

Supplementary materials

Biodiversity of fungi on *Vitis vinifera* L. revealed by traditional and high-resolution culture-independent approaches

Ruvishika S Jayawardena^{1,2,3*} · Witoon Purahong^{4*} · Wei Zhang^{1,3*} · Tesfaye Wubet^{4,5} · Xing-Hong Li^{1,3} · Mei Liu^{1,3} · Wensheng Zhao⁶ · Kevin D. Hyde² · JianHua Liu¹ · JiYe Yan^{1,3}

¹ Institute of Plant and Environment Protection, Beijing Academy of Agriculture and Forestry Sciences, Beijing 100097, People's Republic of China

² Centre of Excellence in Fungal Research, School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand

³ Beijing Municipal Key Laboratory for Environment Friendly Management on Fruit Diseases and Pests in North China, Beijing 100097, People's Republic of China

⁴ Department of Soil Ecology, UFZ-Helmholtz Centre for Environmental Research, Theodor-Lieser-Str. 4, D-06120 Halle (Saale), Germany

⁵ German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany

⁶ College of Agricultural and Biotechnology, China Agricultural University, Beijing 100193, People's Republic of China

* Equally contributed

Table S1 Potential functional group of fungal OTUs identified in this study. In total, 143/226 fungal OTUs were successfully assigned for their functions.

OTU ID	Avg relative abundance	Taxon	Functional group
OTU-1	10.394	<i>Trichothecium</i>	Plant Pathogen
OTU-2	7.046	<i>Aspergillus</i>	Saprotroph
OTU-3	5.065	<i>Nectriaceae</i>	Saprotroph
OTU-4	7.214	<i>Ilyonectria</i>	Saprotroph
OTU-5	5.224	<i>Aspergillus</i>	Saprotroph
OTU-6	0.457	<i>Eurotiales</i>	Saprotroph
OTU-9	5.244	<i>Clonostachys</i>	Plant Pathogen
OTU-11	9.474	<i>Aspergillus</i>	Saprotroph
OTU-12	2.816	<i>Microascus</i>	Saprotroph
OTU-13	3.683	<i>Aspergillus</i>	Saprotroph
OTU-15	0.932	<i>Acrostalagmus luteoalbus</i>	Endophyte
OTU-17	0.779	<i>Hypocreales</i>	Saprotroph
OTU-20	0.710	<i>Ceratobasidium</i>	Ectomycorrhizal
OTU-21	1.782	<i>Aspergillus</i>	Saprotroph
OTU-22	0.602	<i>Chrysosporium</i>	Saprotroph
OTU-24	0.416	<i>Trichocomaceae</i>	Saprotroph
OTU-25	0.627	<i>Hypocreales</i>	Saprotroph
OTU-27	1.237	<i>Eurotiales</i>	Saprotroph
OTU-28	0.234	<i>Aspergillus aculeatus</i>	Plant Pathogen
OTU-30	1.700	<i>Aspergillus</i>	Saprotroph
OTU-31	0.212	<i>Trichocomaceae</i>	Saprotroph
OTU-32	0.523	<i>Lasiodiplodia</i>	Plant Pathogen
OTU-33	0.234	<i>Stromato neurospora</i>	Saprotroph
OTU-35	0.214	<i>Hansfordia</i>	Saprotroph
OTU-36	0.167	<i>Stachybotrys</i>	Saprotroph

OTU ID	Avg relative abundance	Taxon	Functional group
OTU-37	0.314	<i>Cryptococcus</i>	Fungal Parasite-Saprotroph
OTU-38	0.241	<i>Microascus</i>	Saprotroph
OTU-39	0.155	<i>Scopulariopsis</i>	Saprotroph
OTU-40	0.158	<i>Emericella</i>	Saprotroph
OTU-42	0.264	<i>Phoma</i>	Plant Pathogen-Saprotroph
OTU-43	0.180	<i>Penicillium citrinum</i>	Plant Pathogen
OTU-44	0.102	<i>Fusarium</i>	Plant Pathogen-Saprotroph
OTU-48	0.046	<i>Emericella</i>	Saprotroph
OTU-49	0.066	<i>Hypocreales</i>	Saprotroph
OTU-50	0.106	<i>Ampelomyces</i>	Endophyte-Saprotroph
OTU-51	0.043	<i>Lecanicillium</i>	Animal Pathogen
OTU-52	0.041	<i>Coniocessia</i>	Saprotroph
OTU-53	0.040	<i>Penicillium</i>	Saprotroph
OTU-57	0.020	<i>Aspergillus</i>	Saprotroph
OTU-58	0.043	<i>Dactylellina</i>	Saprotroph
OTU-61	0.039	<i>Rhodosporidium</i>	Saprotroph
OTU-62	0.050	<i>Eupenicillium</i>	Saprotroph
OTU-63	0.021	<i>Marasmius</i>	Saprotroph
OTU-64	0.027	<i>Nectriaceae</i>	Saprotroph
OTU-65	0.023	<i>Hypocreales</i>	Saprotroph
OTU-66	0.034	<i>Fusarium</i>	Plant Pathogen-Saprotroph
OTU-69	0.019	<i>Simplicillium</i>	Animal Pathogen
OTU-72	0.018	<i>Penicillium</i>	Saprotroph
OTU-73	0.025	<i>Aspergillus terreus</i>	Saprotroph
OTU-76	0.012	<i>Eurotiales</i>	Saprotroph
OTU-84	0.009	<i>Phaeoacremonium</i>	Plant Pathogen
OTU-85	0.008	<i>Aplosporella</i>	Plant Pathogen
OTU-86	0.025	<i>Davidiella</i>	Saprotroph

OTU ID	Avg relative abundance	Taxon	Functional group
OTU-88	0.008	<i>Tricoderma</i>	Saprotroph
OTU-89	0.011	<i>Paecilomyces</i>	Saprotroph
OTU-90	0.012	<i>Penicillium chrysogenum</i>	Plant Pathogen
OTU-92	0.007	<i>Hypocreales</i>	Saprotroph
OTU-93	0.008	<i>Monographella</i>	Plant Pathogen
OTU-94	0.023	<i>Aspergillus</i>	Saprotroph
OTU-95	0.007	<i>Talaromyces</i>	Saprotroph
OTU-96	0.009	<i>Conioliariella</i>	Saprotroph
OTU-97	0.008	<i>Nectriaceae</i>	Saprotroph
OTU-99	0.007	<i>Trichocomaceae</i>	Saprotroph
OTU-100	0.008	<i>Penicillium</i>	Saprotroph
OTU-101	0.005	<i>Lecanicillium</i>	Animal Pathogen
OTU-105	0.008	<i>Chaetomium</i>	Saprotroph
OTU-106	0.006	<i>Mortierella</i>	Saprotroph
OTU-107	0.010	<i>Myrothecium</i>	Saprotroph
OTU-109	0.008	<i>Hypocreales</i>	Saprotroph
OTU-110	0.004	<i>Humicola</i>	Saprotroph
OTU-112	0.004	<i>Cladosporium</i>	Endophyte-Plant Pathogen
OTU-113	0.006	<i>Claviceps</i>	Plant Pathogen
OTU-116	0.006	<i>Aspergillus</i>	Saprotroph
OTU-118	0.003	<i>Penicillium</i>	Saprotroph
OTU-119	0.004	<i>Bionectriaceae</i>	Saprotroph
OTU-120	0.008	<i>Hypocreaceae</i>	Saprotroph
OTU-121	0.003	<i>Cladosporium</i>	Endophyte-Plant Pathogen
OTU-122	0.003	<i>Chaetomium</i>	Saprotroph
OTU-123	0.003	<i>Spiromyces</i>	Saprotroph
OTU-124	0.003	<i>Eurotiales</i>	Saprotroph

OTU ID	Avg relative abundance	Taxon	Functional group
OTU-126	0.005	<i>Penicillium</i>	Saprotroph
OTU-127	0.002	<i>Botrytis</i>	Plant Pathogen
OTU-129	0.003	<i>Phoma</i>	Plant Pathogen-Saprotroph
OTU-130	0.004	<i>Volutella</i>	Plant Pathogen
OTU-134	0.004	<i>Ophiocordyceps</i>	Animal Pathogen
OTU-136	0.002	<i>Penicillium</i>	Saprotroph
OTU-137	0.003	<i>Volutella</i>	Plant Pathogen
OTU-139	0.001	<i>Spiromastix</i>	Saprotroph
OTU-142	0.001	<i>Lophiostoma</i>	Saprotroph
OTU-143	0.001	<i>Aspergillus</i>	Saprotroph
OTU-144	0.002	<i>Clonostachys</i>	Plant Pathogen
OTU-146	0.002	<i>Cadophora</i>	Endophyte
OTU-148	0.002	<i>Papulaspora</i>	Fungal Parasite-Saprotroph
OTU-150	0.001	<i>Chrysosporium</i>	Saprotroph
OTU-151	0.001	<i>Gymnascella</i>	Saprotroph
OTU-152	0.002	<i>Eurotiales</i>	Saprotroph
OTU-153	0.002	<i>Geomyces</i>	Saprotroph
OTU-154	0.003	<i>Neurospora</i>	Saprotroph
OTU-155	0.002	<i>Thielavia</i>	Saprotroph
OTU-156	0.001	<i>Trichocomaceae</i>	Saprotroph
OTU-157	0.001	<i>Hypocreales</i>	Saprotroph
OTU-159	0.002	<i>Xylaria</i>	Endophyte-Saprotroph
OTU-160	0.003	<i>Hypocreales</i>	Saprotroph
OTU-161	0.001	<i>Arthrographis</i>	Saprotroph
OTU-162	0.002	<i>Fusarium</i>	Plant Pathogen-Saprotroph
OTU-163	0.001	<i>Penicillium</i>	Saprotroph
OTU-164	0.003	<i>Scopulariopsis</i>	Saprotroph
OTU-166	0.028	<i>Trichocomaceae</i>	Saprotroph

OTU ID	Avg relative abundance	Taxon	Functional group
OTU-167	0.092	<i>Microascus</i>	Saprotroph
OTU-168	0.002	<i>Penicillium</i>	Saprotroph
OTU-170	0.001	<i>Arachnomyces</i>	Saprotroph
OTU-171	0.001	<i>Cylindrocarpon</i>	Plant Pathogen
OTU-172	0.001	<i>Penicillium</i>	Saprotroph
OTU-175	0.001	<i>Aspergillus</i>	Saprotroph
OTU-177	0.001	<i>Chaetomium</i>	Saprotroph
OTU-179	0.001	<i>Chaetomium</i>	Saprotroph
OTU-180	0.155	<i>Nectriaceae</i>	Saprotroph
OTU-183	0.001	<i>Pseudallescheria</i>	Saprotroph
OTU-184	0.002	<i>Kernia</i>	Saprotroph
OTU-185	0.001	<i>Microascus</i>	Saprotroph
OTU-187	0.001	<i>Phialosimplex</i>	Saprotroph
OTU-190	0.001	<i>Podospora communis</i>	Saprotroph
OTU-191	0.001	<i>Devriesia</i>	Plant Pathogen
OTU-194	0.001	<i>Nectriaceae</i>	Saprotroph
OTU-199	0.001	<i>Aspergillus</i>	Saprotroph
OTU-202	0.001	<i>Hypocreales</i>	Saprotroph
OTU-205	0.001	<i>Leptosphaeria</i>	Plant Pathogen
OTU-207	0.002	<i>Rhodotorula</i>	Saprotroph
OTU-208	2.108	<i>Eurotiales</i>	Saprotroph
OTU-210	0.001	<i>Metarhizium</i>	Animal Pathogen
OTU-211	0.001	<i>Kernia</i>	Saprotroph
OTU-218	0.004	<i>Nectriaceae</i>	Saprotroph
OTU-220	0.004	<i>Cladosporium</i>	Endophyte-Plant Pathogen
OTU-225	0.001	<i>Derxomyces</i>	Fungal Parasite-Saprotroph
OTU-227	0.001	<i>Saccharomycetales</i>	Saprotroph
OTU-228	0.040	<i>Aspergillus</i>	Saprotroph

OTU ID	Avg relative abundance	Taxon	Functional group
OTU-232	0.001	<i>Hansfordia</i>	Saprotroph
OTU-235	0.001	<i>Apodus</i>	Saprotroph
OTU-238	0.001	<i>Myrothecium</i>	Saprotroph
OTU-240	0.001	<i>Cladosporium</i>	Endophyte-Plant Pathogen
OTU-249	0.001	<i>Lentinus</i>	Saprotroph
OTU-255	0.001	<i>Microdochium</i>	Endophyte-Plant Pathogen
OTU-257	0.001	<i>Hydnum</i>	Ectomycorrhizal

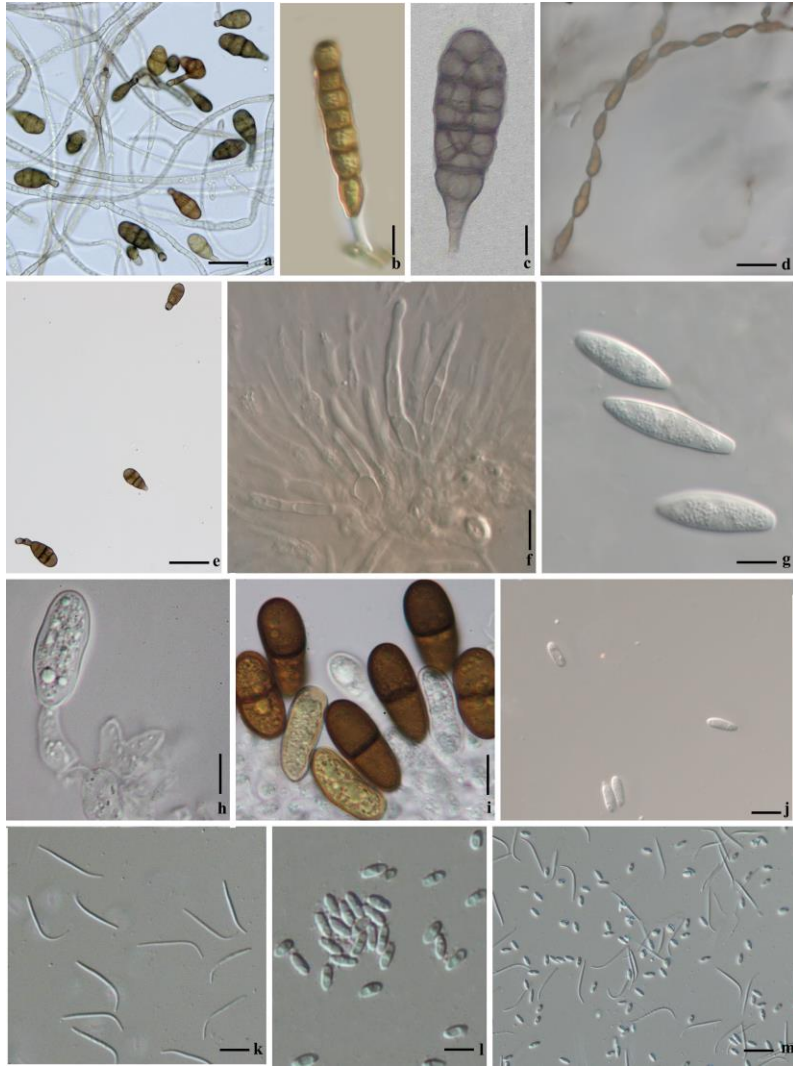


Fig. S1a. Morphology of species identified in this study. **a–d** Conidia of *Alternaria alternate*. **e** Conidia of *Alternaria vitis*. **f** Conidiophore of *Botryosphaeria dothidea*. **g** Conidia of *Botryosphaeria dothidea*. **h** Conidiogenous cell of *Dothiorella sarmentorum*. **i** Mature conidia of *Dothiorella sarmentorum*. **j** Conidia of *Didymella pomorum*. **k** β conidia of *Diaporthe eres*. **l** α conidia of *Diaporthe eres*. **m** α and β conidia of *Diaporthe eres*. Scale bars: a, d–i = 20 μm , j–m = 10 μm .



Fig. S1b Morphology of species identified in this study. **a** Conidiogenous cells of *Albifimbria verrucaria*. **b** Conidia of *Albifimbria verrucaria*. **c** Conidiogenous cells of *Albifimbria viridis*. **d** Conidia of *Albifimbria viridis*. **e** Chlamydospores of *Epicoccum nigrum*. **f** Spores of *Epicoccum nigrum*. **g–i** Macronematous conidiophores and conidial chains *Cladosporium cladosporioides*. **j** Conidiogenous cells of *Coniella vitis*. **k** Conidia of *Coniella vitis*. **l** Conidiophore of *Bipolaris maydis*. **m–n** Conidia of *Bipolaris maydis*. **o** Conidia on conidiophores of *Botrytis cinerea*. Scale bars g, i, l, o = 50 µm, a–f, h, j–k, m–n = 10 µm.

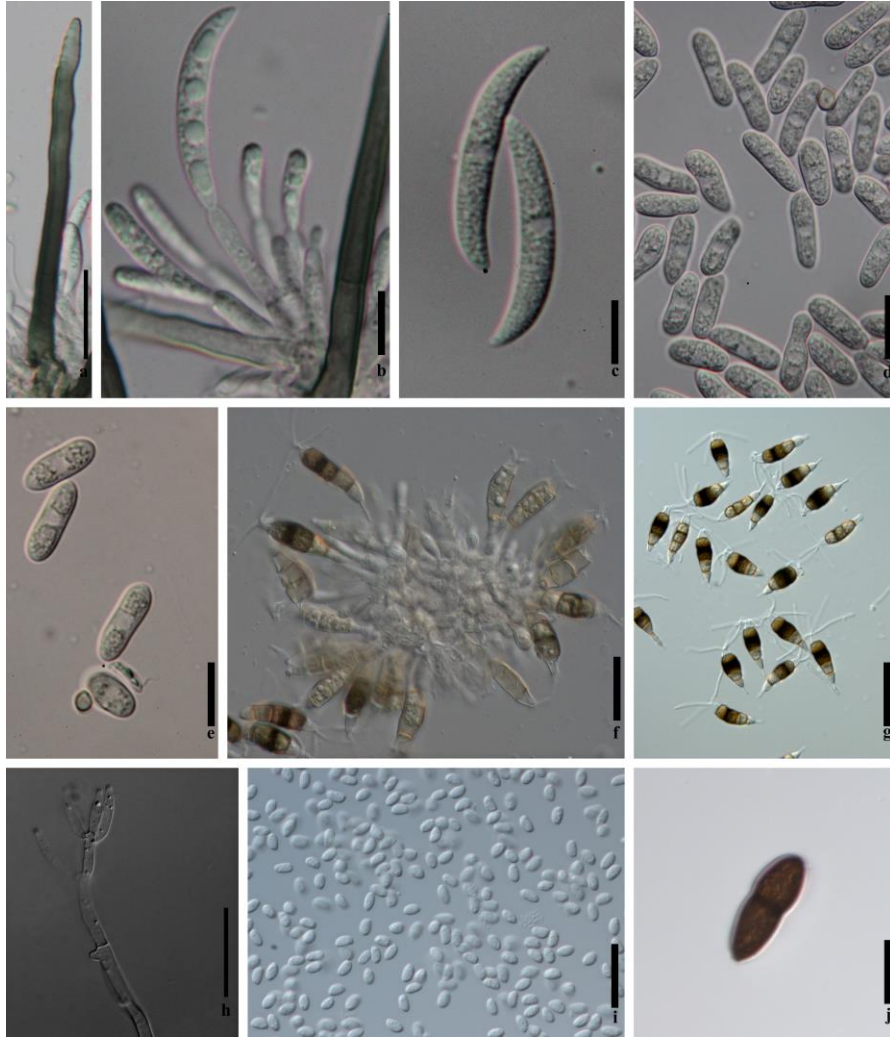


Fig. S1c Morphology of species identified in this study **a** Setae of *Colletotrichum truncatum*. **b** Conidiophores of *Colletotrichum truncatum*. **c** Conidia of *Colletotrichum truncatum*. **d** Conidia of *Colletotrichum viniferum*. **e** Conidia of *Colletotrichum hebeiense*. **f** Conidiogenous cells and conidia of *Neopestalotiopsis vitis*. **g** Conidia of *Neopestalotiopsis clavispora*. **h** Conidiophores and conidiogenous cells of *Clonostachys rosea*. **i** Conidia of *Clonostachys rosea*. **j** Ascospore of *Clonostachys rosea*. Scale bars: a–b, h =20 μm , c–g, i–j =10 μm .

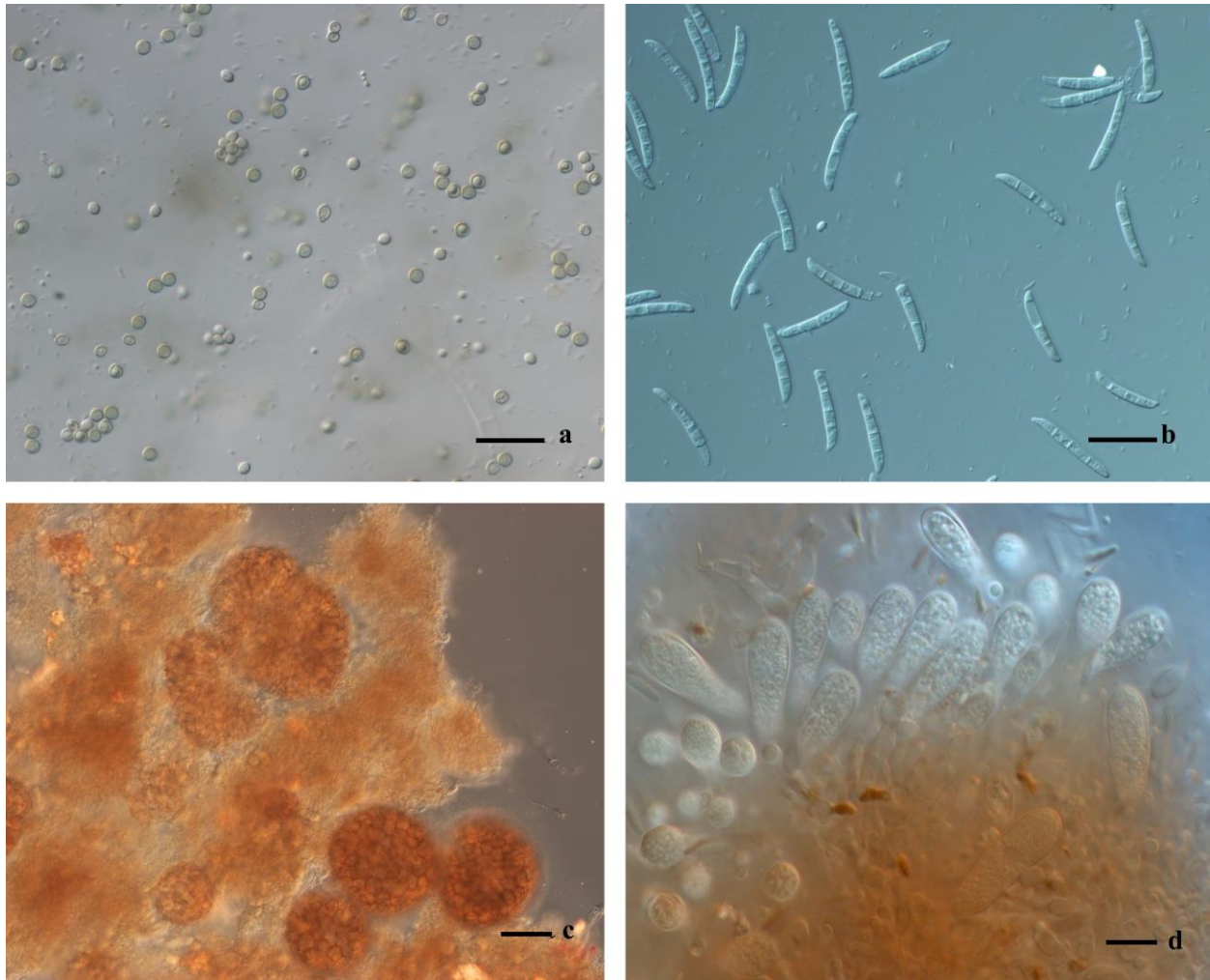


Fig. S1d Morphology of species identified in this study **a** Conidia of *Talaromyces purpurogenus*. **b** Conidia of *Fusarium oxysporum*. **c** *Minimedusa* sp. **d** *Peniophora* sp. Scale bars c–d =50 μm , a–b=10 μm .

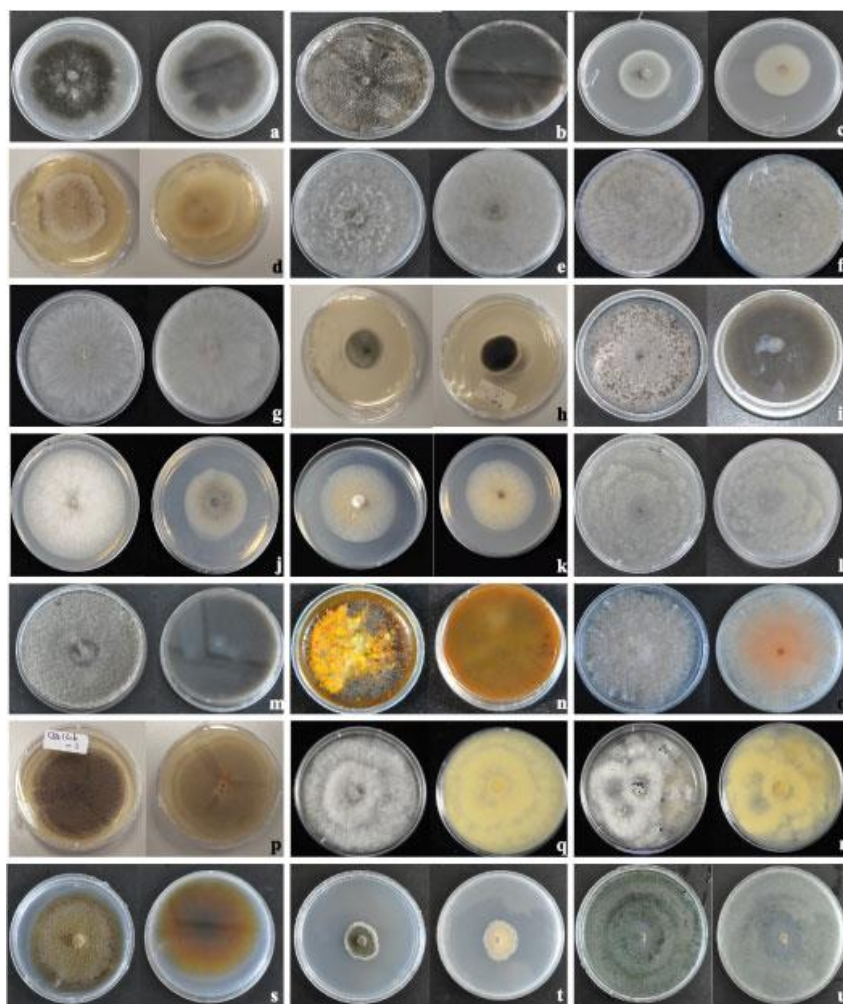


Fig. S2 Forward and reverse views of colonies **a** *Alternaria alternata*. **b** *Alternaria vitis*. **c** *Aspergillus niger*. **d** *Bipolaris maydis*. **e** *Botryosphaeria dothidea*. **f** *Botrytis cinerea*. **g** *Coniella vitis*. **h** *Cladosporium cladosporioides*. **i** *Colletotrichum truncatum*. **j** *Colletotrichum hebeiense*. **k** *Colletotrichum viniferum*. **l** *Diaporthe eres*. **m** *Dothiorella sarmentorum*. **n** *Epicoccum nigrum*. **o** *Fusarium oxysporum*. **p** *Mucor racemosus*. **q** *Neopestalotiopsis clavispora*. **r** *Neopestalotiopsis*

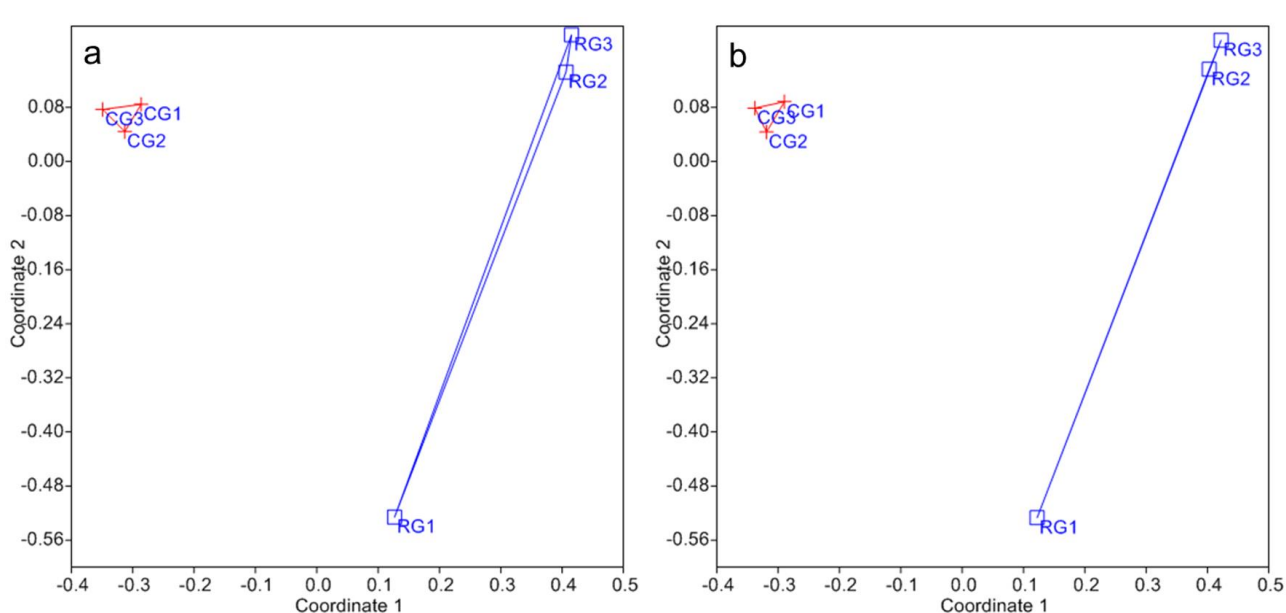


Fig. S3 Nonmetric Multidimensional Scaling (NMDS) ordinations of (a) all fungal OTUs (2D stress = 0.19) and (b) all fungal OTUs detected in two locations (2D stress = 0.18) of two grape cultivars: (CarbanateGernischet (CG1-3) and Red Globe (RG1- 3)).

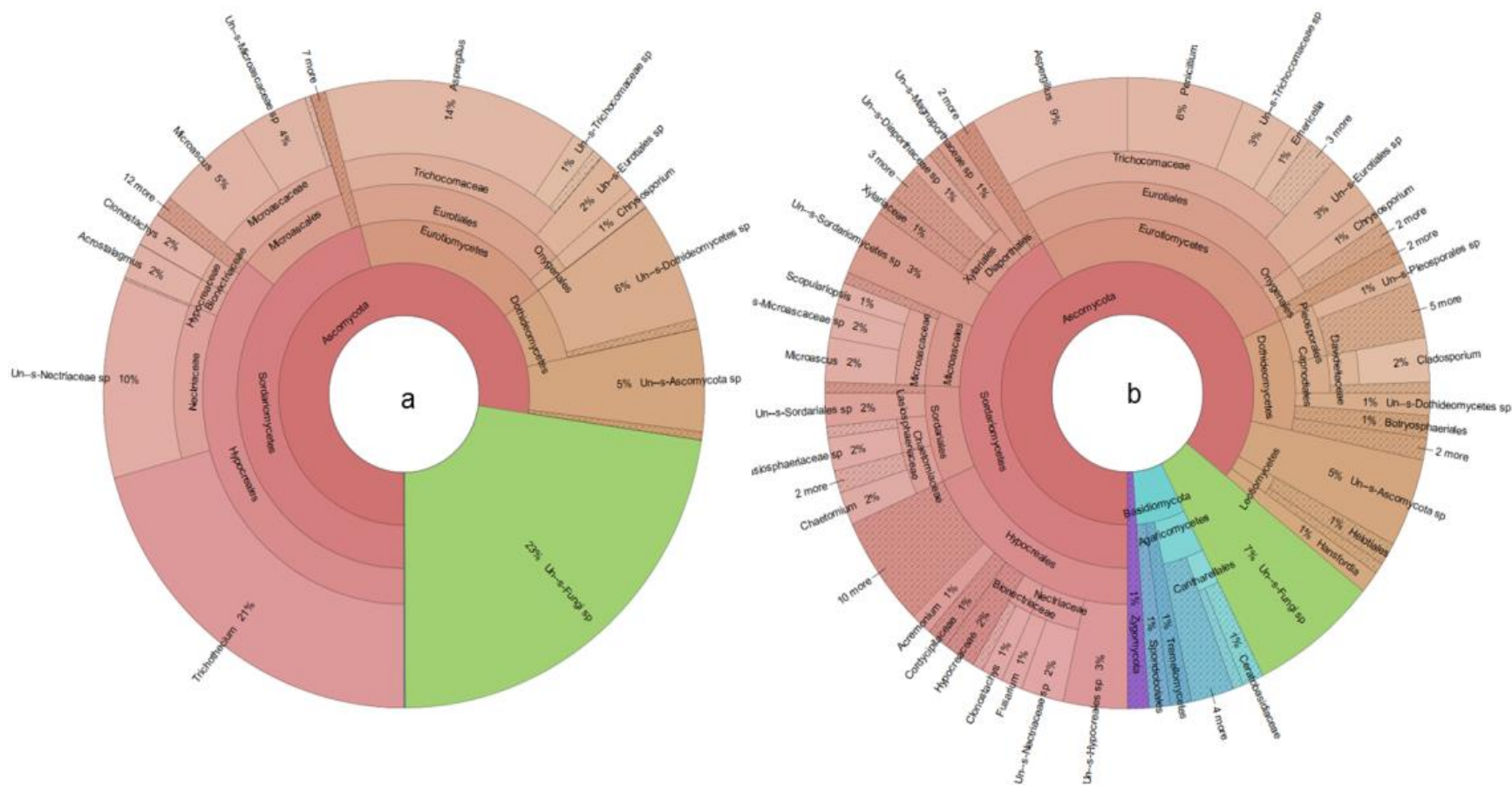


Figure S4 Fungal Community composition in Carbanate Gernischet based on relative abundance (a) and presence/absence (b) data

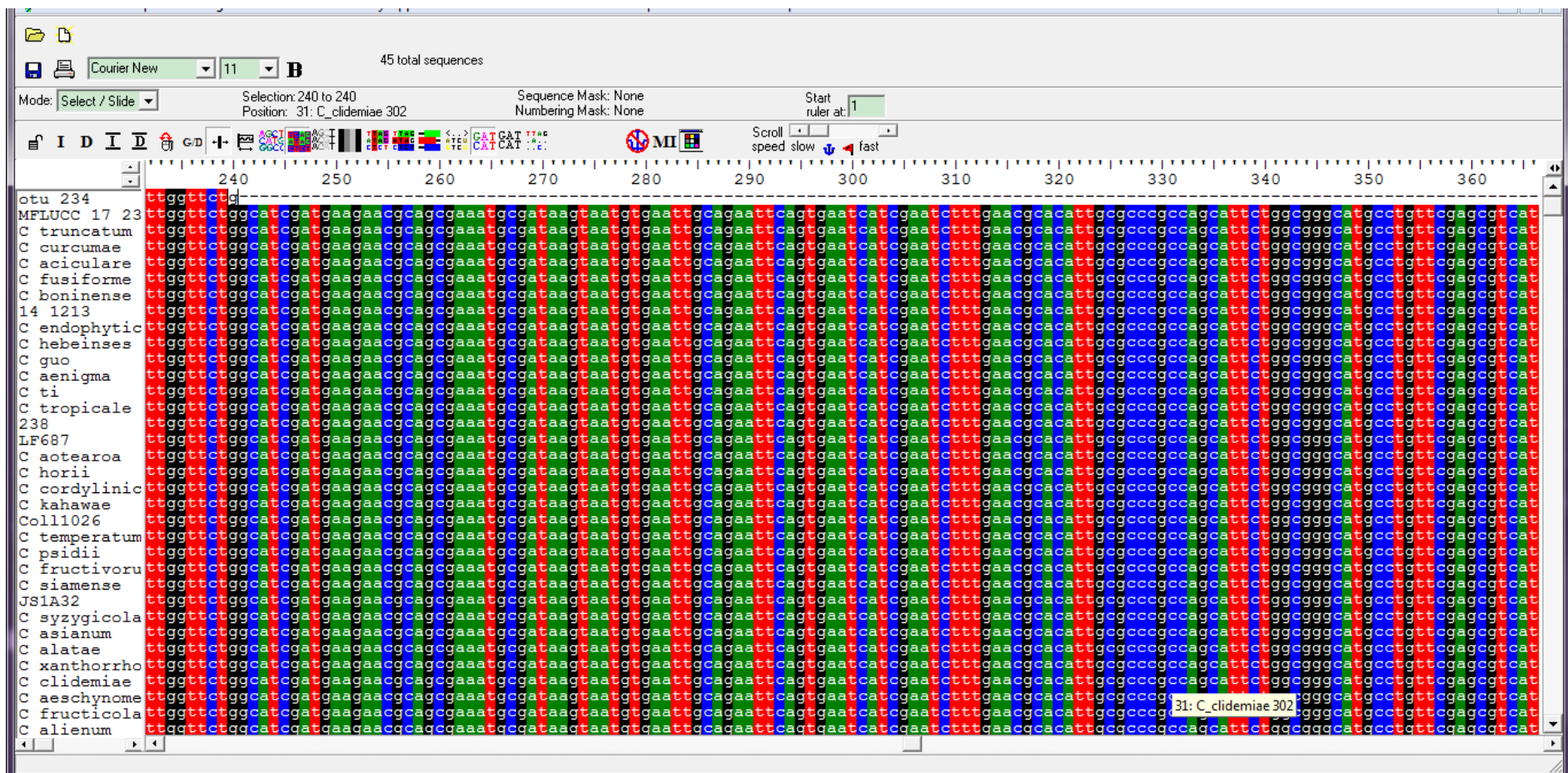


Fig. S6 Alignment of the sequences

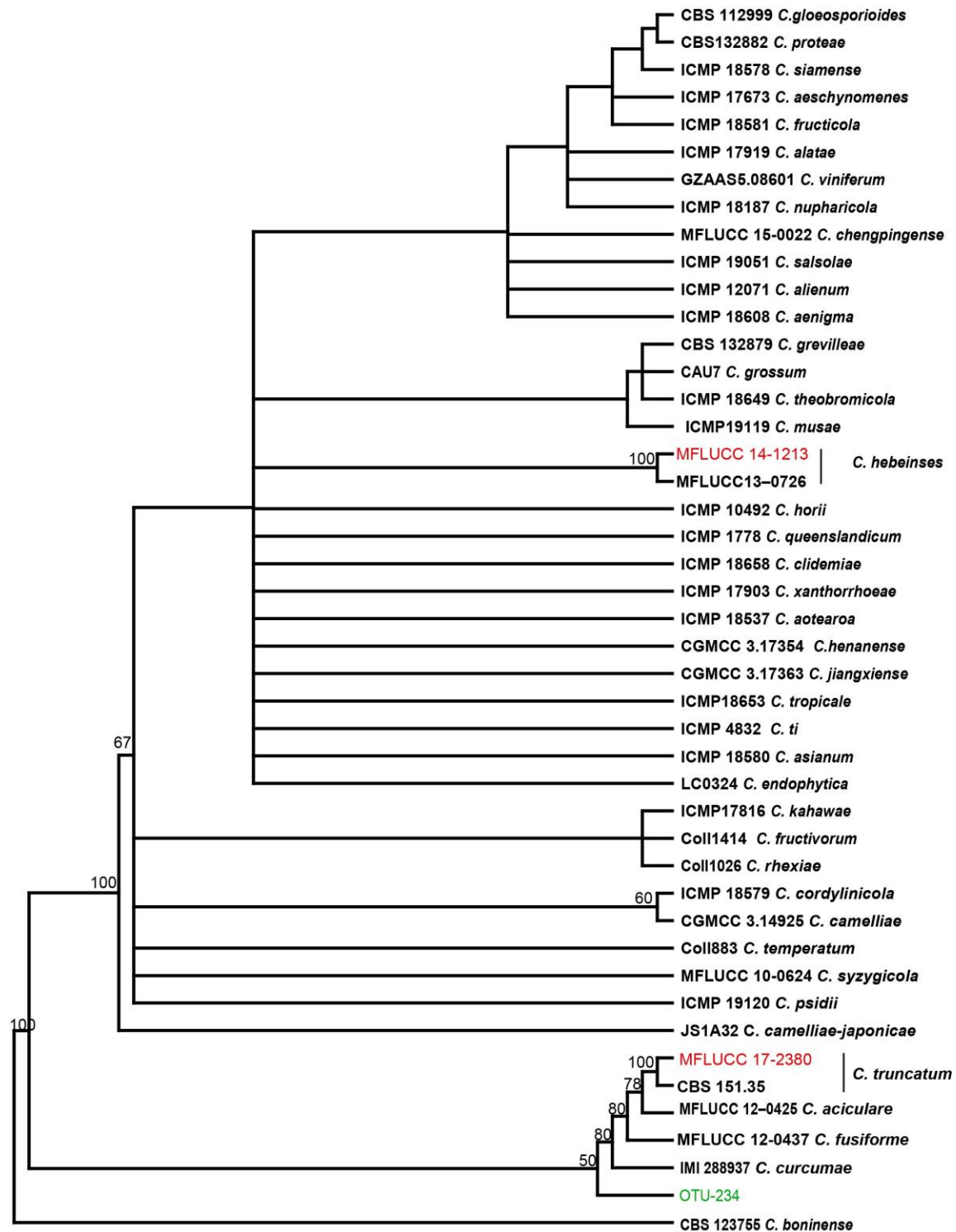


Fig. S7 One of ten most parsimonious trees obtained from a heuristic search for ITS sequence data of taxa from *Colletotrichum*. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches. Ex-type strains are in bold. Strains obtained in this study are in red and OUT is in green. The tree is rooted with *Colletotrichum boninense* CBS 123755.

