

Supplementary Materials: Six Feet under Microbiota: Microbiologic Contamination and Toxicity Profile in Three Urban Cemeteries from Lisbon, Portugal

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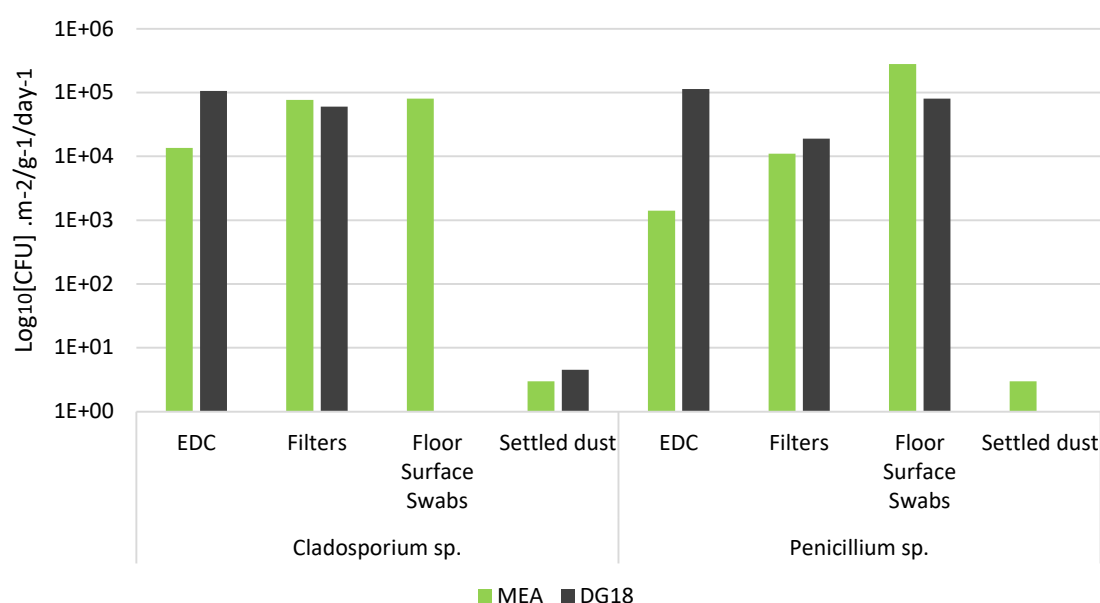


Figure S1. The prevalent fungal genera on MEA and DG18 in samples from different matrices (EDC: CFU.m⁻².day⁻¹; Fillters and Swabs CFU.m⁻²; Settled dust: CFU.g⁻¹).

Table S1. Assessment of species diversity (Shannon's and Simpson's indices) in each sampling method.

Method	Fungi	Culture media	Diversity indices	
		MEA (CFU. m ⁻² .day ⁻¹ /m ⁻² /g ⁻¹)	Shannon Index (H)	Simpson Index (D)
EDC	<i>Alternaria</i> sp.	530.786	1.03	1.86
	<i>Aureobasidium</i> sp.	110.157		
	<i>C.sitophila</i>	114.157		
	<i>Chrysosporium</i> sp.	13571.639		
	<i>F. verticilloides</i>	2441.614		
	<i>A. section Fumigati</i>	106.157		
	<i>A. section Nigri</i>	424.628		
	<i>Penicillium</i> sp.	1404.042		
	<i>Trichoderma</i> sp.	106.157		
	<i>Ulocladium</i> sp.	116.157		

FILTER	<i>Allternaria</i> sp.	500	0.95	1.67
	<i>Aureobasidium</i> sp.	500		
	<i>C.sitophila</i>	4000		
	<i>Chrysonilia</i> sp.	500		
	<i>Chrysosporium</i> sp.	1500		
	<i>Cladosporium</i> sp.	76500		
	<i>A. section Fumigati</i>	500		
	<i>Fusarium equiseti</i>	1000		
	<i>A. section Nidulantes</i>	2000		
Settled Dust	<i>Penicillium</i> sp.	11000	1.33	3.65
	<i>Ulocladium</i> sp.	2000		
	<i>Aureobasidium</i> sp.	1.5		
	<i>Cladosporium</i> sp.	3		
	<i>Penicillium</i> sp.	3		
SWAB	<i>Trichoderma</i> sp.	4	1.13	2.23
	<i>Aureobasidium</i> sp.	10000		
	<i>C.sitophila</i>	40000		
	<i>Chrysosporium</i> sp.	10000		
	<i>Cladosporium</i> sp.	80000		
	<i>A. section Fumigati</i>	20000		
	<i>Penicillium</i> sp.	280000		

Samples were kept refrigerated (-until 4 °C) for a maximum of 24 h before RNA was extracted from the isolated sample (5 mL in air samples and 1.5 ml in surface samples) with the NZY Viral RNA Isolation kit, from Nzytech, according to manufacturer's instructions. One step-RT qPCR was performed using NZYSpeedy One-step RT-qPCR probe Master Mix with primers and probes published by CDC (available on <https://www.cdc.gov/coronavirus/2019-ncov/lab/rt-pcr-panel-primer-probes.html>), which detect two viral gene regions (N1 and N2). qPCR was performed on BioRad CFX96 PCR machine. In each analysis a positive (a SARS-CoV-2 positive sample) and a negative (water) sample was included. Furthermore, in order to detect possible PCR inhibitors an internal control was added to each PCR.

Table S2. Novel Coronavirus (2019-nCoV) Real-time RT-PCR Panel Primers and Probes.

Name	Description	Oligonucleotide Sequence (5'>3')	Label1
2019-nCoV_N1-F	2019-nCoV_N1 Forward Primer	5'-GAC CCC AAA ATC AGC GAA AT-3'	None
2019-nCoV_N1-R	2019-nCoV_N1 Reverse Primer	5'-TCT GGT TAC TGC CAG TTG AAT CTG-3'	None
2019-nCoV_N1-P	2019-nCoV_N1 Probe	5'-FAM-ACC CCG CAT TAC GTT TGG TGG ACC-BHQ1-3'	FAM, BHQ-1
2019-nCoV_N2-F	2019-nCoV_N2 Forward Primer	5'-TTA CAA ACA TTG GCC GCA AA-3'	None
2019-nCoV_N2-R	2019-nCoV_N2 Reverse Primer	5'-GCG CGA CAT TCC GAA GAA-3'	None

2019-nCoV_N2-P	2019-nCoV_N2 Probe	5'-FAM-ACA ATT TGC CCC CAG CGC TTC AG- BHQ1-3'	FAM, BHQ-1
Spike In		TATAA Universal RNA Spike I	FAM

Fungal DNA was extracted using the ZR Fungal/Bacterial DNA MiniPrep Kit (Zymo Research, Irvine, USA) and molecular identification was performed by Real Time PCR (qPCR) using the CFX-Connect PCR System (Bio-Rad). Reactions included 1× iQ Supermix (Bio-Rad, Portugal), 0.5 µM of each primer, and 0.375 µM of TaqMan probe in a total volume of 20 µL. Amplification followed a three-step PCR: 40 cycles with denaturation at 95 °C for 30 s, annealing at 52 °C for 30 s, and extension at 72 °C for 30 s (Supplementary material – Table S3). A non-template control and a positive control consisting of DNA obtained from a reference that belonged to the culture collection of the Reference Unit for Parasitic and Fungal Infections, Department of Infectious Diseases of the National Institute of Health, from Dr. Ricardo Jorge. These strains have been sequenced for ITS, B-tubulin, and Calmodulin.

Table S3. Sequence of primers and TaqMan probes used for real-time PCR.

Fungal Species/Sections Targeted	Sequences	Reference
<i>Flavi</i>		
Forward Primer	5'–GTCCAAGCAACAGGCCAAGT–3'	Mayer, Z.; Bagnara, A.; Färber, P.; Geisen, R. Quantification of the copy number of nor-1, a gene of the aflatoxin biosynthetic pathway by real-time PCR, and its correlation to the cfu of <i>Aspergillus flavus</i> in foods. <i>Int. J. Food Microbiol.</i> 2003, 82, 143–151.
Reverse Primer	5'–TCGTGCATGTTGGTGATGGT–3'	
Probe	5'–TGTCTTGATCGGCGCCCG–3'	
<i>Fumigati</i>		
Forward Primer	5'–CGCGTCCGGTCCTCG–3'	Cruz-Perez, P.; Buttner, M.P.; Stetzenbach, L.D. Detection and quantitation of <i>Aspergillus fumigatus</i> in pure culture using polymerase chain reaction. <i>Mol. Cell. Probes.</i> 2001, 15, 81–88.
Reverse Primer	5'–TTAGAAAAATAAAGTTGGGTGTCCG–3'	
Probe	5'–TGTCACCTGCTCTGTAGGCCCG–3'	
<i>Circumdati</i>		
Forward Primer	5'–CGGGTCTAATGCAGCTCCAA–3'	[12]
Reverse Primer	5'–CGGGCACCAATCCTTTCA–3'	
Probe	5'–CGTCAATAAGCGCTTTT–3'	
<i>Nidulantes</i>		
Forward Primer	5'–CGGCGGGGAGCCCT–3'	United States Environmental Protection Agency (EPA), About the National Exposure Research Laboratory (NERL), (n.d.). Available online: http://www.epa.gov/nerlcwww/moldtech.html
Reverse Primer	5'–CCATTGTTGAAAGTTTTGACTGATCTTA–3'	
Probe	5'–AGACTGCATCACTCTCAGGCATGAAGTTCAG–3'	

In all samples, 38 mycotoxins were analyzed by HPL-MS ((HPLC) Nexera (Shimadzu, Tokyo, Japan) with a mass spectrometry detector API 4000 (Sciex, Foster City, CA, USA). The mycotoxin concentration was calculated using external calibration. The Limits of Detection (LOD) obtained for each mycotoxin with the analytical method used are presented in Table S4.

Table S4. LOD values for the samples analysed.

Type of Sample	Mycotoxins	LOD ($\mu\text{g/kg}$)
EDC	15-Acetyldeoxynivalenol	8
	3-Acetyldeoxynivalenol Aflatoxin B ₁	4
	Aflatoxin B ₂	1
	Aflatoxin G ₁	1
	Aflatoxin G ₂	1
	Aflatoxin M ₁	1
	Deepoxydeoxynivalenol	5
	Deoxynivalenol	8
	Deoxynivalenol-3-glucoside	5
	Diacetoxyscirpenol	2
	Fumonisin B ₁	4
	Fumonisin B ₂	3
	Fusarenon X	10
	Griseofulvin	2
	HT-2 toxin	4
	Mevinolin	7
	Monoacetoxyscirpenol	2
	Mycophenolic acid	3
	Neosolaniol	3
	Nivalenol	4
	Ochratoxin A	2
	Ochratoxin B	2
	Patulin	8
	Roquefortine C	2
	Sterigmatocystin	1
	T-2 tetraol	2
	T-2 toxin	2
	T-2 triol	5
	Zearalanone	2
	Zearalenone	1
	α -Zearalanol	2
	α -Zearalenol	2
	β -Zearalanol	2
	β -Zearalenol	3
Filters	15Acetyldeoxynivalenol	8
	3-Acetyldeoxynivalenol Aflatoxin B ₁	4
	Aflatoxin B ₂	1
	Aflatoxin G ₁	1
	Aflatoxin G ₂	1

	Aflatoxin M ₁	1
	Deepoxydeoxynivalenol	5
	Deoxynivalenol	8
	Deoxynivalenol-3-glucoside	5
	Diacetoxyscirpenol	2
	Fumonisin B ₁	4
	Fumonisin B ₂	3
	Fusarenon X	10
	Griseofulvin	2
	HT-2 toxin	4
	Mevinolin	7
	Monoacetoxyscirpenol	2
	Mycophenolic acid	3
	Neosolaniol	3
	Nivalenol	4
	Ochratoxin A	2
	Ochratoxin B	2
	Patulin	8
	Roquefortine C	2
	Sterigmatocystin	1
	T-2 tetraol	2
	T-2 toxin	2
	T-2 triol	5
	Zearalanone	2
	Zearalenone	1
	α -Zearalanol	2
	α -Zearalenol	1
	β -Zearalanol	3
	β -Zearalenol	2
Settled dust	15Acetyldeoxynivalenol	20
	3-Acetyldeoxynivalenol Aflatoxin B ₁	10
	Aflatoxin B ₂	2
	Aflatoxin G ₁	1
	Aflatoxin G ₂	2
	Aflatoxin M ₁	1
	Deepoxydeoxynivalenol	2
	Deoxynivalenol	11
	Deoxynivalenol-3-glucoside	8
	Diacetoxyscirpenol	2
	Fumonisin B ₁	1
	Fumonisin B ₂	2
	Fusarenon X	12
	Griseofulvin	5
	HT-2 toxin	3
	Mevinolin	11
	Monoacetoxyscirpenol	4
	Mycophenolic acid	6
	Neosolaniol	5
	Nivalenol	7

Ochratoxin A	3
Ochratoxin B	4
Patulin	18
Roquefortine C	5
Sterigmatocystin	2
T-2 tetraol	5
T-2 toxin	3
T-2 triol	10
Zearalanone	2
Zearalenone	2
α -Zearalanol	4
α -Zearalenol	3
β -Zearalanol	4
β -Zearalenol	3
