

## Supplementary Material

**Tab. S1** - List of publications reviewed: lands use types and sites.

SN	Date	Authors	Title of the paper	Land use type considered	Land use types	Place	Country
1	1991	Johnson et al.	Dynamics of vesicular-arbuscular mycorrhizae during old field succession	Primary forest, cropland, abandoned cropland	Primary forest, cropland, abandoned cropland	Minneapolis, Minnesota	USA
2	1994	Fischer et al.	Mycorrhiza inoculum potentials in tropical secondary succession	Bareland, pasture, forest	Bareland, pasture, secondary forest		Costa Rica
3	1997	Jhonson & Wedin	Soil carbon, nutrients, and mycorrhizae during conversion of dry tropical forest to grassland	Tropical forest, Grassland	Primary forest, secondary grassland	southern Guanacaste Province	Costa Rica
4	2002	Turgay and Nonaka	Effect of land-use and management practices on soil ergosterol content in andosols	Farmland and two forest sites	Primary forest, cropland	Japan	Japan
5	2002	Helund	Soil microbial community structure in relation to vegetation management on former agricultural land	agriculture forest and abandoned land	Secondary forest, abandoned land, cropland	Trollehlm estate, Lund, South Sweden	Sweden
6	2002	McLean and Huhta	Microfungal community structure in anthropogenic birch stand in central Finland	Plantation age	Cropland and plantation forest	Central Finland	Finland
7	2003	Oehl et al.	Impact of land use intensity on the species diversity of arbuscular mycorrhizal fungi in agroecosystems of central Europe	Grassland, crop rotation and monocropping	Secondary grassland and cropland	Plain of the upper Rhine River	Switzerland
8	2004	Kalmer & Hedlund	Fungal diversity in set-aside agricultural soil investigated using terminal-restriction fragment length polymorphism	Forest, cropland and abandoned land	Secondary forest, abandoned land and cropland	Sweden	Sweden
9	2004	Mabuhay et al.	Influence of erosion on soil microbial biomass, abundance and community diversity	Eroded and undisturbed (Pine trees)	Primary forest, bareland	Hiroshima Prefecture	Japan
10	2005	Allison et al.	Change in soil microbial community structure in a tallgrass prairie chronosequence	Restoration	Secondary grassland and cropland	Fermilab, Batavia, Illinois, USA	USA
11	2006	Tedersoo et al.	Diversity of community structure of ectomycorrhizal fungi in a wooded meadow	Wooded meadow, forest	Secondary grassland and secondary forest	Tagamoisa, Saaremaa Island, Northwest Estonia	Estonia
12	2006	van der Wal	Fungal biomass development in a chronosequence of land abandonment	Abandoned land and heathland	Secondary shrubland and abandoned land		Scotland
13	2006	Diaz et al.	Are ericoid mycorrhizas a factor in the success of <i>Calluna vulgaris</i> heathland restoration	Heathland and cropland	Secondary shrubland and cropland	Wareham	England
14	2007	Bedini et al.	Effects of long-term land use on arbuscular mycorrhizal fungi and glomalin-related soil protein	Cropland Grassland Forest	Primary grassland, plantation forest and cropland	Cerreto Farm, Sovicille, Italy	Italy
15	2007	Li et al.	Arbuscular mycorrhizal colonization and spore density across different land-use types in a hot and arid ecosystem, Southwest China.	Cropland, Fallow land, undisturbed savanna	Primary grassland, abandoned land and cropland	Yunmou, Southwest China	China
16	2007	Perger et al.	Losses of glomalin-related soil protein under prolonged arable corpping: A chronosequence study in sandy soils of the South African Highveld.	Cropping duration and native grassland	Primary grassland and cropland	Free State Province of South Africa	South Africa
17	2007	Li et al.	Differences of arbuscular mycorrhizal fungal diversity and community between a cultivated land, an old field, and a never-cultivated field in a hot and arid ecosystem of southwest China	Cropland, old field, never cultivated land	Primary grassland, abandoned land, and cropland	Yuanmou	China

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18	2008	Dong et al.	Soil microbial community structure in diverse land use systems: a comparative study using BIOLOG, DGGE, and PLFA analyses.	Tea garden and forest	Primary forest and perennial cropland	Zhejiang Province in Southeast China	China
19	2008	van Ekeren et al.	Soil biological quality after 36 years of ley-arable cropping, permanent grassland and permanent arable cropping.	cropping system with permanent grass or arable land	Primary grassland and cropland	Nederlands	Netherland
20	2008	Guadarrama et al.	Propagules of arbuscular mycorrhizal fungi in a secondary dry forest of Oaxaca, Mexico.	Time elapse after abandonment	Abandoned land and cropland	Nizanda, Oaxaca state, Mexico	Mexico
21	2008	Guo and Han	Soil biochemical properties and arbuscular mycorrhizal fungi as affected by afforestation of rangelands in Northern China.	Rangeland, plantation forest	Plantation forest and pasture	Guyuan county, Northern China	China
22	2008	Hamer et al.	Soil organic matter and microbial community structure in set-aside and intensively managed arable soils in ne-Saxony, Germany	Intensive agriculture, abandonment	Abandoned land and cropland	Kreinitz, NE-Saxony	Germany
23	2008	Kasel et al.	Land use influences soil fungal community composition across central Victoria, south-eastern Australia	Plantation and unimproved pastures	Plantation forest and pasture	central Victoria, south-eastern Australia	Australia
24	2008	Lauber et al.	The influence of soil properties on the structure of bacterial and fungal communities across land-use types.	Hardwood and pine forests, cultivated and livestock pasture lands	Secondary forest, plantation forest, pasture, and cropland	Piedmont region, northwestern South Carolina, USA	USA
25	2008	Rahman et al.	Physical, chemical and microbiological properties of an andisol as related to land use and tillage practice.	No tillage orchard, Conventional tillage Paddy field	Perennial cropland and cropland	Iwate University Agricultural field, Japan	Japan
26	2008	Violi et al.	Disturbance changes arbuscular mycorrhizal fungal phenology and soil glomalin concentrations but not fungal spore composition in Montane rainforests in Veracruz and Chiapas, Mexico.	forests converted to pine-dominant stands, milpas, non-selectively logged forests and/or pastures	Primary forest and plantation forest	Mexico	Mexico
27	2008	Hamer et al.	Microbial activity and community structure in degraded soils on the Loess Plateau of China	Bareland, cropland, Forest	Secondary forest, cropland and bareland		China
28	2009	Bakhsipour et al.	Effect of land use change on status of arbuscular mycorrhizal fungi in some hyrcanian forest soil a case study of Lahidjan region, Iran.	native broadleaf forest two afforested sites	Primary forest and plantation forest	Guilan Province, Northern Iran, Iran	Iran
29	2009	Guo et al.	The influence of land use change on chemical and biological properties of steppe soils in northern china.	native steppe to intensive agriculture intensive agriculture to alfalfa	Primary grassland and cropland	Mongolia Plateau, China	China
30	2009	Hamer et al.	Microbial activity and community structure in degraded soils on the loess plateau of China	Clear cut bare plot, Secondary forest Natural succession, Arable land	Secondary forest, cropland and bareland	Shaanxi Province, P.R. China	China
31	2009	Hamer and Makeschin	Rhizosphere soil microbial community structure and microbial activity in set-aside and intensively managed arable land.	Intensive agricultural land fallow land Natural vegetation	Abandoned land and cropland	Kreinitz, Saxony, NE-Germany	Germany
32	2009	Leal et al.	Occurrence and diversity of arbuscular mycorrhizal fungi in trap cultures from soils under different land use systems in the Amazon, Brazil.	Forest, Old Secondary Forest, Young Secondary Forest, Agroforestry systems, Crops and Pasture	Primary forest, secondary forest, agroforestry, pasture and cropland	western park of Amazon state, Brazil	Brazil
33	2009	Jefwa et al.	Influence of land use types on occurrence of arbuscular mycorrhizal fungi in the high-altitude regions of Mt. Kenya	cropland Perennial cropland, Pasture/fallow, Forest, plantation forest	Primary forest, plantation forest, pasture, abandoned land, perennial cropland, and cropland		Kenya

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34	2009	Zornoza et al.	Changes in soil microbial community structure following the abandonment of agricultural terraces in mountainous areas of eastern Spain.	Undisturbed forest, agricultural, abandoned agricultural	Secondary forest, abandoned land and cropland	province of Alicante (SE Spain)	Spain
35	2010	Carson et al.	Afforestation alters community structure of soil fungi.	Plantation, pasture	Plantation forest and pasture	Esperance, South-West Western Australia	Australia
36	2010	Drenovsky et al.	Land use and climatic factors structure regional patterns in soil microbial communities.	Forest, grasslands, cropland	Primary forest, secondary grassland, and cropland	California	USA
37	2010	Lumini et al.	Disclosing arbuscular mycorrhizal fungal biodiversity in soil through a land-use gradient using a pyrosequencing approach.	Vineyard, meadow, pasture, Oak forest	Secondary forest, secondary grassland, pasture, and perennial cropland	Berchidda site, Northern hills of Sardinia, Italy	Italy
38	2010	Oehl et al.	Soil type and land use intensity determine the composition of arbuscular mycorrhizal fungal communities.	Grassland pasture and arable land	Secondary grassland, pasture, and cropland	Rhine Valley	Switzerland
39	2010	Snoeck et al.	Temporal changes in VAM fungi in the cocoa agroforestry systems of central Cameroon.	Secondary forest chronosequence in cocoa agroforests, fallow land	Secondary forest, agroforestry, and abandoned land	Central province of Cameroon.	Cameroon
40	2010	Verbruggen et al.	Positive effects of organic farming on below-ground mutualists: large-scale comparison of mycorrhizal fungal communities in agricultural soils.	Agricultural land Semi-natural grassland	Secondary grassland and cropland	Netherlands	Netherlands
41	2010	Postma-Blaauw et al.	Soil biota community structure and abundance under agricultural intensification and extensification	conversion of grassland to arable land fertilization Monoculture and crop rotation	Secondary grassland and cropland	De Bovenbuurt	Netherlands
42	2011	Banning et al.	Soil microbial community composition as affected by restoration practices in California grassland	perennial and annual grassland, tilled bareland	Secondary grassland and bareland	Santa Lucia Mountains in Upper Carmel Valley	USA
43	2011	Gast et al.	Spatial scaling of arbuscular mycorrhizal fungal diversity is affected by farming practice	Arable & horticulture	Perennial cropland and cropland	England	England
44	2011	Sturmer et al.	Species richness and spore abundance of arbuscular mycorrhizal fungi across distinct land uses in Western Brazilian Amazon.	pristine forest, old secondary forest, young secondary forest, agroforestry system, crop, and pasture	Primary forest, secondary forest, pasture, agroforestry, and cropland	Amazon state Brazil	Brazil
45	2011	Grantina et al.	The influence of the land use on abundance and diversity of soil fungi: comparison of conventional and molecular methods of analysis	Forest, former agricultural land; agricultural land – meadow; agricultural land – conventional arable land	Secondary forest, abandoned land, and cropland	Jelgava, Cesis and Valka district	Latvia
46	2011	Covacevich and Berbara	Indigenous arbuscular mycorrhizae in areas with different successional stages at a tropical dry forest biome in Brazil	secondary grassland and pasture	Secondary grassland and pasture	Minas Gerais State	Brazil
47	2011	Mehring et al.	Impact of forest organic farming change on soil microbial C turnover using C-13 of phospholipid fatty acids	Secondary forest, primary forest, organic farming, Conventional farming	Primary forest, secondary forest, and cropland	São Paulo	Brazil
48	2012	Costa et al.	Diversity of filamentous fungi in different systems of land use.	Conventional Cassava monoculture Atlantic forest	Primary forest and cropland	Pernambuco, Brazil	Brazil
49	2012	Fokom et al.	Glomalin related soil protein, carbon, nitrogen and soil aggregate stability as affected by land use variation in the humid forest zone of south Cameroon.	forest, fallow land, cultivated system	Secondary forest, abandoned land, and cropland	Metet, Cameroon	Cameroon

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50	2012	G'Cortes et al.	Arbuscular mycorrhizal fungal (AMF) communities and land use change: the conversion of temperate forests to avocado plantations and maize fields in central Mexico.	Forest, avocado plantation maize field	Secondary forest, perennial cropland, and cropland	State of Michoacan in Central Mexico	Mexico
51	2012	Hryniewicz et al.	Correspondence of ectomycorrhizal diversity and colonisation of willows ( <i>Salix</i> spp.) grown in short rotation coppice on arable sites and adjacent natural stands	Arable land and adjacent natural forest	Primary forest cropland	Uppsala, Sweden	Sweden
52	2012	Jefwa et al.	Impact of land use types and farming practices on occurrence of arbuscular mycorrhizal fungi (AMF) Taita-Taveta district in Kenya.	maize, horticulture, fallow,napier, planted forests, and indigenous forests	Primary forest, plantation forest, secondary grassland, abandoned land, perennial cropland, and cropland	Taita-Taveta, Southeast Kenya	Kenya
53	2012	Munchane et al.	Effect of land use system on arbuscular mycorrhiza fungi in Maasai Mara ecosystem, Kenya	protected and unprotected grassland and woodland, intensified monocropping systems and subsistence farming systems	Secondary grassland, woodland, and cropland	MME, boundary of Kenya and Tanzania	Kenya
54	2012	Orgiazzi et al.	Unravelling soil fungal communities from different Mediterranean land-use backgrounds	Tillage and non-tillage vineyard meadow Oak forest	Secondary forest, secondary grassland, and perennial cropland	Sardinia, Italy	Italy
55	2012	Potthast et al.	Land-use change in a tropical mountain rainforest region of southern Ecuador affects soil microorganisms and nutrient cycling.	forest- pasture – abandoned pasture	Primary forest, pasture, and abandoned land	Southern Ecuador	Ecuador
56	2012	Sene et al.	The abundance and diversity of legume-nodulating rhizobia and arbuscular mycorrhizal fungal communities in soil samples from deforested and man-made forest systems in a semi-arid Sahel region in Senegal.	Deforested area and planted forest	Secondary forest and plantation forest	Bandia in Coastal, Senegal	Senegal
57	2012	Yurkov et al.	Assessment of yeast diversity in soils under different management regimes.	Forest plot and grassland plot	Secondary forest and secondary grassland		Germany
58	2012	Zangaro et al.	Root colonization and spore abundance of arbuscular mycorrhizal fungi in distinct successional stages from an Atlantic rainforest biome in southern Brazil	Grassland, Shrubland, Secondary forest, Mature forest	Primary forest, secondary forest, secondary shrubland, and secondary grassland		Brazil
59	2012	Yamashita et al.	Changes in community structure of wood-inhabiting aphyllporaceous fungi after clear-cutting in a cool temperate zone of Japan: Planted conifer forest versus broad-leaved secondary forest	Secondary forest and Planted forest	Secondary forest and plantation forest		Japan
60	2013	Bonfim et al.	Arbuscular mycorrhizal fungi in the Brazilian Atlantic forest: a gradient of environmental restoration	Native forest and planted forest with different age	Primary forest and secondary forest	Brazil	Brazil
61	2013	Dai et al.	Impact of land use on arbuscular mycorrhizal fungal communities in rural Canada	Cropland, Natural areas, seminatural areas,	Primary forest and cropland	Alberta, Manitoba, Saskatchewan, USA	USA
62	2013	Dinesh and Chaudhuri	Soil biochemical/microbial indices as ecological indicators of land use change in mangrove forests	Mangroove sites and plantation sites	Secondary forest and plantation forest	South Andaman Islands, India	India
63	2013	Fracetto et al.	Impact of Amazon land use on the community of soil fungi	Secondary forest, agriculture Pasture, Agroforestry	Secondary forest, cropland, pasture, and perennial cropland	Amazonas State, Brazil	Brazil
64	2013	Hazard et al.	The role of local environment and geographical distance in determining community composition of arbuscular mycorrhizal fungi at the landscape scale	Pasture, agriculture, Forest, plantation	Secondary forest, plantation forest, pasture, and cropland	Ireland	Ireland

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65	2013	Leal et al.	Switch of tropical amazon forest to pasture affects taxonomic composition but not species abundance and diversity of arbuscular mycorrhizal fungal community	Pasture and foerst site	Primary forest and pasture	Brazil	Brazil
66	2013	Li et al.	Succession of plant and soil microbial communities with restoration of abandoned land in the loess plateau, china	Regenerated forest Abandoned plots	Secondary forest and abandoned land	Lvliang Mountains, China	China
67	2013	Sousa et al.	Arbuscular mycorrhizal fungi within agroforestry and traditional land use systems in semi-arid northeast Brazil	Traditional agriculture, pasture, intercropping	Pasture, perennial cropland, and cropland	State of Paraiba, Brazil	Brazil
68	2013	Ying et al	Effects of land utilization patterns on soil microbial communities in an acid red soil based on DNA and PLFA analyses	Restoration, degradation, cropland, pine	Primary forest, secondary forest, and cropland	Hunan Province of China	China
69	2013	Lupatini et al.	Land-use change and soil type are drivers of fungal and archaeal communities in the Pampa biome	Native forest Plantation forest Grassland Cropland	Primary forest, plantation forest, secondary grassland, and cropland	Rio Grande do Sul	Brazil
70	2013	Yu et al.	Fungal and Bacterial Communities in the Rhizosphere of <i>Pinus tabulaeformis</i> Related to the Restoration of Plantations and Natural Secondary Forests in the Loess Plateau, Northwest China	secondary forest and plantation forest	Secondary forest and plantation forest	Ziwuling Region, Heshui County, Gansu Province	China
71	2014	Fichtner et al.	Effects of anthropogenic disturbances on soil microbial communities in oak forests persist for more than 100 years	Former arable, Former heathland Ancient forest	Primary forest and cropland	Saxony, NW Germany	Germany
72	2014	Gherghel et al.	Former land use and host genotype influence the mycorrhizal colonization of poplar roots	Plantation with different plant clone	Secondary forest, secondary grassland, and cropland	Hannoversch Münden, Germany	Germany
73	2014	Jansa et al.	Soil and geography are more important determinants of indigenous arbuscular mycorrhizal communities than management practices in Swiss agricultural soils	Cropland Grassland	Secondary grassland and cropland		Switzerland
74	2014	Lisboa et al.	The match between microbial community structure and soil properties is modulated by land use types and sample origin within an integrated agroecosystem	Plantation, Improved pasture, Degraded pasture	Plantation forest and pasture	Goiás State, Brazil	Brazil
75	2014	Melo et al.	Species composition of arbuscular mycorrhizal fungi differ in semi-natural and intensively managed pastures in an isolated oceanic island (Terceira, Azores)	Seminatura and intensive	Secondary forest cropland	Terceira island, Azorean archipeloga,Portugal	Portugal
76	2014	Moora et al	Anthropogenic land use shapes the composition and phylogenetic structure of soil arbuscular mycorrhizal fungal communities	Intensive, sustainable, grassland Forested, plantation	Primary forest Plantation forest secondary grassland Cropland	Estonia	Estonia
77	2014	Pereira et al.	Diversity of arbuscular mycorrhizal fungi in Atlantic forest areas under different land uses	Natural forest, plantation forest, Rubber plantation, cropland,	Primary forest Plantation forest Perennial cropland Cropland	Agronomic Institute of Pernambuco, Brazil	Brazil
78	2014	Sharmah and Jha	Diversity of arbuscular mycorrhizal fungi in undisturbed forest, slash-and-burn field, and monoculture forest of Indo-Burma megadiverse region	pristine undisturbed forest slash-and-burn field monoculture forest	Primary forest Secondary forest	Karbi Anglong Hills, Assam, India	India
79	2014	Smith et al.	Microbial community structure varies across soil organic matter aggregate pools during tropical land cover change	active pastures secondary forests growing on abandoned pastures primary reference forest	Primary forest, secondary forest, secondary grassland	Sierra de Cayey of Southeastern Puerto Rico	Puerto Rico
80	2014	Wang et al.	Spatio-temporal dynamics of arbuscular mycorrhizal fungi associated with glomalin-related soil protein and soil enzymes in different managed semiarid steppes	non-grazed overgrazed restored grassland	Secondary grassland pasture	Inner Mongolia Plateau, Northern China	China

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81	2014	Kerfahi et al.	The Impact of Selective-Logging and Forest Clearance for Oil Palm on Fungal Communities in Borneo	Unlogged forest Once and twice logged forest Oil palm plantation	Secondary forest perennial cropland	Sabah, Malaysian Borneo	Borneo
82	2014	Xiang et al.	Land use influences arbuscular mycorrhizal fungal communities in the farming-pastoral ecotone of northern China	Grassland Farmland	Primary grassland cropland	China	China
83	2014	Glinka et al.	Environmental Controls on Fungal Community Composition and Abundance Over 3 Years in Native and Degraded Shrublands	Native shrubland, Disturb shrubland, Pasture	Primary shrubland secondary shrubland pasture	central Florida	USA
84	2014	Lagerlof et al.	Land-use intensification and agroforestry in the Kenyan highland: Impacts on soil microbial community composition and functional capacity		Agroforestry, planted forest, agricultural field, eroded land		Kenya
85	2015	Bainard et al.	Arbuscular mycorrhizal fungal communities are influenced by agricultural land use and not soil type among the Chernozem great groups of the Canadian prairies	Cropland and roadsides	abandoned land and cropland	Province of Saskatchewan, Canada	Canada
86	2015	Bordoloi et al.	Distribution of arbuscular mycorrhizal fungi associated with different land use systems of Arunachal Pradesh of Eastern Himalayan region	Forest, fallow, plantation forest and tea garden, agricultural land and home garden	Secondary forest abandoned land plantation forest perennial cropland cropland	Papum Pare District, Arunachal Pradesh, India	India
87	2015	Castaneda et al.	Comparison of soil microbial communities inhabiting vineyards and native sclerophyllous forests in central Chile	Vineyard and native forest	Primary forest, perennial cropland	Central Chile	Chile
88	2015	Ciccolini et al.	Land-use intensity and soil properties shape the composition of fungal communities in Mediterranean peaty soils drained for agricultural purposes	high intensity (maize monoculture) low intensity (extensive grassland) zero intensity (agricultural soil left abandoned)	abandoned land, cropland	Massaciuccoli Lake basin, Pisa, Italy	Italy
89	2015	Furrazola et al.	Functionality of arbuscular mycorrhizal fungi in three plant communities in the managed floristic reserve San Ubaldo-Sabanalamar, Cuba	Seminatural savannah Recovering savannah Agroecosystem of low input	Secondary grassland agroforestry	Cuba	Cuba
90	2015	Ma et al.	Soil moisture and land use are major determinants of soil microbial community composition and biomass at a regional scale in northeastern China	Rangeland, Rangeland grazed, woodland, returned cropland, farmland, rice field	Rangeland/woodland, cropland	Jilin Province, Inner Mongolia, China	China
91	2015	McGuire et al.	Responses of soil fungi to logging and oil palm agriculture in Southeast Asian tropical forests	primary forest forest regenerating from logging oil palm plantation	Primary forest, secondary forest, and perennial cropland	Peninsular Malaysia	Malaysia
92	2015	Tardy et al.	Land use history shifts in situ fungal and bacterial successions following wheat straw input into the soil	Grassland and cropland	Secondary grassland and cropland	Lusignan, France	France
93	2015	Thomson et al.	Soil conditions and land use intensification effects on soil microbial communities across a range of European field sites	Woodland, Grassland, Unfertilized forest, Fertilized forest, Permanent grassland, long term abandoned grassland, Unimproved grassland, improved grassland	Woodland, secondary forest, primary grassland, secondary grassland, and cropland	Different area within Europe	
94	2015	Valyi et al.	Land-use intensity and host plant identity interactively shape communities of arbuscular mycorrhizal fungi in roots of grassland plants	Grasslands with low input to fertilized, grazed and mown meadows and pastures	Secondary grassland and pasture	central Germany	Germany

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95	2015	Wang et al.	Role and variation of the amount and composition of glomalin in soil properties in farmland and adjacent plantations with reference to a primary forest in north-eastern China	Primary forest Plantation forest farmland	Primary forest, plantation forest, and cropland	China	China
96	2015	Wong et al.	The incorporation of fungal to bacterial ratios and plant ecosystem effect traits into a state-and-transition model of land-use change in semi-arid grasslands	Grassland and agricultural land	Primary grassland, pasture, and cropland	Australia	Australia
97	2015	Smith et al.	Successional and seasonal variations in soil and litter microbial community structure and function during tropical postagricultural forest regeneration: a multiyear study	Secondary forest and Primary forest	Primary forest and secondary forest		Puerto Rico
98	2015	Pellegrino et al.	Agricultural abandonment in Mediterranean reclaimed peaty soils: long-term effects on soil chemical properties, arbuscular mycorrhizas and CO <sub>2</sub> flux	Abandoned land and cropland	Abandoned land and cropland	Migliarino-San Rossore-Massaciuccoli (Pisa, Italy)	Italy
99	2015	Song et al.	Effects of historical logging on soil microbial communities in a subtropical forest in southern China	Primary forest, secondary forest and plantation forest	Primary forest, secondary forest, and plantation forest	Zhejiang province	China
100	2015	Tardy et al.	Shifts in microbial diversity through land use intensity as drivers of carbon mineralization in soil	Secondary grassland and abandoned field	Secondary grassland and abandoned land		
101	2015	Aldezabal et al.	Impact of grazing abandonment on plant and soil microbial communities in an Atlantic mountain grassland	secondary grassland and pasture	Secondary grassland and pasture	Northern Spain	Spain
102	2015	Smith et al.	Successional and seasonal variations in soil and litter microbial community structure and function during tropical postagricultural forest regeneration: a multiyear study	Secondary forest and Primary forest	Primary forest and secondary forest		Puerto Rico
103	2015	Krashevskaja et al.	Impact of tropical lowland rainforest conversion into rubber and oil palm plantations on soil microbial communities	Secondary forest, Agroforestry, perennial cropland (oil palm and rubber)	Secondary forest, perennial cropland, and agroforestry	Sumatra	Indonesia
104	2016	Xiao et al.	Effects of vegetation type and soil depth on soil microbial communities on the loess plateau of china	Cropland, natural grassland, broadleaf forest, coniferous forest	Secondary forest, secondary grassland, and cropland	China	China
105	2016	Zhang et al.	Alterations in soil microbial community composition and biomass following agricultural land use change	Woodland, planted shrubland, cropland, uncultivated land	Woodland, secondary shrubland, abandoned land, and cropland	Danjiangkou Reservoir region	China
106	2016	Mueller et al.	Land use change in the amazon rain forest favours generalist fungi	Primary forest, pasture of various age Secondary forest of various age	Primary forest, secondary forest, and pasture	Amazon rainforest, Brazil	Brazil
107	2016	Bachelot et al.	Long-lasting effects of land use history on soil fungal communities in second-growth tropical rain forests	second-growth tropical forest	Secondary forest and perennial cropland	Puerto Rico	Puerto Rico
108	2016	Fernandes et al.	Occurrence and species richness of mycorrhizal fungi in soil under different land use.	No tillage, pasture, coffee plantation Riparian forest	Primary forest, pasture, and perennial cropland	Universidade Federal de Goiás, Jataí, Brazil	Brazil
109	2016	Kerfahi et al.	Rainforest conversion to rubber plantation may not result in lower soil diversity of bacteria, fungi, and nematodes	Old growth forest rubber plantation	Primary forest and perennial cropland	Malaysia	Malaysia
110	2016	Xue et al.	Soil fungal and bacterial responses to conversion of open land to short-rotation woody biomass crops	Conversion of open land to woody plantation	Plantation forest and abandoned land	Michigan and Wisconsin, USA	USA
111	2016	Creamer et al.	Grassland to woodland transitions: dynamic response of microbial community structure and carbon use patterns	Grassland, woody cluster, grove sites	Secondary grassland and woodland	southern Texas, USA	USA
112	2016	Palta et al.	The effect of different land uses on arbuscular mycorrhizal fungi in the Northwestern Black Sea region	forest, gap in forest, and pasture	Secondary forest and pasture	Black Sea region in Turkey	Turkey
113	2016	Wakelin et al.	Soil physicochemical properties impact more strongly on bacteria and fungi than conversion of grassland to oil palm	Grassland, Oil palm plantation	Secondary grassland and perennial cropland	Oro Province, Papua New Guinea	Papua New Guinea

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114	2016	Islas et al.	Can soil properties and agricultural land use affect arbuscular mycorrhizal fungal communities indigenous from the Argentinean pampas soils?	Agriculture and near pristine	Primary forest and cropland	Buenos Aires Province, Argentina	Argentina
115	2016	Holland et al.	Evaluating the diversity of soil microbial communities in vineyards relative to adjacent native ecosystems	Native sites and vineyard	Primary forest and perennial cropland	South Central British Columbia, Canada	Canada
116	2016	Voříšková et al.	Effect of past agricultural use on the infectivity and composition of a community of arbuscular mycorrhizal fungi	abandoned field, semi natural grassland	Secondary grassland and abandoned land	northern Bohemia, Czech Republic	Czech Republic
117	2016	Terjo et al.	Disturbance and land use effect on functional diversity of the arbuscular mycorrhizal fungi	Pasture and milpa	Pasture and cropland	Biosphere Reserve Los Tuxtlas in Mexico	USA
118	2016	Oliveira et al.	Conversion of forest into irrigated pasture and changes in the chemical and biological properties of the soil	Pasture and natural vegetation	Primary forest and pasture	State of Ceará, Brazil	Brazil
119	2016	Leon et al.	Symbiont dynamics during ecosystem succession: co-occurring plant and arbuscular mycorrhizal fungal communities	Secondary grassland and primary grassland	Primary grassland and secondary grassland		Estonia
120	2016	Voříšková et al.	Effect of past agricultural use on the infectivity and composition of a community of arbuscular mycorrhizal fungi	Abandoned land and grassland	Secondary grassland and abandoned land		Czech Republic
121	2016	Liang et al.	Effect of vegetation types on soil arbuscular mycorrhizal fungi and nitrogen-fixing bacterial communities in a karst region	Grassland, shrubland, secondary forest, Primary forest	Primary forest, secondary forest, secondary shrubland and secondary grassland	Guangxi autonomous region of southwest China	China
122	2016	Henry et al.	Characterization of ectomycorrhizal communities of <i>Asteropeia mchersonii</i> seedlings spontaneously growing in natural forest and in open disturbed areas	Natural forest and disturbed forest	Primary forest and secondary forest		Madagascar
123	2016	Disyatat et al.	Community structure and dynamics of ectomycorrhizal fungi in a dipterocarp forest fragment and plantation in Thailand	Secondary forest and plantation forest	Secondary forest and plantation forest	Nan Province	Thailand
124	2017	Bainard et al.	Plant communities and soil properties mediate agricultural land use impacts on arbuscular mycorrhizal fungi in the mixed prairie ecoregion of the North American Great Plains	Annual cropland, roadside, Tame grassland Native grassland	Primary grassland, secondary grassland, and cropland	Southwestern Saskatchewan, North American Great Plains	USA
125	2017	Bhattachariya et al.	Comparative evaluation of three contrasting land use systems for soil carbon, microbial and biochemical indicators in North-Western Himalaya	Agriculture, horticulture and agroforestry	Perennial cropland and cropland	Pantnagar, India	India
126	2017	Castaneda et al.	Metagenomic analysis exploring taxonomic and functional diversity of soil microbial communities in Chilean vineyards and surrounding native forests	vineyard and surrounding forest	Secondary forest and perennial cropland		Chile
127	2017	Chmolowska et al.	Functioning grouped soil microbial communities according to ecosystem type, based on comparison of fallows and meadows in the same region	Fallow and meadows	Secondary grassland and abandoned land	Polish Western Carpathians, Poland	Poland
128	2017	He et al.	Differential responses of soil microbial community to four-decade long grazing and cultivation in a semi-arid grassland	Grazing field and wheat field	Pasture and cropland	Inner Mongolia, China	China
129	2017	Xu et al.	Land use alters arbuscular mycorrhizal fungal communities and their potential role in carbon sequestration on the Tibetan Plateau	Arable fields, grasslands and forests	Secondary forest, secondary grassland, and cropland	Nyingchi region, Tibetan Plateau	China
130	2017	French et al.	Conversion of grassland to arable decreases microbial diversity and alters community composition	grassland cropland	Secondary grassland and cropland	England	England
131	2017	Yang et al.	Links between soil fungal diversity and plant and soil properties on the loess plateau	artificial forest, natural shrub; artificial grassland, natural grassland, and slop cropland,	Secondary forest, primary shrubland, primary grassland, secondary grassland, and cropland	Loess Plateau, China	China

SN	Date	Authors	Title of the paper	Land use type considered	Land use types	Place	Country
132	2017	Xiang et al.	Changes in soil microbial community and its effect on carbon sequestration following afforestation on the loess plateau, China	Shrubland and cropland	Secondary shrubland and cropland	Ningxia autonomous region, China	China
133	2017	Honnay et al.	Plant community reassembly on restored semi-natural grasslands lags behind the assembly of the arbuscular mycorrhizal fungal communities	Restoration gradient	Primary grassland, secondary grassland, and plantation grassland	Belgium	Belgium
134	2017	Xiao et al.	Changes in microbial communities and respiration following the re-vegetation of eroded soil	Abandoned cropland and secondary grassland	Secondary grassland and abandoned land	Gansu Province, China	China
135	2017	Manoharan et al.	Agricultural management practices influence AMF diversity and community composition with cascading effects on plant productivity	farmland four different agricultural practices as well as permanent pasture grasslands	Pasture and cropland	Scania, southern Sweden	Sweden
136	2017	Xu et al.	Soil microbial community responses to long-term land use intensification in subtropical grazing lands	gradient of management intensities ranging from native rangeland, silvopasture, to improved bahiagrass pasture.	Rangeland and pasture	Florida, USA	USA
137	2017	Tian et al.	Land-use types and soil chemical properties influence soil microbial communities in the semiarid loess plateau region in China	Five land-use types representing natural and planted forests	Primary forest and plantation forest	Shaanxi Province, Central Part of Loess Plateau	China
138	2017	Zhang et al.	Impacts of conversion from secondary forests to larch plantations on the structure and function of microbial communities	70 years old forest and 40 years larch plantation	Secondary forest and plantation forest	Liaoning Province, Northeast China	China
139	2017	Ali et al.	Variation in soil physical, chemical and microbial parameters under different land uses in Bagrot valley, Gilgit, Pakistan	different land use gradient	Primary forest, pasture, and cropland	Karakoram Range, Gilgit, Pakistan	Pakistan
140	2017	Szoboszlay et al.	Impact of land-use change and soil organic carbon quality on microbial diversity in soils across Europe	Secondary forest secondary grassland cropland	Secondary forest, secondary grassland, and cropland		10 countries
141	2017	Liu et al.	Forest conversion induces seasonal variation in microbial $\beta$ -diversity	Primary forest and Plantation forest	Primary forest, plantation forest	Huitong county, Hunan province, China.	China
142	2017	Dang et al.	Effects of stand age and soil properties on soil bacterial and fungal community composition in Chinese pine plantations on the Loess Plateau	Abandoned land, Plantation forest and secondary forest	Secondary forest, plantation forest, and abandoned land		China
143	2017	Zhang et al.	Natural succession on abandoned cropland effectively decreases the soil erodibility and improves the fungal diversity	Cropland and secondary grassland	Secondary grassland and cropland		China
144	2017	Zhang et al.	Diversity of root-associated fungi of <i>Vaccinium mandarinorum</i> along a human disturbance gradient in subtropical forests, China	Primary forest, secondary forest, Plantation forest	Primary forest, secondary forest, and plantation forest		China
145	2017	Edirisinghe and Madawala	Arbuscular mycorrhizal fungal dynamics following change of land use from mature forest to Eucalyptus plantation	Mature forest and Plantation forest	Primary forest and plantation forest	Matale District	Sri-Lanka
146	2017	Birhane et al.	Changes in arbuscular mycorrhiza fungi spore density and root colonization of woody plants in response to enclosure age and slope position in the highlands of Tigray, Northern Ethiopia	Secondary grassland and pasture	Secondary grassland and pasture	Tigray region, Northern Ethiopia	Ethiopia
147	2017	Pankova et al.	Arbuscular mycorrhizal fungi and associated microbial communities from dry grassland do not improve plant growth on abandoned field soil	Secondary grassland and abandoned land	Secondary grassland, and abandoned land	Northern Bohemia	Czech Republic

SN	Date	Authors	Title of the paper	Land use type considered	Land use types	Place	Country
148	2017	Wang et al.	Conversion of rainforest into agroforestry and monoculture plantation in China: Consequences for soil phosphorus forms and microbial community	natural old growth forests, young rubber plantation, mature rubber plantation and rubber agroforestry systems	Primary forest and perennial cropland	Aisha country, Hainan province	China
149	2018	Peerawat et al.	Rubber plantation ageing controls soil biodiversity after land conversion from cassava	annual cropland and perennial cropland	Perennial cropland and cropland		Thailand
150	2018	Monkai et al.	Natural forests maintain a greater soil microbial diversity than that in rubber plantations in Southwest China	Natural forest, rubber plantation of different age	Primary forest and perennial cropland	Xishuangbanna, Yunnan Province, China	China
151	2018	Cai et al.	Land-use type strongly shapes community composition, but not always diversity of soil microbes in tropical China	Primary forest, secondary forest, plantation, perennial crops (Rubber and Plukenetia)	Primary forest, secondary forest, plantation forest, and perennial cropland	Xishuangbanna, southwest China	China
152	2018	Ren et al. 2018	Differential soil microbial community response to the linkage of soil organic carbon fractions with respiration across land-use change	Plantation, abandoned land and cropland	Plantation, abandoned land, and cropland	Ansai County, Shaanxi Province	China
153	2018	Soka and Ritchie	Arbuscular mycorrhizal spore composition and diversity associated with different land uses in a tropical savanna landscape, Tanzania	pasture and agriculture land	Pasture and cropland	Serengeti National Park (SNP), Tanzania	Tanzania
154	2018	Cerqueira et al.	Amazon basin pasture soils reveal susceptibility to phytopathogens and lower fungal community dissimilarity than forest	pasture and forest	Primary forest and pasture	Mutum-Paraná River Basin	Brazil
155	2018	Yang et al.	The influence of tree species on soil properties and microbial communities following afforestation of abandoned land in northeast China	Plantation and Abandoned land	Plantation forest and abandoned land	Baoshan district, Shuangyashan city, Heilongjiang province	China
156	2018	Hui et al.	Over twenty years farmland reforestation decreases fungal diversity of soils, but stimulates the return of ectomycorrhizal fungal communities	Forest sites and agricultural sites	Primary forest, secondary forest, and cropland	Wuying, northeast China	China
157	2018	Li et al.	Land-use change alters patterns of soil biodiversity in arid lands of northwestern China	Grassland, plantation and cropland	Primary grassland, secondary shrubland, plantation forest, and cropland	Linze County, Gansu Province, northwestern China	China
158	2018	Sepp et al.	Effect of land use on arbuscular mycorrhizal fungal communities in Estonia	semi-natural grazed dry calcareous grassland, overgrown ungrazed calcareous grassland, semi-natural wooded meadow (haymaking once per year), farmyard lawn, boreonemoral mixed forest, and clear-cut sites of boreonemoral forest	Secondary forest and secondary grassland	Lõu, Uisu, Ridala, Tagamõisa, Nedrema, Tummelka, Voorbahi, Koeru, Vapramäe, Vahuküla, Ao	Estonia
159	2018	Zhang et al.	Linking soil bacterial and fungal communities to vegetation succession following agricultural abandonment	cropland, secondary grassland, secondary shrubland, secondary forest	Secondary forest, secondary shrubland, secondary grassland cropland	South aspect of Qinling Mountains, central China	China
160	2018	McGee et al.	Determinants of Soil Bacterial and Fungal Community Composition Toward Carbon-Use Efficiency Across Primary and Secondary Forests in a Costa Rican Conservation Area	Primary forest and secondary forest	Primary forest and secondary forest		Costa Rica
161	2018	Li et al.	Soil microbial community restoration in Conservation Reserve Program semi-arid grasslands	cropland, secondary grassland, rangeland	Secondary grassland, rangeland, and cropland	West Texas, USA	USA

SN	Date	Authors	Title of the paper	Land use type considered	Land use types	Place	Country
162	2018	Zhang et al.	Interactions of soil bacteria and fungi with plants during long-term grazing exclusion in semiarid grasslands	Pasture and Secondary grassland	Secondary grassland, and pasture	Ningxia Autonomous Region of China.	China
163	2018	Stover et al.	Soil disturbance changes arbuscular mycorrhizal fungi richness and composition in a fescue grassland in Alberta Canada	Secondary grassland and Native grassland	Primary grassland and secondary grassland	Alberta, Canada	Canada
164	2018	Upton et al.	Belowground response of prairie restoration and resiliency to drought	Grassland and cropland	Secondary grassland and cropland	Boone County, Iowa	USA
165	2018	Boeraeve et al.	The impact of spatial isolation and local habitat conditions on colonization of recent forest stands by ectomycorrhizal fungi	Young forest and ancient forest	Primary forest and secondary forest	Northern Belgium	Belgium
166	2018	Guillou et al.	Tillage intensity and pasture in rotation effectively shape soil microbial communities at a landscape scale	Cropland and Pasture	Pasture and cropland	Brittany, Western France	France
167	2018	Krashevskaya et al.	Micro-decomposer communities and decomposition processes in tropical lowlands as affected by land use and litter type	Forest, palm and rubber plantation	Primary forest and perennial cropland	Jambi Province, Southeast Sumatra, Indonesia	Indonesia
168	2018	Nkuekam et al.	Arable agriculture changes soil microbial communities in the South African Grassland Biome	Agricultural land, natural grassland	Primary grassland and cropland	Mpumalanga Province	South Africa
169	2018	Yang et al.	Grazing practices affect the soil microbial community composition in a Tibetan alpine meadow	Secondary grassland and pasture	Secondary grassland and pasture	Maqu, Gansu, China	China
170	2019	Brinkmann	Intensive tropical land use massively shifts soil fungal communities	Rain forest to Plantation	Primary forest and plantation forest	Jambi Province of Sumatra, Indonesia	Indonesia
171	2019	Zheng et al.	Soil multifunctionality is affected by the soil environment and by microbial community composition and diversity	Cropland, Grassland, and forest	Secondary forest, pasture, and cropland	central Enns valley, Styria, Austria	Austria
172	2019	Wang et al.	Higher temporal turnover of soil fungi than bacteria during long-term secondary succession in a semiarid abandoned farmland	Cropland to Secondary forest (successional gradient)	Secondary forest and cropland		China
173	2019	Grau et al.	Encroachment of shrubs into subalpine grasslands in the Pyrenees modifies the structure of soil fungal communities and soil properties	Grassland to Shrubland	Secondary shrubland and secondary grassland		Spain
174	2019	Reyes et al.	Arbuscular mycorrhizal fungi along secondary forest succession at the eastern periphery of Amazonia: Seasonal variability and impacts of soil fertility	Young secondary forest to old forest	Primary forest and secondary forest		Brazil
175	2019	Zhao et al.	Dynamics of soil microbial communities following vegetation succession in a karst mountain ecosystem, Southwest China	Grassland to shrubland to secondary forest, Plantation forest and Natural forest	Primary forest, secondary forest, plantation forest, shrubland, grassland		China
176	2019	Wang et al.	Effects of grassland afforestation on structure and function of soil bacterial and fungal communities	Grassland, forest and transition zone between grassland and forest	Secondary forest and secondary grassland	Heshui County, Gansu Province, China	China
177	2019	Qiao et al.	Priming alters soil carbon dynamics during forest succession	Grassland, young forest and old-growth forest	secondary forest and secondary grassland	Yunnan Province of southwestern China	China
178	2019	Makiola et al.	Land use is a determinant of plant pathogen alpha- but not beta-diversity	Natural forest, planted forest, secondary grassland, Perennial cropland	Primary forest, plantation forest, secondary grassland, and perennial cropland		New Zealand
179	2019	Song et al.	Tropical forest conversion to rubber plantation in southwest China results in lower fungal beta diversity and reduced network complexity	Natural forest and Rubber plantation	Primary forest and perennial cropland	Xishuangbanna, Yunnan, China	China
180	2019	Ma et al.	The Variation of the Soil Bacterial and Fungal Community Is Linked to Land Use Types in Northeast China	Cropland, agro-pastoral, Plantation forest	Plantation forest, pasture, and cropland	Northeast China	China

SN	Date	Authors	Title of the paper	Land use type considered	Land use types	Place	Country
181	2019	Sui et al.	Land use change effects on diversity of soil bacterial, Acidobacterial and fungal communities in wetlands of the Sanjiang Plain, northeastern China	wetland, Forest and Cropland	Plantation forest, wetland, and cropland	Sanjiang Plain	China
182	2019	Hui et al.	Karst rocky desertification does not erode ectomycorrhizal fungal species richness but alters microbial community structure	Eroded shrubland and old forest	Primary forest and secondary shrubland	Yunnan, China	China
183	2019	Nautiyal et al.	Role of glomalin in soil carbon storage and its variation across land uses in temperate Himalayan regime	Forest, perennial cropland, and cropland	Primary forest, perennial cropland and cropland	Tehri district of Uttarakhand, India	India
184	2020	Yan et al.	Change in composition and potential functional genes of soil bacterial and fungal communities with secondary succession in <i>Quercus liaotwigensis</i> forests of the Loess Plateau, western China	Cropland to secondary forest	Secondary forest and cropland	Fuxian county	China
185	2020	Liu et al.	Changes in soil microbial community structure during long-term secondary succession	Grassland to shrubland to secondary forest	Secondary forest, secondary shrubland, and secondary grassland		China
186	2020	Sousa et al.	Dynamics of soil microbiological attributes in integrated crop-livestock systems in the cerrado-amazonia ecotone	Cropland forest and pasture with crop	Primary forest, pasture, and cropland		Brazil
187	2020	Flores-Rentería et al.	Changes in the Abundance and Composition of a Microbial Community Associated with Land Use Change in a Mexican Tropical Rain Forest	Primary forest, secondary forest, Pasture, and cropland	Primary forest, secondary forest, pasture, and cropland	Los Tuxtlas Tropical Biology Station	Mexico
188	2020	Berkelmann et al.	Unravelling the effects of tropical land use conversion on the soil microbiome	Rainforest and perennial cropland	Primary forest and Perennial cropland	the Bukit Duabelas National Park in midwest Sumatra	Indonesia
189	2020	Yang et al.	Comparison of soil microbial community between planted woodland and natural grass vegetation on the Loess Plateau	planted woodland and restored grassland	Plantation forest and Secondary grassland	Gansu province of China	China
190	2020	Liu et al.	Long-term forest succession improves plant diversity and soil quality but not significantly increase soil microbial diversity: Evidence from the Loess Plateau	Farmland, grassland, shrubland, pioneer forest, climax forest	Primary forest, secondary forest, secondary shrubland, secondary grassland, and cropland	Gansu province of China	China

**Tab. S2** – List of publications reviewed: fungal guilds, fungal parameters and method used.

SN	Authors	Fungal guild	Fungal parameters	Methods used	Methods used to assay
1	Johnson et al.	AM	Spore density; VAM infectivity	Spore analysis	Spore morphology
2	Fischer et al.	AM	Propagules density	Propagules	Spore morphology
3	Jhonsen & Wedin	AM	Spore count; richness; diversity	Spore analysis	Spore morphology
4	Turgay and Nonaka	Total	Ergosterol content	Ergosterol content	Ergosterol content
5	Helund	Total and AM	PLFA content, root colonization	PLFA, Root colonization	PLFA + Root colonization
6	McLean and Huhta	Total	Community composition, Ergosterol content	Cultural method (MEA); Ergosterol content	Anamorph morphology + Ergosterol content
7	Oehl et al.	AM	Abundance; species richness; diversity; root colonization	Spore analysis	Spore morphology + Root colonization
8	Kalmer & Hedlund	Total	Species richness; Community composition	DNA method (TRFLP)	TRFLP + Root colonization
9	Mabuhay et al.	Total	Colony forming unit	Culture method	Anamorph morphology
10	Allison et al.	Total	PLFA content	PLFA	PLFA
11	Tedersoo et al.	ECM	Diversity of ECM, community composition	ECM root tips assay, DNA method (sanger sequencing)	Mt + sequencing
12	van der Wal	Total	PLFA content	PLFA	PLFA
13	Diaz et al.	EM	Root colonization	Root colonization	Root colonization
14	Bedini et al.	AM	Community composition; GRSP content	Spore analysis, Glomalin protein	Spore morphology + GRSP
15	Li et al.	AM	Root colonization; Spores density	Root colonization, Spore analysis	Spore morphology + Root colonization
16	Perger et al.	AM	GRSP content	Glomalin protein	GRSP
17	Li et al.	AM	Spore density, Species richness, community composition	Spore analysis	Spore morphology
18	Dong et al.	Total	Diversity; PLFA content	DNA method (DGGE), PLFA	DGGE + PLFA
19	van Ekeren et al.	Total	PLFA content, % of hyphal length	PLFA, Fungal hyphal count	PLFA
20	Guadarrama et al.	AM	Root colonization; Total mycelium length; Infective propagules	Root colonization, Extraradical mycelium, Spore and propagules analysis	Spore morphology + Root colonization
21	Guo and Han	AM	Spore density; Mycorrhizal infection	Root colonization, Spore analysis	Spore morphology + Root colonization
22	Hamer et al.	Total	PLFA content	PLFA	PLFA
23	Kasel et al.	Total	Community composition	DNA method (TRFLP)	TRFLP
24	Lauber et al.	Total	Abundance (qPCR)	DNA method (qPCR and sanger sequencing)	qPCR + Sanger sequencing
25	Rahman et al.	Total	Community composition	PLFA ; DNA method (DGGE)	PLFA + DGGE
26	Violi et al.	AM	AMF richness; AMF sporulation; GRSP content	Spore analysis; Glomalin protein	Spore morphology + GRSP
27	Hamer et al.	Total	PLFA content	PLFA	PLFA
28	Bakhshipour et al.	AM	Spore density; root colonization	Spore analysis	Spore morphology + Root colonization
29	Guo et al.	AM	Spore density	Spore analysis	Spore morphology + Root colonization
30	Hamer et al.	Total	community profile (fungi)	PLFA	PLFA + DGGE
31	Hamer and Makeschin	Total	PLFA content	PLFA	PLFA
32	Leal et al.	AM	Spore abundance; Spore density	Trap culture, spore analysis	Spore morphology
33	Jefwa et al.	AM	Richness, diversity	Trap culture, spore analysis	Spore morphology
34	Zornoza et al.	Total	PLFA content	PLFA	PLFA
35	Carson et al.	Total	Community composition	DNA method (ARISA)	ARISA
36	Drenovsky et al.	Total	PLFA content	PLFA	PLFA
37	Lumini et al.	AM	OTUs richness; diversity; community composition	DNA method (Pyrosequencing)	NGS
38	Oehl et al.	AM	Spore density; community composition; root colonization	Trap culture and spore analysis	Spore morphology + Root colonization

SN	Authors	Fungal guild	Fungal parameters	Methods used	Methods used to assay
39	Snoeck et al.	AM	Spore density; diversity	Spore analysis	Spore morphology
40	Verbruggen et al.	AM	Root colonization; richness; community composition	DNA method (TRFLP)	TRFLP + Root colonization
41	Postma-Blaauw et al.	Total	Abundance	Microscopy	Anamorph morphology
42	Banning et al.	Total	PLFA content	PLFA	PLFA
43	Gast et al.	AM	Root colonization; richness (TRF richness); community composition	DNA method (TRFLP)	TRFLP + Root colonization
44	Sturmer et al.	AM	Richness; diversity; abundance; community composition	Spore analysis	Spore morphology
45	Grantina et al.	Total	Diversity; Abundance (qPCR); colony forming unit	culture method, DNA method (qPCR)	Anamorph morphology + qPCR
46	Covacevich and Berbara	AM	Spore density; root colonization	Spore analysis	Spore morphology + Root colonization
47	Mehring et al.	Total	PLFA content	PLFA	PLFA
48	Costa et al.	Total	Richness, diversity, Equitability; Dominance, community composition	Culture method, DNA method (DGGE)	Anamorph morphology + DGGE
49	Fokom et al.	AM	Spore density; GRSP content	Spore, Glomalin protein	Spore morphology + GRSP
50	G'Cortes et al.	AM	Species richness; Community composition	Spore analysis	Spore morphology
51	Hryniewicz et al.	ECM	Root colonization; Community composition	Morphotyping, DNA method (sanger sequencing)	Mt+ sequencing + Root colonization
52	Jefwa et al.	AM	Richness; diversity; abundance; community composition	Spore morphology	Spore morphology
53	Munchane et al.	AM	Species richness, community composition; Spore density, Diversity; Inoculum potential	Spore morphology	Spore morphology
54	Orgiazzi et al.	Total	Community composition	DNA method (Pyrosequencing)	NGS
55	Potthast et al.	Total	PLFA content	PLFA	PLFA
56	Sene et al.	AM	Propagules number; root colonization	Trap culture, spore analysis	Spore morphology + Root colonization
57	Yurkov et al.	Yeast	Diversity; community composition	DNA method (Sanger sequencing)	Sequencing
58	Zangaro et al.	AM	Spore density; root colonization; Frequency of occurrence of AM taxa	Spore analysis, root analysis	Spore morphology
59	Yamashita et al.	Total	Community composition	Fruitbodies	Sporocarps
60	Bonfim et al.	AM	Spore density; diversity	Spore analysis, Glomalin protein	Spore morphology + GRSP
61	Dai et al.	AM	Richness; diversity; community composition	Culture method, DNA method (Sanger sequencing)	Sequencing
62	Dinesh and Chaudhuri	Total	Ergosterol content	Ergosterol content	Ergosterol content
63	Fracetto et al.	Total	Community composition, richness, diversity	DNA method (DGGE)	DGGE
64	Hazard et al.	AM	Community composition	DNA method (TRFLP)	TRFLP
65	Leal et al.	AM	Spore abundance; frequency occurrence	Spore analysis	Spore morphology
66	Li et al.	Total	Diversity, abundance, community composition	DNA method (qPCR and TRFLP)	qPCR + TRFLP
67	Sousa et al.	AM	Spore density, root colonization, Infective propagules number, GRSP content	Spore analysis, Glomalin protein, root colonization	Spore morphology + GRSP + Root colonization
68	Ying et al.	Total	Abundance, PLFA content, qPCR	DNA method (TRFLP), PLFA, qPCR	TRFLP + PLFA + qPCR
69	Lupatini et al.	Total	OUT richness; community composition	DNA method (RISA)	ARISA
70	Yu et al.	Total	Richness; diversity; community composition	DNA method (DGGE and Sequencing)	DGGE + Sequencing
71	Fichtner et al.	Total	PLFA content	PLFA	PLFA
72	Gherghel et al.	ECM and AM	Richness; diversity; root colonization	Morphotyping, DNA method (RFLP + sanger sequencing)	Mt+ RFLP+ Sequencing
73	Jansa et al.	AM	Community composition, abundance (qPCR)	DNA method (qPCR)	qPCR
74	Lisboa et al.	Total and AM	PLFA content	PLFA	PLFA

SN	Authors	Fungal guild	Fungal parameters	Methods used	Methods used to assay
75	Melo et al.	AM	Diversity, richness, community composition and spore density	Spore analysis	Spore morphology
76	Moora et al.	AM	Community composition, Phylogenetic diversity	DNA method (Pyrosequencing)	NGS
77	Pereira et al.	AM	Community composition, Diversity	Spore analysis	Spore morphology
78	Sharmah and Jha	AM	Community composition, Frequency and relative abundance, Spore density	Spore analysis	Spore morphology
79	Smith et al.	Total	PLFA content	PLFA	PLFA
80	Wang et al.	AM	Root colonization and extra-radical hyphal length density, Spore density, species richness, diversity	Root colonization, spore analysis, Glomalin protein	Spore morphology + GRSP + Root colonization
81	Kerfahi et al.	Total	Diversity, Community composition, Relative abundance	DNA method (Pyrosequencing)	NGS
82	Xiang et al.	AM	Hyphal length density, Root colonization, Richness	Root colonization, DNA method (Pyrosequencing)	Root colonization + NGS
83	Glinka et al.	Total	Hyphal abundance, Fungal richness and community composition	DNA method (TRFLP)	TRFLP
84	Lagerlof et al.	Total	PLFA content	PLFA	PLFA
85	Bainard et al.	AM	community composition	DNA method (sequencing)	Sequencing
86	Bordoloi et al.	AM	Diversity, community composition	Spore analysis	Spore morphology
87	Castaneda et al.	Total	community composition	DNA method (T-RFLP)	TRFLP
88	Ciccolini et al.	Total and AM	phylogenetic diversity, abundance, community composition	DNA method (Sanger sequencing)	Sequencing
89	Furrazola et al.	AM	Root colonization, Extraradical mycelial biomass, spore density	Root colonization, Extraradical AMF mycelial biomass, spore analysis	Spore morphology + Root colonization
90	Ma et al.	Total	PLFA content	PLFA	PLFA
91	McGuire et al.	Total	Abundance, community composition	DNA method (Illumina Miseq)	NGS
92	Tardy et al.	Total	Diversity, community composition	DNA method (Pyrosequencing)	NGS
93	Thomson et al.	Total	Community composition	DNA method (T-RFLP)	TRFLP
94	Valyi et al.	AM	Community composition; dominance structure, nestedness, indicator species analysis	DNA method	TRFLP
95	Wang et al.	AM	GRSP content	Glomalin protein	GRSP
96	Wong et al.	Total	PLFA content	PLFA	PLFA
97	Smith et al.	Saprophytic, ECM and AM	PLFA content	PLFA	PLFA
98	Pellegrino et al.	AM	colonization, diversity, community composition	Root analysis, DNA method (Sanger sequencing)	Root colonization + Sequencing
99	Song et al.	Total	PLFA content	PLFA	PLFA
100	Tardy et al.	Total	Richness, Diversity and community composition	DNA method (Pyrosequencing)	NGS
101	Aldezabal et al.	Total	Diversity	DGGE method	DGGE
102	Smith et al.	Total	PLFA content	PLFA	PLFA
103	Krashevskaya et al.	Total	PLFA content	PLFA	PLFA
104	Xiao et al.	Total	Community composition, PLFA content	DNA method (DGGE), PLFA	DGGE + PLFA
105	Zhang et al.	Total	PLFA content	PLFA	PLFA
106	Mueller et al.	Total	Diversity and community composition; niche breadth	DNA method (Illumina Miseq)	NGS
107	Bachelot et al.	Total	community composition; diversity (evenness)	DNA method (Illumina Miseq)	NGS
108	Fernandes et al.	AM	Spore density; diversity, frequency and richness	Spore analysis	Spore morphology
109	Kerfahi et al.	Total	Abundance; Diversity; Community composition	DNA method (Illumina Miseq)	NGS
110	Xue et al.	AM	Community composition	DNA method (Pyrosequencing)	NGS

SN	Authors	Fungal guild	Fungal parameters	Methods used	Methods used to assay
111	Creamer et al.	Total	PLFA content	PLFA	PLFA
112	Palta et al.	AM	Root colonization	Root colonization, Spore analysis	Root colonization + Spore morphology
113	Wakelin et al.	Total	Community composition	DNA method (TRFLP)	TRFLP
114	Islas et al.	AM	Diversity, Community composition	Spore analysis, DNA method (DGGE)	DGGE
115	Holland et al.	Total	Community composition	DNA method (Pyrosequencing)	NGS
116	Voříšková et al.	AM	Root colonization, infectivity, richness, community composition	DNA method (TRFLP)	TRFLP
117	Terjo et al.	AM	Abundance, Spore viability, root colonization and capacity to infect, Mycorrhizal infective potential (MIP)	AMF spore abundance, Capacity to infect Colonization on trap plants Mycorrhizal infective potential	Spore morphology
118	Oliveira et al.	AM	Spore density	Spore analysis	Spore morphology
119	Leon et al.	AM	VT richness, Community composition	DNA method (Pyrosequencing)	NGS
120	Voříšková et al.	AM	Root colonization, AM infectivity, richness, community composition	DNA method (TRFLP)	TRFLP
121	Liang et al.	AM	Log copies number Relative abundance	DNA method (TRFLP)	TRFLP
122	Henry et al.	ECM	Abundance, community composition	Morphotypes (Sanger sequencing)	Mt + Sequencing
123	Disyatat et al.	ECM	Abundance, Community composition and richness	Fruitbodies assay and root tip assay	Sporocarps + Mt
124	Bainard et al.	AM	AM fungal communities Abundance of particular fungal genera	DNA method (Pyrosequencing)	NGS
125	Bhattachariya et al.	AM	GRSP content	Glomalin protein	GRSP
126	Castaneda et al.	Total	Abundances Diversity indices	DNA method (Pyrosequencing)	NGS
127	Chmolewska et al.	Total and AM	PLFA content, root colonization	PLFA, root analysis	PLFA + Root colonization
128	He et al.	Total	Colony forming unit	Culture method	Anamorph morphology
129	Xu et al.	AM	Diversity and abundance, community composition	DNA method (Pyrosequencing)	NGS
130	French et al.	Total	Richness, community composition	DNA method (Illumina Miseq)	NGS
131	Yang et al.	Total	Diversity, community composition	DNA method (Illumina Miseq)	NGS
132	Xiang et al.	Total	PLFA content	PLFA	PLFA
133	Honnay et al.	AM	Richness, diversity, community composition	Spore analysis	Root colonization
134	Xiao et al.	Total	Diversity, abundance (qPCR), community composition	DNA method (qPCR and Illumina Miseq)	qPCR + NGS
135	Manoharan et al.	AM	Diversity, community composition	DNA method (Pyrosequencing)	NGS
136	Xu et al.	Total	PLFA content	PLFA	PLFA
137	Tian et al.	Total	Abundance, community composition	DNA method (Ion torrent)	NGS
138	Zhang et al.	Total	Community composition	DNA method (Illumina Miseq)	NGS
139	Ali et al.	Total	ITS copy number	DNA method (qPCR)	qPCR
140	Szoboszlay et al.	Total	ITS copy number	DNA method (qPCR and Pyrosequencing)	qPCR + NGS
141	Liu et al.	Total	Abundance, community composition	DNA method (Illumina Miseq)	NGS
142	Dang et al.	Total	Diversity, relative abundance, Community composition	DNA method (Illumina Miseq)	NGS
143	Zhang et al.	Total, AM, ECM and saprophytic	Diversity, relative abundance, community composition	DNA method (Illumina Miseq)	NGS
144	Zhang et al.	EM	Richness, relative abundance, Community composition	DNA method (Illumina Miseq)	NGS
145	Edirisinghe and Madawala	AM	Richness, spore density	Spore analysis	Spore morphology

SN	Authors	Fungal guild	Fungal parameters	Methods used	Methods used to assay
146	Birhane et al.	AM	Root colonization, spore density	Spore analysis, root colonization	Spore morphology + Root colonization
147	Pankova et al.	AM	Extraradial mycelium, root colonization, community composition	Soil analysis, root analysis, DNA method (TRFLP)	TRFLP + Root colonization + Spore morphology
148	Wang et al.	Total	PLFA content	PLFA	PLFA
149	Peerawat et al.	Total	Abundance, community composition	DNA method (Pyrosequencing)	NGS
150	Monkai et al.	Total	PLFA content	PLFA	PLFA
151	Cai et al.	Total	Richness, diversity, community composition	DNA method (Illumina Miseq)	NGS
152	Ren et al. 2018	Total	Diversity, abundance, community composition	DNA method (Illumina Miseq)	NGS
153	Soka and Ritchie	AM	Diversity, spore density	Spore analysis	Spore morphology
154	Cerqueira et al.	Total	Diversity, richness, community composition	DNA method (Illumina Miseq)	NGS
155	Yang et al.	Total	PLFA content	PLFA	PLFA
156	Hui et al.	Total	Diversity, richness, abundance, community composition	DNA method (Illumina Miseq)	NGS + qPCR
157	Li et al.	Total	Richness, diversity, community composition	DNA method (Illumina Miseq)	NGS
158	Sepp et al.	AM	Richness, community composition	DNA method (Pyrosequencing)	NGS
159	Zhang et al.	Total	Diversity, community composition	DNA method (Illumina Miseq)	NGS
160	McGee et al.	Total	Relative abundance, community composition	DNA method (Illumina Miseq)	NGS
161	Li et al.	Total and AM	Abundance	PLFA	PLFA
162	Zhange et al.	Total	Richness, diversity, relative abundance, community composition	DNA method (Illumina Miseq)	NGS
163	Stover et al.	AM	Richness, diversity, community composition	DNA method (Pyrosequencing)	NGS
164	Upton et al.	Total	Richness, diversity, community composition	DNA method (Illumina Miseq)	NGS
165	Boeraeve et al.	ECM	Richness, diversity, relative abundance, community composition	DNA method (Illumina Miseq)	NGS
166	Guillou et al.	Total	Richness, diversity	DNA method (Pyrosequencing)	NGS
167	Krashevska et al.	Total	PLFA content	PLFA	PLFA
168	Nkuekam et al.	Total	Richness, diversity, relative abundance	DNA method (Illumina Miseq)	NGS
169	Yang et al.	Total	Richness, diversity, community composition	DNA method (Illumina Miseq)	NGS
170	Brinkmann	Total	Richness, diversity, Community composition, indicator species	DNA method (Pyrosequencing)	NGS
171	Zheng et al.	Total	Relative abundance, community composition	DNA method (Illumina Miseq)	NGS
172	Wang et al.	Total	Abundance, community composition	DNA method (Illumina Miseq)	NGS
173	Grau et al.	Total and AM	Richness, community composition	DNA method (Ion torrent)	NGS
174	Reyes et al.	AM	Glomalin content, Spore density	Glomalin protein, Spore analysis	Spore morphology + GRSP
175	Zhao et al.	Total	PLFA content	PLFA	PLFA
176	Wang et al.	Total	Richness, diversity, relative abundance of trophic group, community composition	DNA method (Illumina Miseq)	NGS
177	Qiao et al.	Total	PLFA content	PLFA	PLFA
178	Makiola et al.	Pathogenic	Diversity, community composition	DNA method (Illumina Miseq)	NGS
179	Song et al.	Total	Relative abundance, diversity, community composition	DNA method (Illumina Miseq)	NGS
180	Ma et al.	Total	Relative abundance, community composition	DNA method (Illumina Miseq)	NGS
181	Sui et al.	Total	Richness, diversity, community composition	DNA method (Illumina Miseq)	NGS
182	Hui et al.	Total and ECM	richness, diversity, community composition	DNA method (Illumina Miseq)	NGS
183	Nautiyal et al.	AM	Glomalin content	Glomalin protein	GRSP

<b>SN</b>	<b>Authors</b>	<b>Fungal guild</b>	<b>Fungal parameters</b>	<b>Methods used</b>	<b>Methods used to assay</b>
184	Yan et al.	Total	Diversity, community composition	DNA method (Illumina Miseq)	NGS
185	Liu et al.	Total	Diversity, relative abundance, community composition ITS copy number	PLFA, DNA method (qPCR and Illumina Miseq)	PLFA + qPCR + NGS
186	Sousa et al.	Total	Colony forming unit	Culture method	NA
187	Flores-Rentería et al.	Total	PLFA content	PLFA	PLFA
188	Berkelmann et al.	Total	Diversity, relative abundance, community composition	DNA method (Illumina Miseq)	NGS
189	Yang et al.	Total	Relative abundance, diversity	DNA method (Illumina Miseq)	NGS
190	Liu et al.	Total	Richness, diversity, relative abundance, community composition	DNA method (Illumina Miseq)	NGS

**Tab. S3** - List of publications reviewed: parameters analyzed. (I): increase; (D): decrease; (V): varying; (ND): no difference; (SC): significant change.

SN	Authors	Species / OTUs richness	Diversity	Abundance	Community composition	Root colonization	Spore density	Infective propagule number	PLFA content	Soil ergosterol content	Gene copy number	Glomalin related proteins	% hyphal length	Colony forming unit
1	Johnson et al.						V	V						
2	Fischer et al.					V								
3	Jhonsen & Wedin	ND	ND				ND							
4	Turgay and Nonaka								D					
5	Helund								D					
6	McLean and Huhta				SC					D				
7	Oehl et al.	D	D	D		D								
8	Kalmer & Hedlund	V			SC									
9	Mabuhay et al.													D
10	Allison et al.								D					
11	Tedersoo et al.	D			SC									
12	van der Wal								D					
13	Diaz et al.					D								
14	Bedini et al.						V					D		
15	Li et al.					V	I							
16	Perger et al.											D		
17	Li et al.	I	I		SC		V							
18	Dong et al.								V					
19	van Ekeren et al.								ND				ND	
20	Guadarrama et al.					V	V	V						
21	Guo and Han						D	D						
22	Hamer et al.								V					
23	Kasel et al.				SC									
24	Lauber et al.				SC						D			
25	Rahman et al.								D					
26	Violi et al.	V					D					D		
27	Hamer et al.								V					
28	Bakhshipour et al.					D	D							
29	Guo et al.						D							
30	Hamer et al.								I					
31	Hamer & Makeschin							V						
32	Leal et al.			V			V							
33	Jefwa et al.			V		V								
34	Zornoza et al.								D					
35	Carson et al.				SC									
36	Drenovsky et al.								V					
37	Lumini et al.	V		V	SC									

SN	Authors	Species / OTUs richness	Diversity	Abundance	Community composition	Root colonization	Spore density	Infective propagule number	PLFA content	Soil ergosterol content	Gene copy number	Glomalin related proteins	% hyphal length	Colony forming unit
38	Oehl et al.	V	D		SC	ND	I							
39	Snoeck et al.		D				D							
40	Verbruggen et al.	D			SC	D								
41	Postma-Blaauw et al.											D		
42	Banning et al.								D					
43	Gast et al.	V			SC	V								
44	Sturmer et al.	D	V	V			V							
45	Grantina et al.		V								D			V
46	Covacevich and Berbara				ND	I								
47	Mehring et al.								D					
48	Costa et al.	D	D		SC									
49	Fokom et al.						D					D		
50	G'Cortes et al.	D			SC									
51	Hryniewicz et al.				SC	D								
52	Jefwa et al.	V	V		V		D							
53	Munchane et al.	I	I			V	I	I						
54	Orgiazzi et al.	D			SC									
55	Potthast et al.								ND					
56	Sene et al.	I	I					D						
57	Yurkov et al.	I	D		SC									I
58	Zangaro et al.					D	I							
59	Yamashita et al.				SC									
60	Bonfim et al.		V	V	SC		ND							
61	Dai et al.	V	V	V	SC									
62	Dinesh and Chaudhuri								D					
63	Fracetto et al.	D	D		SC									
64	Hazard et al.	V			ND									
65	Leal et al.	ND	ND		SC		I							
66	Li et al.	ND	ND		SC						V			
67	Sousa et al.					ND	ND					V		
68	Ying et al.				SC				I		ND			
69	Lupatini et al.	V			SC									
70	Yu et al.	V	V		SC									
71	Fichtner et al.								V					
72	Gherghel et al.	V	V			V								
73	Jansa et al.			V	SC						D			
74	Lisboa et al.								SC					

SN	Authors	Species / OTUs richness	Diversity	Abundance	Community composition	Root colonization	Spore density	Infective propagule number	PLFA content	Soil ergosterol content	Gene copy number	Glomalin related proteins	% hyphal length	Colony forming unit
75	Melo et al.	ND	ND		SC		ND							
76	Moora et al.	V			SC									
77	Pereira et al.		V		SC									
78	Sharmah and Jha			V	SC		D							
79	Smith et al.								I					
80	Wang et al.	V	V			V	D					D	D	
81	Kerfahi et al.	D		D	SC									
82	Xiang et al.	D	D			I							D	
83	Glinka et al.	V			SC								V	
84	Lagerlof et al.								ND					
85	Bainard et al.				SC									
86	Bordoloi et al.	V	D											
87	Castaneda et al.	ND	ND	V	ND									
88	Ciccolini et al.			ND	SC									
89	Furrazola et al.					D								
90	Ma et al.								D					
91	McGuire et al.	D	ND	D										
92	Tardy et al.	I	ND		SC									
93	Thomson et al.	ND			ND									
94	Valyi et al.				SC									
95	Wang et al.											V		
96	Wong et al.								V					
97	Smith et al.								I					
98	Pellegrino et al.	I	I		SC	D								
99	Song et al.								V					
100	Tardy et al.	ND			SC									
101	Aldezabal et al.		ND											
102	Smith et al.								V					
103	Krashevskaya et al.								V					
104	Xiao et al.				SC									
105	Zhange et al.								D					
106	Mueller et al.	V		V	SC									
107	Bachelot et al.	D	D		SC									
108	Fernandes et al.	D	D			D	D							
109	Kerfahi et al.	D	D	V										
110	Xue et al.	V	V											
111	Creamer et al.								D					
112	Palta et al.					I								
113	Wakelin et al.				ND									
114	Islas et al.		D		SC	I	D					D		

SN	Authors	Species / OTUs richness	Diversity	Abundance	Community composition	Root colonization	Spore density	Infective propagule number	PLFA content	Soil ergosterol content	Gene copy number	Glomalin related proteins	% hyphal length	Colony forming unit
115	Holland et al.		ND	V	SC									
116	Voříšková et al.	V			SC			I						
117	Terjo et al.					D	D	I						
118	Oliveira et al.						V							
119	Leon et al.	D			SC									
120	Voříšková et al.	I			SC	D		D						
121	Liang et al.			V	SC						D			
122	Henry et al.			V										
123	Disyatat et al.	D				D								
124	Bainard et al.	D	D		SC									
125	Bhattachariya et al.										V			
126	Castaneda et al.		D											
127	Chmolowska et al.					D			D					
128	He et al.													ND
129	Xu et al.	V	V	V	SC							V		
130	French et al.	D		V										
131	Yang et al.	D			SC									
132	Xiang et al.								V					
133	Honnay et al.	D	D		SC									
134	Xiao et al.		D	ND	SC						I			
135	Manoharan et al.		D	V	SC									
136	Xu et al.								V					
137	Tian et al.		ND	V	SC									
138	Zhang et al.			ND	SC									
139	Ali et al.										D			
140	Szoboszlay et al.										D			
141	Liu et al.			D	SC									
142	Dang et al.		V	V	SC									
143	Zhang et al.	V	V	V	SC									
144	Zhang et al.	D		V	SC									
145	Edirisinghe and Madawala	ND	D			D	D							
146	Birhane et al.						D							
147	Pankova et al.				SC	I								
148	Wang et al.								V					
149	Peerawat et al.			V	SC				D					
150	Monkai et al.								D					
151	Cai et al.	Varying	V		SC									
152	Ren et al. 2018		ND	ND	SC									
153	Soka and Ritchie		V				V							

SN	Authors	Species / OTUs richness	Diversity	Abundance	Community composition	Root colonization	Spore density	Infective propagule number	PLFA content	Soil ergosterol content	Gene copy number	Glomalin related proteins	% hyphal length	Colony forming unit
154	Cerqueira et al.	I	I	V	SC									
155	Yang et al.								D					
156	Hui et al.	V	I	D	SC						D			
157	Li et al.	I			SC									
158	Sepp et al.	ND			SC									
159	Zhang et al.	V	V	V	SC									
160	McGee et al.			V	SC									
161	Li et al.								D					
162	Zhange et al.	I	I	V	SC									
163	Stover et al.	D	I		SC									
164	Upton et al.	D	D		SC									
165	Boeraeve et al.	D		V	SC									
166	Guillou et al.	D	D											
167	Krashevskaya et al.								V					
168	Nkuekam et al.	D	D											
169	Yang et al.	I		V	SC									
170	Brinkmann	V	V	V	SC									
171	Zheng et al.			V	SC									
172	Wang et al.			V	SC									
173	Grau et al.	V			SC									
174	Reyes et al.						V					ND		
175	Zhao et al.								V					
176	Wang et al.	V	V	V	SC									
177	Qiao et al.								V					
178	Makiola et al.	I			SC									
179	Song et al.	D	ND	V	SC									
180	Ma et al.			V	SC									
181	Sui et al.	V	ND	V	SC									
182	Hui et al.	ND	ND		SC									
183	Nautiyal et al.											D		
184	Yan et al.		D		SC									
185	Liu et al.	V	V	V	SC						D			
186	Sousa et al.													V
187	Flores-Rentería et al.							D						
188	Berkelmann et al.		I	V	SC									
189	Yang et al.	D	D											
190	Liu et al.	V	V		SC									

**Tab. S4** - List of publications reviewed: geographic and environmental variables.

SN	Authors	Latitude	Longitude	Altitude	Soil type	Climate	Precipitation	Temperature
1	Johnson et al.							
2	Fischer et al.	10°26'N	83°59'E				4000 mm	24 °C
3	Jhonson & Wedin	10°30' N	85°21' W		Tropepts	Tropical	1000 to 2200 mm	33 to 38 °C
4	Turgay and Nonaka	37.50469° N	138.8654° E	3 m			40 and 278 mm	18.1 and 9.1°C
5	Helund	55° 45' N	13° 15' E					
6	McLean and Huhta							
7	Oehl et al.				Calcaric Regosols. Haplic Luvisols Haplic Alisol Rendzic Leptosol	Temperate	650 to 850 mm	9.5°C
8	Kalmer & Hedlund							
9	Mabuhay et al.					Warm-temperate monsoon		
10	Allison et al.							
11	Tedersoo et al.	58° 27' N	22° 00' E		Entisol and classified as Fluvent soil.	Sub-Mediterranean	930 mm	15°C
12	van der Wal							
13	Diaz et al.	50°42'N	2°12'W					
14	Bedini et al.							
15	Li et al.	25° 23' to 26° 06' N	101° 35' to 102° 06' E					
16	Perger et al.			1350 and 1800 m				
17	Li et al.	25°23'–26°06'N	101°35'–102°06'E				629 mm	21.9°C
18	Dong et al.	30° 11' N	120° 05' E			Subtropical wet monsoon climate	1500 mm	16°C
19	van Ekeren et al.	50° 59' N	03° 49' E					
20	Guadarrama et al.	16° 39' N	95° 00' W		lithosols		1000 mm	25°C
21	Guo and Han					Continental climate		
22	Hamer et al.				Cambisol		550 mm and 600 mm	– 8.4°C and 9.8°C
23	Kasel et al.	37° 90' S	145o 80' E	400 m to 420 m				
24	Lauber et al.	34.5°N	82° W		Kaolinitic		1250 mm	15.9°C
25	Rahman et al.	39.7°N	141.16°E	135 m	Andisol		1052 mm	14.7 °C
26	Violi et al.							
27	Hamer et al.							
28	Bakhshipour et al.	37° 08' N to 37o 12' N	50° 02' E				1850 mm	18°C
29	Guo et al.	41° 52' N	115° 50' E	1353 m	sandy Calciustoll (Kastanozems)		426 mm	16°C
30	Hamer et al.							
31	Hamer and Makeschin				Cambisol			
32	Leal et al.	4° 21' and 4° 26' S	69° 36' and 70° 1' W			Tropical humid and super humid	2562 mm	25.7°C
33	Jefwa et al.							

SN	Authors	Latitude	Longitude	Altitude	Soil type	Climate	Precipitation	Temperature
34	Zornoza et al.							
35	Carson et al.	33° 52' S	121° 53' E		arenosol	Mediterranean	619 mm	12°C to 21.8°C
36	Drenovsky et al.							
37	Lumini et al.	40° 30' 13.37" N	9° 47' 00.56" E	275 m to 300 m	Hyromorphic and Granitic soil with a loamy sand texture	Mesomediterranean subhumid phytoclimatic	862 mm	13.8°C
38	Oehl et al.				Cambisol, Leptosols,	Temperate	700 – 1000 mm	8.0 – 9.5°C
39	Snoeck et al.	2.1° – 5.8° N	10.5° – 16.2° E	600 – 800 m	unsaturated, ferrallitic, clayey-sandy	hot and humid	1542 mm	25°C
40	Verbruggen et al.							
41	Postma-Blaauw et al.	51° 59' N	5° 40' E					
42	Banning et al.	121° 31' 0' N	36° 12' 30' W			Mediterranean	540 mm	5.5 °C in summer and 13.0 °C in winter
43	Gast et al.							
44	Sturmer et al.	4° 21' to 4° 26' S	69° 36' to 70° 1' W		Inceptisols		2562 mm	25.7°C
45	Grantina et al.							
46	Covacevich and Berbara	43° 97' 02'' S	14° 64' 09'' W				660 mm	18 °C
47	Mehring et al.	23° 39' S–23° 47' S	46° 55' W–47° 6' W	800–1,000 m	Ferralsol		1,700 mm	15°C
48	Costa et al.						1700 mm	
49	Fokom et al.	3° 25" N	11° 44" E	227 m	ferrallitic classified mainly as typic kandiuult soil		1500 mm	24.5°C
50	G'Cortes et al.				humic andosols		1000 – 1200 mm	> 15°C
51	Hryniewicz et al.	59° 49' N	17° 40' E					
52	Jefwa et al.	2° 15' and 2° 30' S	38° 15' and 38° 30' E	1500 m	Humic Nitisols		440 mm at plains to 1900 mm	14°C and 19.5°C
53	Munchane et al.							
54	Orgiazzi et al.	40° 30' 13.3" N	9° 47' 00.56" E	275 to 300 m	Leptic Cambisols	Meso-mediterranean, subhumid phytoclimatic belt	862 mm	13.8°C
55	Potthast et al.	3° 58' S	79° 04' W	1890 m	Cambisol		2176 mm	15.3°C
56	Sene et al.						400 to 700 mm	
57	Yurkov et al.							
58	Zangaro et al.	23° 27' S	51° 15' W		Rhodic Ferralsol	Cfa-mesothermic, with hot summers, an undefined dry season	1,600 mm	21 °C
59	Yamashita et al.	36° 50'–57' N	140° 32'–37' E	580–820 m			1910 mm	10.7 °C
60	Bonfim et al.							
61	Dai et al.				podzol			
62	Dinesh and Chaudhuri	10° 30' – 13° 42' N	92° 14' – 94° 16' E		Entisols			
63	Fracetto et al.	4° 20' and 4° 26' S	69° 36' and 70° 2' W				2562 mm	25.7°C
64	Hazard et al.							
65	Leal et al.							
66	Li et al.	37° 45' – 37° 59' N	111° 21' – 111° 37' E					
67	Sousa et al.	7° 12' 23" S	36° 49' 25" W	520 m	Fluvent		558 mm	26°C

SN	Authors	Latitude	Longitude	Altitude	Soil type	Climate	Precipitation	Temperature
68	Ying et al.	28° 55' N	111° 26' E					
69	Lupatini et al.							
70	Yu et al.	35°03'–36°37' N	108°10'–109°18' E	1211–1453 m	calcareous cinnamon soil		587.6 mm	7.4°C
71	Fichtner et al.	53° 15' N	9° 58' E	70 – 150 m	Podzols	Humid suboceanic climate	811 mm	8.4°C
72	Gherghel et al.							
73	Jansa et al.							
74	Lisboa et al.							
75	Melo et al.							17.5°C
76	Moora et al.				Gleyic luvisol			
77	Pereira et al.	07° 38' 20" S	034° 57' 10" W			Ams' type-rainy tropical monsoon with dry summer	2000 mm	24°C
78	Sharmah and Jha	25° 45' and 26° 35' N	92° 45' and 93° 54' E	232 m	sandy loam	Sub-tropical monsoonal climate	1235 mm	
79	Smith et al.	18° 01' N	66° 05' W		Kaolinitic, isothermic Humic Hapludox in the Los Guineos soil series		2000 mm	21.5°C
80	Wang et al.	43° 55' N	116° 31' E	1201 m	Calcic Chernozems		350 mm	– 0.4°C
81	Kerfahi et al.	4° 58' N	117° 48' E					
82	Xiang et al.							
83	Glinka et al.	27° 11' N	81° 21' W				1324 ± 29.59 mm	
84	Lagerlof et al.	1° 04' N	34° 04' E	1900 m	Reddish sandy clay loams developed from basalt and ashes and rich in organic matter		1300 mm	18 °C
85	Bainard et al.	51 and 56° N	106 and 110° W		Chernozem order and the Vertisol order			
86	Bordoloi et al.	26° 55' N – 28° 40' N	92° 40' E – 94° 21' E			Humid tropical climate	1100 to 1600 mm	12 to 37°C
87	Castaneda et al.							
88	Ciccolini et al.	43° 49' N	10° 19' E		Histosol	Mediterranean		
89	Furrazola et al.							
90	Ma et al.	43° 12' – 44° 36' N	114° 34' – 124° 18' E			Continental monsoon climate	237 to 472 mm	1.3° to 6.8°C
91	McGuire et al.	2° 5' N	102° 18' W	80 m		aseasonal	1788 mm	22.7°C and 33.2°C
92	Tardy et al.							
93	Thomson et al.							
94	Valyi et al.							
95	Wang et al.							
96	Wong et al.							
97	Smith et al.	18° 01' N	66° 05' W					21.5 °C
98	Pellegrino et al.	43° 49' N	10° 19' E		Peaty soil	Mediterranean		
99	Song et al.	29° 10' 19" – 29° 17' 41" N	118° 03' 50" – 118° 11' 12" E				1793 mm	16.5 °C
100	Tardy et al.					Mediterranean to Temperate bioclimatic		

SN	Authors	Latitude	Longitude	Altitude	Soil type	Climate	Precipitation	Temperature
101	Aldezabal et al.	42°59'48"N	2°06'51"W			Oceanic climate	1400 mm	12.4 °C
102	Smith et al.				Very-fine, kaolinitic, isothermic Humic Hapludox	Subtropical wet forest life zone	2184 mm	21.5 °C
103	Krashevska et al				Acrisols and in the Harapan region by loam Acrisols			
104	Xiao et al.							
105	Zhang et al.							
106	Mueller et al.	10°10'18.71" S	62°47'15.67" W					
107	Bachelot et al.							
108	Fernandes et al.	17° 56' 35" S	51° 43' 38" W	672 m	Red Latosol		1650 to 1800 mm	22° C
109	Kerfahi et al.				Ultisol			
110	Xue et al.	45°46'20"N	87°11'43"W					
111	Creamer et al.	27°40'N	98°12'W		Typic Argiustolls			
112	Palta et al.							
113	Wakelin et al.					Humid tropical climate	~2300 mm	
114	Islas et al.							
115	Holland et al.				Inceptisol and Mollisol			
116	Voříšková et al.	50°30'2.627"N	14°18'57.45"E					
117	Terjo et al.				Andisol	Warm and humid	4700 mm	
118	Oliveira et al.	3°44'32" S	38°34'39" W		Typic Hapludult	Tropical wet, very hot, with most rainfall occurring in the summer and autumn	1600 mm	23 °C to 29 °C
119	Leon et al.				rendzic leptosol	mild-maritime	500–700 mm	17°C and –5°C
120	Voříšková et al.	50°30'2.627"N	14°18'57.45"E					
121	Liang et al.	24° 44' to 25° 33' N	107° 51' to 108° 43' E			subtropical mountainous monsoon	1389 mm	18.5 °C
122	Henry et al.	18°52'19"S	48°19'22"E	1000 m	Oxisol	altitudinal wet tropical	1700 mm	25 °C
123	Disyatat et al.	18°34' N	100°46'E				1200 mm	
124	Bainard et al.	49.048717° and 49.730422°	-107.586917° and -108.026867°	795 m and 955 m	Chernozem			
125	Bhattachariya et al.	29° N	79° 29' E	243.8 m		Sub-humid and sub-tropical climate zone	1400 mm	1° to 9° C
126	Castaneda et al.							
127	Chmolowska et al.	49° 25' 17" N	20° 57' 33" E	600 m			890 mm	4° C
128	He et al.							
129	Xu et al.	26°52'-30°40' N	92°09'-98°47' E	3000 m			600 to 800 mm	7 to 16 °C
130	French et al.							4.9–7.6 °C 12.5–17.6 °C
131	Yang et al.	36°23'-37°17'N	108°45'-110°28'E	900 and 1500 m	loessal soil (Chinese classification)		497 mm	5 to 9°C
132	Xiang et al.	35°59'–36°02' N	106°26'–106°30' E	1534–1822 m	Entisols	sub-arid	419.1 mm	6.9 °C
133	Honnay et al.							

SN	Authors	Latitude	Longitude	Altitude	Soil type	Climate	Precipitation	Temperature
134	Xiao et al.	34°36'–34°37'N	105°42'–105°43'E			Semi-arid	496–628 mm	10.7 °C
135	Manoharan et al.							
136	Xu et al.	27°23'76"N	82°56'11"W		Ona fine sand	subtropical climate	1206 mm	21.5 °C
137	Tian et al.	36°25.40'N	109°31.53'E	1353 m		semiarid	504.7 mm	10.1 °C
138	Zhang et al.	41°51' N	124°54' E	500 ~ 1100 m	Udalfs	continental monsoon climate	700 to 850 mm	4.7 °C
139	Ali et al.				Chalt Volcanic Group			
140	Szoboszlay et al.							
141	Liu et al.							
142	Dang et al.	35°28'0 –36°02'0 N	109°38'0 –110°12'0 E	1200 m	Orthic Primosols	Warm and temperate	611.8 mm	8.6 °C
143	Zhang et al.	36°46' N	109°16' E			Semiarid	510 mm	8.8 °C
144	Zhang et al.	29°10'19.4"N–29°17'41.4"N	118°03'49.7"E– 118°11'12.2"E		Red soil with granite or deeply weathered granite as parent rock	Subtropical	1793 to 1960 mm	15.3 °C
145	Edirisinghe and Madawala						1750 – 2500 mm	24 to 28 °C
146	Birhane et al.			2232 to 2937 m	Luvissols (Alfissols), Regosols (Entissols), Cambisols (Inceptissols) and Calcisols (Aridisols)	Tropical semi-arid		
147	Pankova et al.	50°30'2.627"N	14°18'57.45"E					
148	Wang et al.	19°18'N	109°38'E		Oxisols		1940 mm.	22.7 °C
149	Peerawat et al.	13°41'N	101°04'E		Kabin Buri series	Tropical monsoon climate,	1328 mm	28.1 °C
150	Monkai et al.	22° 04'–22° 17'N	100° 32'–100° 44'E	600 to 800 m		Tropical monsoon climate	1106 mm	21.3 °C
151	Cai et al.	21°56'N	101°15'E	560 m		southwest monsoon	1500 mm	22.9 °C
152	Ren et al. 2018	36°51'41.23"–36°52'50.87"N	109°19'49.20" – 109°21'46.46"E		Calcaric Cambisols	Temperate semiarid	510 mm	8.8 °C
153	Soka and Ritchie	2°19'57.27"S	34°49'55.75"E		Chromi-Luvic Phaeozems, Eutric Leptosols, Eutric- Pellic Vertisols, Mollic Solonetz and Vitric Andisols	Tropical	1050 to 550 mm	24° to 27 °C 15° to 21 °C
154	Cerqueira et al.					Aw (Koppen's classification)	1600 to 1900 mm	20 °C
155	Yang et al.	46°21'–46°37'N	131°16'–131°42'E			temperate monsoon climate	620 mm	3.4 °C (22 °C maximum in July and –18 °C minimum in January)
156	Hui et al.	48.11 N	129.14 E	400 to 800 m				
157	Li et al.	39°21' N,	100°07' E	1384 m		temperate, arid, and continental, with cold winters and hot, dry summers	116.8 mm	7.6 °C
158	Sepp et al.							
159	Zhang et al.					subtropical humid zone and warm temperate zone	950 to 1200 mm	11.8 °C

SN	Authors	Latitude	Longitude	Altitude	Soil type	Climate	Precipitation	Temperature
160	McGee et al.	10° 27' 05.7" N	84° 16' 24.32" W		Oxisols	humid Atlantic		27 °C
161	Li et al.					semi-arid climate		
162	Zhange et al.	36°10'–36°17'N	106°21'–106°27'E		Montane gray-cinnamon soil.	semi-arid climate	425 mm	7 °C
163	Stover et al.	49°09'N	113°08'W		Chernozem soils with predominantly calcareous soil		808 mm	–1.3 to 10.6 °C
164	Upton et al.						700 to 900 mm	10 to 11 °C
165	Boeraeve et al.							
166	Guillou et al.	48°00' N	2°49' O					
167	Krashevskaya et al.	2°0'57"S	102°45'12"E					
168	Nkuekam et al.			>3300 m	Humic clays to poorly structured sands		400 mm to >1200 mm	
169	Yang et al.	33°38'N	101°53'E	3,500 m	mollic cryic cambisols	Cold humid-alpine		1.2°C
170	Brinkmann			< 100 m		Tropical	2332 mm	26.9 °C
171	Zheng et al.	47° 29'N	14° 6'E	690 m	Luvisols (limestone, L) and Cambisols (silicate, S)		980 mm	7.2 °C
172	Wang et al.	35°03'–36°37'N	108°10'–109°08'E		Cambisols		576.7 mm	10 °C
173	Grau et al.	42°35'32.9"N 42°39'53.9"N	01°04'28.8"E 00°50'07.8"E	1800–1900 2000–2100		Atlantic Continental, with Atlantic influence	800–900* 600–800**	8 to 10 °C
174	Reyes et al.	2° 23' 51" S	44° 24' 16" W	32 m	Typic Haplaustox	humid-tropical	2370 mm	
175	Zhao et al.	107°52'–108°05'N	25°09'–25°20'E	550–850 m		subtropical humid monsoon	1389 mm	15 °C
176	Wang et al.	35°03'–36°07'N	108°10'–109°18'E	1211–1453 m	Inceptisols		587 mm	10 °C
177	Qiao et al.	24° 38'–24° 58' N	103° 11'–103° 29' E				970 mm	16.2 °C
178	Makiola et al.			<1000 m				
179	Song et al.	21°54'– 21°59'N	101°13'–101°17'E				1493 mm	21.8 °C
180	Ma et al.						560mm	1.9 °C
181	Sui et al.	47°35'N	133°31'E					
182	Hui et al.	23° 48' N	103° 45' E		mollic inceptisols	subtropical monsoon climate	815.8 mm	18.6 °C
183	Nautiyal et al.	30°18.759'N	78°24.680'E	1800 m	silty loam and rich in organic carbon and nitrogen	Temperate	1383 mm	
184	Yan et al.	36°04'–36°05'N	109°08'–109°11'E	1157–1396 m		Temperate, continental monsoon	576.7 mm	9 °C
185	Liu et al.	35°03'–36°37'N	108°10'–109°18'E	1,211–1,453 m	calcareous brown soil (Ustalfs)		587 mm	7.4°C
186	Sousa et al.	12°03'58"S	55°21'07" W					
187	Flores-Rentería et al.	18°10' and 18°45'N	94°42' and 95°27'W	150–530 m	Andosols		4700 mm	27 °C
188	Berkelmann et al.							
189	Yang et al.	35°42'N	107°37'E		loessal	Sub-humid climate	556.5 mm	9.3 °C
190	Liu et al.	35°03'–36°37' N	108°10'–109°18'E	1211–1453 m	Loessial soil (Calcic Cambisols)		500 mm to 620 mm	7 °C to 8 °C

**Tab. S5** - Impact of particular land use change on soil fungi. Abbreviations of land-use types: (PF) Primary forest; (SF) Secondary forest; (PL) Plantation forest; (PS) Primary shrubland; (SS) Secondary shrubland; (PG) Primary grassland; (SG) Secondary grassland; (WL/RL) Woodland or Rangeland; (PA) Pasture; (AL) Abandoned land; (AF) Agroforestry; (PC) Perennial cropland; (CR) Cropland; (others) bareland/eroded land.

Land-use change		Fungal parameters							
PF and SF	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
	Decrease	1	1						2
	Increase	1	1			1	3		6
	No change							2	2
	Varying			3			2		5
	Significant change				2				2
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>		<b>number of results</b>
	Decrease	1	1	1		4	1		8
	Increase	2	2			2			6
	No change	2	1			1	1		5
Varying	1		4					5	
Significant change				8				8	
PF and PL	<b>ECM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>			<b>number of results</b>
	Decrease	1							1
	Increase					1			1
	No change								0
	Varying			2					2
	Significant change				2				2
	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
	Decrease	3	2			3	3	2	13
	Increase			1					1
	No change	3	2		1		1		7
Varying								0	
Significant change				2				2	
<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>			<b>number of results</b>	
Decrease	4	1	1		1			7	
Increase								0	
No change		2						2	
Varying			3		1			4	
Significant change				5				5	
PF and SG	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Gene copy number</b>	<b>number of results</b>
	Decrease							1	1

<b>Land-use change</b>		<b>Fungal parameters</b>							
	Increase	1				1	1	3	
	No change	2	2		1		2	7	
	Varying			1				1	
	Significant change				2			2	
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Community composition</b>	<b>PLFA content</b>			<b>number of results</b>	
	Decrease				1			1	
	Increase	1	1		1			3	
	No change	1		1				2	
	Varying			1				1	
	Significant change							0	
<b>PF and PA</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
	Decrease	1	1			1			3
	Increase	1					4		5
	No change	1	2			1			4
	Varying	1		3			2		6
	Significant change				1				1
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>Colony forming unit</b>	<b>number of results</b>
	Decrease	1					1		2
	Increase	1	1			1			3
	No change					2			2
	Varying			2				1	3
	Significant change				2				2
<b>PF and PC</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
	Decrease	2	2			1	2	1	8
	Increase								0
	No change	1	1			1			3
	Varying								0
	Significant change				1				1
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>		<b>number of results</b>
	Decrease	4	1			1			6
	Increase	4	1			1			6
	No change	4	5		1	1			11
	Varying			6		1			7
	Significant change				5				5
	<b>ECM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>			<b>number of results</b>
	Decrease								0

Land-use change		Fungal parameters								
	Increase	1							1	
	No change								0	
	Varying								0	
	Significant change	1							1	
<b>PF and CR</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>	
	Decrease	1					2	2	5	
	Increase	1	1				1	3	6	
	No change	3	2						5	
	Varying				3	1	1		5	
	Significant change				3				3	
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>Colony forming unit</b>	<b>number of results</b>	
	Decrease	2	2	1				1	2	8
	Increase						1		3	
	No change	1					1	1	3	
	Varying	2		2				2	6	
	Significant change				7				7	
	<b>ECM</b>	<b>Community composition</b>		<b>Root colonization</b>					<b>number of results</b>	
	Decrease			1					1	
	Increase								0	
	No change								0	
	Varying								0	
	Significant change	1							1	
<b>SF and PL</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Spore density</b>			<b>number of results</b>	
	Decrease	2	2				1	5		
	Increase	1	1						2	
	No change				1				1	
	Varying							0		
	Significant change				1				1	
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>number of results</b>		
	Decrease	2							1	3
	Increase							0		
	No change	1					1	2		
	Varying	1	2	5	1	1	1	11		
	Significant change				5				5	
	<b>ECM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>			<b>number of results</b>	
	Decrease	1				1			2	

<b>Land-use change</b>		<b>Fungal parameters</b>							
Increase		0							
No change		0							
Varying		0							
Significant change		0							
<b>SF and SG</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
Decrease		1	1					1	4
Increase		1	1			2			4
No change		1					1		2
Varying		1	1	2					4
Significant change					4				4
Total		Species / OTUs richness	Diversity	Abundance	Community composition	PLFA content	Gene copy number	colony forming unit	number of results
Decrease		1	2			1	2		6
Increase		3	3					1	7
No change		1	1			1			3
Varying				3					3
Significant change					9				9
ECM		Species / OTUs richness	Diversity	Abundance	Community composition	Root colonization			number of results
Decrease		1				1			2
Increase									0
No change									0
Varying									0
Significant change									0
<b>SF and PA</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
Decrease		2	1						3
Increase		1				2			3
No change									0
Varying				3			1		4
Significant change					2				2
Total		Species / OTUs richness	Diversity	Abundance	Community composition	PLFA content	Gene copy number		number of results
Decrease						1	1		2
Increase						1			1
No change				2					2
Varying		1							1
Significant change					2				2
<b>SF and PC</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Spore density</b>		<b>number of results</b>
Decrease		2	1				1		4

Land-use change		Fungal parameters							
	Increase	1		1			1		
	No change			1			1		
	Varying	1		1			2		
	Significant change			1			1		
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>number of results</b>	
	Decrease	5	3	1				9	
	Increase						0		
	No change	1					1		
	Varying			1	1		2		
	Significant change			5			5		
<b>SF and CR</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
	Decrease	3	2	1	2		1	2	12
	Increase	1							1
	No change	1		1	1	2			
	Varying	1	1						
	Significant change			2					2
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>Colony forming unit</b>	<b>number of results</b>
	Decrease	2	2			3	2	9	
	Increase	1				1	2		
	No change	2	2			1		5	
	Varying	1		4	2		1	1	9
	Significant change			11					11
	<b>ECM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>			<b>number of results</b>
	Decrease	1			1				2
	Increase							0	
	No change							0	
	Varying							0	
	Significant change							0	
<b>PL and CR</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>	
	Decrease	1	1	1		2	1	6	
	Increase	2	1			1	4		
	No change					1	1	2	
	Varying							0	
	Significant change			3				3	
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>Ergosterol content</b>	
	Decrease					1		1	2

Land-use change		Fungal parameters							
	Increase	3	1						4
	No change		1	1		1		0	3
	Varying			2					2
	Significant change					7			7
<b>PG and CR</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
	Decrease		1			1	4	2	9
	Increase	2	1			1			4
	No change								0
	Varying			1					1
	Significant change					2			2
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>hyphal length</b>	<b>number of results</b>
	Decrease	2	1			1			4
	Increase	1							1
	No change	1			1	1		1	4
	Varying								0
	Significant change					2			2
<b>SG and PA</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>% hyphal length</b>	<b>number of results</b>
	Decrease	2	1			2	1	1	6
	Increase	2				2			4
	No change		1		1	0			2
	Varying	1	1		2				4
	Significant change			4					4
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>		<b>number of results</b>
	Decrease								0
	Increase	2							2
	No change		1						1
	Varying		1	2					3
	Significant change					2			2
<b>SG and CR</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
	Decrease	5	4			2	1	1	14
	Increase	2	2			1	3		8
	No change	1				2	1		4
	Varying			3					3
	Significant change					8			8
	<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>number of results</b>
	Decrease	5	3			1	4	1	15

<b>Land-use change</b>		<b>Fungal parameters</b>						
Increase	1							1
No change	2	4		1				7
Varying			2					2
Significant change				9				9
<b>ECM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>			<b>number of results</b>
Decrease		1			1			2
Increase								0
No change	2							2
Varying		1	1					2
Significant change				1				1
<b>PA and CR AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
Decrease	2	2			2			6
Increase	1	1						2
No change		1		1	4		1	7
Varying			3		1			4
Significant change				3				3
<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>colony forming unit</b>	<b>number of results</b>
Decrease	1	1			2	2		6
Increase								0
No change							1	1
Varying			2				1	3
Significant change				2				2
<b>AL and CR AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>PLFA content</b>	<b>Glomalin related proteins</b>	<b>number of results</b>
Decrease	1	1		2	4	1	1	10
Increase	2	1			1			4
No change	3	2		2	2			9
Varying				1				1
Significant change			5					5
<b>Total</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>	<b>Colony forming unit</b>	<b>number of results</b>
Decrease	1				3	1		5
Increase			1					1
No change					1			1
Varying		1	1		1		1	4
Significant change				3				3
<b>ECM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>			<b>number of results</b>
Decrease								0

<b>Land-use change</b>		<b>Fungal parameters</b>								
Increase										0
No change										0
Varying										0
Significant change										0
<b>PC and CR</b>	<b>AM</b>	<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>Root colonization</b>	<b>Spore density</b>	<b>Glomalin related proteins</b>	<b>number of results</b>	
	Decrease	1						1	2	
	Increase					2			2	
	No change	4	2			1	2	1	10	
	Varying	1				1		1	3	
	Significant change				3				3	
<b>Total</b>		<b>Species / OTUs richness</b>	<b>Diversity</b>	<b>Abundance</b>	<b>Community composition</b>	<b>PLFA content</b>	<b>Gene copy number</b>		<b>number of results</b>	
	Decrease					2			2	
	Increase								0	
	No change								0	
	Varying			1					1	
	Significant change				1				1	

**Tab. S6** - Summary of Tab. S5.

Land use change	Fungal group	Quantitative parameters								species/OTU composition					
		number of studies	number of results	negative	positive	no/varying	% negative	% positive	% no/varying	number of studies	number of results	change	no change	% change	%no change
PF-SF	AM	8	15	2	6	7	13	40	47	2	2	2	0	100	0
	ECM	3	4	1	1	2	25	25	50	2	2	2	0	100	0
	TOT	13	24	8	6	10	33	25	42	8	8	8	0	100	0
PF-PL	AM	7	21	13	1	7	62	5	33	2	2	2	0	100	0
	TOT	8	13	0	7	6	0	54	46	5	5	5	0	100	0
PF-SG	AM	5	12	1	3	8	8	25	67	2	2	2	0	100	0
	TOT	6	7	1	3	3	14	43	43	0	0	0	0	0	0
PF-PA	AM	6	18	3	5	10	17	28	56	1	1	1	0	100	0
	TOT	7	10	2	3	5	20	30	50	2	2	2	0	100	0
PF-PC	AM	4	11	8	0	3	73	0	27	1	1	1	0	100	0
	TOT	12	30	6	6	18	20	20	60	6	6	5	1	83	17
	ECM	1	1	0	1	0	0	100	0	0	1	1	1	0	100
PF-CR	AM	11	21	5	6	10	24	29	48	3	3	3	0	100	0
	TOT	13	20	9	3	9	45	15	45	7	7	7	0	100	0
	ECM	1	1	1	0	0	100	0	0	1	1	1	0	100	0
SF-PL	AM	4	8	5	2	1	63	25	13	1	1	1	0	100	0
	TOT	10	16	3	0	13	19	0	81	6	6	5	1	83	17
	ECM	1	2	2	0	0	100	0	0	0	0	0	0	0	0
SF-SG	AM	6	14	4	2	6	29	14	43	4	4	4	0	100	0
	TOT	13	19	6	7	6	32	37	32	9	9	9	0	100	0
	ECM	2	4	3	0	1	75	0	25	1	1	1	0	100	0
SF-PA	AM	6	10	3	3	4	30	30	40	2	2	2	0	100	0
	TOT	5	6	2	1	3	33	17	50	2	2	2	0	100	0
SF-PC	AM	3	8	4	1	3	50	13	38	2	2	1	1	50	50
	TOT	7	12	9	0	3	75	0	25	5	5	5	0	100	0
SF-CR	AM	8	20	12	1	7	60	5	35	3	3	2	1	67	33
	TOT	19	25	9	2	14	36	8	56	11	11	11	0	100	0
	ECM	1	3	3	0	0	100	0	0	0	0	0	0	0	0
PL-CR	AM	7	12	6	4	2	50	33	17	3	3	3	0	100	0
	TOT	8	11	2	4	5	18	36	45	7	7	7	0	100	0
PG-CR	AM	7	14	9	4	1	64	29	7	2	2	2	0	100	0

Land use change	Fungal group	Quantitative parameters								species/OTU composition					
		number of studies	number of results	negative	positive	no/varying	% negative	% positive	% no/varying	number of studies	number of results	change	no change	% change	%no change
SG-PA	TOT	6	9	4	1	4	44	11	44	3	3	2	1	67	33
	AM	6	16	6	4	6	38	25	38	4	4	4	0	100	0
	TOT	4	6	0	2	4	0	33	67	2	2	2	0	100	0
SG-CR	AM	13	29	14	8	7	48	28	24	8	8	8	0	100	0
	TOT	15	25	15	1	9	60	4	36	10	10	9	1	90	10
	ECM	2	6	2	0	4	33	0	67	1	1	1	0	100	0
PA-CR	AM	9	19	6	2	11	32	11	58	4	4	3	1	75	25
	TOT	9	10	6	0	4	60	0	40	2	2	2	0	100	0
AL-CR	AM	12	24	10	4	10	42	17	42	5	5	5	0	100	0
	TOT	9	11	5	1	5	45	9	45	3	3	3	0	100	0
	AM	8	17	2	2	13	12	12	76	3	3	3	0	100	0
PC-CR	TOT	2	3	2	0	1	67	0	33	1	1	1	0	100	0