

**TABLE S1** Meteorological information.

<b>Assay</b>	<b>Sampling date</b>	<b>Temperature* (Max. - Min.) [°C]</b>	<b>Relative humidity* (Max. - Min.) [%]</b>	<b>Barometric pressure* (Max. - Min.) [hPa]</b>	<b>Wind speed<sup>a</sup> (Max. wind gust) [m/s]</b>	<b>Wind direction<sup>b</sup></b>	<b>Precipitation<sup>c</sup> [mm]</b>	<b>Total insolation [h] (% insolation)</b>
A	2-9/Dec 2015	16.6 – 3.7	90 – 46	957.0 – 949.4	0.75 (4.70)	N	0.0	6.0 (64%)
B	9-16/Dec 2015	15.5 – 5.1	88 - 61	958.2 – 943.2	0.90 (8.30)	N	0.2	3.6 (38%)
C	16-23/Dec 2015	15.4 – 4.5	96 – 49	956.0 – 944.6	0.64 (8.61)	N	0.0	6.5 (70%)
M	20-27/Jul 2015	37.6 – 20.0	92 – 29	941.5 – 934.6	1.83 (8.80)	W	3.6	12.8 (88%)

\* Maximum and minimum values measured during the sampling time

<sup>a</sup> Average of the sampling time

<sup>b</sup> Predominant during sampling time

<sup>c</sup> Total registered

**TABLE S2** Statistical comparison between NGS and morphological assignation for pollen. Concordance Correlation Coefficient (CCC) was determined to analyze the agreement between both methods. The results of relative abundance from NGS analyses were corrected to match 100% to compare only those pollen types that were identified by microscopy.

Sample A1				Sample B1				Sample C1			
Pollen type	Morpho. (%)	NGS (%)	NGS (% corrected)	Pollen type	Morpho. (%)	NGS (%)	NGS (% corrected)	Pollen type	Morpho. (%)	NGS (%)	NGS (% corrected)
Artemisia	0.33	0.06	0.09	Artemisia	0.67	0.20	0.30	Artemisia	0.36	0.40	0.54
Compositae	0.66	0.24	0.37	Compositae	0.34	0.10	0.15	Compositae	0.18	0.10	0.14
Fabaceae	0.66	2.00	3.10	Cheno./Amar.	1.35	0.01	0.03	Cheno./Amar.	0.54	0.00	0.00
Quercus	0.99	0.30	0.46	Fabaceae	0.67	1.00	1.53	Fabaceae	0.54	1.00	1.36
Fraxinus	0.66	0.50	0.77	Quercus	2.69	0.40	0.61	Alnus	0.18	0.04	0.05
Eucalyptus	0.33	0.00	0.00	Fraxinus	1.01	0.10	0.15	Quercus	2.14	2.00	2.72
Cupress./Taxac.	89.77	37.00	57.00	Olea	1.01	0.00	0.00	Fraxinus	1.61	1.00	1.36
Pinaceae	0.33	0.00	0.00	Populus	0.34	2.00	3.06	Cupress./Taxac.	89.46	60.00	81.82
Poaceae	1.65	6.00	9.23	Cupress./Taxac.	81.82	52.00	79.70	Pinaceae	0.71	0.00	0.00
Platanus	0.66	1.00	1.54	Pinaceae	1.35	0.00	0.00	Poaceae	1.07	3.00	4.10
Urticaceae	2.31	16.00	24.61	Poaceae	3.03	5.00	7.66	Urticaceae	2.86	5.00	6.82
Unidentified	1.65	1.91	2.94	Urticaceae	4.38	4.00	6.13	Unidentified	0.36	0.79	1.10
Total	100.00	65.01	100.00	Unidentified	1.35	0.44	0.67	Total	100.00	73.33	100.00
				Total	100.00	65.25	100.00				
	CCC		0.84						CCC		0.99
				CCC			0.96				

**TABLE S3** Statistical comparison between NGS and morphological assignation for fungal spores. Concordance Correlation Coefficient (CCC) was determined to analyze the agreement between both methods. The group “Others” was removed to reduce the uncertainty and the relative abundance were corrected to match 100% in both methods.

Sample A1					Sample B1					Sample C1				
Morphological type	Morpho. (%)	Morpho. (% corrected)	NGS (%)	NGS (% corrected)	Morphological type	Morpho. (%)	Morpho. (% corrected)	NGS (%)	NGS (% corrected)	Morphological type	Morpho. (%)	Morpho. (% corrected)	NGS (%)	NGS (% corrected)
Davidiella = Cladosporium (C. herbarum + C. cladosporoides)	26.83	76.48	35.00	64.87	Davidiella = Cladosporium (C. herbarum + C. cladosporoides)	46.02	88.19	35.00	67.92	Davidiella = Cladosporium (C. herbarum + C. cladosporoides)	55.13	89.39	45.00	77.80
Polythrincium (= Mycosphaerella)	0.08	0.23	0.02	0.04	Polythrincium (= Mycosphaerella)	0.06	0.11	0.00	0.00	Polythrincium (= Mycosphaerella)	0.11	0.17	0.00	0.00
Epicoccum	0.46	1.31	2.00	3.71	Epicoccum	0.11	0.21	5.00	9.70	Epicoccum	0.29	0.47	2.00	3.46
Alternaria	1.31	3.73	12.00	22.24	Alternaria	0.56	1.07	8.00	15.52	Alternaria	0.42	0.67	7.00	12.10
Drechslera	0.69	1.97	0.50	0.93	Drechslera	0.17	0.32	0.00	0.00	Drechslera	0.35	0.57	0.00	0.00
Chaetomium	0.69	1.97	1.00	1.85	Spegazzinia	0.45	0.86	0.06	0.12	Curvularia	0.03	0.05	0.01	0.01
Xylariales	0.46	1.31	0.20	0.37	Chaetomium	0.34	0.64	0.70	1.36	Tetraploa	0.03	0.05	0.00	0.00
Arthrinium	0.69	1.97	0.10	0.19	Fusarium	0.56	1.07	0.30	0.58	Spegazzinia	0.09	0.15	0.01	0.02
Khuskia	0.69	1.97	0.01	0.02	Xylariales	0.28	0.54	0.20	0.39	Chaetomium	0.29	0.47	0.70	1.21
Psathyrellaceae	1.16	3.31	0.50	0.93	Arthrinium	0.34	0.64	0.01	0.02	Xylariales	0.03	0.05	0.20	0.35
Bovista	0.54	1.54	0.80	1.48	Khuskia	0.73	1.40	0.03	0.06	Arthrinium	0.62	1.00	0.06	0.10
Ganoderma	0.15	0.43	0.03	0.06	Beltrania	0.00	0.00	0.00	0.00	Khuskia	0.38	0.62	0.01	0.01
Boletales	0.23	0.66	0.30	0.56	Psathyrellaceae	1.06	2.04	0.50	0.97	Beltrania	0.03	0.05	0.01	0.02
Thelephoraceae	0.39	1.11	0.09	0.17	Bovista	0.17	0.32	0.50	0.97	Psathyrellaceae	0.86	1.40	0.90	1.56
Pucciniomycetes	0.15	0.43	0.40	0.74	Ganoderma	0.28	0.54	0.06	0.12	Bovista	1.02	1.65	0.60	1.04
Ustilaginomycetes	0.54	1.54	1.00	1.85	Thelephoraceae	0.17	0.32	0.07	0.14	Ganoderma	0.32	0.52	0.05	0.09
Total	35.08	100.00	53.95	100.00	Pucciniomycetes	0.17	0.32	0.80	1.55	Boletales	0.09	0.15	0.30	0.52
	CCC			0.94	Ustilaginomycetes	0.73	1.40	0.30	0.58	Thelephoraceae	0.34	0.55	0.20	0.35
					Total	52.19	100.00	51.53	100.00	Pucciniomycetes	0.11	0.17	0.30	0.52
						CCC			0.94	Ustilaginomycetes	1.12	1.82	0.50	0.86
										Total	61.67	100.00	57.84	100.00
											CCC			0.98

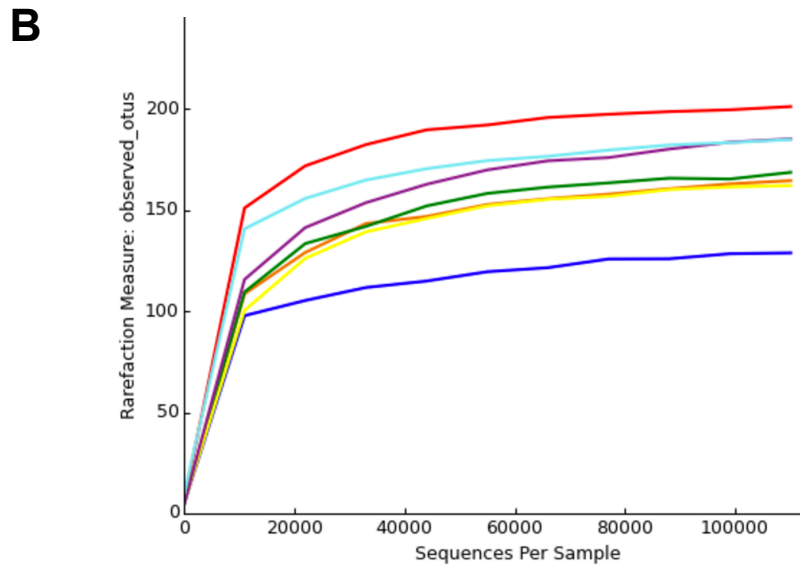
**TABLE S4** Complete morphological classification of fungal propagules.

Phylum	Class	Order	Family	Genus	Morphological spore type / hypha	Sample A1		Sample B1		Sample C1				
						Total	%	Total	%	Total	%			
Ascomycota	Dothideomycetes	Capnodiales	Davidiellaceae	<i>Davidiella</i> =	C. herbarum	390	15.03	957	17.87	1297	19.97			
			Mycosphaerellaceae	<i>Cladosporium</i>	C. cladosporioides	306	11.8	1507	28.15	2284	35.16			
				<i>Cercospora</i>	Cercospora	0	0	12	0.22	0	0			
				<i>Passalora</i>	Passalora	0	0	0	0	0	0			
			Pleosporales	Pleosporaceae	<i>Polythrincium</i>	Polythrincium	2	0.08	3	0.06	7	0.11		
					<i>Epicoccum</i>	Epicoccum nigrum	12	0.46	6	0.11	19	0.29		
					<i>Alternaria</i>	Alternaria	34	1.31	30	0.56	27	0.42		
				<i>Drechslera</i> = <i>Pyrenophora</i>	Drechslera	18	0.69	9	0.17	23	0.35			
				<i>Curvularia</i>	Curvularia	0	0	0	0	2	0.03			
				<i>Stemphylium</i>	Stemphylium	18	0.69	12	0.22	10	0.15			
		<i>Pleospora</i>		Pleospora	4	0.15	24	0.45	19	0.29				
		<i>Pithomyces</i>		Pithomyces	28	1.08	18	0.34	14	0.22				
		Leptosphaeriaceae		Leptosphaeria	10	0.39	60	1.12	26	0.4				
		Sporormiaceae		Sporormiella	0	0	0	0	0	0				
		Tetraplospora	Tetraploa	0	0	0	0	2	0.03					
		Eurotiomycetes	Eurotiales	Trichocomaceae	<i>Aspergillus</i>	Aspergillaceae	22	0.85	105	1.96	463	7.13		
					<i>Penicillium</i>	0	0	0	0	0	0			
				incertae sedis	<i>Periconia</i>	Periconia	4	0.15	3	0.06	5	0.08		
					Dothideales	Dothioraceae	<i>Aureobasidium pullulans</i>	Torula	20	0.77	9	0.17	19	0.29
					Microthyriales	Microthyriaceae	0	0	24	0.45	6	0.09		
		incertae sedis	Monodictys	4	0.15	15	0.28	11	0.17					
		Leotiomycetes	Erysiphales	Erysiphaceae	<i>Blumeria</i>	Oidium	0	0	33	0.62	8	0.12		
				Helotiales	Sclerotiniaceae	<i>Botrytis</i> = <i>Botryotina</i>	Botrytis	56	2.16	24	0.45	64	0.99	
			Sordariomycetes	Sordariales	Chaetomiaceae	<i>Chaetonium</i>	Chaetonium	18	0.69	18	0.34	19	0.29	
				Hypocreales	Nectriaceae	<i>Fusarium</i>	Fusarium	0	0	30	0.56	0	0	
				Xylariales	Xylariaceae	<i>Xylaria</i>	Xylaria	12	0.46	15	0.28	2	0.03	
					Diatrypales	Diatrypaceae	0	0	0	0	0	0		
incertae sedis	Arthrinium			Arthrinium	18	0.69	18	0.34	40	0.62				
	<i>Khuskia</i>			Nigrospora	18	0.69	39	0.73	25	0.38				
Pezizomycetes	Pezizales		Ascobolaceae	<i>Ascobolus</i>	Ascobolus	0	0	0	0	0				
incertae sedis	Beltrania		0	0	0	0	2	0.03						
Basidiomycota	Agaricomycetes	Agaricales	Psathyrellaceae	Basidiospores	266	10.25	279	5.21	269	4.14				
			Agaricaceae	<i>Bovista</i>	Coprinus	30	1.16	57	1.06	56	0.86			
		Strophariaceae	<i>Bovista</i>	Bovista	14	0.54	9	0.17	66	1.02				
			<i>Agrocybe</i>	Agrocybe	6	0.23	15	0.28	4	0.06				
		Ganodermatale: Ganodermataceae	<i>Ganoderma</i>	Ganoderma	4	0.15	15	0.28	21	0.32				
		Boletales	Boletaceae	<i>Boletus</i>	Boletus	6	0.23	0	0	6	0.09			
		Thelephorales	Thelephoraceae	<i>Thelephora</i>	Thelephora	10	0.39	9	0.17	22	0.34			
		Pucciniales	Puccinia	4	0.15	9	0.17	7	0.11					
		Ustilaginomycetes	Ustilaginales	<i>Ustilago</i>	Ustilago	14	0.54	39	0.73	73	1.12			
		Exobasidiomycetes	Tilletiales	Tilletiaceae	<i>Tilletia</i>	Tilletia	0	0	0	0	2	0.03		
Myxomycota	Unidentified				Myxomycetes	320	12.34	287	5.36	314	4.83			
					simple-hyaline	142	5.47	408	7.62	92	1.42			
					uniseptate-hyaline	20	0.77	184	3.44	12	0.18			
					fragmo-hyaline	0	0	15	0.28	4	0.06			
					filiform-hyaline	0	0	0	0	0	0			
					helico-hyaline	0	0	15	0.28	5	0.08			
					simple-brown	224	8.64	573	10.7	544	8.37			
					uniseptate-brown	120	4.63	140	2.61	131	2.02			
					fragmo-brown	60	2.31	69	1.29	52	0.8			
					muriform-brown	30	1.16	21	0.39	20	0.31			
					hyphae hyaline	4	0.15	12	0.22	0	0			
					hyphae brown	326	12.57	200	3.74	385	5.93			
					<b>TOTAL</b>					2594	100	5354	100	6496
<b>OTHERS TOTAL</b>					1684		2560		2490					

**FIG S1**

**A**

Amplicon ITSD	Assay A		Assay B		Assay C		M0
	A1	A2	B1	B2	C1	C2	M0
No. reads (2x300)	144655	195875	157699	187428	180709	174039	200333
No. sequences after pairing and quality filtering	117666	157030	130384	156554	149210	143120	160245
No. sequences after minimal OTUs filtering ( $n \geq 5$ )	112196	149903	123867	149414	142114	136830	146744
No. sequences unassigned (final data for grouped analyses)	2313 (2.06%)	2858 (1.91%)	549 (0.44%)	888 (0.59%)	1117 (0.79%)	1027 (0.75%)	11672 (7.95%)
No. of OTUs (final data for grouped analyses)	201	133	166	176	188	166	187
No. of OTUs after filtering each pair for statistics ( $n \geq 5$ )	182	114	136	130	140	133	161
No. sequences for rarefaction (PCoA and statistics)				110000			



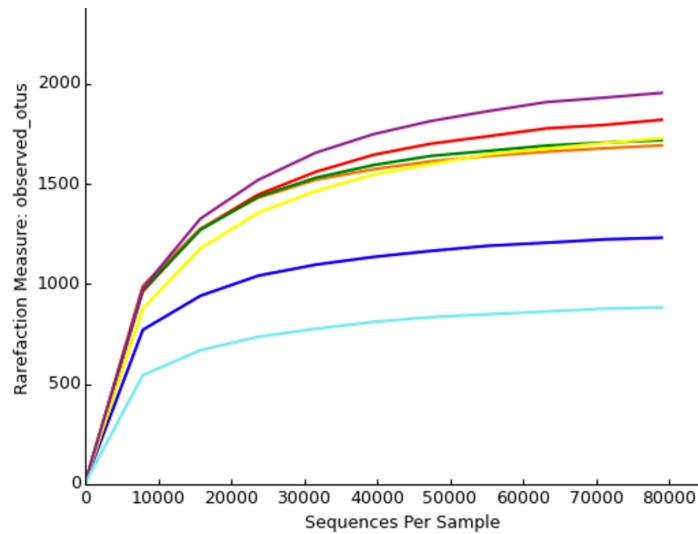
**FIG S1 (A)** Sequence information from NGS processing (Plants). **(B)** Rarefaction curves.

**FIG S2**

**A**

Amplicon ITS	Assay A		Assay B		Assay C		M0
	A1	A2	B1	B2	C1	C2	M0
No. reads (2x300)	201288	161241	142778	14229	196958	18471	188725
No. sequences after pairing and quality filtering	182927	143950	128244	142294	177575	166028	153966
No. sequences assigned	181442	142822	127249	128028	176150	164708	153281
No. sequences after additional filtering (plant sequences removed)	157668	119497	80396	88239	122290	116277	142618
No. sequences after minimal OTUs filtering ( $n \geq 5$ )	156903	119063	79819	87655	121273	115586	142376
No. sequences unassigned (final data for grouped analyses)	5941 (3.8%)	5897 (4.95%)	4982 (6.24%)	5328 (6.08%)	6079 (5.01%)	5590 (4.83%)	5858 (4.11%)
No. of OTUs (final data for grouped analyses)	1916	1270	1693	1731	2033	1788	924
No. of OTUs after filtering each pair for statistics ( $n \geq 5$ )	1258	942	1367	1396	1286	1169	673
No. sequences for rarefaction (PCoA and statistics)				79000			

**B**



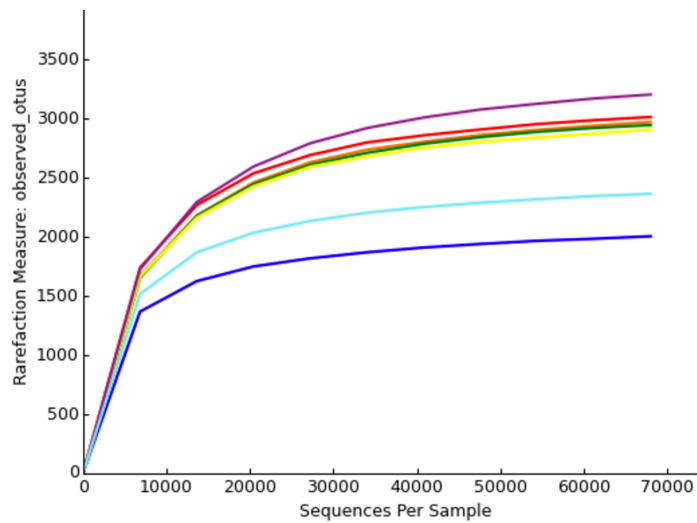
**FIG S2 (A)** Sequence information from NGS processing (Fungi). **(B)** Rarefaction curves.

**FIG S3**

**A**

Amplicon 16S	Assay A		Assay B		Assay C		M0
	A1	A2	B1	B2	C1	C2	M0
No. reads (2x300)	130996	105725	136187	150081	125804	143440	177074
No. sequences after pairing and quality filtering	116418	92797	122076	132508	113244	128593	162756
No. sequences assigned	109404	87977	115222	124764	106753	121112	154014
No. sequences after additional filtering (chloroplast and mitochondria sequences removed)	94847	72482	84663	92914	71820	80844	153221
No. sequences after minimal OTUs filtering ( $n \geq 5$ )	91881	71079	81771	90044	68012	74662	133091
No. sequences unassigned (final data for grouped analyses)	421 (0.45%)	365 (0.51%)	478 (0.57%)	577 (0.63%)	509 (0.73%)	515 (0.65%)	378 (0.28%)
No. of OTUs (final data for grouped analyses)	3088	2013	3021	3223	3210	2932	2481
No. of OTUs after filtering each pair for statistics ( $n \geq 5$ )	2334	1747	2332	2297	2498	2373	1940
No. sequences for rarefaction (PCoA and statistics)	68000 sequences						

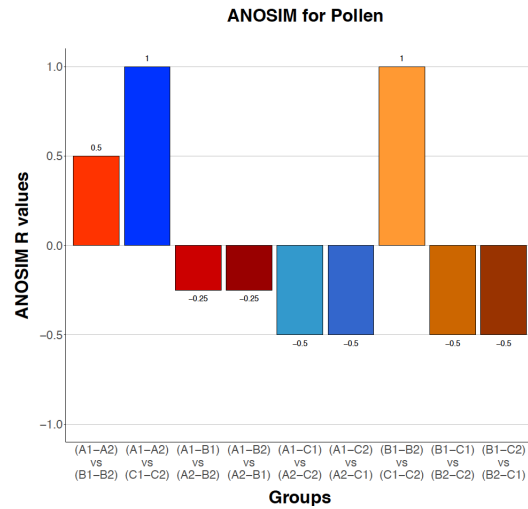
**B**



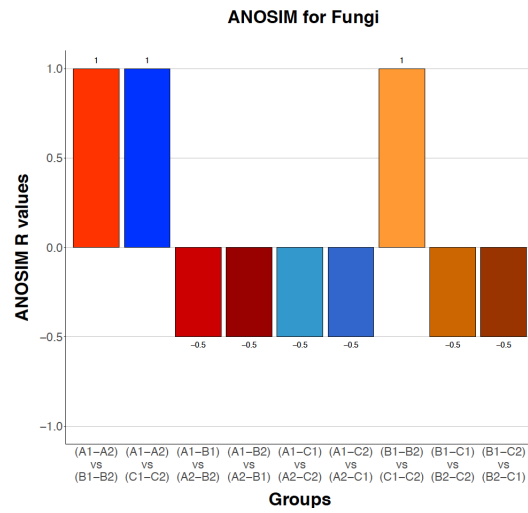
**FIG S3 (A)** Sequence information from NGS processing (Bacteria). **(B)** Rarefaction curves.

FIG S4

A



B



C

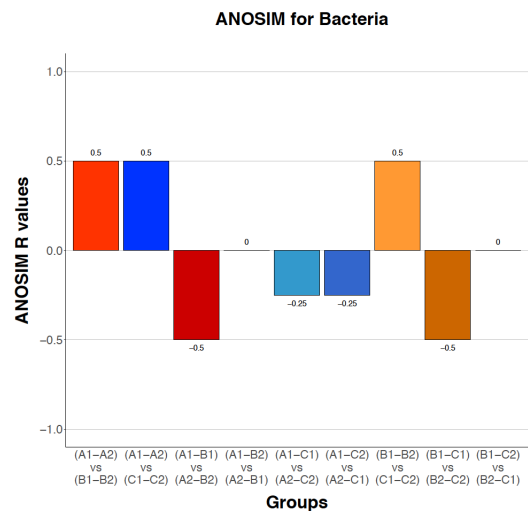


FIG S4.- ANOSIM R values determined for different group combinations between replicates for pollen (A), fungi (B), and bacteria (C).