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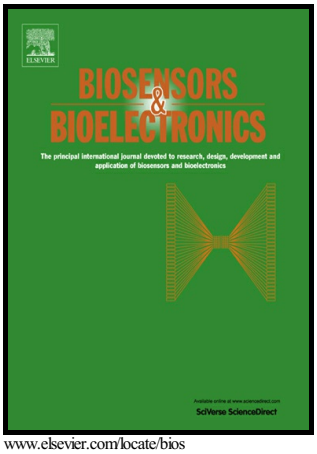

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A Label-Free and High-Efficient GO-based Aptasensor for Cancer Cells Based on Cyclic Enzymatic Signal Amplification

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Abstract: A label-free and high-efficient graphene oxide (GO)-based aptasensor was developed for the detection of low quantity cancer cells based on cell-triggered cyclic enzymatic signal amplification (CTCESA). In the absence of target cells, hairpin aptamer probes (HAPs) and dye-labeled linker DNAs stably coexisted in solution, and the fluorescence was quenched by the GO-based Förster resonance energy transfer (FRET) process. In the presence of target cells, the specific binding of HAPs with the target cells triggered a conformational alternation, which resulted in linker DNA complementary pairing and cleavage by nicking endonuclease-strand scission cycles. Consequently, more cleaved fragments of linker DNAs with more the terminal labeled dyes could show the enhanced fluorescence because these cleaved DNA fragments hardly combine with GOs and prevent the FRET process. Fluorescence analysis demonstrated that this GO-based aptasensor exhibited selective and sensitive response to the presence of target CCRF-CEM cells in the concentration range from 50 to 10^5 cells. The detection limit of this method was 25 cells, which was approximately 20 times lower than the detection limit of normal fluorescence aptasensors without amplification. With high sensitivity and specificity, it provided a simple and cost-effective approach for early cancer diagnosis.

Keywords: Cancer Cells; Enzymatic Signal Amplification; Fluorescence Assay; Graphene Oxide; Hairpin Aptamer Probe

1. Introduction

The development of a method to detect cancer cells at their early stage with high selectivity and sensitivity is a key challenge in cancer prevention, diagnosis and treatment (Wu and Qu 2015). By measuring the specific cellular levels in routine blood test, doctors can find early sign of cancer for people with no symptom and increase the chance of cure (Savage 2011; Yu et al. 2013). Flow cytometry (Schamhart et al. 2003), immunohistochemistry (Singh et al. 2004) and polymerase chain reaction (PCR) (Xenidis et al. 2006) are tradition technique for cancer cell analysis. However, they require complicated operation, long treating time and costly instrument, which