Real-time detection of SARS-CoV-2 in clinical samples via ultrafast ligation-dependent RNA transcription amplification

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Name		Sequence (5'-3')
Promoter probe		
Reporter probe		CCCCCACAAGTCACACACCTTCACAAATCTTAAA
Reporter probe		UCCUACAAUTUACAUCTIUACAAATUTTAAA
(no terminator)		CCGCCGGACAAGTGACAGCTTGACAAATGTTAAA
(no terminator)		
T7 promoter	20-nt	TAATACGACTCACTATAGGG
	22-nt	CCTAATACGACTCACTATAGGG
	24-nt	TTCCTAATACGACTCACTATAGGG
	26-nt	CCTTCCTAATACGACTCACTATAGGG
Molecular beacon	MB1	FAM- CCGCCGGACAAGGAGGCTGGAGTCAACCGGCGG -DABCYL
	MB2	FAM-AGTATACCTGCAGTGACTCTTAAGATCCAGGTATACT-DABCYL
	MB3	FAM-ACCTTCTATAGCAAACACCATTGTCACACTCCACCTCAGCCTAT
		AGAAGGT-DABCYL
	MB4	FAM-ACTATAGGTATACAACCTACTACCTCACCCTATAGT-DABCYL
aRT_PCR primer set	F	GTGATGTAGAAAACCCTCACC
(°I R898678 2)	R	
(11(0)0070.2)	ĸ	
	F3	TGCTTCAGTCAGCTGATG
	B3	TTAAATTGTCATCTTCGTCCTT
qRT-LAMP primer set	FIP	TCAGTACTAGTGCCTGTGCCCACAATCGTTTTTAAACGGGT
(°LR898678.2)	BIP	TCGTATACAGGGCTTTTGACATCTATCTTGGAAGCGACAACAA
	LF	CTGCACTTACACCGCAA
	LB	GTAGCTGGTTTTGCTAAATTCC
RNA fragment with SARS-		AUGCCACAACUGCUUAUGCUAAUAGUGUUUUUAACAUUUGUCAAGC UGUCACGGCC
CoV-2 orflab gene specific		
sequence (°OQ117226.1)		
RNA fragment with SARS- CoV <i>orf1ab</i> gene specific sequence (°MN312831.1)		^d AUGC <i>U</i> ACAACUGCUUAUGCUAAUAGUGU <i>C</i> UUUAACAUUUGUCAAG CUGU <i>U</i> AC <i>A</i> GCC

Supplementary Information

Table S1. Sequences of nucleic acids used in this work

^a Sequences marked in red and blue were the sequence complementary to the part of the target RNA and T7 promoter binding site, respectively.

^b Sequences marked in orange, green, and red were the VSV terminator, the sequence consistent with the loop part of the MB, and the sequence complementary to the part of the target RNA, respectively. ^c GenBank accession number.

^d The portion in italic type represented the nucleotides variation compared to the RNA fragment with SARS-CoV-2 *orf1ab* gene specific sequence.

Procedure of qRT-PCR and qRT-LAMP

The reaction system of qRT-PCR with a total volume of 20 µL consists of 2 µL sample, 0.4 µL dNTPs (10 mM each), 0.8 µL forward and backward primer (10 µM each), 0.3 µL Tag DNA polymerase (5 U/µL), 1.3 µL 10× Tag buffer, 0.5 µL EvaGreen Dye, 0.2 µL HiScript II Reverse Transcriptase (200 U/µL), 1.3 µL 5× HiScript II Buffer, 0.2 µL Murine RNase inhibitor (40 U/µL), 0.08 MgSO₄ solution (100 mM) and 12.12 µL DEPC-treated water. The reaction procedure included reverse transcription at 55°C for 5 min, denaturation at 95°C for 3 min, and 40 cycles consisting of 95°C for 10 s, and 58°C for 15 s for amplification. qRT-LAMP was performed by adding 2.5 µL sample, 4 µL dNTPs (10 mM each), 1 µL F3 and B3 (10 µM each), 0.8 µL FIP and BIP (100 µM each), 0.4 µL LF and LB (100 µM each), 0.5 µL Bst 2.0 WarmStart DNA polymerase (8000 U/mL), 2.5 µL 10× ThermoPol reaction buffer, 0.5 µL MgSO₄ solution (100 mM), 0.625 µL EvaGreen Dye, 0.3 µL HiScript II Reverse Transcriptase (200 U/µL) and 11.875 µL DEPC-treated water into a total volume of 25 µL at 65°C for 45 min. Both qRT-PCR and qRT-LAMP assays were carried out by a CFX Connect[™] Real-Time PCR System (Bio-Rad, CA, USA). The fluorescence signal of the qRT-PCR was read after each thermal cycling, while that of the qRT-LAMP was monitored at 1-min intervals.



SARS-CoV-2 AUGCCACAACUGCUUAUGCUAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCC SARS-CoV AUGCUACAACUGCUUAUGCUAAUAGUGUCUUUAACAUUUGUCAAGCUGUUACAGCC

Fig.S1. Capability of SCAN to distinguish RNA with similar sequence to the target. The concentration of the RNA fragments was 1 μ M. The portion in italic type represented the ligation site of the two probes (between the two nucleotides), while the variation nucleotides of the RNA fragment with SARS-CoV *orf1ab* gene specific sequence were marked in red. NTC represented no template control.