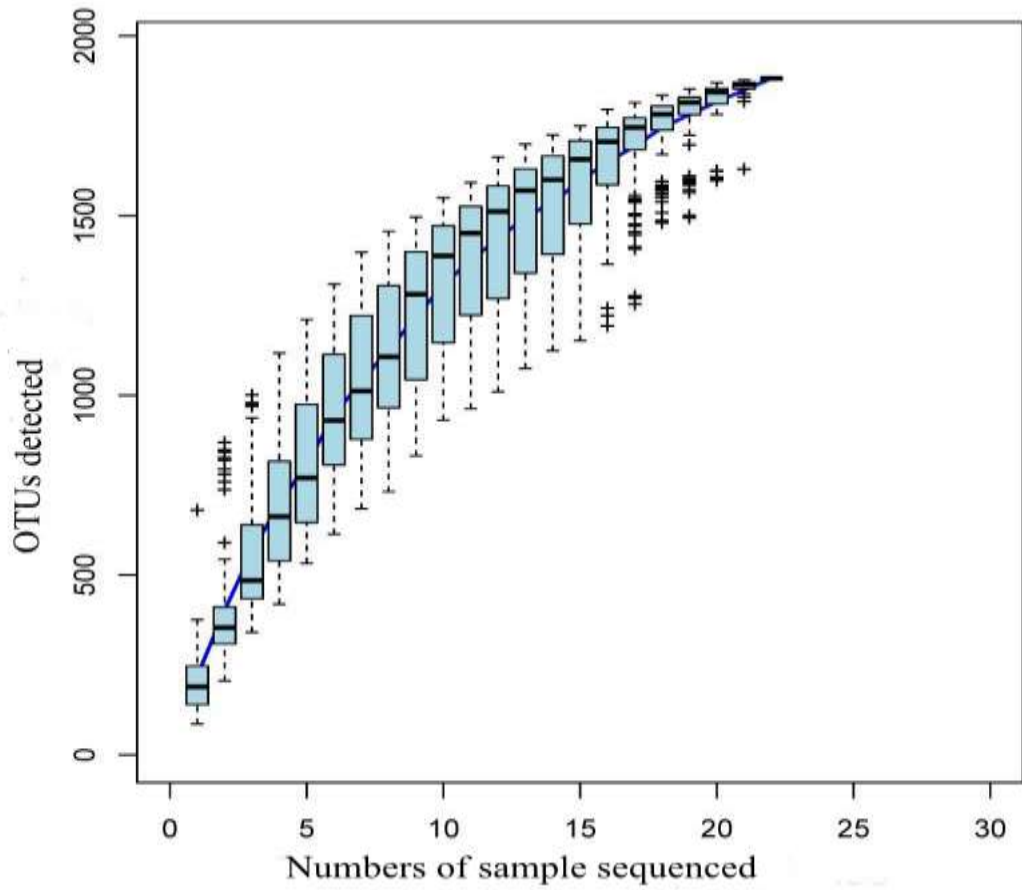


Appendix A Sequencing data statistics of DNA samples

Accession no.	Raw data number	Mean length of raw data	Clean data number	Mean length of clean data	OUT number
XY1	84589	336.3	83977	289.1	376
XY2	120354	298.9	118904	254.9	674
XY3	98326	330.3	97751	283.5	306
XY4	72095	336.8	71473	293.5	156
XY5	72956	338.0	72297	294.5	140
XY6	60927	335.7	60285	292.1	139
XR1	75323	275.6	74388	231.6	86
XR2	71873	292.8	70810	248.8	119
XR3	72319	336.6	71110	295.0	175
XR4	74649	315.6	72971	274.8	264
XR5	74587	309.5	73355	267.1	189
XR6	75543	312.3	74840	268.6	150
QL1	73304	332.1	71694	292.0	257
QL2	77920	327.4	76233	287.0	216
QL3	75218	288.2	74056	244.1	221
QL4	74315	321.6	73357	278.7	171
QL5	75874	282.9	74555	239.5	220
AS1	76628	276.7	74970	234.0	170
AS2	74235	329.9	72715	288.2	230
AS3	71150	289.6	69898	245.5	257
AS4	75777	334.8	74306	293.8	233
AS5	75633	289.9	74281	246.8	237
Sum	1703595	-	1692504	-	4986

Appendix B Community richness and diversity indices for individuals and geographical groups

Group	Sample_ID	Chao1 index	ACE_index	Shannon_index	Simpson index	Coverage
XY	XY1	537.013	568.819	0.470	0.871	0.998
	XY2	709.892	735.100	1.629	0.357	0.999
	XY3	412.419	468.632	0.639	0.762	0.999
	XY4	401.286	1108.106	0.296	0.916	0.999
	XY5	298.913	532.470	0.158	0.960	0.999
	XY6	294.217	531.540	0.352	0.885	0.999
Mean	-	442.290	657.445	0.591	0.792	0.999
SD	-	158.518	238.370	0.534	0.223	0.000
CV/%	-	35.84	36.26	90.44	28.18	0.00
XR	XR1	123.273	133.505	0.559	0.739	0.999
	XR2	215.130	220.331	0.814	0.520	0.999
	XR3	297.229	328.668	0.137	0.970	0.999
	XR4	365.020	374.302	0.835	0.642	0.999
	XR5	321.028	519.834	1.077	0.498	0.999
	XR6	373.250	738.055	0.766	0.533	0.999
Mean	-	282.488	385.782	0.698	0.650	0.999
SD	-	96.580	217.475	0.321	0.181	0.000
CV/%	-	34.19	56.37	45.94	27.88	0.00
QL	QL1	414.200	665.219	0.331	0.910	0.998
	QL2	353.500	457.519	0.482	0.825	0.999
	QL3	349.886	537.592	1.305	0.388	0.999
	QL4	361.778	672.207	0.802	0.614	0.999
	QL5	349.419	586.991	1.190	0.414	0.999
	Mean	-	365.757	583.906	0.822	0.630
SD	-	27.530	90.190	0.426	0.236	0.000
CV/%	-	7.53	15.45	51.83	37.38	0.02
AS	AS1	236.500	281.669	1.228	0.400	0.999
	AS2	343.957	491.306	0.668	0.776	0.999
	AS3	394.948	453.648	0.919	0.472	0.998
	AS4	354.727	444.925	0.298	0.922	0.999
	AS5	389.630	630.981	1.298	0.371	0.998
	Mean	-	343.953	460.506	0.882	0.588
SD	-	63.932	124.783	0.413	0.246	0.000
CV/%	-	18.59	27.10	46.78	41.86	0.00

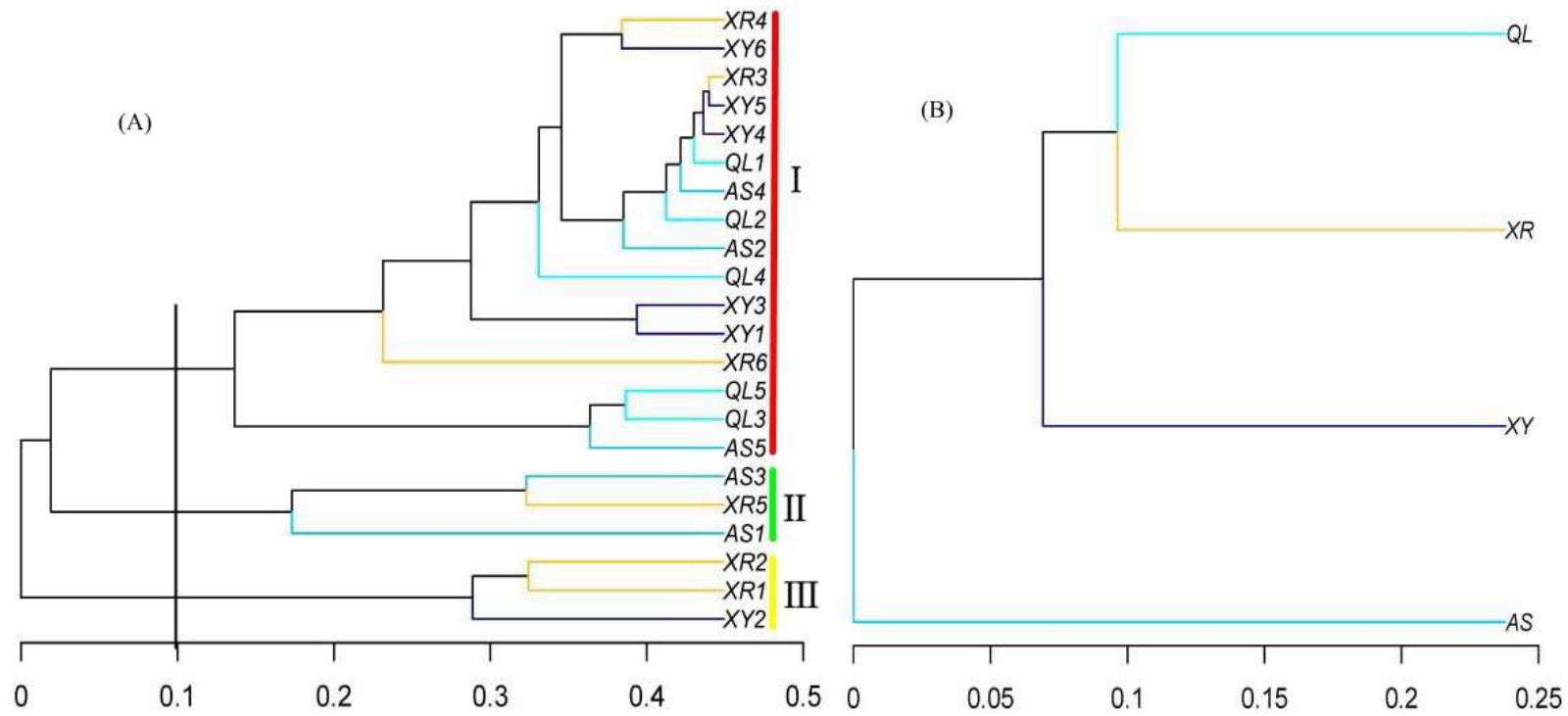


Appendix C Species accumulation curves.

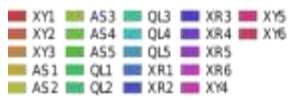
Appendix D Species taxonomy and community ratio at genus level

Genus	Community Ratio/%																					Mean	
	XY1	XY2	XY3	XY4	XY5	XY6	XR1	XR2	XR3	XR4	XR5	XR6	QL1	QL2	QL3	QL4	QL5	AS1	AS2	AS3	AS4		AS5
<i>Sporisorium</i> ^a	95.57	42.02	88.92	96.75	98.05	94.35	10.72	33.94	98.65	78.70	66.23	64.71	95.38	90.68	43.40	76.33	38.93	15.77	87.92	45.54	96.13	45.14	68.36
<i>Fusarium</i>	0.02	48.41	2.32	0.72	0.00	0.00	85.67	65.05	0.16	0.03	1.60	0.01	0.04	0.52	6.87	18.38	0.04	0.21	4.58	0.61	0.10	0.12	10.70
<i>Magnaporthe</i>	0.00	0.01	7.39	0.00	0.00	0.00	0.08	0.00	0.44	0.00	0.00	0.00	0.00	0.00	47.67	0.00	51.22	0.00	0.06	0.00	0.00	40.15	6.68
<i>Verticillium</i>	0.01	0.03	0.00	0.88	0.85	1.31	0.02	0.02	0.06	4.86	0.04	0.02	0.12	0.15	0.22	0.06	0.03	0.06	0.19	0.10	0.41	0.07	0.43
<i>Cercospora</i>	0.06	0.09	0.10	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.06	0.05	0.01	0.00	0.24	0.00	0.10	0.00	0.27	7.60	0.39
<i>Epicoccum</i>	1.55	0.37	0.01	0.47	0.11	0.04	0.00	0.00	0.00	0.06	0.11	0.21	0.36	0.19	0.05	0.00	0.02	0.05	0.04	0.00	0.01	0.11	0.17
<i>Cladosporium</i>	0.01	0.36	0.01	0.04	0.06	0.01	0.00	0.00	0.02	0.58	0.36	0.02	0.15	0.66	0.05	0.67	0.82	0.00	0.01	0.01	0.01	0.00	0.18
<i>Curvularia</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.99	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.03	0.05	1.20	0.46	0.17
<i>Ramichloridium</i>	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.04	0.01	0.08	0.02	0.21	0.11	1.21	0.01	0.03	1.11	0.13
<i>Plectosphaerella</i>	0.97	0.05	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.03	0.10	0.86	0.01	0.05	0.28	0.00	0.02	0.07	0.11
<i>Bipolaris</i>	0.02	0.17	0.00	0.00	0.00	1.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.09
<i>Leninula</i>	0.06	0.91	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05
<i>Ustilago</i> ^a	0.12	0.03	0.04	0.12	0.12	0.08	0.01	0.04	0.09	0.09	0.06	0.07	0.12	0.09	0.04	0.07	0.03	0.01	0.13	0.04	0.08	0.04	0.07
<i>Candida</i>	0.04	0.22	0.01	0.00	0.01	0.01	0.00	0.00	0.06	0.26	0.00	0.01	0.05	0.03	0.00	0.02	0.01	0.00	0.06	0.03	0.13	0.02	0.04
<i>Alternaria</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.95	0.00	0.00	0.00	0.00	0.00	0.04
<i>Saitozyma</i>	0.13	0.02	0.00	0.06	0.00	0.01	0.00	0.00	0.00	0.10	0.00	0.01	0.03	0.01	0.04	0.03	0.03	0.00	0.00	0.00	0.01	0.01	0.02
<i>Mortierella</i>	0.01	0.14	0.05	0.00	0.00	0.00	0.01	0.04	0.03	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.02	0.00	0.02
<i>Aspergillus</i>	0.04	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.09	0.00	0.00	0.01	0.01	0.00	0.01	0.01	0.00	0.03	0.01	0.08	0.01	0.02
<i>Dissoconium</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.04	0.06	0.01	0.01	0.24	0.00	0.00	0.00	0.00	0.00	0.02
<i>Nigrospora</i>	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.19	0.00	0.00	0.00	0.01
Others	0.21	1.56	0.12	0.05	0.04	0.09	0.00	0.20	0.04	0.37	0.34	0.05	0.31	0.26	0.13	0.14	0.55	0.13	0.26	0.08	0.20	0.30	0.25
Unclassified	1.03	5.41	0.94	0.86	0.73	2.39	3.48	0.67	0.34	14.79	29.20	34.83	3.19	7.14	1.31	3.36	6.59	83.58	4.78	53.41	1.22	4.74	12.00

List only the genera with top 20, the remaining genera were merged to ‘Others’ and unclassified fungus were merged to ‘Unclassified’; Superscript letter ‘a’ showing the smut genera that discovered in all samples.



Appendix E Bray crutis distance of all accessions and merged groups. Bray crutis distance clustering of twenty-two accessions (A) and four geographical groups (B).



Appendix F Phylogenetic tree topology of communities. Different pie colors respect the community richness ratio among all accessions