Supplemental Text for

Mycosands: Fungal diversity and abundance in beach sand and recreational waters - relevance to human health

Table S1: Number of samples by matrix (sand or water) per country:

Country	AU	IE	FR	GR	IL	IT	LT	NL	PT	RO	SL	RS	TR	Total
Sand	9	31	19	51	17	13	10	13	34	80	4	9	82	372
Water	0	31	19	45	0	1	10	1	34	80	4	9	82	316

Note: AU=Australia (Sydney), IE=Ireland, FR=France, GR=Greece, IL=Israel, IT=Italy, LT=Lithuania, NL=Netherlands, PT=Portugal, RO=Romania, SL=Slovenia, RS=Serbia, TR=Turkey

Table S2: Number of sampling events per country for sand samples per region

Sand - number of samples														
Country	AU	IE	FR	GR	IL	IT	LT	NL	PT	RO	SL	RS	TR	Total
Black Sea	0	0	0	0	0	0	0	0	0	80	0	0	0	80
Mediterranean	0	0	15	19	17	13	0	0	0	0	9	4	82	159
Northwest Europe	0	51	16	0	0	0	10	13	0	0	0	0	0	90
Southwest Europe	0	0	0	0	0	0	0	0	34	0	0	0	0	34
Sydney (Australia)	9	0	0	0	0	0	0	0	0	0	0	0	0	9

Note: AU=Australia (Sydney), IE=Ireland, FR=France, GR=Greece, IL=Israel, IT=Italy, LT=Lithuania, NL=Netherlands, PT=Portugal, RO=Romania, SL=Slovenia, RS=Serbia, TR=Turkey

Table S3: Number of sampling events per country for water samples per region

Water - number of samples											
Country	IE	FR	GR	IT	LT	NL	PT	RO	SL	RS	TR	Total
Black Sea	0	0	0	0	0	0	0	80	0	0	0	80
Mediterranean	0	15	19	1	0	0	0	0	9	4	82	130
Northwest Europe	45	16	0	0	10	1	0	0	0	0	0	72
Southwest Europe	0	0	0	0	0	0	34	0	0	0	0	34

Note: AU=Australia (Sydney), IE=Ireland, FR=France, GR=Greece, IL=Israel, IT=Italy, LT=Lithuania, NL=Netherlands, PT=Portugal, RO=Romania, SL=Slovenia, RS=Serbia, TR=Turkey

Table S4: Relative humidity per region

Variable	Median (range) in %				P value
	Mediterranean (N=159)	Northwest Europe (N=90)	Southwest Europe (N=34)	Sydney, Australia (N=9)	
Relative humidity	64.0 (19.0, 98.0)	78.0 (60.0, 97.0)	70.0 (25.0, 96.0)	60.0 (60.0, 67.0)	< 0.001

Table S5: Number of samples with fungi in sand samples by country (CFU/g)

	AU (N=9)	FR (N=31)	GR (N=19)	IE (N=51)	IL (N=17)	IT (N=13)	LT (N=10)	NL (N=13)	PT (N=34)	RO (N=80)	RS (N=4)	SL (N=9)	TR (N=82)	Total (N=372)
Sand														
Fungi (all)														
N	9	31	19	51	17	13	10	13	34	80	4	9	82	372
Mean (SD)	624.1	46.5	1051.1	61.1	158.6	78.2	1127.4	144.2	542.6	208.5	310.0	1203.9	308.8	321.3
	(527.3)	(168.3)	(1010.6)	(99.8)	(214.8)	(104.6)	(1122.4)	(338.5)	(1181.9)	(340.7)	(301.7)	(450.0)	(366.9)	(610.3)
Median(Range)	366.7	0.0	650.0	20.0	40.0	16.7	1002.5	15.0	90.8	72.5	262.5	1166.7	166.7	89.2
	(83.3,1533.3)	(0.0,928.3)	(57.5,3365.0)	(0.0,581.7)	(5.0,647.0)	(0.0,300.0)	(3.3,3497.5)	(0.0,1207.5)	(1.7,6400.0)	(0.5,2170.0)	(16.7,698.3)	(630.0,2268.3)	(0.0,1583.3)	(0.0,6400.0)
Aspergillus spp														
N	6	31	19	51	15	13	10	2	34	0	4	9	70	264
Mean (SD)	296.7	15.9	716.2	5.5	73.7	21.8	3.2	40.0	107.5	NA	123.3	367.0	84.3	117.5
	(425.3)	(38.0)	(867.6)	(9.3)	(139.0)	(38.1)	(3.2)	(49.5)	(261.5)		(103.2)	(188.5)	(153.3)	(325.6)
Median(Range)	48.3	0.0	310.0	1.7	5.0	0.0	2.5	40.0	1.7	NA	124.2	323.3	33.3	5.0
	(0.0,943.3)	(0.0,156.7)	(50.0,2930.0)	(0.0,40.0)	(0.0,430.0)	(0.0,116.7)	(0.0,10.0)	(5.0,75.0)	(0.0,900.0)		(16.7,228.3)	(116.7,748.3)	(0.0,833.3)	(0.0,2930.0)
Aspergillus section Fumigati														
N	0	31	13	0	9	13	10	2	8	0	0	0	20	106
Mean (SD)	NA	10.0	60.2	NA	7.2	10.3	3.1	13.8	2.1	NA	NA	NA	13.3	15.4
		(26.4)	(137.3)		(10.9)	(22.1)	(3.1)	(15.9)	(5.9)				(37.3)	(54.5)
Median(Range)	NA	0.0	0.0	NA	0.0	0.0	2.5	13.8	0.0	NA	NA	NA	0.0	0.0
		(0.0,91.7)	(0.0,425.0)		(0.0,25.0)	(0.0,66.7)	(0.0,10.0)	(2.5,25.0)	(0.0,16.7)				(0.0,166.7)	(0.0,425.0)
Aspergillus section Nigri														
N	3	0	19	0	6	13	0	2	34	0	0	9	64	150
Mean (SD)	568.9	NA	174.2	NA	46.7	11.5	NA	26.2	46.4	NA	NA	2.8	54.6	70.6
	(471.1)		(245.3)		(107.0)	(21.9)		(33.6)	(164.5)			(8.3)	(155.4)	(184.7)
Median(Range)	723.3	NA	95.0	NA	2.5	0.0	NA	26.2	0.0	NA	NA	0.0	0.0	0.0
	(40.0,943.3)		(5.0,950.0)		(0.0,265.0)	(0.0,66.7)		(2.5,50.0)	(0.0,833.3)			(0.0,25.0)	(0.0,833.3)	(0.0,950.0)
Candida spp														
N	6	0	0	51	12	0	10	1	10	24	4	9	28	155
Mean (SD)	31.1	NA	NA	29.2	19.3	NA	1.0	5.0	2.2	4.6	27.1	6.7	19.0	17.8
	(51.8)			(85.1)	(38.3)		(2.4)	(NA)	(6.9)	(11.0)	(26.7)	(11.2)	(54.0)	(56.7)
Median(Range)	0.0	NA	NA	1.7	5.0	NA	0.0	5.0	0.0	0.0	29.2	0.0	0.0	0.0
	(0.0,123.3)			(0.0,555.0)	(0.0,105.0)		(0.0,7.5)	(5.0,5.0)	(0.0,21.7)	(0.0,40.0)	(0.0,50.0)	(0.0,30.0)	(0.0,250.0)	(0.0,555.0)

Candida albicans														
N	0	0	0	0	6	0	0	0	0	4	4	0	5	19
Mean (SD)	NA	NA	NA	NA	1.7 (2.6)	NA	NA	NA	NA	5.0 (10.0)	27.1 (26.7)	NA	3.3 (7.5)	8.2 (15.9)
Median(Range)	NA	NA	NA	NA	0.0 (0.0,5.0)	NA	NA	NA	NA	0.0 (0.0,20.0)	29.2 (0.0,50.0)	NA	0.0 (0.0,16.7)	0.0 (0.0,50.0)
Candida parapsilosis														
N	3	0	0	0	6	0	0	0	0	4	0	9	0	22
Mean (SD)	41.1 (71.2)	NA	NA	NA	4.2 (3.8)	NA	NA	NA	NA	7.5 (15.0)	NA	5.6 (10.1)	NA	10.4(26.7)
Median(Range)	0.0 (0.0,123.3)	NA	NA	NA	5.0 (0.0,10.0)	NA	NA	NA	NA	0.0 (0.0,30.0)	NA	0.0 (0.0,30.0)	NA	0.0 (0.0,123.3)
Candida glabrata														
N	0	0	0	51	0	0	0	0	0	0	0	0	0	51
Mean (SD)	NA	NA	NA	0.6 (1.8)	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.6 (1.8)
Median(Range)	NA	NA	NA	0.0 (0.0,8.3)	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0 (0.0,8.3)
Candida tropicalis														
N	0	0	0	51	0	0	0	0	0	0	0	9	0	60
Mean (SD)	NA	NA	NA	3.1 (8.1)	NA	NA	NA	NA	NA	NA	NA	1.1 (3.3)	NA	2.8 (7.6)
Median(Range)	NA	NA	NA	0.0 (0.0,41.7)	NA	NA	NA	NA	NA	NA	NA	0.0 (0.0,10.0)	NA	0.0 (0.0,41.7)
Candida dubliniensis														
N	0	0	0	34	0	0	5	0	0	0	0	0	0	39
Mean (SD)	NA	NA	NA	37.2 (93.4)	NA	NA	0.5 (1.1)	NA	NA	NA	NA	NA	NA	32.5 (87.9)
Median(Range)	NA	NA	NA	3.3 (0.0,516.7)	NA	NA	0.0 (0.0,2.5)	NA	NA	NA	NA	NA	NA	1.7(0.0,516.7)
Rhodotorula spp														
N	9	8	12	0	9	0	10	0	28	8	4	9	50	147
Mean (SD)	57.4 (59.6)	1.2(1.9)	43.3(143.8)	NA	2.2(2.6)	NA	19.5(43.1)	NA	0.2 (0.7)	13.2(37.5)	15.8 (29.5)	16.5(49.4)	183.0 (320.7)	73.0 (207.7)
Median(Range)	40.0 (0.0,166.7)	0.0 (0.0,5.0)	0.0 (0.0,500.0)	NA	0.0 (0.0,5.0)	NA	0.0 (0.0,130.0)	NA	0.0 (0.0,3.3)	0.0 (0.0,106.0)	1.7 (0.0,60.0)	0.0 (0.0,148.3)	0.0 (0.0,1333.3)	0.0 (0.0,1333.3)

Cryptococcus spp														
N	6	4	0	0	5	0	10	0	10	0	4	0	0	39
Mean (SD)	40.6 (53.2)	125.0 (250.0)	NA	NA	14.0 (25.8)	NA	3.2 (7.0)	NA	0.2 (0.5)	NA	38.3 (41.3)	NA	NA	25.7 (83.3)
Median(Range)	13.3 (0.0,110.0)	0.0 (0.0,500.0)	NA	NA	5.0 (0.0,60.0)	NA	0.0 (0.0,22.5)	NA	0.0 (0.0,1.7)	NA	35.0 (0.0,83.3)	NA	NA	0.0 (0.0,500.0)
Fusarium spp														
N	9	0	13	0	3	0	10	3	34	0	4	9	35	120
Mean (SD)	51.1 (40.6)	NA	22.3 (47.0)	NA	16.7 (28.9)	NA	2.5 (4.2)	36.7 (36.4)	4.2 (12.6)	NA	19.6 (25.7)	295.7 (107.3)	39.0 (86.3)	43.2 (94.0)
Median(Range)	33.3 (6.7, 123.3)	NA	0.0 (0.0, 150.0)	NA	0.0 (0.0, 50.0)	NA	0.0 (0.0, 10.0)	25.0 (7.5, 77.5)	0.0 (0.0, 68.3)	NA	10.8 (0.0, 56.7)	228.3 (180.0, 428.3)	16.7 (0.0, 400.0)	0.8 (0.0, 428.3)
Yeast														
N	9	8	15	51	17	0	10	2	28	52	4	9	56	261
Mean (SD)	105.6 (62.8)	63.7 (177.6)	44.7 (131.7)	29.2 (85.1)	18.9 (35.9)	NA	150.2 (393.9)	3.8 (1.8)	1.0 (4.2)	7.3 (19.5)	106.7 (112.5)	23.1 (48.2)	178.6 (316.5)	63.2 (187.0)
Median(Range)	123.3 (16.7,190.0)	0.0 (0.0,503.3)	0.0 (0.0,500.0)	1.7 (0.0,555.0)	5.0 (0.0,110.0)	NA	11.2 (0.0,1265.0)	3.8 (2.5,5.0)	0.0 (0.0,21.7)	0.0 (0.0,106.0)	90.0 (0.0,246.7)	0.0 (0.0,148.3)	0.0 (0.0,1333.3)	0.0 (0.0,1333.3)
Allergenic														
N	0	0	0	51	0	0	0	0	18	4	0	0	6	79
Mean (SD)	NA	NA	NA	27.5 (35.6)	NA	NA	NA	NA	970.7 (1507.2)	244.8 (160.2)	NA	NA	0.0 (0.0)	251.3 (808.7)
Median(Range)	NA	NA	NA	15.0 (0.0,170.0)	NA	NA	NA	NA	252.5 (50.0,6400.0)	310.0 (9.0,350.0)	NA	NA	0.0 (0.0,0.0)	21.7 (0.0,6400.0)
Dematiaceous fungi														
N	9	31	19	0	17	13	10	13	34	0	0	9	82	237
Mean (SD)	10.7 (13.5)	0.1 (0.6)	34.7 (89.7)	NA	1.2 (3.8)	15.4 (50.7)	258.8 (803.3)	27.7 (75.8)	71.0 (142.0)	NA	NA	7.2 (12.4)	17.1 (63.8)	32.9 (180.6)
Median(Range)	3.3 (0.0,36.7)	0.0 (0.0,3.3)	0.0 (0.0,350.0)	NA	0.0 (0.0,15.0)	0.0 (0.0,183.3)	1.7 (0.0,2545.0)	0.0 (0.0,275.0)	15.0 (0.0,600.0)	NA	NA	0.0 (0.0,31.7)	0.0 (0.0,416.7)	0.0 (0.0,2545.0)
Dermatophytes														
N	0	0	0	51	0	0	0	1	24	8	0	0	6	90
Mean (SD)	NA	NA	NA	4.4 (8.7)	NA	NA	NA	7.5 (NA)	7.6 (34.0)	25.0 (53.5)	NA	NA	34.7 (32.7)	9.1 (26.6)
Median(Range)	NA	NA	NA	1.7 (0.0,53.3)	NA	NA	NA	7.5 (7.5,7.5)	0.0 (0.0,166.7)	0.0 (0.0,150.0)	NA	NA	20.8 (0.0,83.3)	0.0 (0.0,166.7)

Table S6: Number of samples with fungi in water samples by country (CFU/ml)

		FR (N=31)	GR (N=19)	IE (N=45)	IT (N=1)	LT (N=10)	NL (N=1)	PT (N=34)	RO (N=79)	RS (N=4)	SL (N=9)	TR (N=82)	Total (N=315)
Water													
Fungi (all)													
N		31	19	45	0	10	0	34	79	4	9	82	313
Mean (SD)		7.5	8.5	39.5	NA	13.9	NA	13.5	5.2	159.6	12.4	23.2	18.6
		(32.4)	(18.1)	(236.8)		(28.1)		(26.0)	(9.9)	(154.3)	(37.2)	(43.6)	(96.4)
Median(Range)		0.0	0.0	1.7	NA	2.5	NA	4.2	0.0	161.7	0.0	0.0	0.0
		(0.0,181.7)	(0.0,62.0)	(0.0,1591.7)		(0.0,91.7)		(0.0,131.7)	(0.0,55.0)	(5.0,310.0)	(0.0,111.7)	(0.0,250.0)	(0.0,1591.7)
***Aspergillus* spp**													
N		31	19	45	0	10	0	34	0	4	0	70	213
Mean (SD)		7.4	4.8	0.8	NA	0.3	NA	3.4	NA	98.3	NA	10.0	7.4
		(32.5)	(15.5)	(2.3)		(1.1)		(14.9)		(94.2)		(25.7)	(26.8)
Median(Range)		0.0	0.0	0.0	NA	0.0	NA	0.0	NA	93.3	NA	0.0	0.0
		(0.0,181.7)	(0.0,62.0)	(0.0,13.3)		(0.0,3.3)		(0.0,83.3)		(5.0,201.7)		(0.0,133.3)	(0.0,201.7)
Aspergillus* section *Fumigati													
N		31	13	0	0	10	0	0	0	0	0	20	74
Mean (SD)		4.1	1.5	NA	NA	0.2	NA	NA	NA	NA	NA	0.8	2.3
		(16.1)	(5.5)			(0.5)						(3.7)	(10.9)
Median(Range)		0.0	0.0	NA	NA	0.0	NA	NA	NA	NA	NA	0.0	0.0
		(0.0,90.0)	(0.0,20.0)			(0.0,1.7)						(0.0,16.7)	(0.0,90.0)
Aspergillus* section *Nigri													
N		3	19	0	0	0	0	34	0	0	0	64	120
Mean (SD)		1.1	2.6	NA	NA	NA	NA	2.5	NA	NA	NA	2.5	2.5
		(1.9)	(8.1)					(14.3)				(7.8)	(9.9)
Median(Range)		0.0	0.0	NA	NA	NA	NA	0.0	NA	NA	NA	0.0	0.0
		(0.0,3.3)	(0.0,30.0)					(0.0,83.3)				(0.0,41.7)	(0.0,83.3)
***Candida* spp**													
N		0	14	45	0	10	0	0	24	4	0	0	97
Mean (SD)		NA	1.4	37.5	NA	0.2	NA	NA	0.1	3.8	NA	NA	17.8
			(3.6)	(236.0)		(0.8)			(0.4)	(4.4)			(160.9)
Median(Range)		NA	0.0	0.0	NA	0.0	NA	NA	0.0	3.3	NA	NA	0.0

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12
Candida albicans												
N	0	0	45	0	0	0	0	0	4	0	0	49
Mean (SD)	NA	NA	3.8 (25.3)	NA	NA	NA	NA	NA	3.8 (4.4)	NA	NA	3.8 (24.3)
Median(Range)	NA	NA	0.0 (0.0,170.0)	NA	NA	NA	NA	NA	3.3 (0.0,8.3)	NA	NA	0.0 (0.0,170.0)
Candida parapsilosis												
N	0	2	0	0	0	0	0	0	0	0	0	2
Mean (SD)	NA	6.0 (8.5)	NA	NA	NA	NA	NA	NA	NA	NA	NA	6.0 (8.5)
Median(Range)	NA	6.0 (0.0,12.0)	NA	NA	NA	NA	NA	NA	NA	NA	NA	6.0 (0.0,12.0)
Candida glabrata												
N	0	12	45	0	0	0	0	0	0	0	0	57
Mean (SD)	NA	0.2 (0.7)	0.1 (0.3)	NA	NA	NA	NA	NA	NA	NA	NA	0.1 (0.4)
Median(Range)	NA	0.0 (0.0,2.5)	0.0 (0.0,1.7)	NA	NA	NA	NA	NA	NA	NA	NA	0.0 (0.0,2.5)
Candida tropicalis												
N	0	0	45	0	0	0	0	4	0	0	0	49
Mean (SD)	NA	NA	2.6 (13.6)	NA	NA	NA	NA	0.2 (0.5)	NA	NA	NA	2.4 (13.0)
Median(Range)	NA	NA	0.0 (0.0,90.0)	NA	NA	NA	NA	0.0 (0.0,1.0)	NA	NA	NA	0.0 (0.0,90.0)
Candida dubliniensis												
N	0	0	30	0	5	0	0	0	0	0	0	35
Mean (SD)	NA	NA	46.0 (241.6)	NA	0.5 (1.1)	NA	NA	NA	NA	NA	NA	39.5 (223.7)
Median(Range)	NA	NA	0.0 (0.0,1325.0)	NA	0.0 (0.0,2.5)	NA	NA	NA	NA	NA	NA	0.0 (0.0,1325.0)
Rhodotorula spp												
N	0	12	0	0	10	0	28	7	4	0	50	111
Mean (SD)	NA	0.8 (1.9)	NA	NA	0.8 (2.4)	NA	1.1 (4.8)	0.7 (1.9)	12.1 (19.0)	NA	9.3 (40.0)	5.1 (27.4)
Median(Range)	NA	0.0 (0.0,5.0)	NA	NA	0.0 (0.0,7.5)	NA	0.0 (0.0,25.0)	0.0 (0.0,5.0)	4.2 (0.0,40.0)	NA	0.0 (0.0,250.0)	0.0 (0.0,250.0)

***Cryptococcus* spp**												
N	0	0	0	0	0	0	0	0	0	0	0	0
Mean (SD)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Median(Range)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
***Fusarium* spp**												
N	0	0	0	0	0	0	34	0	4	0	35	73
Mean (SD)	NA	NA	NA	NA	NA	NA	0.0 (0.3)	NA	4.6 (5.3)	NA	1.4 (6.2)	1.0 (4.6)
Median(Range)	NA	NA	NA	NA	NA	NA	0.0 (0.0, 1.7)	NA	4.2 (0.0, 10.0)	NA	0.0 (0.0, 33.3)	0.0 (0.0, 33.3)
Yeast												
N	0	15	45	0	10	0	28	51	4	0	56	209
Mean (SD)	NA	2.0 (3.7)	37.5 (236.0)	NA	1.0 (2.4)	NA	1.1 (4.8)	0.5 (2.1)	28.3 (46.8)	NA	8.3 (37.9)	11.3 (111.4)
Median(Range)	NA	0.0 (0.0,12.0)	0.0 (0.0,1585.0)	NA	0.0 (0.0,7.5)	NA	0.0 (0.0,25.0)	0.0 (0.0,10.0)	7.5 (0.0,98.3)	NA	0.0 (0.0,250.0)	0.0 (0.0,1585.0)
Allergenic												
N	0	0	45	0	0	0	18	4	0	0	0	67
Mean (SD)	NA	NA	2.0 (2.6)	NA	NA	NA	16.2 (30.7)	0.5 (1.0)	NA	NA	NA	5.7 (17.0)
Median(Range)	NA	NA	1.7 (0.0,13.3)	NA	NA	NA	5.8 (0.0,131.7)	0.0 (0.0,2.0)	NA	NA	NA	1.7 (0.0,131.7)
Dematiaceous fungi												
N	31	19	0	0	10	0	34	0	0	9	82	185
Mean (SD)	0.1 (0.3)	0.1 (0.6)	NA	NA	0.5 (1.1)	NA	2.5 (5.0)	NA	NA	12.4 (37.2)	1.5 (8.4)	1.8 (10.1)
Median(Range)	0.0 (0.0,1.7)	0.0 (0.0,2.5)	NA	NA	0.0 (0.0,2.5)	NA		NA	NA	0.0 (0.0,111.7)	0.0 (0.0,66.7)	0.0 (0.0,111.7)
Dermatophytes												
N	0	0	45	0	0	0	0	0	0	0	0	45
Mean (SD)	NA	NA	0.0 (0.3)	NA	NA	NA	NA	NA	NA	NA	NA	0.0 (0.3)
Median(Range)	NA	NA	0.0 (0.0,1.7)	NA	NA	NA	NA	NA	NA	NA	NA	0.0 (0.0,1.7

Table S7: Opportunistic dematiaceous fungi isolated from sand and water during the study

Human disease	Fungal genera detected in beach sand with known pathogenic potential
Subcutaneous inf.	*Alternaria, Bipolaris, Cladophialophora, Cladosporium, Curvularia, Exophiala, Exserohilum, Fonsecaea, Microsphaeropsis, Phaeoacremonium, Phialophora, Phoma, Pyrenochaeta, Sporothrix*
Cutaneous inf.	*Alternaria, Chaetomium, Cladosporium, Cladophialophora, Exophiala, Exserohilum, Hortaea, Phialophora, Phoma, Scopulariopsis*
Endophthalmitis	*Microsphaeropsis, Pyrenochaeta*
Deep tissue inf.	*Cladophialophora, Exophiala, Fonsecaea, Microsphaeropsis, Pyrenochaeta*
Mycetoma	*Cladophialophora, Curvularia, Exophiala, Madurella, Neopyrenochaeta, Pyrenochaeta*
Allergic response	*Alternaria, Cladosporium*
Asthma	*Alternaria, Cladosporium*
Sinusitis	*Alternaria, Bipolaris, Coniochaeta, Curvularia, Epicoccum, Exserohilum*
Onychomycosis	*Alternaria, Curvularia, Scopulariopsis*
Keratitis	*Alternaria, Bipolaris, Curvularia, Exserohilum, Phialophora*
Peritonitis	*Aureobasidium, Bipolaris, Curvularia*
Neurotropic inf.	*Bipolaris, Chaetomium, Cladophialophora, Exophiala, Exserohilum, Fonsecaea*
Endocarditis	*Curvularia, Phialophora*
Systemic inf.	*Aureobasidium, Chaetomium, Curvularia, Exophiala, Phaeoacremonium, Pseudallescheria, Sporothrix*
Chromoblastomycosis	*Aureobasidium, Cladophialophora, Fonsecaea, Phialophora*
Phaeohyphomycosis	*Cladophialophora, Exophiala, Fonsecaea*
Pulmonary inf.	*Alternaria, Aureobasidium, Chaetomium, Cladophialophora, Curvularia, Exophiala, Pseudallescheria, Sporothrix*

Table S8: Pairs of primers and respective PCR conditions:

Region	Primer pair	Amplification (100ng DNA, 50ng of each primer, 2-3µl MgCl₂ (50mM), 1.25-5µl dNTPs (10nM), water, and buffer)	Cluster
ITS1-4*	ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') ITS4 (5'-TCCTCCGCTTATTGATATGC-3')	-Initial denaturation: 3min 97°C, Denaturation: 45s 95°C, Annealing: 45s 55°C, Extension: 45s 72°C, No. of cycles: 35, Final extension: 8min 72°C	'g,p'
		Initial denaturation: 5min 94°C, Denaturation: 5s 95°C, Annealing: 30s 54°C, Extension: 1min 72°C, No. of cycles: 35, Final extension: 10min 72°C	'c'
		Initial denaturation: 2min 95°C, Denaturation: 5s 95°C, Annealing: 15s 55°C, Extension: 10s 72°C, No. of cycles: 40, Final extension: 8min 72°C	'l'
		Initial denaturation: 4min 30s 95°C, Denaturation: 30s 95°C, Annealing: 30s 48°C, Extension: 1min 72°C, No. of cycles: 40, Final extension: 3min 72°C	'a,b,m,r,x,y,z', 'h,j,o'
		Initial denaturation: 15min 95°C, Denaturation: 1min 95°C, Annealing: 30sec 56°C, Extension 1min 72°C, No. Of cycles: 3, Final extension: 5min 72°C	'w'
	ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') ITS2 (5'-CCTCCGCTTATTGATATGCTTAGG-3')	Initial denaturation: 15min 95°C, Denaturation: 1min 95°C, Annealing: 30sec 56°C, Extension 1min 72°C, No. Of cycles: 39, Final extension: 5min 72°C	'w'
	SR6R (5'-AAGTATAAGTCGTAACAAGG-3') LR1 (5'-GGTTGGTTTCTTTCCT-3')	Initial denaturation: 3min 97°C, Denaturation: 35s 94°C, Annealing: 45s 50°C, Extension: 45s 72°C, No. of cycles: 30, Final extension: 7min 72°C	'g,p', 'i,Þ'
	ITS2 (5-GCTGCGTTCTTCATCGATGC-3') ITS4 (5-TCCTCCGCTTATTGATATGC-3')	Initial denaturation: 3min 95°C, Denaturation: 40s 95°C, Annealing: 40s 51°C, Extension: 40s 72°C, No. of cycles: 35, Final extension: 7min 72°C	'h,j,o','e'
	ITS3 (5'-GCATCGATGAAGAACGCAGC -3') ITS4 (5'-TCCTCCGCTTATTGATATGC-3')	Initial denaturation: 2min 95°C, Denaturation: 30s 95°C, Annealing: 30s 55°C, Extension: 30s 72°C, No. of cycles: 35, Final extension: 5min 72°C	'q'
		Initial denaturation: 15min 95°C, Denaturation: 1min 95°C, Annealing: 30sec 56°C, Extension 1min 72°C, No. Of cycles: 39, Final extension: 5min 72°C	'w'
Barcoding*	AL33F/EF1-1018F (5' GAYTTCATCAAGAACATGAT 3') AL33R/ EF1-1620R (5' GACGTTGAADCCRACRTTGTC 3')	Initial denaturation: 5min 94°C, Denaturation: 50s 94°C, Annealing: 50s 48°C, Extension: 50s 72°C, No. of cycles: 40, Final extension: 7min 72°C	'g,p', 'i,Þ'
		Initial denaturation: 15min 95°C, Denaturation: 1min 95°C, Annealing: 30sec 56°C, Extension 1min 72°C, No. Of cycles: 39, Final extension: 5min 72°C	'w'
	RPBF (5' GAYGAYCGKGAYCAYTTCGG 3') RPBR (5' CCCATRGCYTGYTTRCCCAT 3')	Initial denaturation: 5min 94°C, Denaturation: 30s 94°C, Annealing: 45s 50°C, Extension: 90s 50°C, No. of cycles: 35, Final extension: 5min 72°C	'g,p', 'i,Þ'
Yeasts (D1/D2)	NL1 (5'- GCATATCAATAAGCGGAGGAAAAG –3') NL4 (5'– GGTCCGTGTTTCAAGACGG –3')	Initial denaturation: 5min 94°C, Denaturation: 5s 95°C, Annealing: 30s 54°C, Extension: 1min 72°C, No. of cycles: 35, Final extension: 10min 72°C	'c'
		Initial denaturation: 15min 95°C, Denaturation: 1min 95°C, Annealing: 30sec 56°C, Extension 1min 72°C, No. Of cycles: 39, Final extension: 5min 72°C	'w'
		Initial denaturation: 2min 95°C, Denaturation: 45s 95°C, Annealing: 30s 52°C, Extension: 2min 72°C, No. of cycles: 30, Final extension: 4min 72°C	'n', 'i,Þ'

Cladosporium	ACT-512F (5'-ATGTGCAAGGCCGGTTTCGC-3') ACT-738R (5'-TACGAGTCCTTCTGGCCCAT-3')	Initial denaturation: 3min 94°C, Denaturation:30s 94°C, Annealing: 30s 55°C, Extension: 5min 72°C, No. of cycles: 7, Denaturation:30s 94°C, Annealing: 30s 53°C, Extension: 45s 72°C, No. of cycles: 25, Final extension: 5min 72°C	'n'
Aspergillus spp. and *Penicillium* spp.	Bt2b (5'-ACCCTCAGTGTAGTGACCCTTGGC-3') Bt2a (5'-GGTAACCAAATCGGTGCTGCTTTC-3')	Initial denaturation: 5min 94°C, Denaturation: 5s 95°C, Annealing: 30s 60°C, Extension: 1min 72°C, No. of cycles: 35, Final extension: 10min 72°C	'c'
		Initial denaturation: 15min 95°C, Denaturation: 1min 95°C, Annealing: 30sec 56°C, Extension 1min 72°C, No. Of cycles: 39, Final extension: 5min 72°C	'w'
		Initial denaturation: 2min 95°C, Denaturation: 45s 95°C, Annealing: 45s 60°C, Extension: 90s 72°C, No. of cycles: 30, Final extension: 4min 72°C	'n'
Fusarium spp.	EF1 (5'–ATGGGTAAGGA(A/G)GACAAGAC–3') EF2 (5'–GGA(G/A)GTACCAGT(G/C)ATCATGTT–3')	Initial denaturation: 2min 94°C, Denaturation:40s 94°C, Annealing: 40s 60°C, Extension: 2min 72°C, No. of cycles: 8 (each cycle 1°C lower T), Denaturation:45s 94°C, Annealing: 90s 53°C, Extension: 2min 72°C, No. of cycles: 36, Final extension: 10min 72°C	'n'
black yeasts and other moulds*	ITS4 (5'-TCCTCCGCTTATTGATATGC-3) ITS5 (5'-GGAAGTAAAAGTCGTAACAAGG-3')	Initial denaturation: 1min 94°C, Denaturation: 35s 94°C, Annealing: 53s 55°C, Extension: 30s 72°C, No. of cycles: 30 (each cycle 1°C lower T), Final extension:10 min 72°C	'n'

*Reviewed *in* Hoang MTV, Irinyi L, Chen SCA, Sorrell TC, the ISHAM Barcoding of Medical Fungi Working Group, Meyer W (2019). Dual DNA barcoding for the molecular identification of the agents of invasive fungal infections. Frontiers in Microbiology.10: article number 1647. http://doi.org/10.3389/fmicb.2019.01647

Table S9: Details on Identifications per laboratory cluster – Materials and Methods

Region	Cluster	Primary identification approach	Secondary identification approach	Tertiary Identification approach	DNA Extraction	Quality control
Southwest Europe	a,b,m,r,x,y,z	Macro and Microscopic analysis	VITEK 2 (Biomérieux) (for yeasts)	Molecular Identification with ITS2-ITS4 for moulds	PCR Template Preparation Kit (Roche Diagnostics GmbH)	ISO 15189 accredited
Northwest Europe	c	Macro and Microscopic analysis	MALDI-ToF (Bruker) (for yeast and filamentous fungi)	Molecular Identification with ITS2-ITS4, D1-D2 and Bt2a-Bt2b, if Maldi biotyper Logscore <1.9	QIAamp DNA Mini kit	ISO 15189 accredited
Mediterranean	d	Macro and Microscopic analysis	MALDI-ToF (Bruker) (for yeast and filamentous fungi)	n.a.	n.a.	JCI Hospital Accredited, API (for External Quality Assessment)
Mediterranean	e	Macro and Microscopic analysis	MALDI-ToF MS (Biomérieux)	ITS2-ITS4	Qiagen DNA minikit	ISO 15189 accredited
Black Sea	f	Macro and Microscopic analysis	MALDI-ToF MS (Bruker) (for yeasts and common filamentous fungi)	Molecular Identification with ITS2-ITS4 for moulds	n.a.	ISO 15189 accredited
Sydney, Australia	g,p	MALDI-ToF MS for yeast (Bruker)	ITS1/2, elongation factor 1 alpha(TEF1α) and RNA polymerase II gene (RPB2)	n.a.	phenol:chloroform:isoaml alcohol (25:24:1)	Speciation specialist
Mediterranean	h,j,o	Macro and Microscopic analysis	API ID32C assimilation kit for yeasts (bioMérieux), MALDI-ToF VITEK SYSTEM, IVD, v. 3.2, (Biomérieux)	Molecular Identification With ITS2-ITS4 for moulds	QIAGEN DNeasy Power Soil Pro Kit	UK NEQAS external quality programme, JCI HospC8:H12ital Accredited (site j)
Mediterranean	i,Þ	Macro and Microscopic analysis	MALDI-ToF MS (Bruker) (for yeasts and common filamentous fungi)	Molecular Identification sequencing of ITS Barcoding region (for yeasts not in the MALDI-ToF MS database & rare moulds)	Phenol/chloroform	ISO 15189 accredited
Mediterranean	k	Macro and Microscopic analysis	MALDI-ToF (Bruker) With two data bases: Bruker & MSI	Molecular Identification with ITS 1-5-8, ITS2	Phenol/chloroform	ISO 17025 accredited
Northwest Europe	l	Macro and Microscopic analysis	Candida ID agar (94382) for yeasts	Molecular Identification with ITS1-ITS4 for moulds	QIAGEN DNeasy PowerSoil Pro Kit for moulds and Phenol/Chloroform for Yeasts	Reference strains
Mediterranean	n	Macro and Microscopic analysis	Molecular Identification: NL1 & NL4 (yeasts), ACT-512F & ACT-738R (*Cladosporium*), Bt2b & Bt2a (*Aspergillus*, *Penicillium*), EF1 & EF2 (*Fusarium*), ITS4-ITS5 (for black yeasts & other moulds)	n.a.	Phenol/chloroform and, PrepMan Ultra reagent	Speciation specialist
Northwest Europe	q	Macro and Microscopic analysis	Molecular Identification with ITS3-ITS4 (White et al., 1990)	n.a.	QIAGEN DNeasy PowerSoil Pro Kit	Identification of reference strains (Genebank sequence database).
Northwest Europe	s	Macro and Microscopic analysis	MALDI-ToF MS (Bruker) (for yeasts)	n.a.	n.a.	ISO 15189 accredited
Mediterranean	t	Macro and Microscopic analysis	Vitek and Auxacolor (for yeasts)	n.a.	n.a.	UK NEQAS external quality programme
Mediterranean	u	Macro and Microscopic analysis	MALDI-ToF MS (Bruker) (for yeasts and filamentous fungi)	n.a.	n.a.	UK NEQAS external quality programme
Mediterranean	v	Macro and Microscopic analysis	MALDI-ToF MS (for yeasts and filamentous fungi)	n.a.	n.a.	UK NEQAS external quality programme
Mediterranean	w	Macro and Microscopic analysis	MALDI-ToF MS (for yeasts and filamentous fungi)	Molecular Identification when Maldi biotyper Logscore <1.9 with ITS1-ITS2, ITS3-ITS4, ITS1-ITS4, Translation elongation factor (TEF 1-a), Beta-tubuline2, D1D2 regions (LSU)	QIAGEN Eazy One	ISO 15189 accredited for Secondary and Tertiary approach