

Sensitive and rapid detection of pathogenic bacteria from urine samples using multiplex recombinase polymerase amplification

Junge Chen,^{a,†} Youchun Xu,^{a,b,†} He Yan,^a Yunzeng Zhu,^a Lei Wang,^{b,c} Yan Zhang,^c Ying Lu^a and Wanli Xing^{a,b,*}

Supplementary materials

Figure S1. Pre-treatment of spiked urine samples. (A) The structure of the filter-based pipette for enrichment of bacteria. (B) First, the three-way switch was placed on a position to connect the tip and the white syringe. When we pressed and then released the white syringe, a volume of 5 mL urine was steadily sucked into the syringe through a 0.22 μm filter by the bounce of the spring in white syringe, and the bacteria were thus captured and enriched on the membrane. (C) After that, we rotated the three-way switch for 90° to connect the tip with the blue syringe. (D) The bacterial suspension was injected into the chip with the pure water stored in the blue syringe.

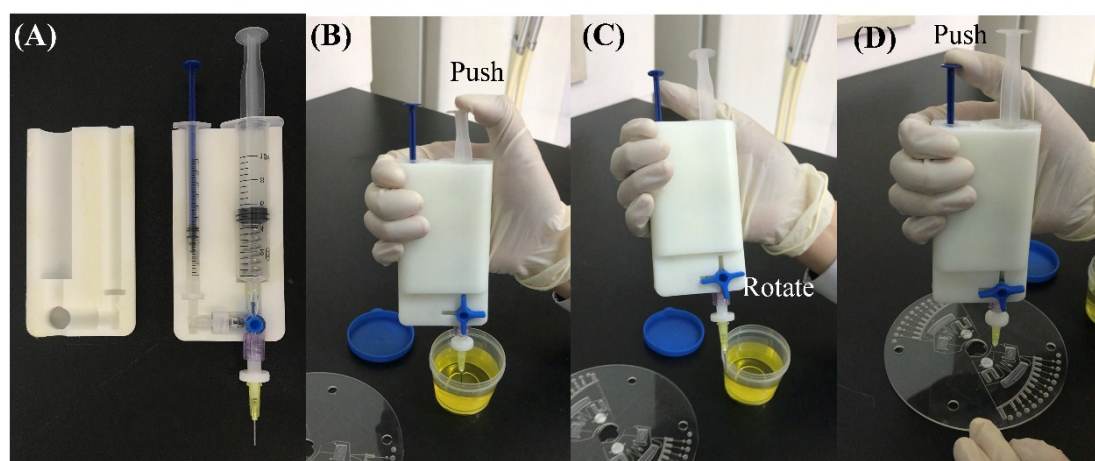


Figure S2. Off-chip RPA detection of five target bacteria (*E. coli*, *S. aureus*, *S. typhimurium*, *P. mirabilis*, and *P. aeruginosa*) in the urine samples. (RFU: relative fluorescence unit; NC: negative control).

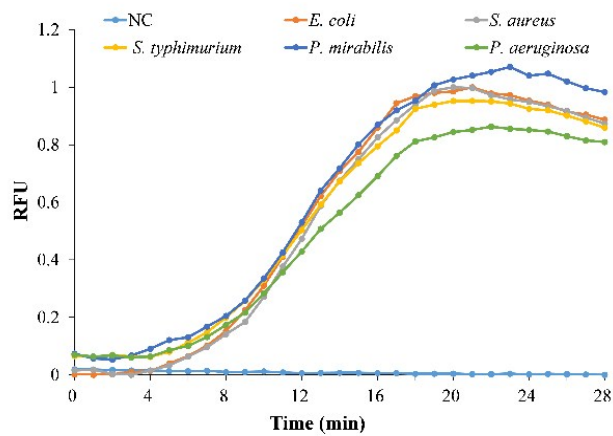


Figure S3. Specificity tests of RPA primers in the tube. (A) Specificity test for detecting *E. coli*. (B) Specificity test for detecting *S. aureus*. (C) Specificity test for detecting *S. typhimurium*. (D) Specificity test for detecting *P. mirabilis*. (E) Specificity test for detecting *P. aeruginosa*.

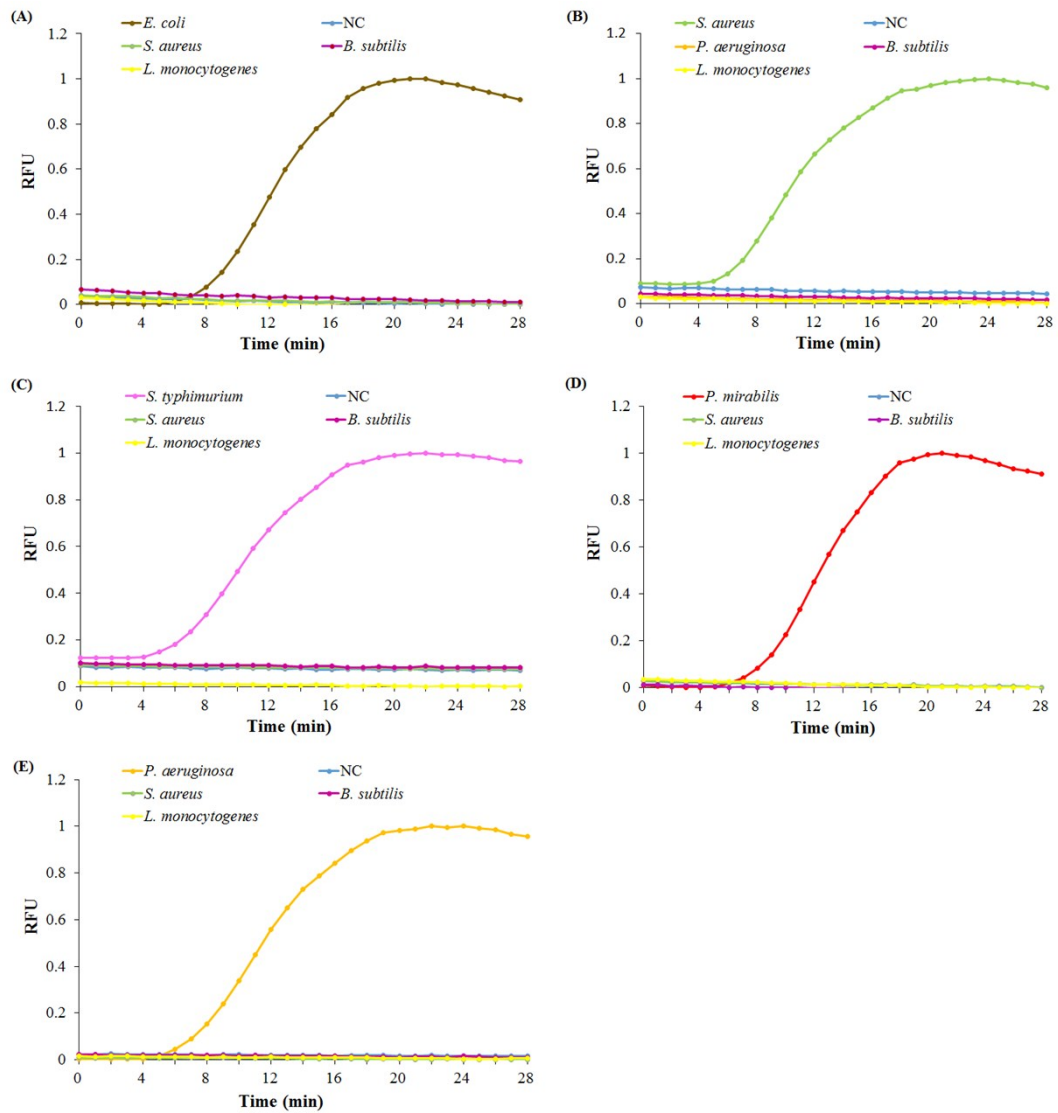


Figure S4. Optimization of bead-beating lysis. (A) Optimization of the rotate speed of magnets for Gram-positive bacteria (*S. aureus*); (B) Optimization of the lysis time for Gram-positive bacteria (*S. aureus*).

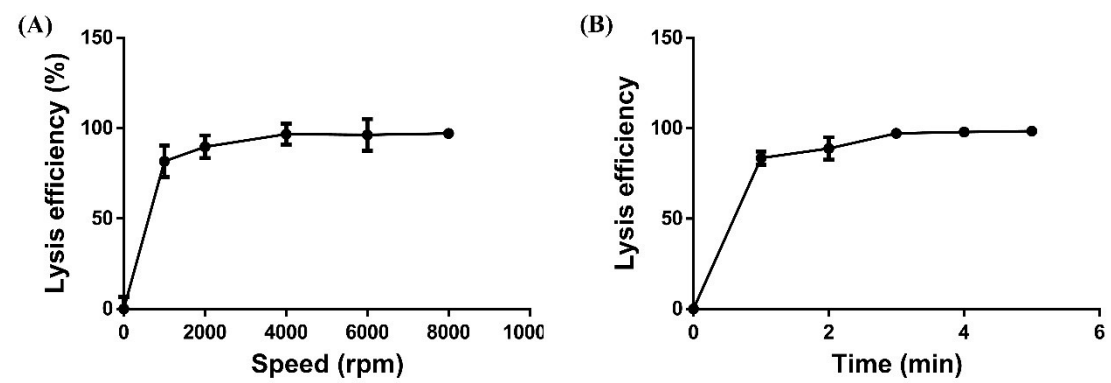


Figure S5. Specificity of on-chip real-time RPA. 10^3 CFU/mL of *E. coli* and *B. subtilis* were spiked in the urine.

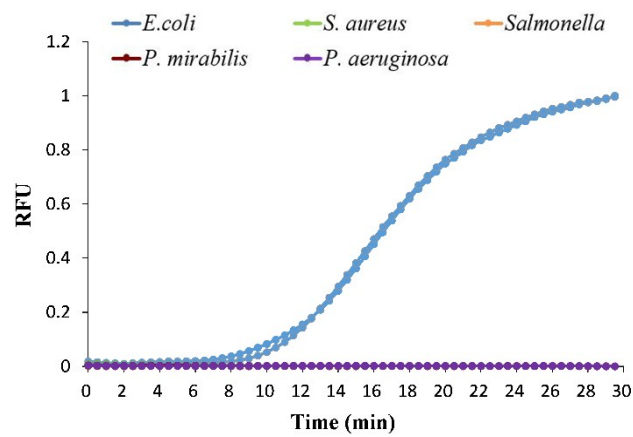


Table S1. Sequences of RPA primers for the various pathogens.

Pathogen	Target gene	Nucleotide sequence 5' to 3'
<i>E. coli</i>	endA	Primer F: GTACGTTTTATTGCGGATGTAAAATTAAGTG Primer R: ATAGACCGGATCTTTAGCGCAGTTTTTAC Probe: GGGCAAAAAAGGCGTTGTTGATCTGCAA-T(FAM)- THF-T(BHQ-1)-GCGGCTATCAGGTGCGC- GGATGAAATTAACGAAG-C6 Spacer
<i>S. aureus</i>	MecA	Primer F: CGATATCGAGGCCCGTGGATTTAGTCGTGA Primer R: GTGACTTCGACACCTTTTTCAAAGGCATGTAC Probe: CGCAAACGTGGCGAAGAATTCTTTTGGTCAA-T(FAM)- THF-A-T(BHQ-1)-GGATGAAATTAACGAAG-C6 Spacer
<i>S. typhimurium</i>	STM4599	Primer F: GTCGAAATCTAGCTAATCTACTGGTTCCTCC Primer R: CTGTGCTGTATTAAGATCATGAAACGCAGTAT Probe: CTGGTGTTTCAGCCAAAACATCAGCAGGCCA- T(FAM)-C-THF-A-T(BHQ-1)-GGCGGCATACAGGC-C6 Spacer
<i>P. mirabilis</i>	ureR	Primer F: GTATATGGTGCAAAAGGTGAGATTTGTATTA Primer R: TTGTAATTCAGTTTCAGACAGTACTAAGGTAT Probe: GATTATTCCTAAATATAGTCAAGTTTCTTG-T(FAM)- THF-A-T(BHQ-1)-GTGACAAATTTTTTC-C6 Spacer
<i>P. aeruginosa</i>	ETA	Primer F: GTGCTGCACTACTCCATGGTCCTGGAGGG Primer R: GTTCGTGGATGAACACCTTGATGTTCGAGG Probe: GAAGGTGGCGTCGAGCCGAACAAGCCGG-T(FAM)-G- THF-GC-T(BHQ-1)-ACAGCTACACGC-C6 Spacer

Table S2. Pre-storage of RPA master mix in real-time RPA chambers.

Reagents	Volume
10 μ M species-specific forward primer	0.42 μ L
10 μ M species-specific reverse primer	0.42 μ L
10 μ M species-specific probe	0.12 μ L
280 mM magnesium acetate	0.50 μ L
50 mg/mL BSA	0.10 μ L

Table S3. Spinning program of the complete assay.

No.	Speed (rpm)	Time (s)	Operation
A	0	180	Cell lysis
B	100	10	Siphon
C	3000	10	Transfer the bacterial lysate into the quantitative chamber
	50	10	Siphon
D	2000	30	Transfer the lysate and RPA master mix into the mixing chamber
	500 ↔ 4000	60	Mixing of bacterial lysate and RPA master mix
	50	10	Siphon
E	1000	30	Pre-distribution of the mixture
F	4000	10	Dispensing of the sample into ten reaction chambers