Supporting Information

A highly sensitive fluorescence biosensor for detection of *Staphylococcus aureus* based on HCR-mediated three-way DNA junction nicking enzyme assisted signal amplification

Chuyan Zhang^a, Zewei Luo^b, Mengfan Wu^c, Wei Ning^a, Ziyi Tian^a, Yixiang Duan^{c, *}, Yongxin Li^{a, *}

a West China School of Public Health and West China Fourth Hospital, Sichuan University, Chengdu 610041, China

b Research Center of Analytical Instrumentation, Key Laboratory of Synthetic and Natural Functional Molecule Chemistry of Ministry of Education, College of Chemistry & Materials Science, Northwest University, Xi'an 710069, China

c Research Center of Analytical Instrumentation, School of Mechanical Engineering, Sichuan University, Chengdu 610065, China.

E-mail: lyxlee2008@hotmail.com

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Table S1 DNA sequences in this study

Name	sequence (5' to 3')					
Т	AAGGTGTAGAGAAATATG GTCCTG (denoted by b* - a*)					
MB	FAM-CCAACG GATCATGG TACCTCAGCG TTGG-Dabcyl (denoted by					
	/-f*-d*-/)					
H1	CAGGAC CATATTTCTCTACACCTT GAT CGCTGAGGTA a					
	GGAAGG AAGGTGTAGAGAAATATG A (denoted by a-b-c-d-e-b*)					
H2	T AAGGTGTAGAGAAATATG GTCCTG CATATTTCTCTACACCTT					
	CCTTCC CCATGATC (denoted by b*- a*-b-e*-f)					
H1-1	CAGGAC CATATTTCTCTACACCTT AT CGCTGAGGTA a GGAAGG					
	AAGGTGTAGAGAAATATG (denoted by a-b-c-d-e-b*)					
H1-2	CAGGAC CATATTTCTCTACACCTT AT CGCTGAGGTA a GGAAGG					
	AAGGTGTAGAGAAATATG A (denoted by a-b-c-d-e-b*)					
H1-3	CAGGAC CATATTTCTCTACACCTT AT CGCTGAGGTA a GGAAGG					
	AAGGTGTAGAGAAATATG TA (denoted by a-b-c-d-e-b*)					
H1-4	CAGGAC CATATTTCTCTACACCTT T CGCTGAGGTA a GGAAGG					
	AAGGTGTAGAGAAATATG A (denoted by a-b-c-d-e-b*)					
H1-5	CAGGAC CATATTTCTCTACACCTT AGAT CGCTGAGGTA a					
	GGAAGGAAGGTGTAGAGAAATATG A (denoted by a-b-c-d-e-b*)					
H1-6	CAGGAC CATATTTCTCTACACCTT AAGAT CGCTGAGGTA a					
	GGAAGGAAGGTGTAGAGAAATATG A (denoted by a-b-c-d-e-b*)					
H2-1	AAGGTGTAGAGAAATATG GTCCTG CATATTTCTCTACACCTT					
	CCTTCC CCATGATC (denoted by b*- a*-b-e*-f)					
H2-2	TA AAGGTGTAGAGAAATATG GTCCTG CATATTTCTCTACACCTT					
	CCTTCC CCATGATC (denoted by b*- a*-b-e*-f)					
1-mismatched strand	AAGGTGTAGAGAAATATGCTCCTG					
2-mismatched strand	AAGGTGTAGAGAAATATGCACCTG					
3-mismatched strand	AAGGTGTAGAGAAATATCCACCTG					
Noncomplementary	TGGCATTATCGATCAGTACCAGCC					
Suanu Forward prime	CCCATTCATCCTCATACCCTT					
Porward prime						
nua ampliaan						
(224 hn)						
(224 bp)						
	GUGIA					

Note: The HCR probes were designed according to complementary base pairing through the simulation of NUPACK software (http://www.nupack.org/). The free end of HCR hairpins is marked in blue. The spacer of H1 is marked in red. The mismatched base is marked in green. The primers were designed using Primer-BLAST tool from the NCBI website online, and the specificity of the sequences was verified by the results of searches against NCBI's non-redundant database using the BLASTN algorithm (https://www.ncbi.nlm.nih.gov/pubmed).



Fig. S1 Sensitivity of the pure HCR strategy for target DNA detection. (A)Fluorescent signal response with different concentrations of target DNA (B)Calibration curves of target DNA concentration with corresponding relative fluorescence intensities. Error bars: the standard deviations of triplicate analyses.



Fig. S2 Various experimental results of aPCR. (A) PAGE analysis. Lane M: DNA marker; Lane 1: traditional PCR of *S. aureus*; Lane 2: aPCR of *S. aureus*; Lane 3: negative control. (B) Simulation studies on the secondary structures of the ssDNA product from aPCR of *S. aureus*.



Fig. S3 Fluorescence response from the proposed strategy to different concentration of *S. aureus* in water $(1.2 \times 10^1 - 1.2 \times 10^6 \text{ cfu/mL})$. The dotted lines represented cut-off value. Error bars: the standard deviations of triplicate analyses.



Fig. S4 Fluorescence response from the proposed strategy to different concentration of *S. aureus* in milk ($1.3 \times 10^1 - 1.3 \times 10^6$ cfu/mL). The dotted lines represented cut-off value. Error bars: the standard deviations of triplicate analyses.

Table S2 Comparison of the proposed assay and other 3WJ-NEASA or HCR-based

Method	Reaction	Operation	Linear range	LOD	Ref.		
	time	procedure					
Fluorescence detection based on 3WJ-	30 min	one-step	100 pM -200	65 pM	1		
NEASA and triplex DNA			nM				
Amperometric detection based on	2.5 h	multi-	1 fM -10 nM	0.33 fM	2		
3WJ-NEANA and flower-like carbon		step					
nanotubes-polyaniline nanohybrid							
Fluorescence detection based on HCR	2h	multi-	0.01- 100	10 pM	3		
and magnetic particles		step	nM				
Fluorescence detection based on four-	1.5 h	one-step	0.2- 60 nM	67 pM	4		
way branched migration HCR							
Chemiluminescence detection of	1.5 h	multi-	0.5- 10 pM	7 pM	5		
DNAzyme and nonlinear HCR		step					
Fluorescence detection based on silver	4.5 h	multi-	10-100 nM	1.18	6		
nanoclusters/graphene oxide and HCR		step		nM			
Fluorescence detection based on	30 min	one-step	10 pM -10	6.7 pM	This		
HCR-mediated 3WJ-NEASA			nM		work		

biosensors for DNA detection

Method	Materials	LOD (cfu/mL)	Ref.
Multiplex PCR	DNA	1.0×10 ⁵ (milk)	7
Multiplex real-time PCR coupled with SDS and PMA	DNA	1.0×10 ² (milk)	8
Immunomagnetic separation via cell binding domain of lysin	antibody	4.0×10 ³ (milk)	9
Competitive ELISA	antibody	1.0×10^4 (culture)	10
Conductometric biosensor based on magnetic analyte	aptamer	4.0×10^3 (tap water)	11
separation			
Microfluidic chip coupled with fluorescent silica nanoparticles	aptamer	2.7×10 ² (water)	12
label			
Fluorescence biosensor based on HCR-mediated 3WJ-	DNA	1.2×10 ¹ (water)	This
NEASA		1.3×10 ² (milk)	work

Table S3 Comparison of previously reported methods for S. aureus detection

Note: SDS, sodium dodecyl sulphate; PMA, propidium monoazide; ELISA, enzyme linked immunosorbent assay.

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