Table S1 – Primers (Universal and species-specific) used for *Candida* species detection and size of fragments separated by agarose gel electrophoresis [57,75,77,78,80,166].

Species	**Target**	**Primer sequences** (F: forward; R: reverse)	**Amplicon size (bp)**	**Annealing temperature (°C)**
C. albicans	ITS	ITS1F: 5′ – TCAACTTGTCACACCAGATTATT – 3′ ITS4R: 5′ – TCCTCCGCTTATTGATATGC – 3′	632[77]	45-55
		CALF: 5′ – AGCTGCCGCCAGAGGTCTAA – 3′ UNI2R: 5′ – TTCTTTTCCTCCGCTTATTG – 3′	583/446[78]	55
	MP65 gene	CA64F: 5′ – AACGGATCCATGTTATTCAAGTCTTTC – 3′ CA64R: 5′ – GGGCTGCAGGTGCTTAGTTAGAGTAA – 3′	1144[57]	60
		CABISF: 5′ – ATGTTATTCAAGTCTTTCGTTACT – 3′ CABISR: 5′ – TGACATTAAATCCAGATAATTGAGC – 3′	467[57]	60
	ITS	CALBF: 5′ – TTTATCAACTTGTCACACCAGA – 3′ CALBR; 5′ – ATCCCGCCTTACCACTACCG – 3′	273[75]	72
C. glabrata	ITS	ITS1F: 5′ – CACGACTCGACACTTTCTAATT – 3′ ITS4R: 5′ – TCCTCCGCTTATTGATATGC – 3′	402[77]	45-55
		CGLF: 5′ – TTGTCTGAGCTCGGAGAGAG – 3′ UNI2R: 5′ – TTCTTTTCCTCCGCTTATTG – 3′	929/839[78]	55
		CGLF: 5′ – TTATCACACGACTCGACACT – 3′ CGLR: 5′ – CCCACATACTGATATGGCCTACAA – 3′	423[75]	72
	MP65 gene	GLA8F: 5′ – GATGTTGTCACTAAGACTGTTCA – 3′ GLA8R: 5′ – AGTAGGAAGACAACTTGGCAAGG – 3′	361[57]	60
C. tropicalis	ITS	ITS2F: 5′ – AAGAATTTAACGTGGAAACTTA – 3′ ITS4R: 5′ – TCCTCCGCTTATTGATATGC – 3′	149[77]	45-55
		CTRF: 5′ – GATTTGCTTAATTGCCCCAC – 3′ UNI2R: 5′ – TTCTTTTCCTCCGCTTATTG – 3′	583/507[78]	55
		CTRF: 5′ – CAATCCTACCGCCAGAGGTTAT – 3′ CTRR: 5′ – TGGCCACTAGCAAAATAAGCGT – 3′	357[75]	72
	MP65	TRPF: 5′ – TTCTGTTGCCAACACC – 3′ TRPR: 5′ – TGCTGTAACCGGACAAA – 3′	257[57]	60
C. parapsilosis	ITS	ITS2F: 5′ – GGCGGAGTATAAACTAATGGATAG – 3′ ITS4R: 5′ – TCCTCCGCTTATTGATATGC – 3′	126[77]	45-55
		CPLF: 5′ – GTCAACCGATTATTTAATAG – 3′ UNI2R: 5′ – TTCTTTTCCTCCGCTTATTG – 3′	570/370[78]	55
		CPAF: 5′ – GCCAGAGATTAAACTCAACCAA – 3′	320/300[75]	72

		CPAR: 5′ – CCTATCCATTAGTTTATACTCCGC – 3′		
	MP65	PAR15F: 5′ – CTTCCGAAGCTAGCCAAGT – 3′ PAR15R: 5′ – GAGGATGAAGTGGAGTCG – 3′	124[57]	60
C. krusei	ITS	CKRF: 5′ – CTGGCCGAGCGAACTAGACT – 3′ UNI2R: 5′– TTCTTTTCCTCCGCTTATTG – 3′	590/169[78]	55
C. guiliermondii	ITS	CGLF: 5′ – TTGGCCTAGAGATAGGTTGG – 3′ UNI2R: 5′ – TTCTTTTCCTCCGCTTATTG – 3′	668/512[78]	55
	MP65	GUILL10F: 5′ – CACCGTGGCTCTTGTTGCT – 3′ GUILL10R: 5′ – AGACTTGGCAGTGGAAACG – 3′	640[57]	60
C. lusitaniae	ITS	CLSF: 5′ – TTCGGAGCAACGCCTAACCG – 3′ UNI2R: 5′– TTCTTTTCCTCCGCTTATTG – 3′	433/329[78]	55
C. dubliniensis	ITS	CDBF: 5′ – CTCAAACCCCTAGGGTTTGG – 3′ UNI2R: 5′ – TTCTTTTCCTCCGCTTATTG – 3′	591/217[78]	55
		CDU F: 5′ – AACTTGTCACGAGATTATTTTT – 3′ CDU R: 5′ – AAAGTTTGAAGAATAAAATGGC – 3′	300[166]	55

Table S2 - List of primers used for Nested PCR. *Candida albicans* A9, *C. dubliniensis* 16F, *C. tropicalis* pk233, *C. tropicalis* NUM5076, *C. parapsilosis* IFO1068, *C. tropicalis* IF01396, *C. krusei* IFO0841, *C. kefyr* IFO0586, *C. guilliermondii* NUM4, *C. glabrata* ATCC2001, *C. lusitaniae* JCM05936 were used in this study. Kanbe (2002) reported that the nucleotide sequence of DNA topoisomerase II gene of *C. tropicalis* pk233 differs from that of *C. tropicalis* IFO1400, and that the nucleotide sequence of DNA topoisomerase II gene of *C. parapsilosis* IFO1068 differs from that of *C. parapsilosis* IFO1396. Therefore, *C. tropicalis* pk233, *C. tropicalis* NUM5076, *C. parapsilosis* IFO1068 and *C. parapsilosis* 1396 were referred to as *C. tropicalis* I, *C. tropicalis* II, *C. parapsilosis* I and *C. parapsilosis* II, respectively. Annealing temperature is 57°C [72].

***Candida* Spp.**	**Specific primers**
C. albicans	CABF59F: 5′ – TTGAACATCTCCAGTTTCAAAGGT – 3′
	CABR110R: 5′ – GTTGGCGTTGGCAATAGCTCTG – 3′
	CADBR125R: 5′ – AGCTAAATTCATAGCAGAAAGC – 3′
C. dubliniensis	CDBF28F: 5′ – AAATGGGTTTGGTGCCAAATTA – 3′
	CDBR110R: 5′ – GTTGGCATTGGCAATAGCTCTA – 3′
	CADBR125R: 5′ – AGCTAAATTCATAGCAGAAAGC – 3′
C. tropicalis I	CTPIF36F: 5′ – GTTGTACAAGCAGACATGGACTG – 3′
	CTPIR68R: 5′ – CAAGGTGCCGTCTTCGGCTAAT – 3′
	CTPIR121R: 5′ – TCAAGGTACAGTTATGGCCAAGTT – 3′
C: tropicalis II	CTPIIF36F: 5′ – CTGGGAAATTATATAAGCAAGTT – 3′
	CTPIIR60R: 5′ – CTTGAGATACTCAATCTTTTATC – 3′
	CTPIIR121R: 5′ – TCAATGTACAATTATGACCGAGTT – 3′
C. parapsilosis I	CPPIF41F: 5′ – TGACAATATGACAAAGGTTGGTA – 3′
	CPPIR61R: 5′ – ACTTTTAAAACTGTTAACCGA – 3′
	CPPIR122R: 5′ – TGTCAAGATCAACGTACATTTAGT – 3′
C. parapsilosis II	CPPIIF41F: 5′ – GGACAACATGACAAAAGTCGGCA – 3′
	CPPIIR69R: 5′ – TTGTGGTGTAATTCTTGGGAG – 3′
	CPPIIR122R: 5′ – GGTAAGGATCAAAGTGCACTTTA – 3′
C. krusei	CKSF35F: 5′ – GAGCCACGGTAAAGAATACACA – 3′
	CKSR57R: 5′ – TTTAAAGTGACCCGGATACC – 3′
	CKSR110R: 5′ – TTTCTCTGGCAATTCCAATCG – 3′
C. kefyr	CKFF35F: 5′ – CTTCCAAAGGTCAGAAGTATGTCC – 3′
	CKFR85R: 5′ – CTTCAAACGGTCTGAAACCT – 3′
	CKFR104R: 5′ – CACGAAATCGTTAGGAACTTCAC – 3′
C. glabrata	CGBF35F: 5′ – CCCAAAAATGGCCGTAAGTATG – 3′
	CGBR103R: 5′ – ATAGTCGCTACTAATATCACACC –3′
	CGBR77R: 5′ – CTGCTTGAAAGAAATATCGGAGAC – 3′
C. guiliermondii	CGLF41F: 5′ – CCCAAAATCACAAAGCTCAAGT – 3′
	CGLR61R: 5′ – TACGACTTGAAGTTGCGAATTG – 3′
	CGLR103R: 5′ – GATGACAATTTTCTCCAGAGGC – 3′
C. lusitaniae	CLTF39F: 5′ – CATGTCGAAATGCAACCCCCCG – 3′
	CLTR119R: 5′ – GCGTACACTTGTGGCCATCTTTA – 3′
	CLTR125R: 5′ – TCATTACCTACGACTTTGAG – 3′

Table S3 - Restriction Fragment Length Polymorphism (RFLP) fragment patterns in oral *Candida* spp. isolates with restriction enzymes. [9,83].

Primer sequence	*ITS1* - (5' – TCCGTAGGTGAACCTGCGG – 3') *ITS4* - (5' – TCCTCCGCTTATTGATATGC – 3')				
	Fragment sizes (bp)				
***Candida* spp.**	***ITS1-ITS4***	***Msp*I**	***Bfa*I**	***Hae*III**	***Dde*I**
C. albicans	535	238-297[9]	-	90, 430[83]	100, 420[83]
C. parapsilosis	520	520[9]	-	40, 110, 390[83]	-
C. tropicalis	524	184-340[9]	-		-
C. krusei	510	249-261[9]	120-200[83]	40, 90, 380[83]	-
C. guiliermondii	608	82-155-371[9]	-		-
C. glabrata	871	314-577[9]	-	200, 650[83]	-
C. lusitaniae	383	117-266[9]	-		-
C. kefyr	721	721[9]	-		-

Table S4 - Oligonucleotide probes used in for *Candida* spp. in non-oral isolates [89].

Species	**Oligonucleotide probe sequence** (Annealing temperature for the following is 55°C)
Positive Control Negative Control	5′ – GCATATCAATAAGCGGAGGA-3′
Universal fungal probe (ITS)	5′ – TTGACCTCRRATCAGGTAGGRATACCCGCTGAACTTAA-3′
C. albicans	5′ – ATTGCTTGCGGCGGTAGCGTCTACCACGTATATCTTCAAAAACGCTTATTTTGCTAGTGGCCACCACAATTTATTTCATA – 3′
C. tropicalis	5′ – AACGCTTATTTTGCTAGTGGCCACCACAATTTATTTCATA – 3′
C. parapsilosis	5′ – TTCCACTCATTGGTACAAACTCCAAAACTTCTTCCAAA – 3′
C. krusei	5′ – GACGCTTGGCGGCCGAGAGCGAGTGTTGCGAGACAACAAA – 3′
C. glabrata	5′ – TAGGTTTTACCAACTCGGTGTTGATCTAGGGAGGGATAAGT – 3′

Table S5 - Primers used in Kasahara for the detection of *Candida* spp. with LAMP. Primers have *ITS2* as the target region [109].

Species	**Primer name**	**Sequence**
C. albicans	F3	5′ – TCTGGTATTCCGGAGGGC – 3′
	B3	5′ – AGTCCTACCTGATTTGAGGT – 3′
	FIP	5′ – CTACCGTCTTTCAAGCAAACCCATGAGCGTCGTTTCTCCCT – 3′
	BIP	5′ – TTGACAATGGCTTAGGTCTAACCAAAAGATATACGTGGTGGACGTTAC – 3′
	LB	5′ – CTCAACACCAAACCCAGCGG – 3′
C. glabrata	F3	5′ – TGGTAGTGAGTGATACTCGTT - 3′
	B3	5′ – CTTAAAGACGTCTGTCTGCC – 3′
	FIP	5′ – GCAGATTAATAGAGAAGCTTGCGCTGAGTTAACTTGAAATTGTAGGCC – 3′
	BIP	5′ – GCGGCGGGGGTTAATACTGTCACAAAACACTCACTTATCCCT – 3′
	LF	5′ – GGTTTTACCAACTCGGTGTTGATCT – 3′
C. parapsilosis group	F3	5′ – CGCCCTTTGGTATTCCAA – 3′
	B3	5′ – CCTCCGCTTATTGATATGCT – 3′
	FIP	5′ – CAAGCAAACCCAGCGTATCGAGCGTCATTTCTCCCTCA – 3′
	BIP	5′ – TTCCACTCATTGGTACAAACTCCAAGTTCAGCGGGTAGTCC – 3′
	LF	5′ - CAACACCAAACCCGAGGGT – 3′
	LB	5′ – CTTCCAAATTCGACCTCAAATCAGG – 3′
C. tropicalis	F3	5′ – TTTGGTATTCCAAAGGGC – 3′
	B3	5′ – AGTCCTACCTGATTTGAGGT – 3′
	FIP	5′ – CCTAGCGTATTGCTCAACACCAAATGCCTGTTTGAGCGTCA – 3′
	BIP	5′ – ACGTGGAAACTTATTTTAAGCGACTATAAATTGTGGTGGCCACTAG – 3′
	LF	5′ – CCGGGGGTTTGAGGGAGAAA – 3′