

Table S1

Oligonucleotide probes used in this study (\* number of reference strains that have had tested)

No	Specificity	Position Code	Sequence [5'-3']	Length (base)	GC (%)	Tm (°C)	* 87	No.
1	Fungi universal	B2	AACTTTCAACAACGGATCTCTTGGTTCT	28	39.3	67.4		
		B3	GCATCGATGAAGAACGCAGCGA	22	54.5	66.5		
		B4	GTGAATCATCGAATCTTTGAACGCACA	27	40.7	66.6		
		B5	ATCTCTTGGTTCTCGCATCGATGAAG	26	46.2	66.7		
		B6	AATCATCGAGTCTTTGAACGCAGCTT	26	42.3	67.2		
2	Filamentous fungi universal	C2	GTTGACCTCGGATCAGGTAGGGAT	24	54.2	66.5		
3	Trichophyton group universal	C3	TTCGAGCGTCATTTCAACCCCTC	23	52.2	66.1		
4	<i>Candida albicans</i> ( <i>C. albicans</i> )	D2	TCTTTGAAACAAACTTGCTTTGGCGG	26	42.3	67.3	4	ATCC 10231
		D3	CCGCCAGAGGTCTAAACTTACAACC	25	52.0	66.7		ATCC 10261
		D4	GACGGTAGTGGTAAGGCGGGAT	22	59.1	66.4		ATCC 20260
		D5	GGCGGTAACGTCCACCACGTAT	22	59.1	67.4		ATCC 18804
5	<i>Candida dubliniensis</i> ( <i>C. dubliniensis</i> )	E2	TGTGTTTTGTTCTGGACAAACTTGCTTTG	29	37.9	68.1	3	MYA-179
		E3	CTGCCGCCAGAGGACATAAACTTAC	25	52.0	67.0		MYA-180
		E4	TAGTGGTATAAGGCGGAGATGCTTGA	26	46.2	67.0		MYA-646
		E5	TCTGGCGTCGCCCATTTTATTCTTC	25	48.0	67.2		
6	<i>Candida glabrata</i> ( <i>C. glabrata</i> )	F2	GGTGTTTTATCACACGACTCGACACT	26	46.2	66.9	4	ATCC 60406
		F3	GGAGTTCTCCCAGTGGATGCAAAC	24	54.2	66.8		ATCC 64677
		F4	GGCCATATCAGTATGTGGGACACG	24	54.2	66.2		ATCC 28226
		F5	AGGTTTTACCAACTCGGTGTTGATCTAG	28	42.9	67.0		ATCC 2001
7	<i>Candida guilliermondii</i> ( <i>C. guilliermondii</i> )	G2	GCTTAACTGCGCGGCGAAAAAC	22	54.5	66.6	4	ATCC 22948
		G3	AGATAGGTTGGGCCAGAGGTTTAAACA	26	46.2	67.4		ATCC 32542
		G4	TCTTAGTCGGAAGTGGCGTTTGCTT	25	48.0	67.4		ATCC 38290
		G5	TCGTTGAATGGTGTGGCGGGAT	22	54.5	67.4		ATCC 6260
8	<i>Candida intermedia</i> ( <i>C. intermedia</i> )	H2	GTGTTGCCTTCCGAAATATCACAGTTG	27	44.4	66.9	3	ATCC 12089
		H3	CAGTTGTCGCAATACGTTACTTCAACTTT	29	37.9	67.1		ATCC 201070 ATCC 36352
9	<i>Candida kefyr</i> ( <i>C. kefyr</i> )	H4	GCGGCCAGTTCTTGATTCTCTGC	23	56.5	67.2	3	ATCC 8572
		H5	AGCTCGTCTCTCCAGTGGACATAAAC	26	50.0	67.8		ATCC 8628
		H6	TTGAAAGTGGCTAGCCGTTGCC	22	54.5	66.5		ATCC 8654
		H7	TCGTGGTAAGCTTGGGTCATAGAGAC	26	50.0	67.6		
10	<i>Candida krusei</i> ( <i>C. krusei</i> )	I2	AGCGGAACGAAAACAACAACACCT	24	45.8	67.1	3	JCM 1608
		I3	ACCTAGTGTGAATTGCAGCCATCG	24	50.0	66.6		JCM 2341
		I4	GACGTGTAAGAGCGTCGGAGC	22	59.1	66.2		JCM 2284
		I5	GCGAGTGTGCGAGACAACAAAAG	25	48.0	67.1		
11	<i>Candida lusitanae</i> ( <i>C. lusitanae</i> )	I6	CTCGAGGCATTCTCGAGGCAT	22	59.1	67.0	3	ATCC 24347
		I7	AGGCGTTGCTCCGAAATATCAACC	24	50.0	66.9		ATCC 24348 ATCC 96040
12	<i>Candida parapsilosis</i> ( <i>C. parapsilosis</i> )	J2	TGGGGCCTGCCAGAGATTAAGT	23	52.2	66.8	4	ATCC 10233
		J3	GTGTTGAGCGATACGCTGGGTTT	23	52.2	66.6		ATCC 14054
		J4	GTTTTTCCACTCATTGGTACAACTCCA	29	37.9	67.0		ATCC 28473 ATCC 28480
13	<i>Candida tropicalis</i> ( <i>C. tropicalis</i> )	J5	ACCGCCAGAGGTTATAACTAAACCAA	27	40.7	66.5	3	ATCC 46535
		J6	GAGCAATACGCTAGGTTTGTGAAAGAA	29	37.9	67.0		ATCC 38773
		J7	ACGCTTATTTGCTAGTGGCCACC	24	50.0	67.1		ATCC 32546

Table S1(continue)

14	<i>Epidermophyton floccosum</i> ( <i>E. floccosum</i> )	K2	TCTCTCTGAATGCTGGACGGTGTC	24	54.2	67.3	3	ATCC 52065
		K3	CTCGCCGAAGGAGTGATTCTCAGA	24	54.2	67.1		ATCC 38486
		K4	TTCCACCGGGGAGAGGAGAAAGG	22	59.1	66.1		ATCC 52063
		K5	ACAAAACCAGCGCCTTCAGGAC	22	54.5	66.4		
15	<i>Microsporum canis</i> ( <i>M. canis</i> )	K6	CCTGAGGGGGACTCTTGTTTCCT	23	56.5	66.5	5	ATCC 52067
		K7	CGCCGGAGGATTACTCTGGAAAAC	24	54.2	66.6		ATCC 42559
16	<i>Arthroderma incurvatum</i> ( <i>A. incurvatum</i> )	L2	TGGGCAATAACCAGCGCCTCTA	22	54.5	66.7	2	ATCC 28327
		L3	TCAGGGATGCATTTCTCTGCGAATC	25	48.0	66.8		ATCC 28328
17	<i>Arthroderma gypseum</i> ( <i>A. gypseum</i> )	L4	GTCCGGGGACAATCAACTCCCT	22	59.1	66.6	3	MYA-892
		L5	AATCCATGAATACTGTTCCGTCTGAGC	27	44.4	67.0		ATCC 24005
		L6	GGCCGGTTTTCTGGCCTAGTTTT	23	52.2	66.7		ATCC 24006
18	<i>Arthroderma benhamiae</i> ( <i>A. benhamiae</i> )	M2	AGCCTCTTTGGGGGCTTTAGCT	22	54.5	66.7	4	ATCC 16781
		M3	ACAGACATCAAAAAATCTTGAAAGCTGT	29	34.5	66.8		ATCC 16782
		M4	CTGGGCGAATGGGCAGTCAAAC	22	59.1	67.1		ATCC 52015
		M5	CTCTGGCCTTCCCCCAAATCTC	22	59.1	65.3		ATCC 52018
19	<i>Arthroderma vanbreuseghemii</i> ( <i>A. vanbreuseghemii</i> )	M6	TCTCTTTAGTGGCTCAACGCTGGA	24	50.0	67.1	2	ATCC 28145
		M7	GGACAGACGCAAAAAAATTCTTTCAGAAG	29	37.9	66.5		ATCC 28146
20	<i>Trichophyton mentagrophytes</i> var. <i>interdigitale</i> ( <i>T. mentagrophytes</i> var. <i>interdigitale</i> )	F9	CCTCTCTTTAGTGGCTAAACGCTGG	25	52.0	66.7	2	IFM 55365
		F10	CGCCCTGGCCTCAAAAATCTGTT	22	54.5	66.3		IFM 55366
21	<i>Trichophyton rubrum</i> ( <i>T. rubrum</i> )	N2	CTTCTGGGAGCCTCGAGCCG	20	70.0	66.6	4	ATCC 52021
		N3	AGACACCAAGAAAAAATTCTCTGAAGAGC	29	37.9	66.6		ATCC 52024
		N4	GAATGGGCAGCCAATTCAGCGC	22	59.1	68.0		ATCC 14001
22	<i>Trichophyton tonsurans</i> ( <i>T. tonsurans</i> )	N5	CGGCGAGCCTCTCTTTATAGCG	22	59.1	65.6	4	ATCC 10218
		N6	CCTCTCTTTATAGCGGCTCAACGC	24	54.2	66.7		ATCC 32504
		N7	GGCTTTCTAGGCGAATGGGCAA	22	54.5	66.1		ATCC 14000
23	<i>Trichophyton verrucosum</i> ( <i>T. verrucosum</i> )	O2	AGGACAGACATCAAAAAATCTTGAAGAGC	29	37.9	66.6	3	ATCC 10217
		O3	AAGCTCGGCTTGTGTGATGGAC	22	54.5	66.0		ATCC 44690
24	<i>Trichophyton violaceum</i> ( <i>T. violaceum</i> )	O4	ACACCAAGGAAAATTCTCTGAAGGGC	26	46.2	67.3	3	ATCC 28943
		O5	CCAAGGAAAATTCTCTGAAGGGCTGT	26	46.2	67.1		ATCC 52319
25	<i>Trichosporon asahii</i> ( <i>T. asahii</i> )	D6	GTTCTACTACTTGACGCAAGTCGAGT	26	46.2	66.2	3	ATCC 58163
		D7	TTGGGCGTCTGCGATTTCTGATC	23	52.2	66.5		ATCC 24787
26	<i>Trichosporon cutaneum</i> ( <i>T. cutaneum</i> )	E6	TGAACTGTTGATTGACTTCGGTCAATTGA	29	37.9	67.8	3	ATCC 62858
		E7	GCGTGTTTAACTTGTCTTATCTGGCG	26	46.2	66.5		MYA-839
27	<i>Cryptococcus neoformans</i> ( <i>C. neoformans</i> )	F6	CAACGGATCTCTTGGCTTCCACA	23	52.2	65.9	4	ATCC 90039
		F7	TTGAGAGTCATGAAAATCTCAATCCCTCG	29	41.4	67.4		ATCC 201110
28	<i>Aspergillus fumigatus</i> ( <i>A. fumigatus</i> )	P2	CCCCTGTCTATCGTACCTTGTGTC	24	54.2	66.6	4	ATCC 01899
		P3	TGAACGCTGTTCTGAAAGTATGCAGT	26	42.3	66.9		ATCC 32902
		P4	GCCAGCCGACACCCAACTTTATT	23	52.2	66.7		ATCC 32967
29	<i>Aspergillus niger</i> ( <i>A. niger</i> )	P5	CCCATCCGTGTCTATTGTACCCTGT	25	52.0	67.3	4	ATCC 28592
		P6	ACACGAACACTGTCTGAAAGCGTG	24	50.0	67.1		ATCC 14113
		P7	CCTGCCGACGTTTTCCAACCAT	22	54.5	66.5		ATCC 32267
								ATCC 32045
								ATCC 24064
								ATCC 1022
								ATCC 14110
								ATCC 32614
								ATCC 208996
								ATCC 7750
								ATCC 16888
								ATCC 9508
								ATCC 64048

**Figure S1.**

**Quantification of PCR-amplified fungus-specific DNA by PCR-DM.**

Fungal DNA amplified from clinical nail samples were quantified via fluorescence intensity as measured by PCR-DM. All samples were prepared in KOH and confirmed by microscopy for fungal elements prior to DNA analysis. KOH+ are samples from patients with onychomycosis(n=106), and KOH- are from non-onychomycosis individuals(n=50). U1-3 are independent fungus universal probes designed to detect all fungi.

