Whole-cell Based Aptamer Selection for Selective Capture of Microorganisms in the Microfluidic Device

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The highly enriched aptamer pools were cloned and sequenced and a total of 40 sequences were obtained. Screened aptamer sequences of eight families without primers are listed in Table S1. The sequence alignment was analyzed using sequence alignment programs ClustalX1.83. The sequences were grouped into eight families based on the homology of the oligonucleotides of individual clones with each group containing similar sequence.

Information on composition and distribution of putative Quadruplex forming G-Rich sequences (QGRS) in nucleotide sequences using QGRS Mapper is listed in Table S2, The result showed that most of aptamer sequence got higher G-scores, which indicated the sequences would be preferable to form a G-quadruplex.

The flow cytometry results of binding assays of aptamers with E. coli cells are shown in Figure S1-S5 for the binding affinity and selectivity. A FC-500 flow cytometer (Beckman coulter Inc., U.S.) was used to assess the binding of the evolved aptamer pools and individual aptamer sequences toward E. coli 11775. The aptamer
pools after the selection were fluorescently tagged via PCR amplification with 5'-FAM modified primers (Invitrogen) and the individual aptamers sequences were obtained with the fluorescent label 5'-FAM from Invitrogen (Shanghai). The DNA aptamers were heated to create folded ssDNA at 95 °C and subsequent fast cooling on ice prior to incubation with the bacteria. The binding affinity of aptamers was determined by incubating 10^8 bacterial cells with 100 pmol FAM-labeled aptamers for 45 min in binding buffer. Cells were then washed once with washing buffer (1 × binding buffer with 0.05% BSA), suspended in 0.5 mL of binding buffer, and subjected to flow-cytometric analysis within 30 min. Forward scatter, side scatter, and fluorescence intensity were measured, and gated fluorescence intensity above background (cells with no aptamer added) was quantified as well.

The detection of bacterial cells in real sample (drinking water) was carried out in the microfluidic device accordingly, and the results are shown in Fig. S6.
Table S1.
Screened aptamer sequences of eight families without primers

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**Table S2.**
Information on composition and distribution of putative Quadruplex forming G-Rich Sequences (QGRS) in nucleotide sequences using QGRS Mapper

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Table S2. Information on composition and distribution of putative Quadruplex forming G-Rich Sequences (QGRS) in nucleotide sequences using QGRS Mapper (continued)

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The table lists all QGRS mapped to sequences of selected aptamers, including information about the position of the QGRS, its distance from 3’ and 5’ splice sites, the actual sequence (underlining the G-groups) and its G-score.
Fig. S1. Flow-cytometric analysis of *E.coli* 11775 binding with aptamers EA1P, EA7P, EA1, EA7. Duplicate analyses were carried out.

Fig. S2. Flow-cytometric analysis of *P.vulgaris* binding with aptamers EA1P, EA7P, EA1, EA7. Duplicate analyses were carried out.
Fig. S3. Flow-cytometric analysis of *B. subtilis* binding with aptamers EA1P, EA7P, EA1, EA7. Duplicate analyses were carried out.

Fig. S4. Flow-cytometric analysis of *E. Coli* DH5α binding with aptamers EA1P, EA7P, EA1, EA7. Duplicate analyses were carried out.
Fig. S5. Flow-cytometric analysis of *E. aerogenes* binding with aptamers EA1P, EA7P, EA1, EA7. Duplicate analyses were carried out.
Fig. S6. Image of detection of bacterial cells in drinking water in microfluidic device: Representative images of *E.Coli* 11775 cells captured (A) and control bacterial cells *B.subtilis* (B) on EA1P aptamer immobilized surface. Representative images of *E.Coli* 11775 cells captured with the random DNA (C) and without DNA immobilized surface (D).