Electronic Supplementary Material (ESI) for Environmental Science: Processes & Impacts.

Supplementary Information

Table S1. PCR based primer specificity testing on 55 different fungal DNAs.

	Fungi	*Aspergillus*	*Penicillium*	*Cladosporium*	*Alternaria*	*Trichoderma*	*Aureobasidium*	*Stachybotrys*	*Tritirachium*	Eurotiales	Saccharomycetales	Mucorales	Basidiomycetes	Ascomycetes
Acremonium antarcticum	+	-	-	-	-	-	-	-	-	x	~	-	-	+
Alternaria alternata	+	-	-	-	+	-	~	-	-	x	~	-	~	+
Alternaria botrytis/oudemansii	+	-	-	-	~	-	-	-	-	-	-	-	~	+
Ampelomyces quisqualis	+	-	-	-	-	§	-	-	-	§	-	-	~	+
Annulohypoxylon cohaerens	+	x	-	-	-	§	-	-	-	-	~	-	~	+
Anthracocystis flocculosa	+	-	-	-	-	-	-	-	-	x	-	-	+	~
Aspergillus niger	+	+	-	-	-	-	-	-	-	+	-	-	-	+
Aspergillus versicolor	+	+	-	-	-	-	-	-	-	+	-	-	-	+
Aureobasidium pullulans	+	-	-	-	-	-	+	-	-	-	-	-	-	+
Bjerkandera adusta	+	-	-	-	-	-	-	-	-	x	-	-	+	+
Botryotinia fuckeliana	+	-	-	-	-	-	-	-	-	+	~	-	-	+
Botrytis cinerea	+	-	-	-	-	-	-	-	-	~	-	-	-	+
Candida albicans	+	-	-	-	-	-	-	-	-	-	+	-	-	+
Cephalotrichum microsporum	+	-	-	-	-	-	-	~	-	-	-	-	-	+
Chaetomium globosum	+	-	-	-	-	-	-	-	-	x	-	-	-	+
Cladosporium herbarum-complex	+	-	-	+	-	-	-	-	-	§	-	-	-	+
Coprinopsis strossmayeri	+	x	§	-	-	§	-	-	§	x	+	§	+	+
Cyphellophora olivacea	+	§	-	-	-	-	-	-	-	x	-	-	-	+
Dacrymyces stillatus	+	-	-	-	~	-	-	-	-	x	-	-	+	+
Didymella	+	-	-	-	-	-	-	-	-	§	-	-	~	+

aliena														
Epicoccum nigrum	+	-	-	-	-	-	-	-	-	-	-	-	~	+
Exophiala dermatitidis	+	-	-	-	-	~	-	-	-	-	-	-	-	§
Exophiala xenobiotica	+	-	-	-	-	-	-	-	-	-	-	-	-	+
Fusarium oxysporum	+	§	-	-	-	-	-	-	-	-	-	-	-	+
Fusarium culmorum	+	-	-	-	-	-	-	-	-	-	-	-	-	+
Gloeophyllum abietinum	+	-	-	-	-	-	-	-	-	-	-	-	+	+
Isaria farinose	+	§	§	-	-	-	-	~	-	-	~	-	§	+
Meyerozyma guilliermondii	+	-	~	-	-	-	-	-	-	+	+	-	-	+
Microascus brevicaulis	+	-	-	-	-	-	-	~	-	x	-	-	-	+
Mucor plumbeus	+	-	-	-	-	-	-	-	-	-	-	+	-	+
Mycosphaerella macrospora	+	-	-	-	-	-	-	-	-	-	-	-	-	+
Neoascochyta exitialis	+	-	-	-	-	-	-	-	-	§	-	-	~	+
Neonectria ditissima	+	-	§	-	-	-	-	-	-	x	-	-	-	+
Paecilomyces variotii	+	+	-	-	-	-	-	-	-	-	~	-	-	+
Paraengyodontium album	+	-	-	-	-	-	-	-	-	-	-	-	-	+
Penicillium citreonigrum	+	-	+	-	-	-	-	-	-	+	-	-	-	+
Penicillium brevicompactum	+	-	+	-	-	-	-	-	-	+	-	-	-	+
Penicillium chrysogenum	+	-	+	-	-	-	-	-	-	+	-	-	-	+
Phoma herbarum	+	-	-	-	-	-	-	-	-	-	-	-	~	+
Pseudogymnoascus pannorum	+	-	-	-	-	-	-	-	-	-	-	-	-	+
Pseudotaeniolina globose	+	-	-	-	-	-	-	-	-	§	-	-	-	+
Pyronema domesticum	+	§	-	+	-	-	~	-	-	x	~	-	§	+
Rhodotorula mucilaginosa	+	-	-	-	-	-	-	-	-	+	-	-	-	~
Sarocladium strictum	+	-	-	-	-	-	-	~	-	-	-	-	-	+
Schizophyllum commune	+	-	-	-	-	-	-	-	-	§	~	-	§	§

Sistotrema brinkmannii	+	§	§	-	-	-	-	-	-	-	~	-	+	+
Solicoccozyma terricola	+	-	-	-	-	-	-	-	-	-	-	-	+	~
Stachybotrys chartarum	+	-	-	-	-	-	-	+	-	-	-	-	-	~
Tilletiopsis washingtonensis	+	-	-	-	-	-	-	-	-	-	~	-	+	+
Trametes versicolor	+	-	-	-	-	-	-	-	-	x	~	-	+	+
Trichocladium asperum	+	-	§	-	-	-	-	-	-	§	-	-	-	+
Trichoderma harzianum	+	-	-	-	-	+	-	-	-	§	-	-	§	+
Tritirachium oryzae	+	-	-	-	-	-	-	-	+	-	~	-	~	~
Ustilago maydis	+	-	-	-	-	-	-	-	-	-	-	-	+	+
Wallemia sebi	+	-	-	-	-	-	-	-	-	-	+	-	+	~

+ positive; - negative; ~ weak band; § different fragment size; x smear;

Table S2. qPCR primer efficiency, qPCR correlation coefficient, coverage of dynamic range and detection limits of the indoor mold detection system’s core assays measured on serial dilutions of fungal DNA standard mixtures.

Primer set	**Efficiency [%]**	**r^2 value**	**Dynamic range**	**Detection limit [pg DNA]**
Fungi	90 – 92	≥ 0.9991	6-log	0.0300
Aspergillus	89 – 94	≥ 0.9975	4-log	0.2143
Penicillium	84 – 94	≥ 0.9970	6-log	0.0021
Cladosporium	92 – 101	≥ 0.9995	6-log	0.0021
Alternaria	91 – 99	≥ 0.9978	6-log	0.0021
Trichoderma	84 – 91	≥ 0.9981	6-log	0.0021
Aureobasidium	84 – 88	≥ 0.9964	6-log	0.0021
Stachybotrys	93 – 95	≥ 0.9989	4-log	0.2143
Tritirachium	90 – 96	≥ 0.9971	6-log	0.0021
Eurotiales	97 – 98	≥ 0.9991	6-log	0.0043
Saccharomycetales	82 – 89	≥ 0.9970	6-log	0.0021
Mucorales	82 – 101	≥ 0.9901	6-log	0.0021

Basidiomycetes	88 – 92	≥ 0.9989	6-log	0.0043
Ascomycetes	83 – 88	≥ 0.9986	5 – 6-log	0.0236

Table S3. Differences on qPCR detection of samples with single fungal DNAs compared to complex DNA mixtures consisting of 13 fungal species illustrated with qPCR measurements conducted with the specific assays.

Assay	**SINGLE Mean [Cq]**	**Std. Dev. [Cq]**	**R^2**	**Eff. [%]**	**MIX Mean [Cq]**	**Std. Dev. [Cq]**	**R^2**	**Eff. [%]**	**Diff. Eff. [%]**
Alternaria	12.61 – 28.02	0.03 – 0.27	0.9996	82.0	12.62 – 26.96	0.02 – 0.22	0.985	92.4	10.4
Aspergillus	11.47 – 23.08	0.01 – 0.12	0.9994	81.9	11.81 – 21.70	0.08 – 0.24	0.992	105.2	23.3
Aureobasidium	15.16 – 28.49	0.05 – 0.15	0.9987	102.0	14.42 – 28.49	0.04 – 0.22	0.985	92.8	-9.2
Basidiomycetes	17.65 – 31.66	0.00 – 0.12	0.9990	92.0	18.25 – 32.28	0.07 – 0.94	0.996	92.8	0.8
Cladosporium	14.97 – 29.71	0.00 – 1.11	0.9914	89.0	14.91 – 28.76	0.01 – 0.35	0.991	96.0	7.0
Hypocreales	18.77 – 31.39	0.03 – 0.63	0.9992	105.6	18.26 – 31.76	0.07 – 0.41	0.999	97.1	-8.5
Mucorales	18.60 – 31.73	0.01 – 0.88	0.9995	102.5	18.59 – 32.11	0.03 – 0.54	0.998	96.3	-6.2
Penicillium	16.88 – 31.12	0.01 – 0.23	0.9998	90.7	16.84 – 30.69	0.01 – 0.35	0.996	95.3	4.6
Pleosporales	17.02 – 32.76	0.09 – 0.23	0.9996	79.9	16.70 – 32.38	0.03 – 0.11	0.993	80.4	0.5
Saccharomycetales	14.68 – 27.72	0.02 – 0.26	0.9995	104.5	16.30 – 30.93	0.02 – 0.17	0.997	88.3	-16.2
Sordariales	15.74 – 29.30	0.03 – 0.25	0.9998	98.1	15.63 – 29.34	0.04 – 0.19	0.992	97.2	-0.9
Trichoderma	15.99 – 29.63	0.02 – 0.20	0.9988	96.0	15.78 – 30.47	0.00 – 0.37	0.990	88.3	-7.8
Tritirachium	15.44 – 29.04	0.03 – 0.23	0.9999	96.2	15.10 – 29.44	0.02 – 0.15	0.992	90.2	-6.0

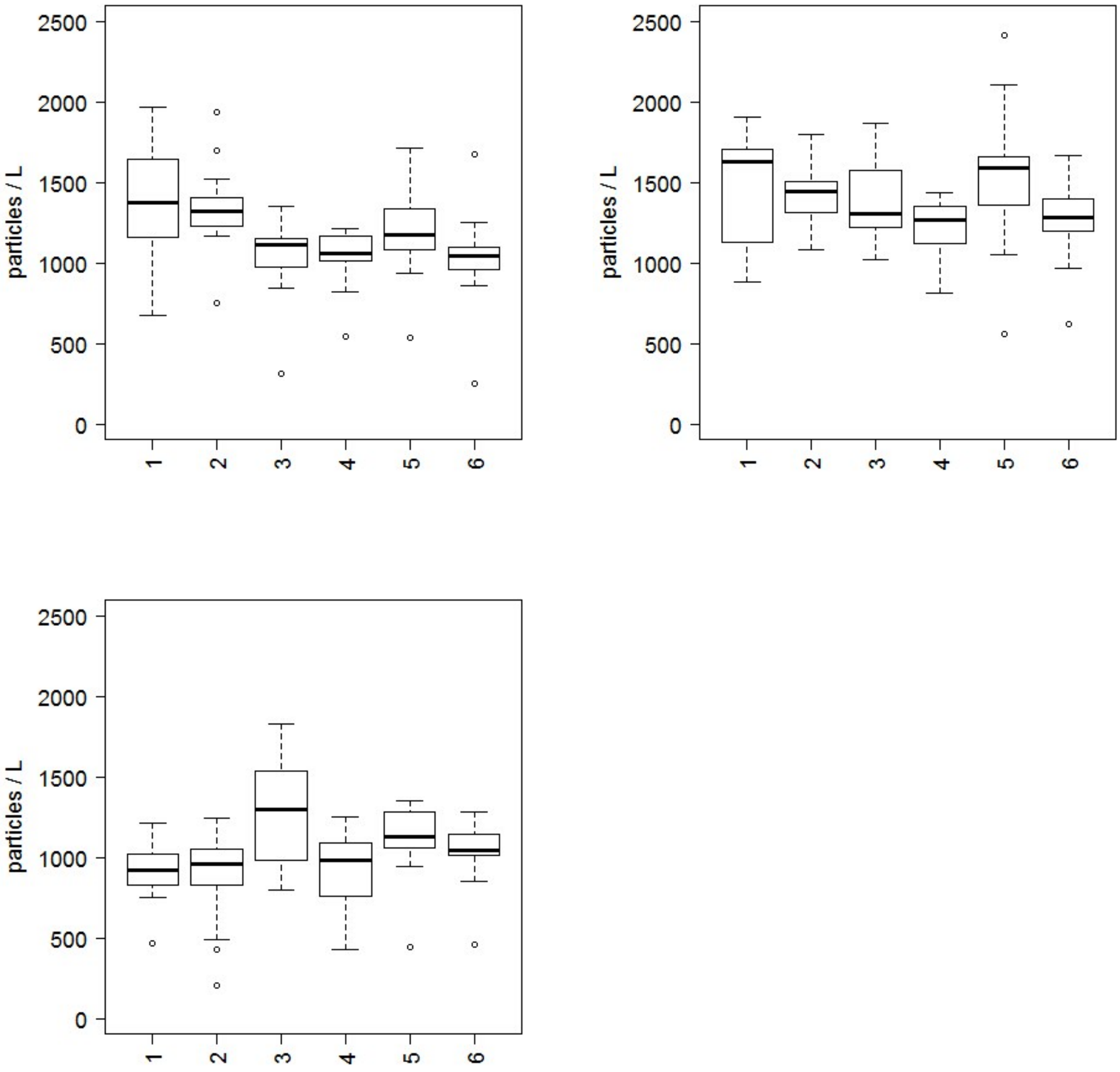

Fig. S1. Particle count deviations within the bioaerosol chamber of 3 independent sampling campaigns (1 upper left; 2 upper right; 3 bottom left) during 6 bioaerosol collections with the Coriolis µ (1-6).

Table S4. Relative abundances in ‰ of the 50 most abundant OTUs in air samples. Samples were taken in October 2015 and January 2016 from an outdoor reference, a vacant office and a wine cellar. At each campaign three samples were collected and subjected to high-throughput sequencing for fungal community analysis. Due to very low airborne fungal particles in the office in October 2015, data were obtained only from one of the three samples. Data from separate samples were combined for the OTU abundance table. Total OTU numbers and Simpson's diversity index (D1=1-D) are shown for combined samples.

Sampling Site		**Oct 2015**			**Jan 2016**		
		Outdoor	**Office**	**Cellar**	**Outdoor**	**Office**	**Cellar**
# samples		3	1	3	3	3	3
# OTUs		173	70	169	199	189	220
1-D		0,65	0,94	0,75	0,82	0,95	0,95
OTU_ID	**Genus**						
OTU_2	*Mycosphaerella*	567,0	38,6	217,7	381,7	82,5	122,0
OTU_1	*Apiotrichum*	31,9	179,1	12,6	49,3	180,6	56,7
OTU_5	*Athelia*	0,1	4,1	402,3	0,0	0,0	1,8
OTU_6	*Bjerkandera*	0,6	0,0	9,5	141,8	31,7	90,0
OTU_7	*Ascochyta*	162,4	0,0	4,8	9,9	36,7	31,1
OTU_19	*Trametes*	0,3	10,7	0,7	95,4	36,6	86,5
OTU_11	*Homophron*	0,2	0,1	190,6	0,0	0,0	1,8
OTU_4	*Pseudeurotium*	11,5	64,7	4,0	20,8	60,2	17,0
OTU_3	*Hyphodiscus*	6,8	57,0	2,7	14,3	38,1	11,0
OTU_8	*Inocybe*	9,8	86,9	2,0	5,3	13,1	7,2
OTU_20	*Daedaleopsis*	0,0	0,0	0,0	2,1	38,1	64,1
OTU_14	*Alternaria*	41,2	0,0	8,5	28,1	1,7	0,9
OTU_15	*Ilyonectria*	5,3	18,6	1,9	8,6	30,4	6,6
OTU_9	*Hyphodiscus*	2,5	40,4	1,9	6,4	12,6	5,9
OTU_13	*Oidiodendron*	4,8	15,4	1,5	6,2	24,3	8,3
OTU_10	*Hyphodiscus*	2,3	25,6	1,2	4,3	17,4	4,4
OTU_16	*Exophiala*	3,1	19,8	0,8	6,4	17,9	4,4
OTU_30	*Penicillium*	0,4	0,0	0,3	0,7	4,1	45,7
OTU_17	*Clavulina*	1,9	25,1	0,5	3,1	14,1	4,0
OTU_27	*Penicillium*	0,2	6,4	6,5	0,3	1,1	22,9
OTU_37	*Penicillium*	0,0	1,0	1,3	2,0	3,8	28,5
OTU_12	*Saitozyma*	3,1	6,0	1,5	4,6	15,9	5,0
OTU_93	*Absidia*	0,0	0,0	5,7	0,0	0,0	30,4
OTU_32	*Mortierella*	1,0	25,1	0,3	2,6	5,2	1,3
OTU_24	*Malbranchea*	0,0	0,0	30,5	0,0	0,0	4,9
OTU_34	*Penidiella*	0,0	13,1	2,2	0,0	0,0	15,5
OTU_29	*Boletus*	5,0	6,3	0,9	2,5	11,9	3,1
OTU_115	*Peniophora*	0,1	0,0	0,0	11,7	1,7	15,6
OTU_67	*Letendraea*	9,4	14,5	4,5	0,4	0,2	0,0
OTU_36	*Zasmidium*	0,0	0,0	5,0	0,0	0,0	23,1
OTU_64	*Aspergillus*	0,0	12,6	6,5	0,0	1,1	5,7
OTU_86	*Aspergillus*	0,1	14,0	4,8	0,2	0,5	5,8
OTU_28	*Aureobasidium*	20,1	0,0	0,0	5,3	0,0	0,1
OTU_21	*Leptodontidium*	2,4	7,3	0,5	3,5	8,6	3,0
OTU_26	*Tetracladium*	1,2	6,1	0,6	2,6	11,0	1,9
OTU_38	*Trichoderma*	2,0	0,0	0,9	4,4	11,6	3,8
OTU_22	*Cryptendoxyla*	0,0	12,4	6,1	0,0	0,0	3,3
OTU_44	*Ischnoderma*	0,0	0,0	0,0	9,4	8,7	3,5
OTU_23	*Fusarium*	1,6	0,9	0,9	3,5	10,5	3,9
OTU_842	*Kendrickiella*	0,1	0,0	0,0	5,4	2,3	13,4
OTU_56	*Fellozyma*	2,1	5,1	0,3	1,7	9,0	2,1
OTU_75	*Tetracladium*	0,7	9,8	0,7	0,8	6,1	2,0
OTU_55	*Xylodon*	0,1	0,0	0,1	7,8	6,2	5,8
OTU_63	*Fusarium*	0,8	12,9	0,1	0,7	3,4	1,8
OTU_45	*Penicillium*	0,0	0,0	8,7	0,0	0,0	11,0
OTU_25	*Pezizales*	1,3	9,3	0,8	2,4	3,6	1,6
OTU_48	*Mycosphaerella*	0,0	0,0	0,4	0,0	0,0	17,5
OTU_1093	*Nectria*	1,4	6,3	0,3	0,8	7,8	1,3
OTU_245	*Fusarium*	0,4	14,2	0,3	0,6	1,8	0,1
OTU_320	*Phialophora*	0,1	14,9	0,0	0,1	0,8	0,7

Table S5. Relative abundences (given in percent from detected abundances within each sample) represented in the heat map of figure 5. Bdl: Below detection limit.

Assay	OUT1 [%]	CEL1 [%]	OFF1 [%]	OUT2 [%]	CEL2 [%]	OFF2 [%]
Aspergillus	Bdl	Bdl	Bdl	Bdl	21.67	Bdl
Penicillium	0.94	6.06	3.57	Bdl	8.58	Bdl
Cladosporium	46.12	5.87	57.99	22.63	5.49	Bdl
Alternaria	2.50	0.30	Bdl	0.89	Bdl	Bdl
Trichoderma	Bdl	Bdl	15.29	Bdl	Bdl	Bdl
Aureobasidium	3.14	Bdl	Bdl	13.94	0.15	Bdl
Stachybotrys	Bdl	Bdl	Bdl	Bdl	Bdl	Bdl
Eurotiales	1.65	16.42	9.73	1.79	35.26	Bdl
Saccharomycetales	Bdl	Bdl	Bdl	Bdl	0.26	Bdl
Mucorales	Bdl	1.36	2.74	Bdl	3.57	Bdl
Basidiomycetes	45.65	69.99	10.68	60.74	25.03	100.00

Table S6. Spearman's rank correlation of qPCR and sequencing data. Nd: Not detected.

Assay	Correlation	*p*-value
Aspergillus	0.78	0.23
Penicillium	0.80	0.33
Cladosporium	*	
Alternaria	1.00	0.08
Trichoderma	*	
Aureobasidium	0.80	0.33
Stachybotrys	Nd	
Eurotiales	1.00	0.08
Saccharomycetales	0.82	0.18
Mucorales	1.00	< 0.01
Basidiomycetes	0.80	0.33

* underrepresented in qPCR or sequencing data