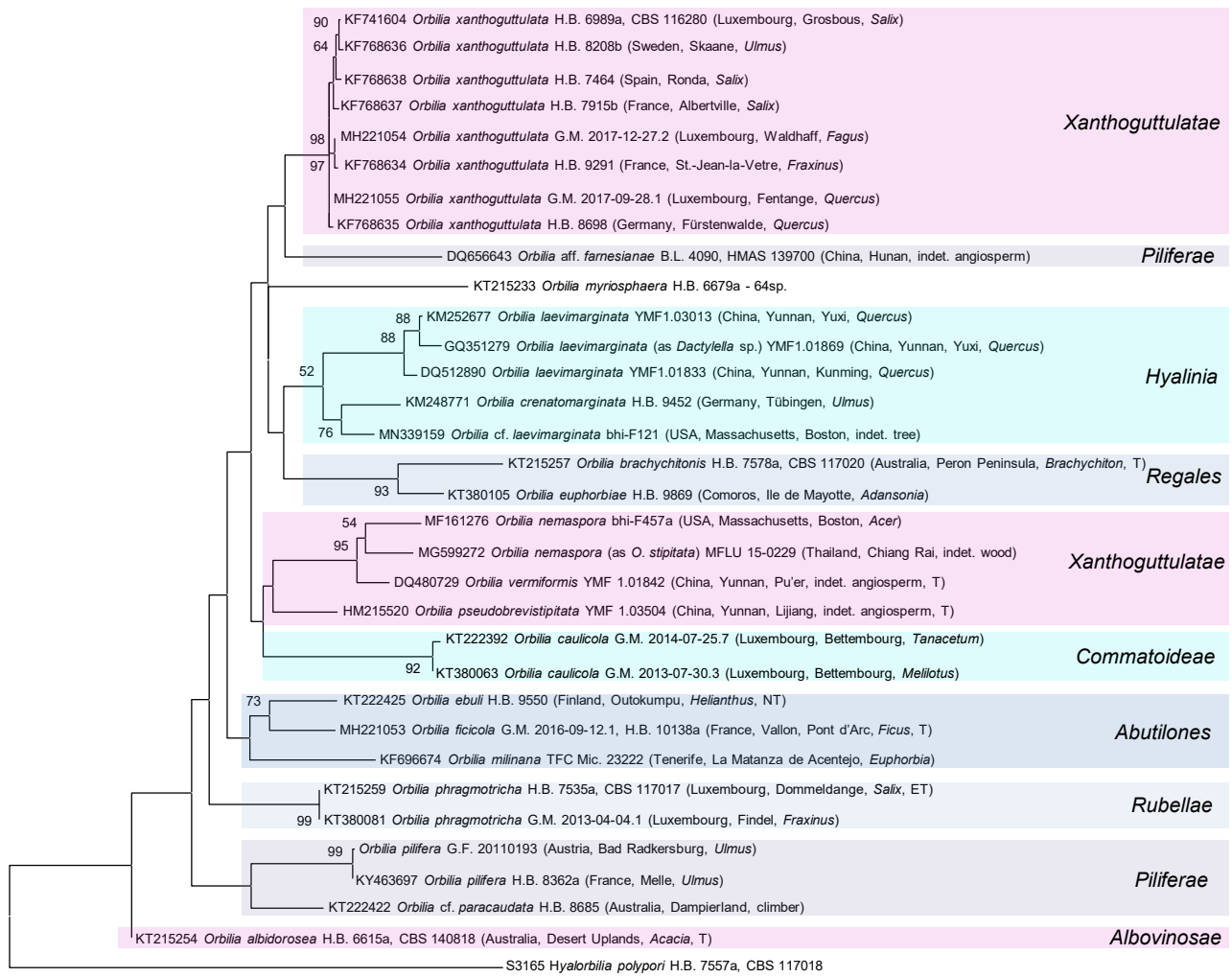
Phylogenetic analysis S11: Phylogram of section *Lentiformes* inferred from ML analysis of LSU (D1–D2) rDNA dataset (26 sequences, 637 positions, aligned with MUSCLE) using the K2+G model in MEGA6 (500 replicates). The tree is rooted with *Tuber borchii* and *Lilapila oculispora*. Asci 8-spored except when otherwise stated; T = type, ET = epitype.



Phylogenetic analysis S12: Phylogram of section *Hemiorbilia* inferred from ML analysis of S1506 intron rDNA dataset (34 sequences, 653 positions, aligned with MUSCLE) using the K2+G model in MEGA6 (500 replicates). The tree is rooted with *Hyalorbilia polyptori*. Asci 8-spored except when otherwise stated; RefSpec = reference specimen, T = type, ET = epitype, TT = toptype.

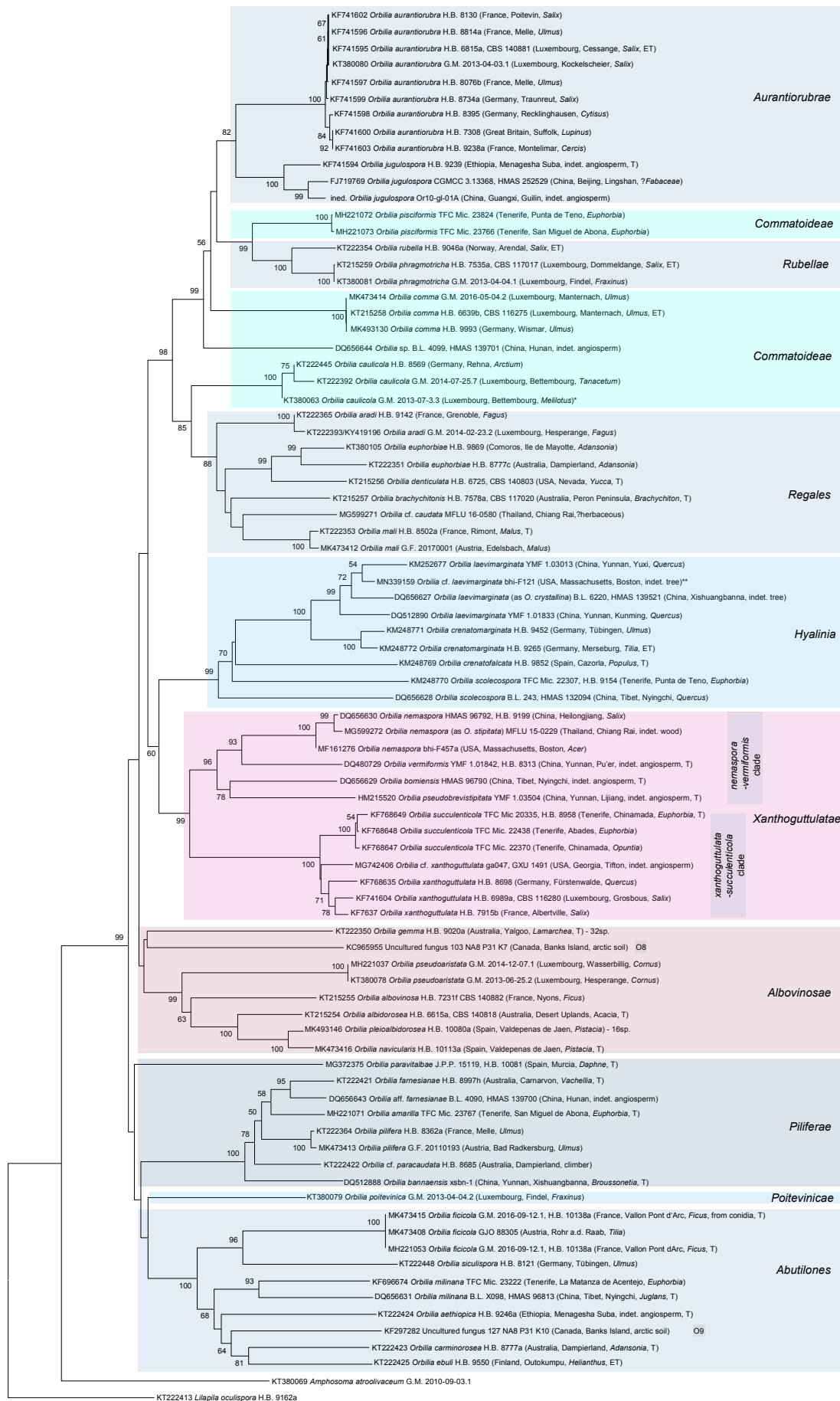


Phylogenetic analysis S13: Phylogram of section *Hemiorbilia* inferred from ML analysis of LSU (D1–D2) rDNA dataset (57 sequences, 638 positions, aligned with MUSCLE) using the K2+G+I model in MEGA7 (500 replicates). An environmental strain from GenBank represents an unidentified species (O2). The tree is rooted with *Lilapila oculispora* and *Orbilia patellarioides*. Asci 8-spored except when otherwise stated; RefSpec = reference specimen, T = type, ET = epitype, TT = topotype, * = without LSU (D2).

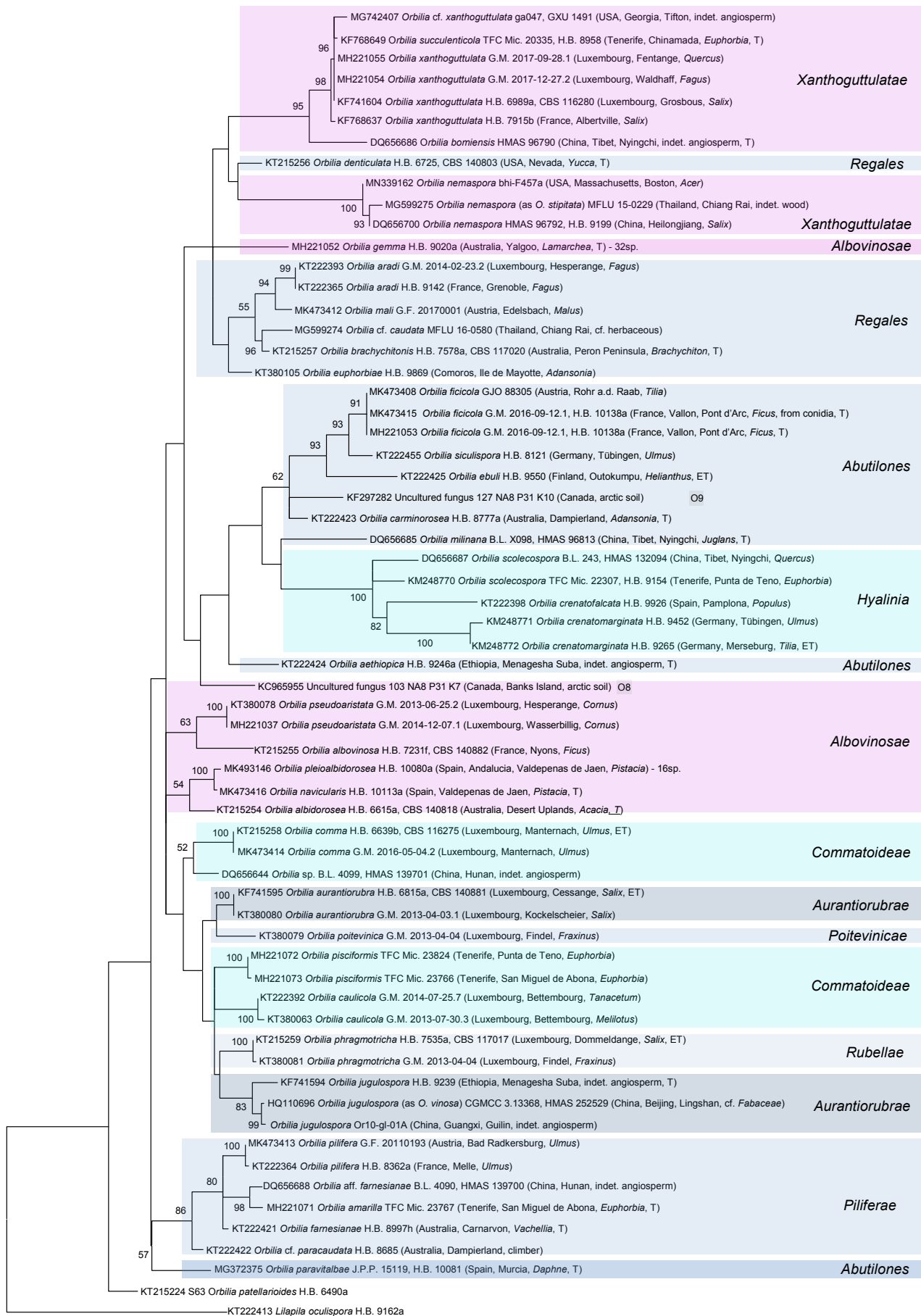


0.2

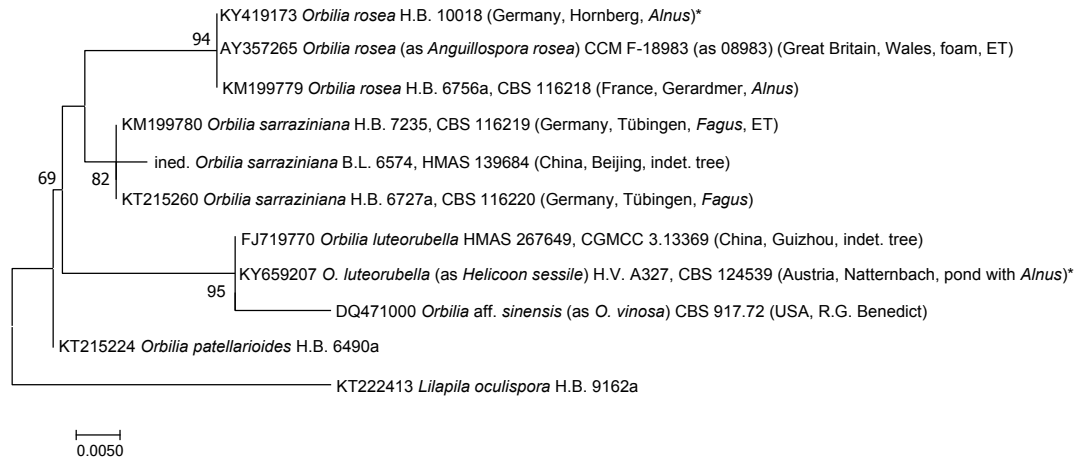
Phylogenetic analysis S14: Phylogram of section *Aurantiourbrae* inferred from ML analysis of S1506 Intron rDNA dataset (33 sequences, 551 positions, aligned with MUSCLE) using the K2+G model in MEGA6 (500 replicates). The tree is rooted with *Hyalorbilia polypori*. Asci 8-spored except when otherwise stated; T = type, ET = epitype, NT = neotype.



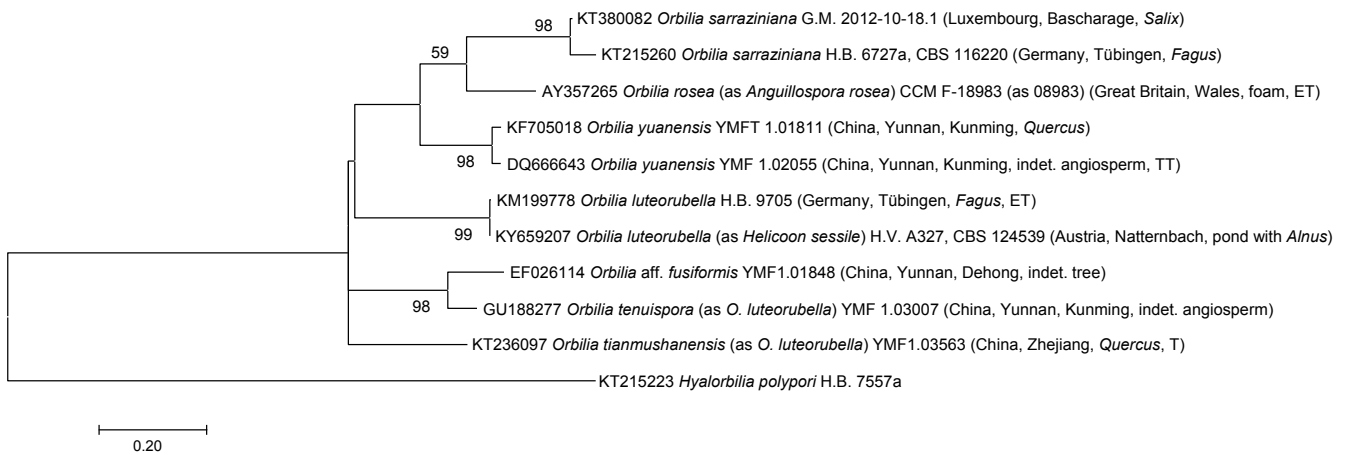
Phylogenetic analysis S15: NJ analysis of section *Aurantiorubrae* based on ITS1-5.8S-ITS2 rDNA dataset (84 sequences, 817 positions, aligned with MUSCLE) using MEGA6 (1000 replicates). Two environmental strains from GenBank are included representing unidentified species (O8, O9). The tree is rooted with *Lilapila oculispora* and *Amphosoma atroolivaceum*. Asci 8-spored except when otherwise stated; T = type, ET = epitype, * = without partial 5.8S and ITS2, ** = without partial ITS2.



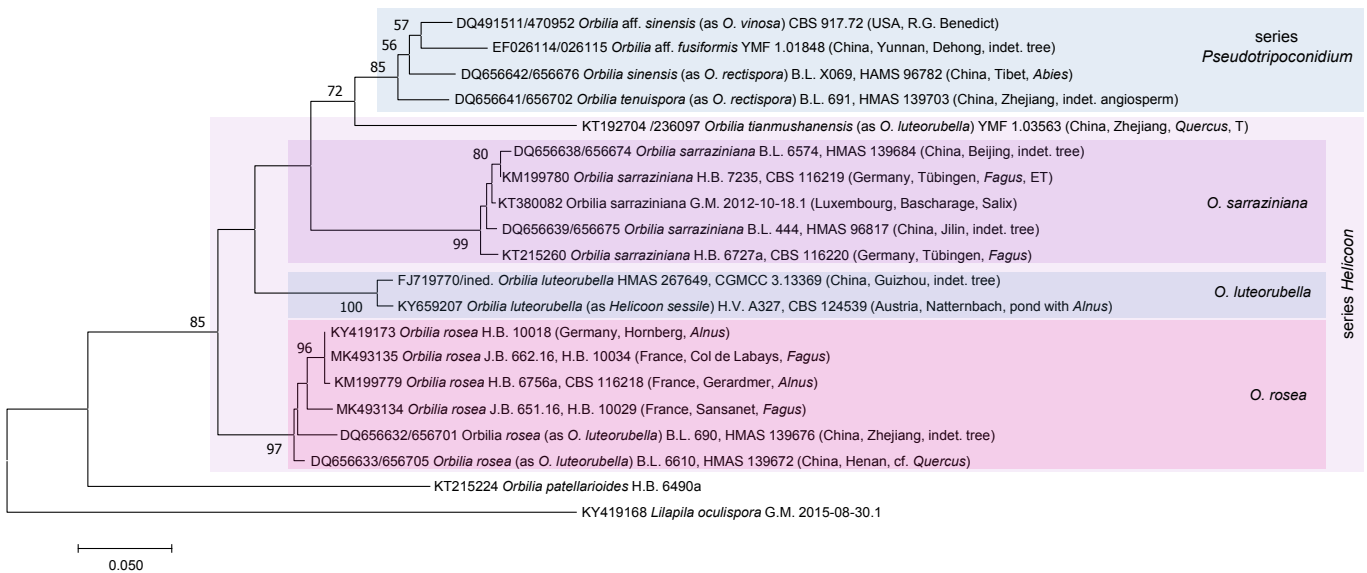
Phylogenetic analysis S16 Phylogram of section *Aurantiorubrae* inferred from ML analysis of LSU (D1–D2) rDNA dataset (63 sequences, 639 positions, aligned with MUSCLE) using the K2+G+I model in MEGA6 (500 replicates). Two environmental strains from GenBank are included representing unidentified species (O8, O9). The tree is rooted with *Lilapila oculispora* and *Orbilia patellarioides*. Asci 8-spored except when otherwise stated; T = type, ET = epitype.



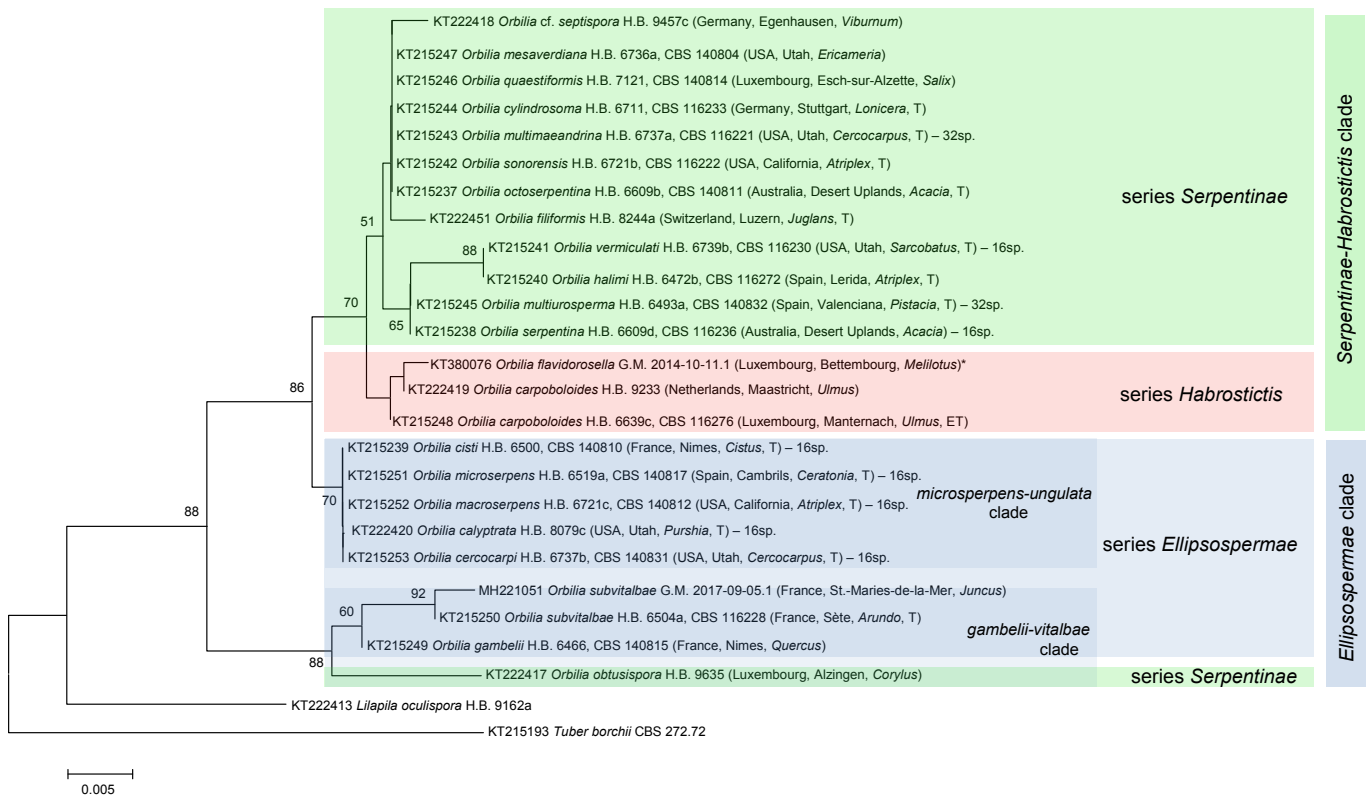
Phylogenetic analysis S17: Phylogram of section *Helicoon* inferred from ML analysis of SSU (V8–V9) rDNA dataset (11 sequences, 288 positions, aligned with MUSCLE) using the K2+G model in MEGA7 (500 replicates). The tree is rooted with *Lilapila oculispora* and *Orbilia patellarioides*. Asci 8-spored in all taxa; ET = epitype, * = without SSU (V8).



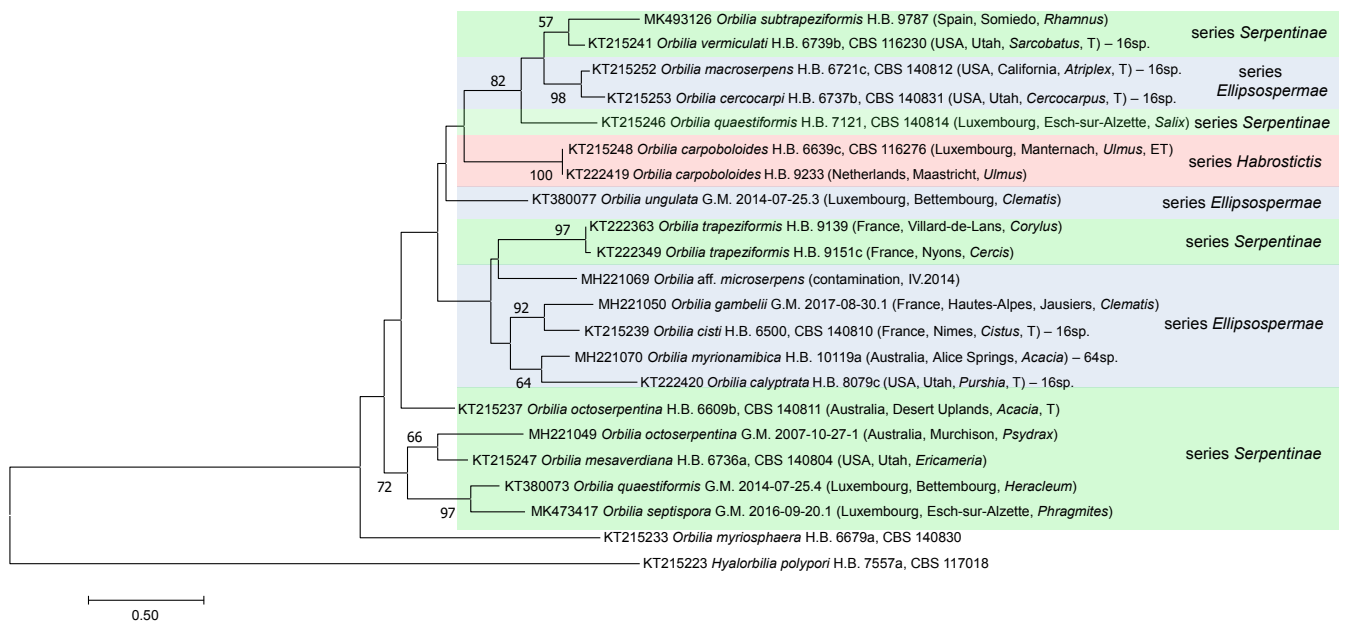
Phylogenetic analysis S18: Phylogram of section *Helicoon* inferred from ML analysis of S1506 Intron rDNA dataset (11 sequences, 1340 positions (514 with more than 2 sequences), aligned with MUSCLE) using the K2+G model in MEGA7 (500 replicates). The tree is rooted with *Hyalorbilia polypori*. Asci 8-spored in all taxa; T = type, ET = epitype, TT = toptype.



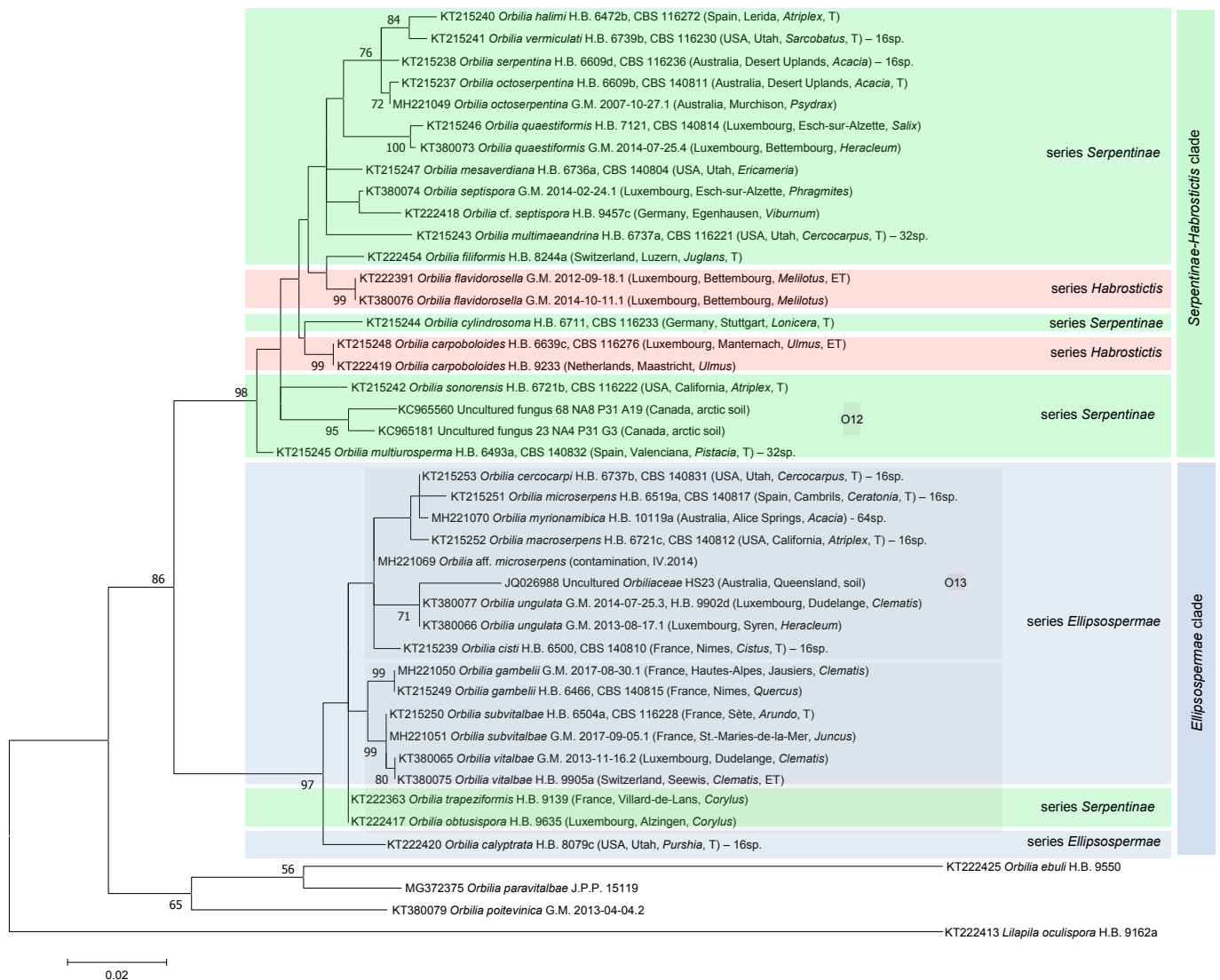
Phylogenetic analysis S19: Phylogram of section *Helicoon* inferred from combined ML analysis of ITS+LSU (D1–D2) rDNA dataset (20 sequences, 1198 positions, aligned with MUSCLE) using the T3+G model in MEGA7 (500 replicates). The tree is rooted with *Lilapila oculispورا* and *Orbilia patellarioides*. Asci 8-spored in all taxa; T = type, ET = epitype.



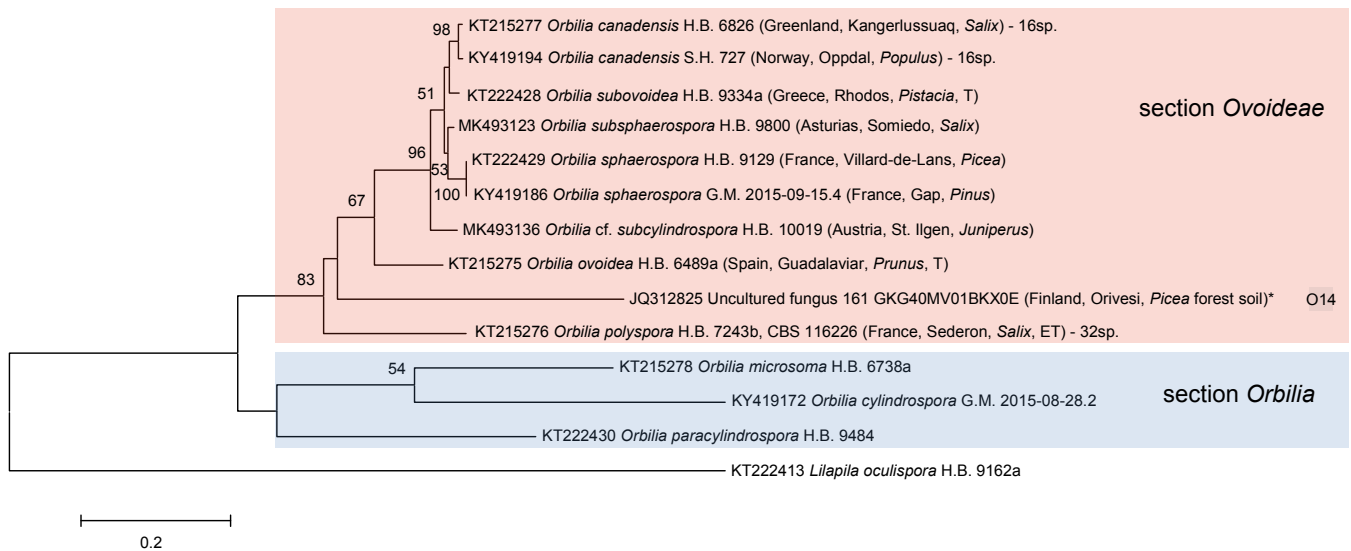
Phylogenetic analysis S20: NJ analysis of section *Habrostrictis* based on SSU (V8–V9) rDNA dataset (26 sequences, 364 positions, aligned with MUSCLE) using MEGA6 (500 replicates). The tree is rooted with *Tuber borchii* and *Lilapila oculispورا*. Asci 8-spored except when otherwise stated; T = type, ET = epitype, * = without SSU (V8).



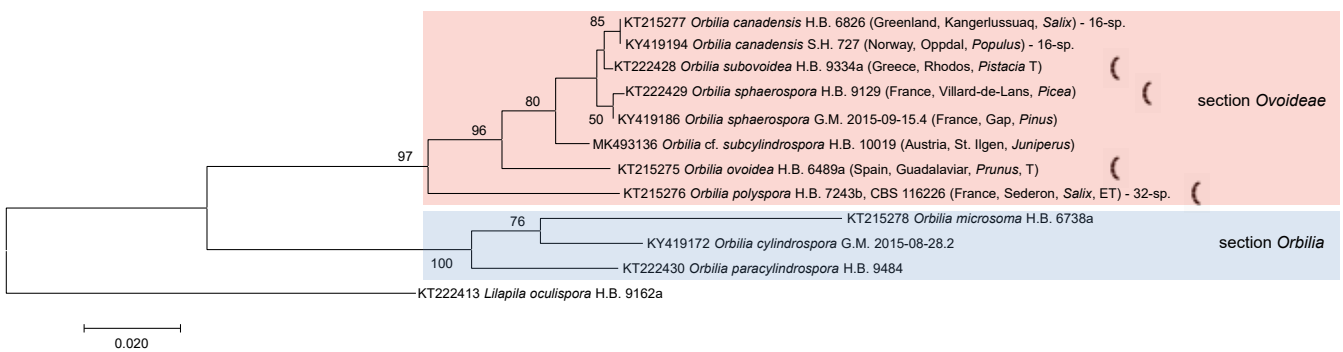
Phylogenetic analysis S21: Phylogram of section *Habrosticktis* inferred from ML analysis of S1506 Intron rDNA dataset (22 sequences, 2146 positions (558 with more than 1 sequence), aligned with MUSCLE) using the T3+G model in MEGA7 (500 replicates). The tree is rooted with *Hyalorbilia polypori* and *Orbilia myriosphaera*. Asci 8-spored except when otherwise stated; T = type, ET = epitype.



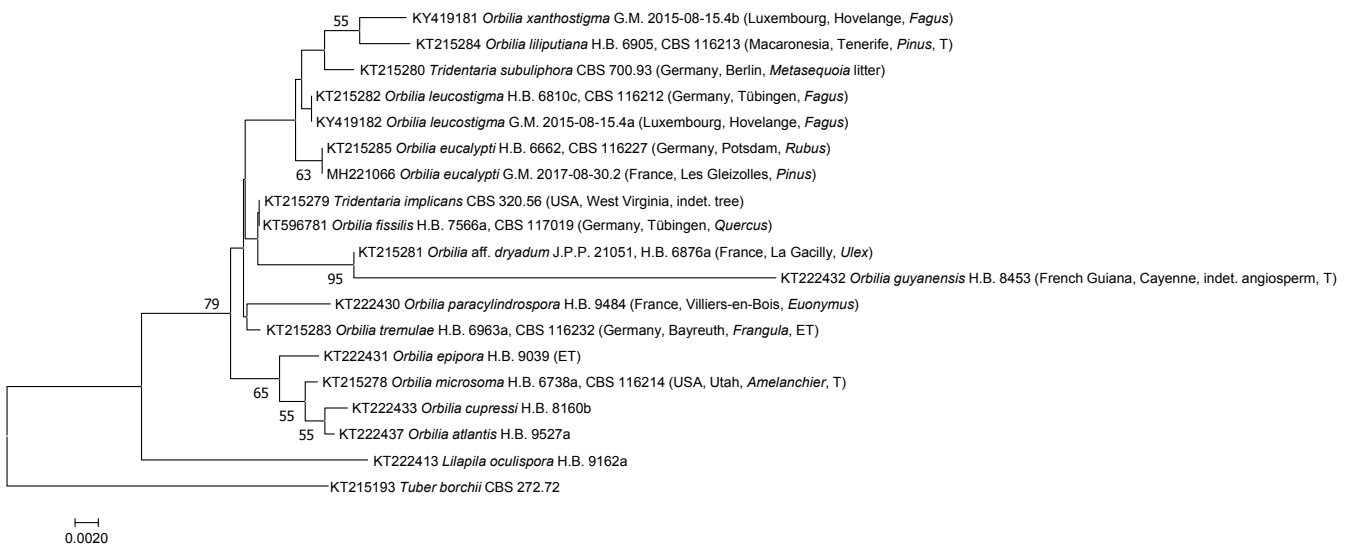
Phylogenetic analysis S22: Phylogram of section *Habrosticktis* inferred from ML analysis of LSU (D1–D2) rDNA dataset (43 sequences, 636 positions, aligned with MUSCLE) using the K2+G+I model in MEGA7 (500 replicates). Three environmental strains from GenBank are included representing two unidentified species (O12, O13). The tree is rooted with *Lilapila oculispora*. Asci 8-spored except when otherwise stated; T = type, ET = epitype.



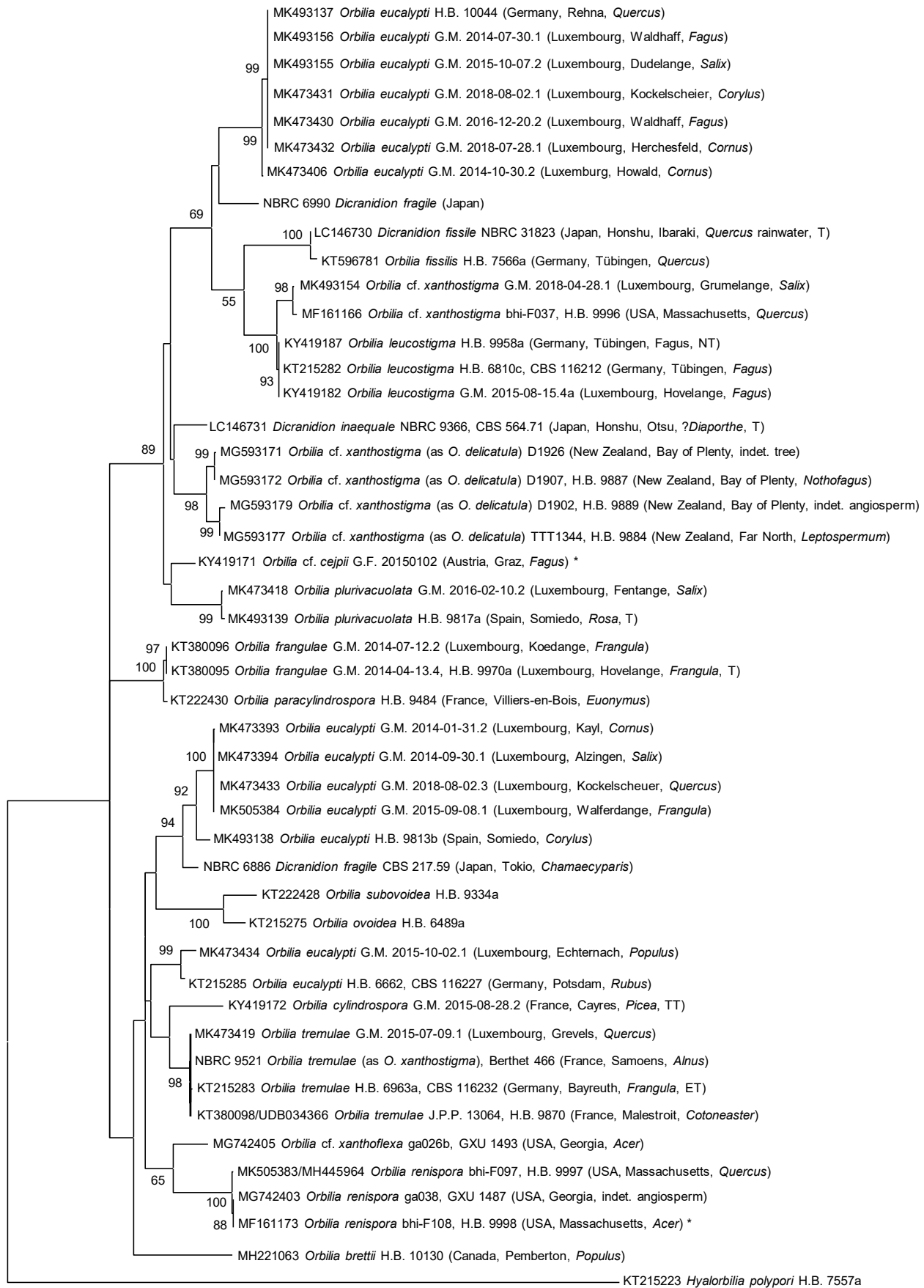
Phylogenetic analysis S23: Phylogram of section *Ovoideae* inferred from ML analysis of ITS1-5.8S-ITS2 rDNA dataset (14 sequences, 625 positions, aligned with MUSCLE) using the K2+G model in MEGA6 (500 replicates). An environmental strain from GenBank represents an unidentified species (O14). The tree is rooted with *Lilapila oculispora*. Asci 8-spored except when otherwise stated; T = type, ET = epitype, * = without ITS1 and partial 5.8S.



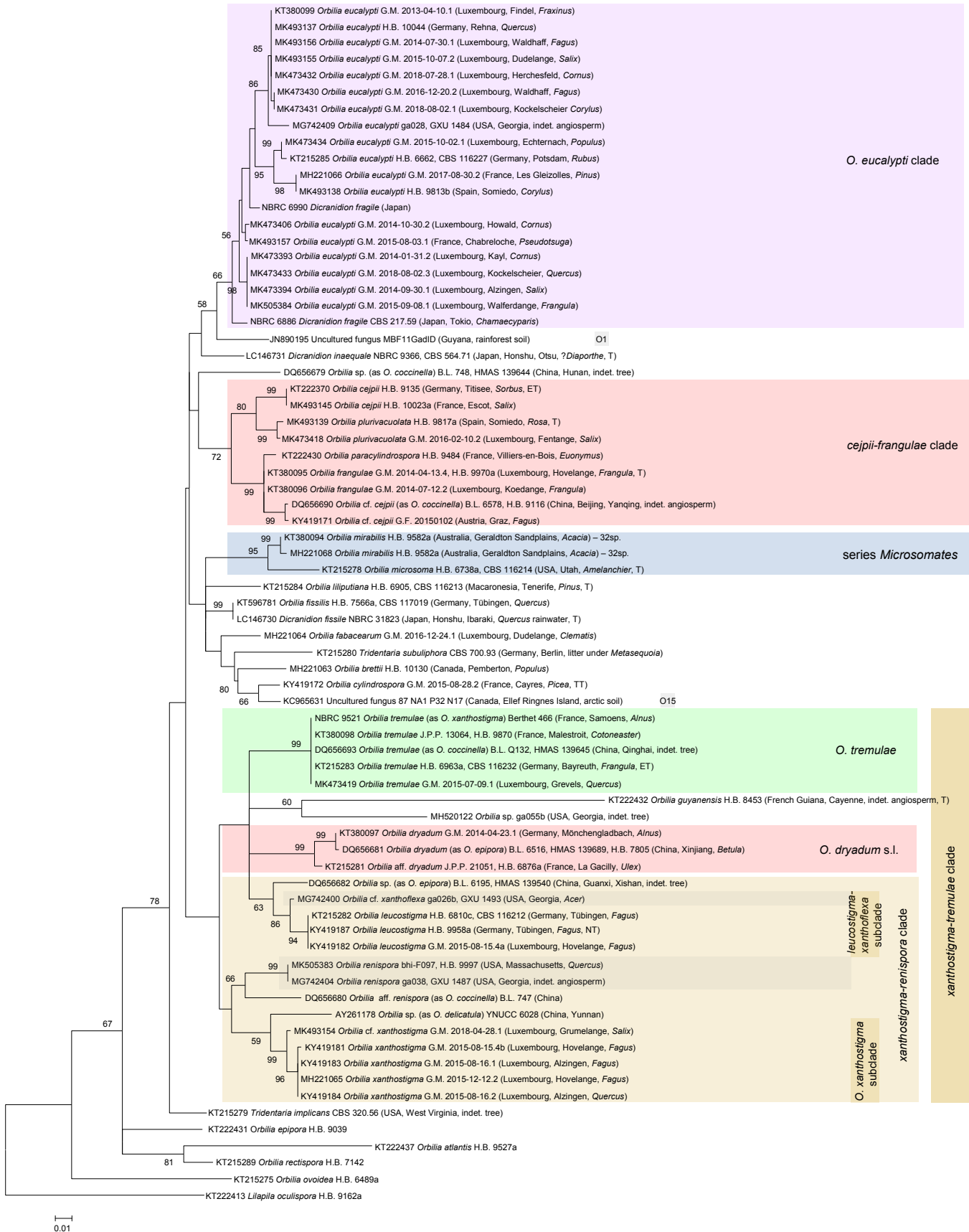
Phylogenetic analysis S24: Phylogram of section *Ovoideae* inferred from ML analysis of LSU (D1–D2) rDNA dataset (12 sequences, 636 positions, aligned with MUSCLE) using the K2+G model in MEGA7 (500 replicates). The tree is rooted with *Lilapila oculispora*. Asci 8-spored except when otherwise stated; T = type, ET = epitype.



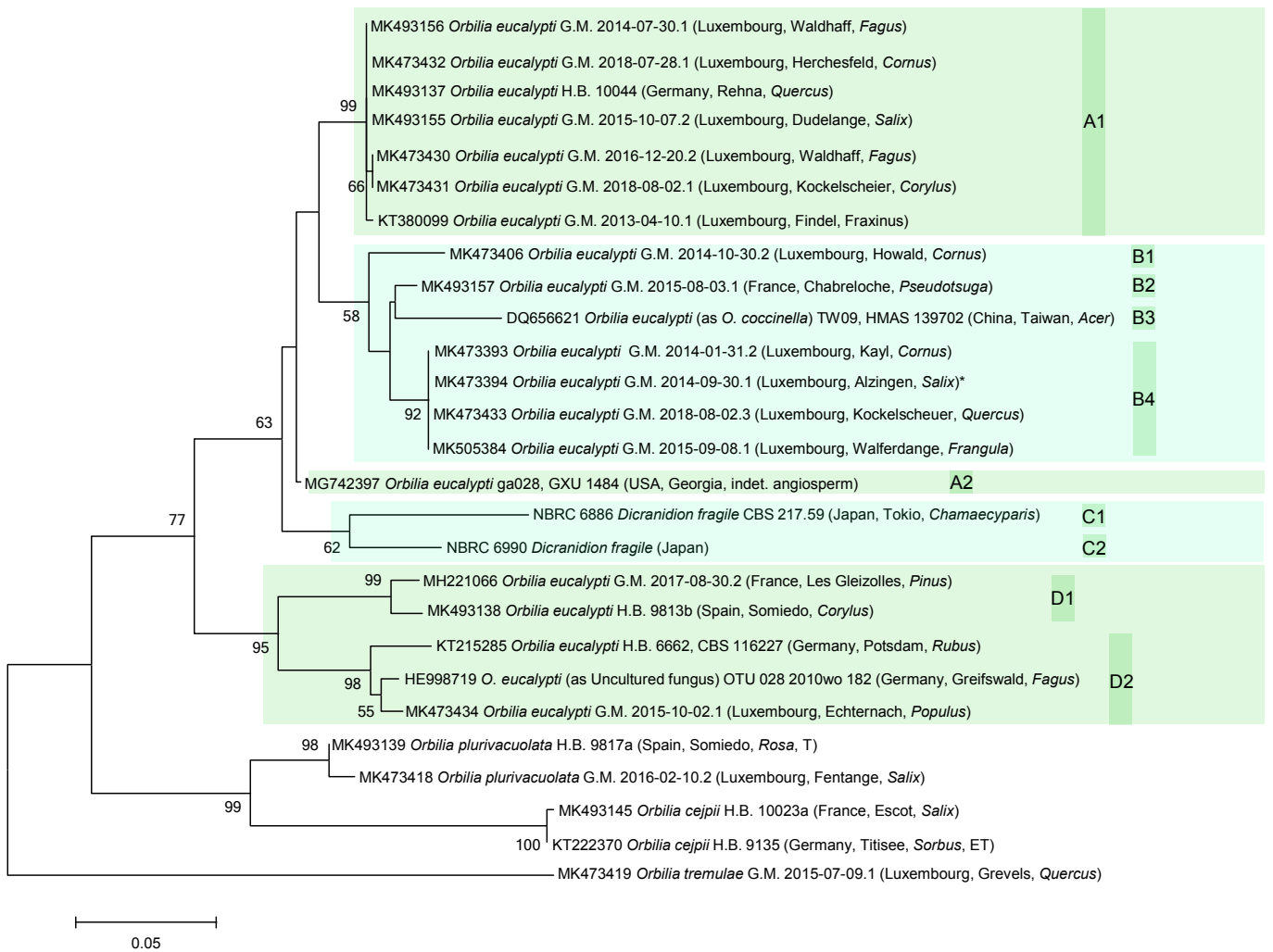
Phylogenetic analysis S25: NJ analysis of section *Orbilia* based on SSU (V8–V9) rDNA dataset (19 sequences, 364 positions, aligned with MUSCLE) using MEGA7 (500 replicates). The tree is rooted with *Tuber borchii* and *Lilapila oculispora*. Asci 8-spored in all taxa; T = type, ET = epitype.



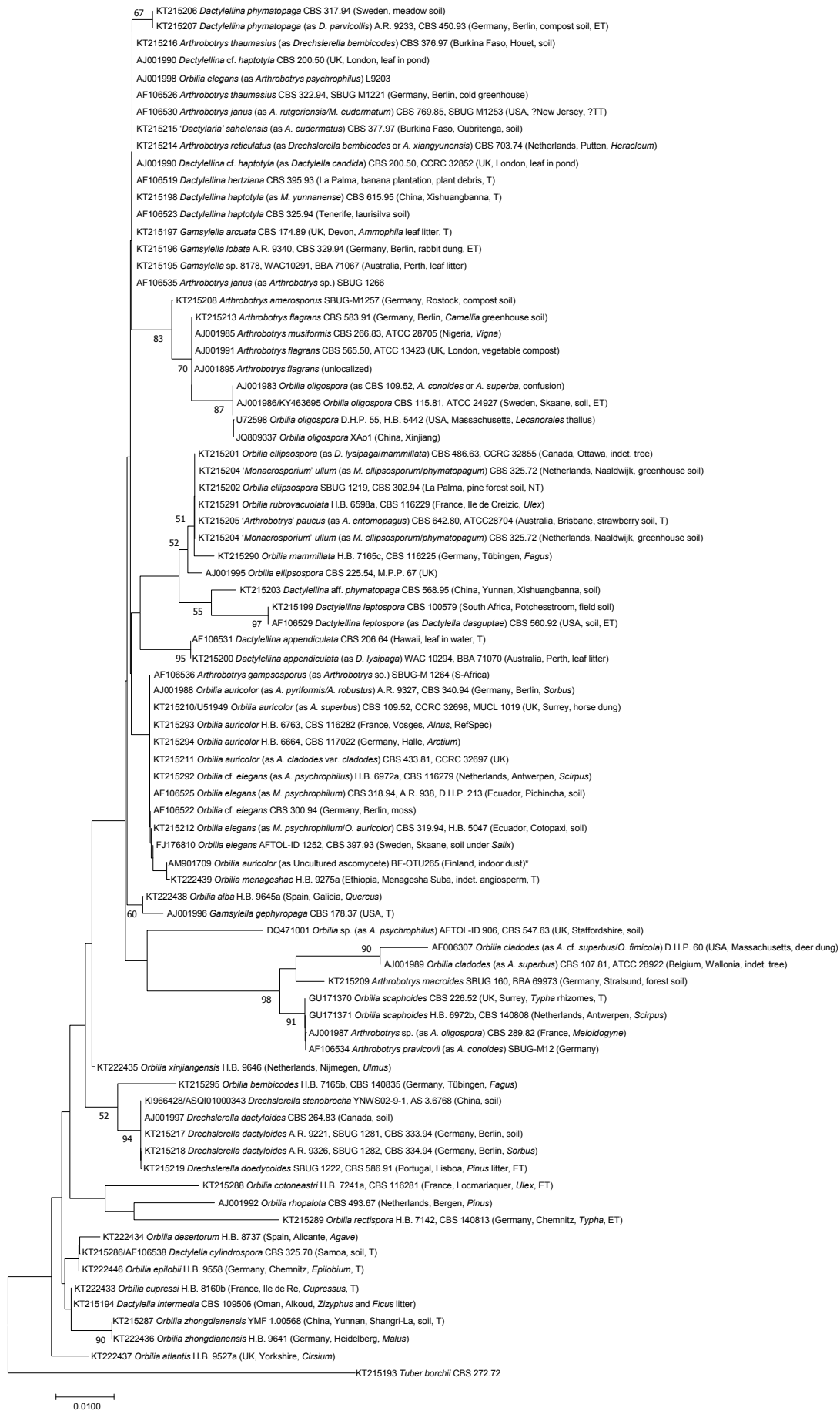
Phylogenetic analysis S26: Phylogram of section *Orbilia* inferred from ML analysis of S1506 Intron rDNA dataset (47 sequences, 1377 positions, aligned with MUSCLE) using the K2+G+I model in MEGA6 (500 replicates). The tree is rooted with *Hyalorbilia polypori*. Asci 8-spored in all taxa; T = type, ET = epitype, NT = neotype, TT = topotype.



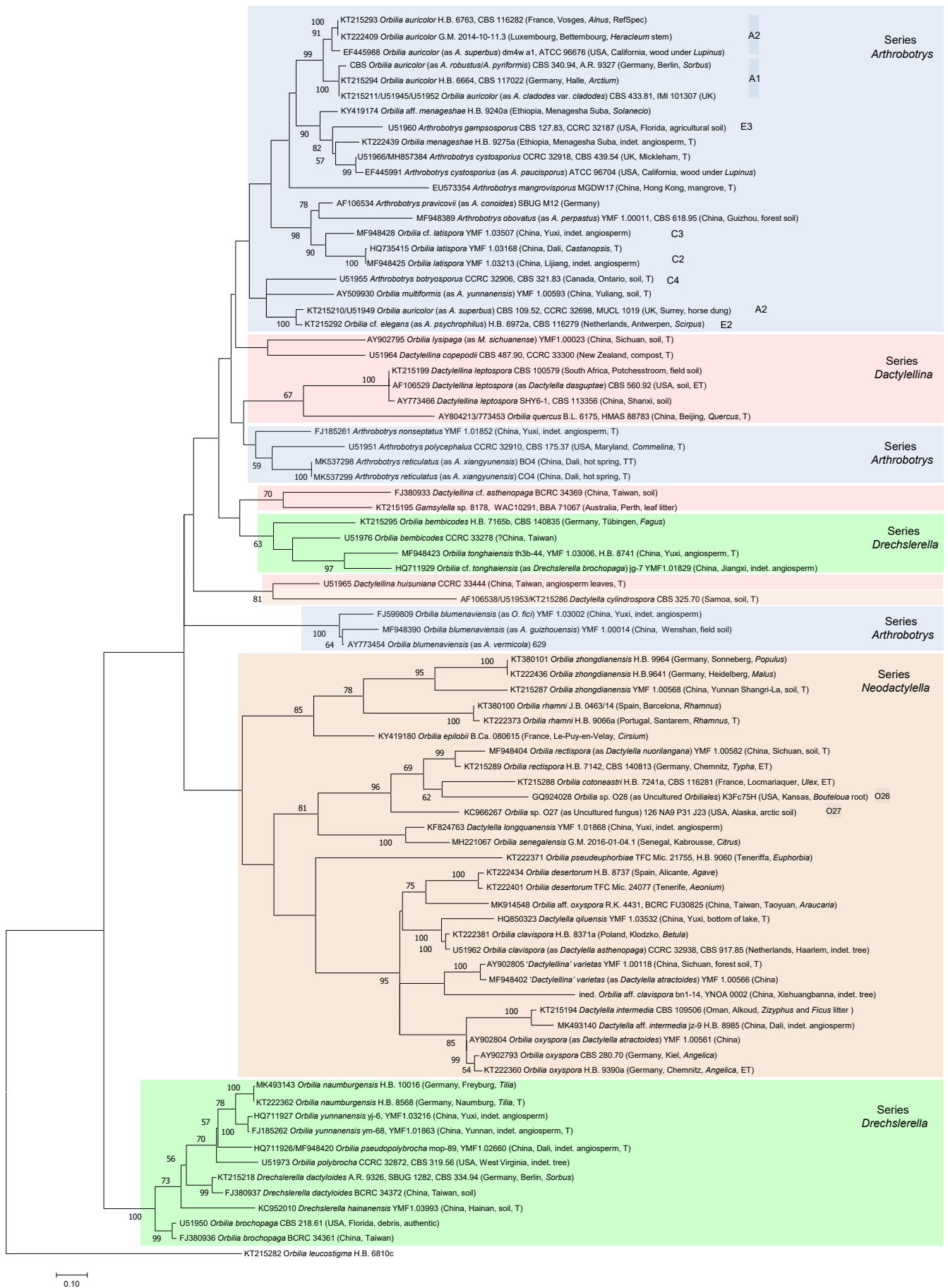
Phylogenetic analysis S27: Phylogram of section *Orbilia* inferred from ML analysis of LSU (D1–D2) rDNA dataset (73 sequences, 641 positions, aligned with MUSCLE) using the TN+G+I model in MEGA7 (500 replicates). Two environmental strains from GenBank are included representing unidentified species (O1, O15). The tree is rooted with *Lilapila oculispora* and *Orbilia ovoidea*. Asci 8-spored except when otherwise stated; T = type, ET = epitype, NT = neotype, TT = topotype.



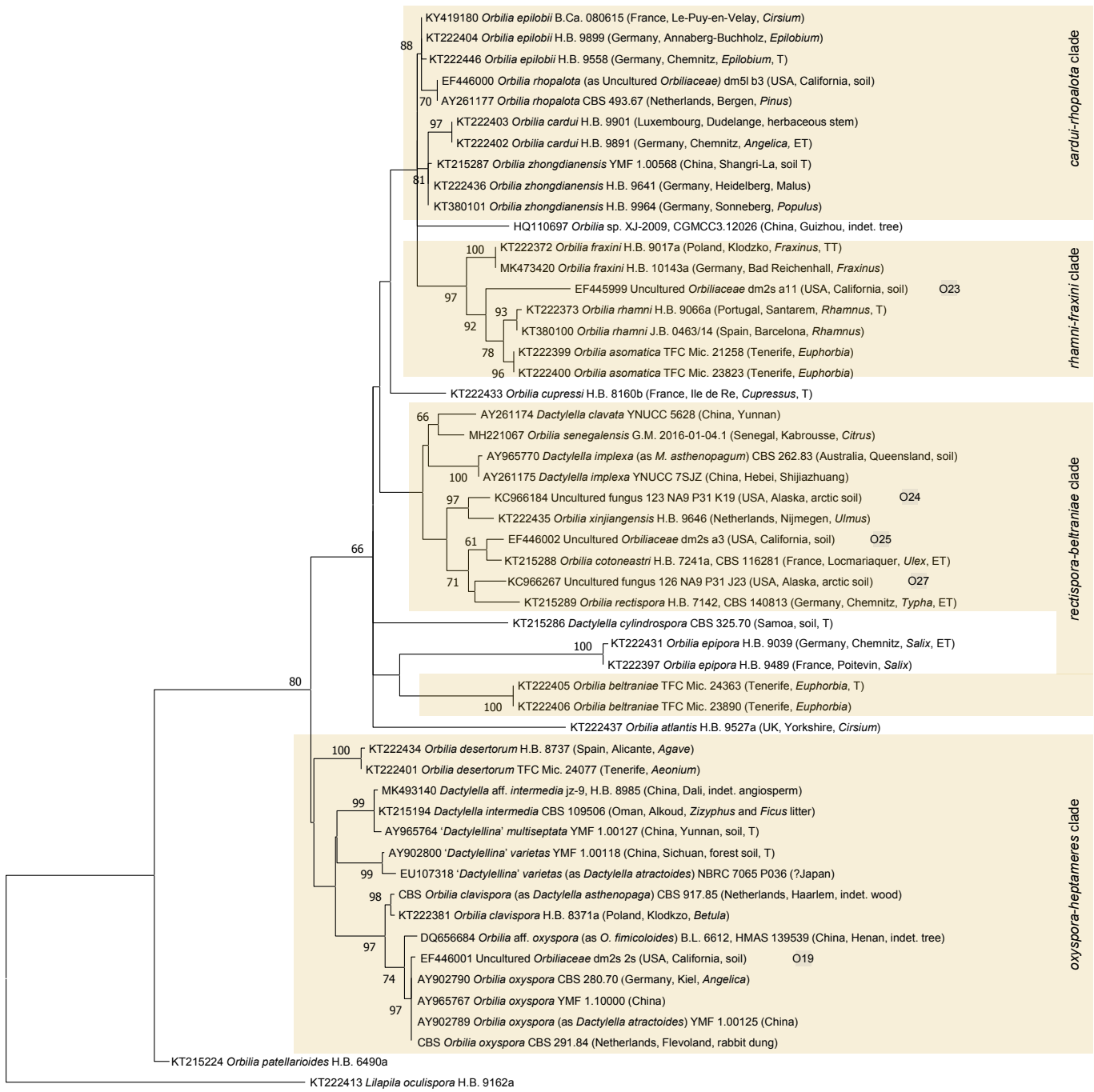
Phylogenetic analysis S28: Phylogram of *Orbilia eucalypti* s.l. inferred from ML analysis of ITS1-5.8S-ITS2 rDNA dataset (27 sequences, 575 positions, aligned with MUSCLE) using the K2+G model in MEGA7 (500 replicates). The tree is rooted with *Orbilia tremulae*, *O. cejpaii*, and *O. plurivacuolata*. Asci 8-spored in all taxa; * = without partial ITS2.



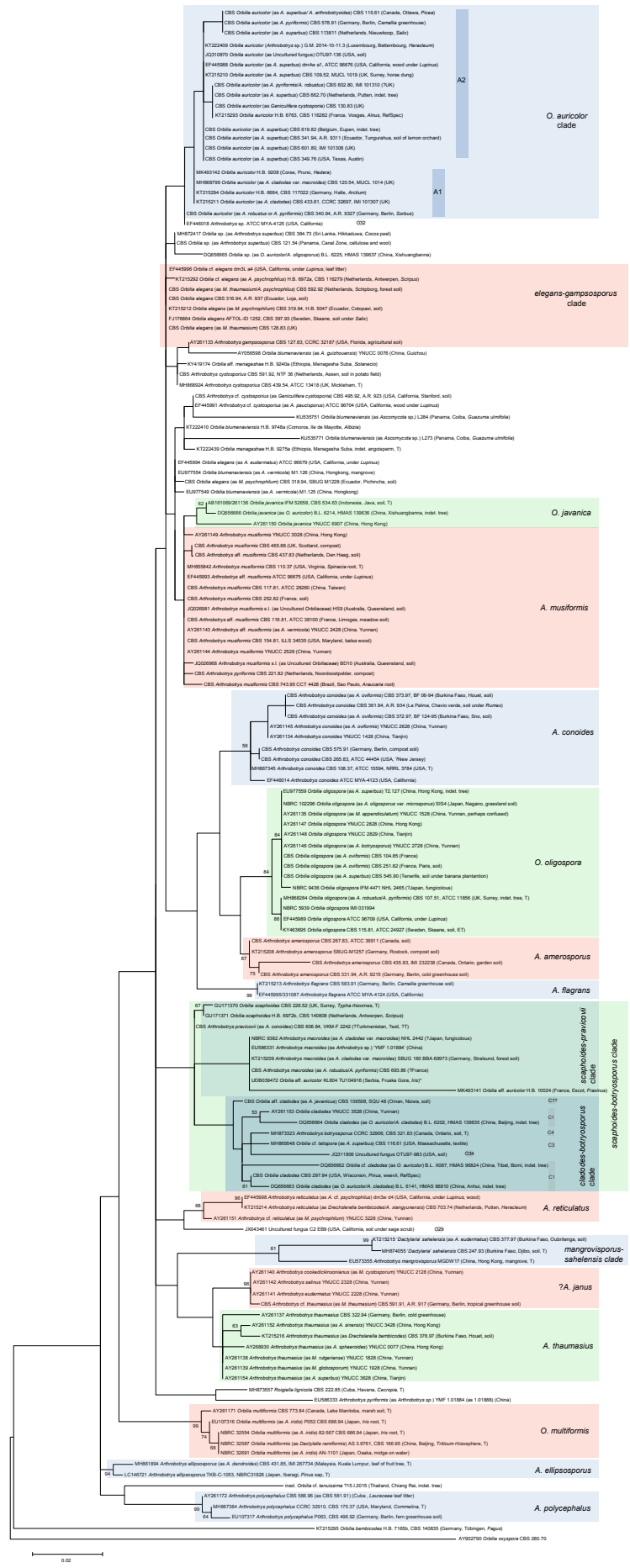
Phylogenetic analysis S29: NJ analysis of section *Arthrobotrys* based on SSU (V8–V9) rDNA dataset (85 sequences, 296 positions, aligned with MUSCLE) using MEGA7 (500 replicates). The tree is rooted with *Tuber borchii*. Asci 8-spored in all teleomorph taxa; T = type, ET = epitype, NT = neotype, TT = topotype. * = without SSU (V8).



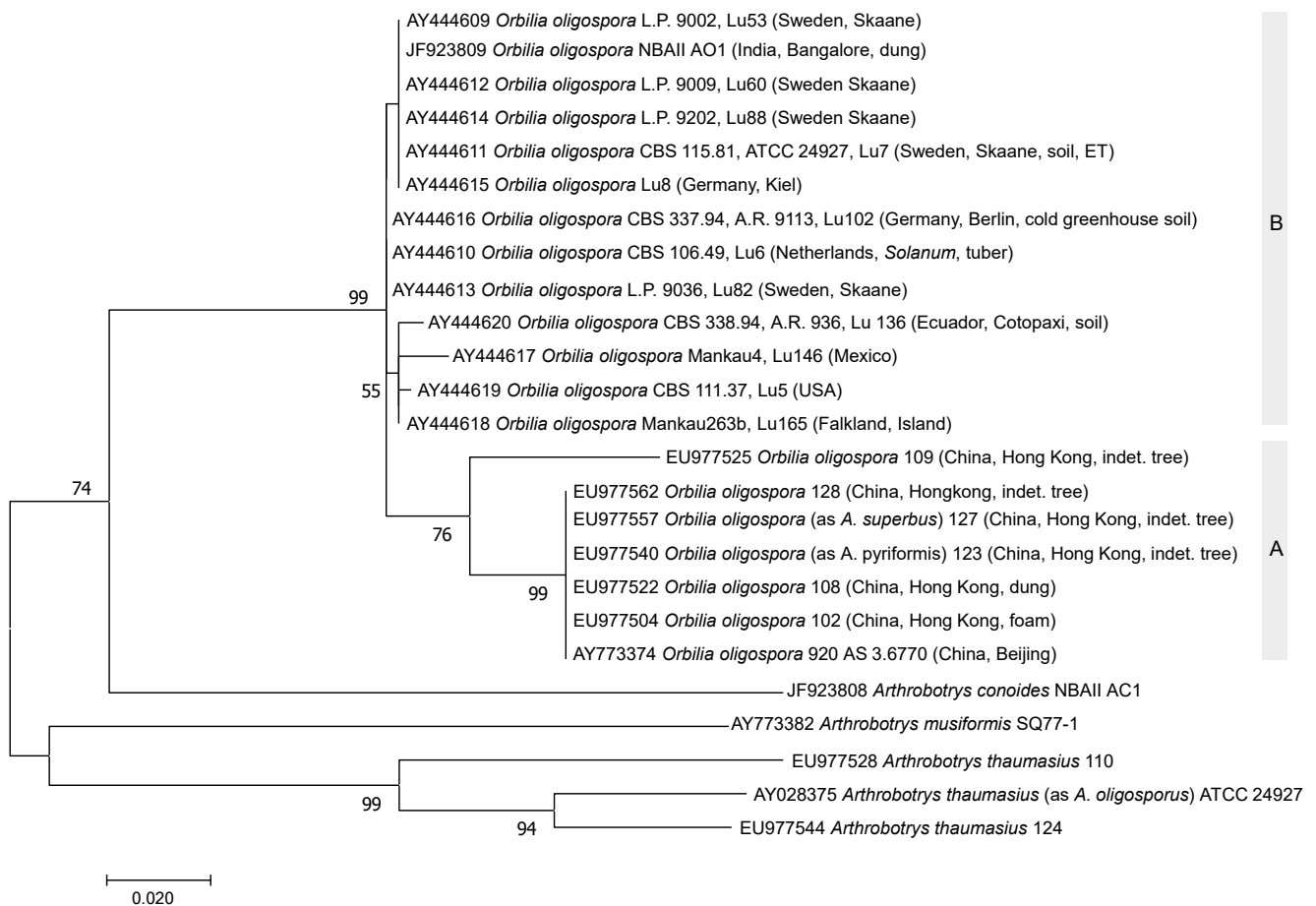
Phylogenetic analysis S30: Phylogram of section *Arthrobotrys* inferred from ML analysis of S1506 Intron rDNA dataset (82 sequences, 560 positions, aligned with MUSCLE) using the K2+G+I model in MEGA7 (500 replicates). Two environmental strains from GenBank are included representing unidentified species (O26, O27). The tree is rooted with *Orbillia leucostigma*. Asci 8-spored in all teleomorph taxa; T = type, ET = epitype.



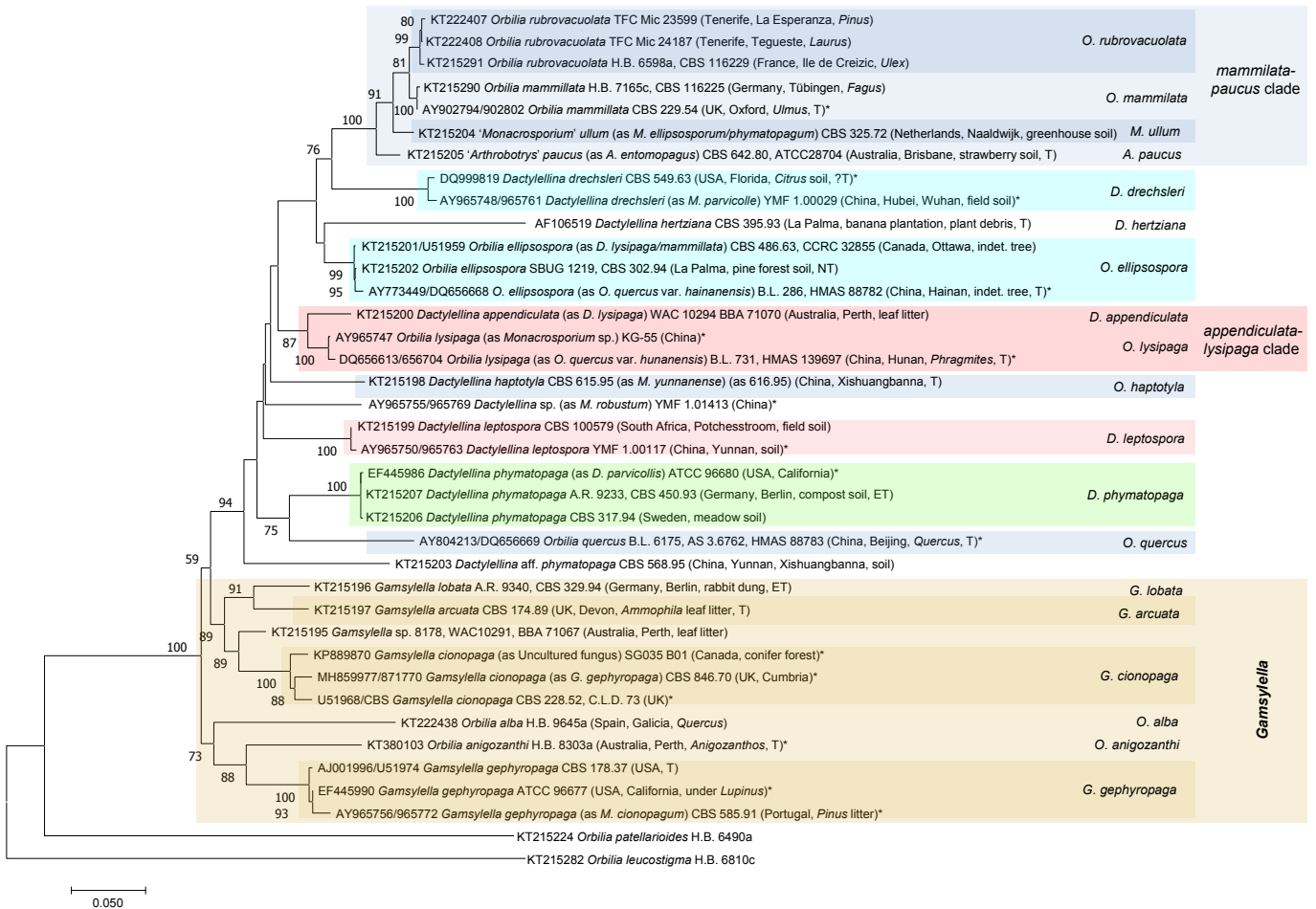
Phylogenetic analysis S31: Phylogram of series *Neodactylella* inferred from ML analysis of LSU (D1–D2) rDNA dataset (52 sequences, 564 positions, aligned with MUSCLE) using the K2+G+I model in MEGA7 (500 replicates). Six environmental strains from GenBank are included, five of them representing unidentified species (O19, O23–O25, O27). The tree is rooted with *Lilapila oculispora* and *Orbilia patellarioides*. Asci 8-spored in all teleomorph taxa; T = type, ET = epitype, TT = topotype.



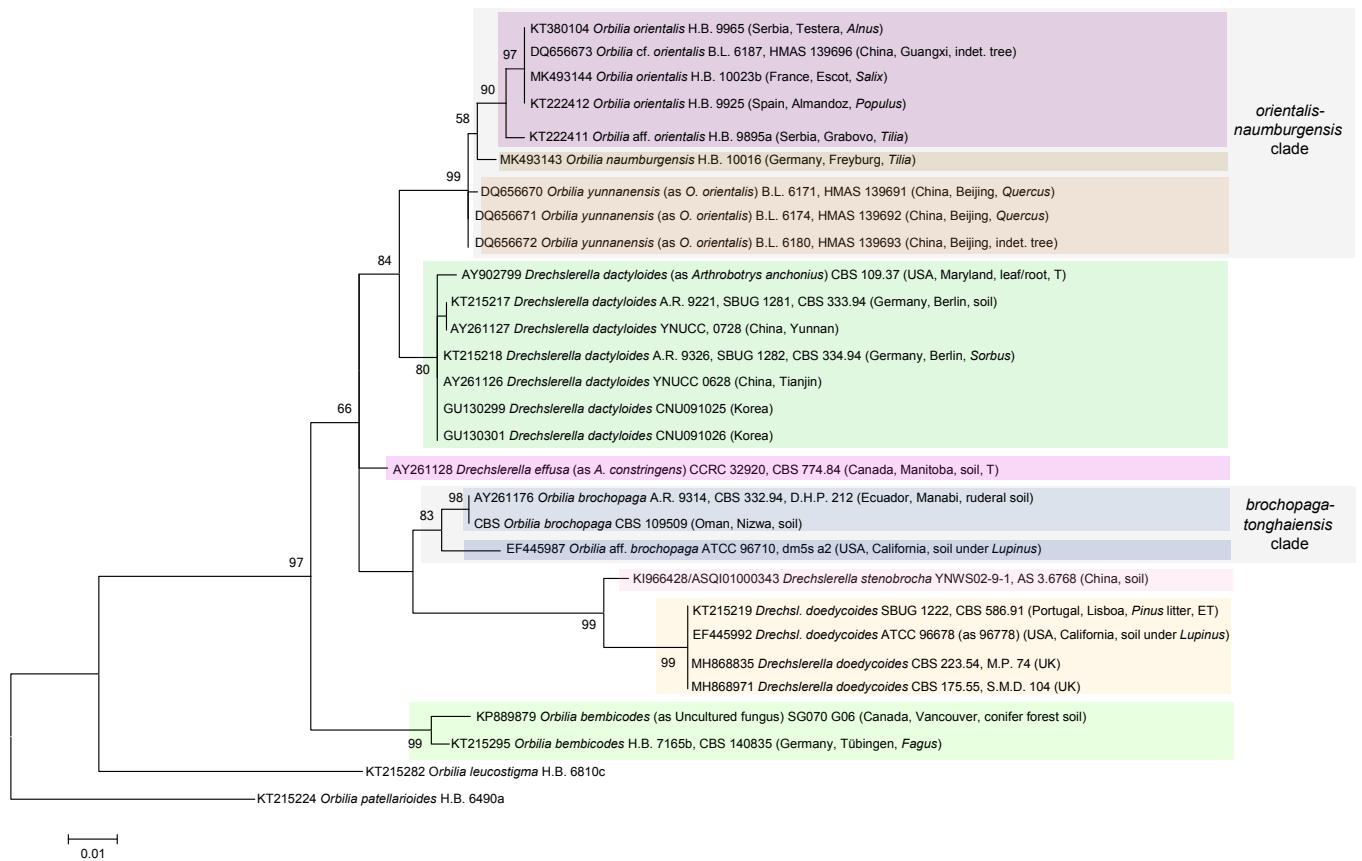
Phylogenetic analysis S32: Phylogram of series *Arthrobotrys* inferred from ML analysis of LSU (D1–D2) rDNA dataset (144 sequences, 593 positions, aligned with MUSCLE) using the K2+G+I model in MEGA7 (500 replicates). Six environmental strains from GenBank are included, three of them representing unidentified species (O29, O32, O34). The tree is rooted with *Orbilia oxyspora* and *O. bembicoides*. Asci 8-spored in all teleomorph taxa; T = type, ET = epitype, * = without LSU (D2).



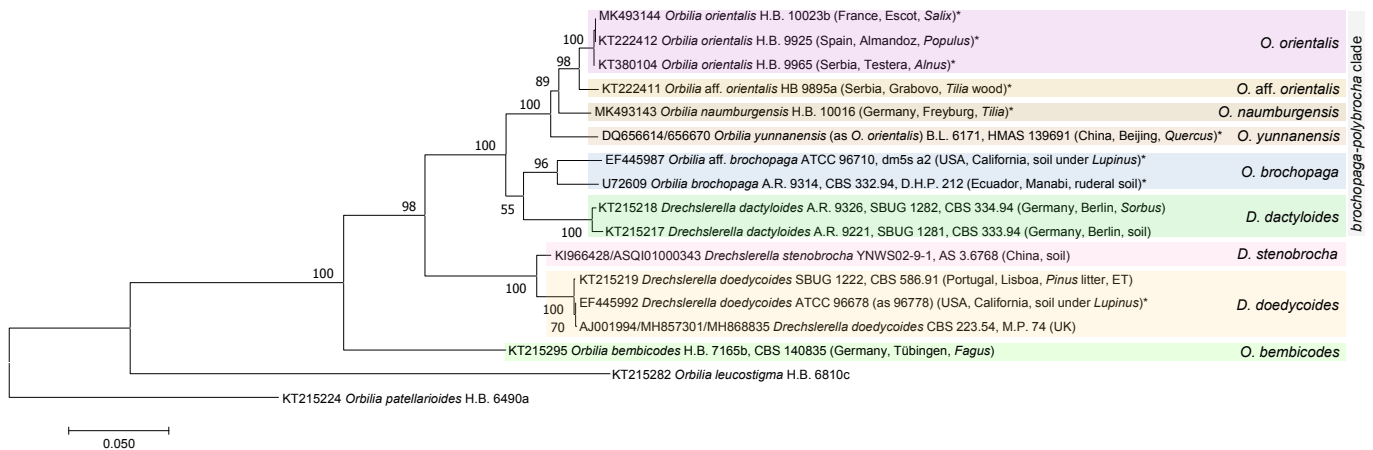
Phylogenetic analysis S34: Phylogram of *O. oligospora* s.l. inferred from ML analysis of *TUBB* dataset (25 sequences, 493 positions, aligned with MUSCLE) using the K2+G model in MEGA6 (500 replicates). The tree is rooted with *Arthrobotrys thaumasius*, *A. musiformis*, and *A. conoides*. ET = epitype.



Phylogenetic analysis S35: Phylogram of series *Dactylellina* and *Gamsylella* inferred from combined ML analysis of SSU (V8–V9)+ITS+LSU (D1–D2) rDNA dataset (38 sequences, 1630 positions, aligned with MAFFT) using the TN+G+I model in MEGA7 (500 replicates). The tree is rooted with *Orbilia leucostigma* and *O. patellarioides*. Asci 8-spored in all teleomorph taxa; T = type, ET = epitype, NT = neotype. * = without SSU.



Phylogenetic analysis S36: Phylogram of series *Drechslerella* inferred from ML analysis of LSU (D1–D2) rDNA dataset (29 sequences, 619 positions, aligned with MUSCLE) using the K2+G model in MEGA6 (500 replicates). The tree is rooted with *Orbilia patellarioides* and *O. leucostigma*. Asci 8-spored in all teleomorph taxa; T = type, ET = epitype.



Phylogenetic analysis S37: Phylogram of series *Drechslerella* inferred from combined ML analysis of SSU (V8–V9)+ITS+LSU (D1–D2) rDNA dataset (17 sequences, 1593 positions, aligned with MUSCLE) using the K2+G+I model in MEGA7. The tree is rooted with *Orbilia patellarioides* and *O. leucostigma*. Asci 8-spored in all teleomorph taxa; ET = epitype, * = without SSU.