ORIGINAL PAPER



Click chemistry reaction-triggered DNA walker amplification coupled with hyperbranched DNA nanostructure for versatile fluorescence detection and drug delivery to cancer cells

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Received: 4 June 2020 / Accepted: 29 September 2020 / Published online: 23 October 2020 © Springer-Verlag GmbH Austria, part of Springer Nature 2020

Abstract

A new DNA hyperbranched hybridization chain reaction (HB-HCR)-amplified fluorescence platform combined with DNA walker was developed for versatile detection of Cu^{2+} , adenosine triphosphate (ATP), and drug delivery to cancer cells. A novel click chemistry reaction-triggered DNA walking machine on magnetic beads (MBs) is introduced for the first time to convert target Cu^{2+} to lots of DNA S3 products. With the help of DNA S3 and H1 on the amino functionalized SiO₂ microsphere, HB-HCR between super hairpin DNA (SH DNA), H3-DNA, and LT-DNA was initiated to assemble a novel dendritic DNA structure with numerous fluorescent Cy5, achieving enormously amplified signal for ultrasensitive detection of Cu^{2+} . Furthermore, this contains large amounts of double-stranded DNA with plentiful GC bases, which can provide many loading sites for chemotherapeutic drug doxorubicin (Dox). The specific binding of ATP to aptamer in the dendritic DNA structure allows for release of Dox, leading to activation of Dox fluorescence for ATP assay. More importantly, this dendritic DNA nanostructure-loaded Dox enters into tumor cells by endocytosis, and then interacts with endogenous ATP, releasing Dox for efficient treatment of cancer cells. Taking advantages of these multiple amplification of HB-HCR on SiO₂ microsphere, click chemistry reaction, DNA walking, and release of Dox, this method enables ultrasensitive detection of Cu^{2+} and ATP as low as 0.1 fM and 1.0 aM, respectively, which can be widely used for accurate detection of biomolecules in clinical diagnosis and biomedical applications.

Keywords Hybridization chain reaction \cdot Click chemistry reaction \cdot DNA walker \cdot Hyperbranched DNA nanostructure \cdot Drug delivery

Introduction

Copper is both an essential trace element and a toxic substance to plants, animals, and humans [1, 2]. Copper toxicosis is very rare compared to its deficiency in plants [3]. This element exhibits high toxicity to microorganisms such as algae, bacteria, viruses, and aquatic animals [4]. In addition, Cu²⁺ is also a significant environmental pollutant [5]. The U.S. Environmental Protection Agency (EPA) has set the safe limit of copper in drinking water at 1.3 mg/L (ca. 20 μ M) [6]. For these reasons, the development of highly selective and sensitive detection methods for Cu²⁺ ion has great significance for environment protection and human health. As the primary energy currency, ATP plays an important role in adjusting cellular metabolizability pathways [7] and various biochemical reaction processes [8, 9]. It has been used as an indicator of living organisms for cell injury and cell viability [10]. Therefore, rapid quantification of the abundant transition metal element Cu²⁺ and the universal energy currency ATP is significant in clinical diagnosis.

To date, many analytical techniques have been developed to achieve effective detection of Cu^{2+} and ATP, such as colorimetry [11, 12], electrochemistry [13, 14], and fluorescence [15, 16]. Among them, fluorescence affords many advantages for high sensitivity, low background, low cost, and wide linear ranges. Moreover, chemistry-based recognition methods, such as specific coordination reagents [17], and Cu (I)-catalyzed

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click chemistry [18] has been used in Cu²⁺ assays. The click reaction displays some advantages, such as high yields, mild reaction conditions, and well-retained framework [19, 20].

In order to improve the detection sensitivity for trace level targets, a series of powerful amplification strategies such as polymerase chain reaction [21], catalyzed assembly hairpin reaction [22], hybridization chain reaction [23], and hyperbranched hybridization chain reaction (HB-HCR) has been developed for detection [24]. Among them, HB-HCR can produce multiple dendritic DNA nanostructures with much high amplification efficiency, and has provided a useful tool for amplified sensing platform in bioanalysis [25, 26]. This dendritic DNA nanostructures with good biocompatibility and stability are also good drug delivery vehicle [27, 28], and the DNA duplex GC base pairs favorably interacts with drug Dox for self-assembly and loading, which has a clear inhibition influence on a wide range of cancers [29, 30].

In this work, we reported a novel HB-HCR cascade amplification method for versatile FL detection of Cu²⁺ and ATP activity based on Cu(I)-catalyzed click chemistry reaction. In the presence of target Cu²⁺, DNA walking amplification based on click chemistry reaction was performed to produce lots of DNA S3. S3 opens H1 on the SiO₂ microspheres, which further initiated HB-HCR to form the dendritic DNA nanostructure with abundant fluorescent signal probes for amplified detection of Cu²⁺. Then, large amounts of Dox were loaded into the double-stranded DNA in the nanostructure, and specific binding of ATP led to release of Dox, generating significantly amplified fluorescence signal for ATP detection. Moreover, the entrance of dendritic DNA nanostructure into cancer cells can be used for both confocal imaging and controllable drug delivery of Dox due to overexpressed ATP in cancer cells. The strategy demonstrated good property with ultrahigh sensitivity for versatile assays of Cu2+, ATP, and clinical treatment of cancer cells.

Experimental section

Assembly of H1 on SiO₂ microsphere

1-Ethyl-3-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC, 12.5 μ L, 100 mM) and Nhydroxysuccinimide (NHS, 12.5 μ L, 25 mM) were added to 25 μ L of 2.0×10^{-7} M H1 DNA to activate the carboxyl group for 1 h, then 18 μ L of aminomodified SiO₂ microspheres were added and incubated for over 6 h (37 °C). To obtain the SiO₂-H1 conjugate, excess H1 was removed by centrifuging the solution.

Fabrication of the dendritic DNA nanostructure for amplified fluorescence detection of Cu²⁺

The obtained DNA (S3) solution and SiO₂-H1 conjugate were uniformly mixed, and incubated for 1.5 h (37 °C), unbound S3 was removed by centrifuging the solution. H2 (50 µL, 0.1 µM) was added to the above SiO₂-H1-S3 mixture, and incubated for 120 min, unbound H2 was removed by centrifuging the solution. Then, 50 μ L of 5.0 × 10⁻⁷ M SH was added to the above mixture and incubated for 120 min to perform the hybridization reaction. Fifty microliters of $5.0 \times$ 10^{-7} M H3 (Cy5-BHO2) was added to the above mixture and incubated for 120 min, then 50 μ L of AS1 (5.0 × 10⁻⁷ M) was added to the above mixture and incubated for 120 min to perform the hybridization reaction. LT and LA are incubated for 1 h to obtain LT/LA. Fifty microliters of 5.0×10^{-7} M LT/ LA was added to the above mixture and incubated for 90 min to perform the hybridization reaction. Finally, 50 μ L of 5.0 \times 10^{-7} M AS2 was added to the above mixture and incubated for 90 min to perform HB-HCR. Unbound DNA was removed by centrifuging the solution, the precipitate was redispersed in 50 μ L of ultrapure water, and the resulting mixtures were immediately subjected to fluorescence measurements.

Fabrication of the dendritic DNA nanostructure with Dox for ATP detection

Ten microliters of 100 μ M Dox and the SiO₂-HB-HCR solution were mixed, and incubated for 3 h (37 °C), then excess Dox were removed by centrifugation; the precipitate was redispersed in 50 μ L of ultrapure water. Ten microliters of various concentration of ATP was added to the above SiO₂-HB-HCR-Dox solution and incubated at 37 °C for 2 h, then the Dox was released. Finally, the fluorescence signal of the mixture solution was measured for assay of target ATP.

Results and discussion

Principle for the HB-HCR-based fluorescence platform for versatile detection of Cu²⁺, ATP, and drug delivery to cancer cells

The part A in Scheme 1 displays the DNA walking amplification process based on click chemistry reaction. The aminomodified DNAzyme and S1 were first linked to the carboxyl magnetic beads by peptide bond. The magnetic beads are mainly used for magnetic separation to produce a large amount of product S3. When target Cu^{2+} and AA are present, Cu^{+} was in situ generated by Cu^{2+} reduction, then click chemistry reaction drove S1 to bind with S2; the hairpin-locked DNAzyme was opened through hybridization with S1 and S2, yielding the "active" DNAzyme, which was then Scheme 1 Schematic illustration for (a) target Cu²⁺-triggered click chemistry reaction and DNA walking amplification process on magnetic beads for generating DNA S3, (b) fabrication of the HB-HCR amplified fluorescence system for detecting target Cu²⁺, (c) fabrication of the HB-HCR amplified fluorescence system for ATP detection, and (d) application of the prepared SiO₂-HB-HCR-Dox for confocal imaging and drug Dox delivery to MCF-7 cells



specifically cleaved by Mg²⁺ at the cleavage site. The released S1/S2 hybridized with another DNAzyme. Due to the DNA walking amplification on the magnetic beads, many S3 products were obtained. The part (B) shows the HB-HCR-based

versatile fluorescence strategy for amplified detection of Cu^{2+} . The carboxyl-modified H1 was first linked to the amino SiO₂ microspheres by covalent bond, then S3 hybridized with H1, and opened green ssDNA of H1 further hybridized with green segment of H2. Subsequently, the red ssDNA of H2 hybridized with red section of SH, and the opened purple ssDNA of SH hybridized with H3, so the cycling processes produced many HCR-1 for the dendritic DNA structure. When the blue ssDNA AS1 was added, the blue segment of SH was opened by hybridization. With addition of the double-stranded substrate LT/LAT, the orange segment of LT hybridized with SH DNA. Subsequently, AS2 is added to dissociate LA strand by displacement reaction, and the above cycling hybridization processes generated abundant HCR-2. Finally, the HB-HCR-based dendritic DNA structure with large amount of fluorescent signal probes (H3) was prepared for amplified detection of target Cu²⁺. In part C, as the dendritic DNA structure contains abundant GC-rich double-stranded DNA, it is used to load a large number of Dox. The specific interaction of ATP with its aptamer destroyed the DNA structure and released Dox, leading to amplified fluorescence signal of free Dox for ATP assay. The fourth part (D) displays the application of the SiO₂-HB-HCR-Dox structure for confocal imaging and drug Dox delivery to MCF-7 cells. After incubation of SiO₂-HB-HCR-Dox with cancer cells, it can enter into the cancer cells by endocytosis. The specific binding of ATP to aptamer resulted in dissociation of dsDNA in the DNA structure, so the released Dox enters the nucleus for cell imaging and treatment of cancer cells. Thus, the novel HB-HCRamplified fluorescence platform coupled with walking amplification was developed for versatile assays of target Cu²⁺, ATP, and drug therapy of cancer cells.

Gel electrophoresis analysis of the DNA walking amplification process and DNA HB-HCR system

The target Cu^{2+} -triggered DNA walking amplification process was characterized by polyacrylamide gel electrophoresis (PAGE). In Fig. 1, lane M is a mark, and lanes 1 to 3 showed S1, S2, and DNAzyme. When S1 was mixed with S2, no new band appeared (lane 4), while the mixture of Cu^{2+} , AA, S1, and S2 showed a bright new band in lane 5, indicating the connection of S2 and S1 based on click chemistry reaction. When Cu^{2+} , AA, S1, S2, and DNAzyme were all mixed, both S1 and S2 hybridize with DNAzyme, generating a clear band (lane 6). By comparison, when Mg²⁺ was added into the mixture of Cu^{2+} , AA, S1, S2, and DNAzyme, a new bright band appeared at the bottom of lane 7, corresponding to the singlestranded DNA (S3) produced by DNAzyme-based shearing. The above results demonstrated the successful formation of the product S3.

The designed HB-HCR system were verified by PAGE. In Fig. 2, lanes 1 to 7 showed H1, H2, SH, H3, AS1, LT, and LA, respectively, when LT was mixed with LA, producing a distinct bright band (lane 8). Lane 9 was AS2, and when AS2 was mixed with LA, an obvious band was obtained (lane 10). In the presence of S3, H1 was opened by hybridization, and a



Fig. 1 Gel electrophoresis analysis of the DNA walking amplification process. Lane 1, 4 μ M S1; lane 2, 100 μ M S2; lane 3, 4 μ M DNAzyme; lane 4, 4 μ M S1 + 100 μ M S2; lane 5, 4 μ M S1 + 100 μ M S2 + 10 μ M Cu²⁺ + 20 μ M AA; lane 6, 4 μ M S1 + 100 μ M S2 + 4 μ M DNAzyme + 10 μ M Cu²⁺ + 20 μ M AA; lane 7, 4 μ M S1 + 100 μ M S2 + 4 μ M DNAzyme + 1 μ M Cu²⁺ + 2 μ M AA + 1 μ M Mg²⁺

new band with higher molecular weight (S3/H1) was obtained in line 11. When H1, S3, and H2 were all present, an obvious higher band (lane 12) was obtained due to further hybridization of S3/H1 with H2. The mixture of H1, S3, H2, and SH showed another new higher band in lane 13 for hybridization of H2 with SH. When H3 was introduced to the mixture of H1, S3, H2, and SH, the purple part of SH DNA further hybridized with H3, and a new distinct band can be observed at higher position in lane 14. By introducing AS1 to the mixture of S3, H1, H2, SH, and H3, SH is further opened by hybridization in the blue section, and a clear new band (HCR-1 DNA branch, lane 15) was obtained. When H1, S3, H2, SH, H3, AS1, and LT/LA were all mixed, the LT in the double-stranded substrate LT/LA is further hybridized with the yellow segment of SH, and a new band with a highest molecular weight was obtained (lane 16). When H1, S3, H2, SH, H3, AS1, LT/LA, and AS2 were all mixed, AS2 hybridized with LA to dissociate it from LT, generating another new band at lower position and DNA branch HCR-2 (lane 17). The above results suggest that the HB-HCR can be performed to fabricate the DNA dendritic structure for assay of S3 (Target Cu²⁺-amplification product). Furthermore, when target ATP and the hyperbranched dendritic DNA solution were all mixed, the double-stranded DNA was dissociated, so several DNA bands with different molecular weight appeared on the lane 18.

The results of Figs. 1 and 2 proved that the designed HB-HCR-based DNA dendritic system can be technically fabricated for amplified assay of target Cu²⁺ and ATP, which can be also used for fluorescence imaging and drug application in cancer cells by releasing Dox from double-stranded DNA.

Fig. 2 Gel electrophoresis analysis of the DNA HB-HCR system. Lane 1, 2 µM H1; lane 2, 2μ M H2; lane 3, 4 μ M SH; lane 4, 4 µM H3; lane 5, 100 µM AS1; lane 6, 4 µM LT; lane7, 4 µM LA; lane 8, 4 μ M LT + 4 μ M LA; lane 9, 4 μ M AS2; lane 10, 4 μ M AS2 + 4 μ M LA; lane 11, 2 μ M H1 + S3; lane 12, 2 µM H1 + S3 + 2 µM H2; lane 13, 2 µM $H1 + S3 + 2 \mu M H2 + 4 \mu M SH;$ lane 14, 2 μ M H1 + S3 + 2 μ M H2 + 4 μ M SH + 4 μ M H3; lane 15, 2 µM H1 + S3 + 2 µM H2 + $4 \mu M SH + 4 \mu M H3 + 4 \mu M$ AS1; lane 16, 2 µM H1 + S3 + $2 \mu M H2 + 4 \mu M SH + 4 \mu M$ H3 + 4 μ M AS1 + 4 μ M LT/LA; lane 17, 2 μ M H1 + S3 + 2 μ M $H2 + 4 \mu M SH + 4 \mu M H3 +$ $4 \mu M AS1 + 4 \mu M LT/LA +$ 4 µM AS2; lane 18, 2 µM H1 + $S3 + 2 \mu M H2 + 4 \mu M SH +$ $4~\mu M~H3 + 4~\mu M~AS1 + 4~\mu M$ $LT/LA + 4 \ \mu M \ AS2 + 1 \ \mu M \ ATP$



Fig. 3 a SEM image of SiO_2 microspheres. b TEM image of SiO_2 microspheres. c TEM image of the dendritic DNA structure on SiO_2 microspheres. d TEM image of the dendritic DNA structure by HB-HCR



Fig. 4 a AFM image of HB-HCR products. b Height profile of HB-HCR products. c AFM image of ATP-HB-HCR products. d Height profile of ATP-HB-HCR products



Characterization of SiO₂ microspheres and HB-HCR process

The functionalized SiO₂ microspheres are used to load a large number of dendritic DNA nanostructure with many signal probes for direct fluorescence detection, and can also be centrifugated to generate precipitates, removing unbound DNA, and isolating Dox that is not embedded in double-stranded DNA. Figure 3a and b shows the SEM and TEM images of SiO₂ microspheres, respectively. The SiO₂ microspheres displayed uniform particle size with an average diameter of about 110 nm, and the surface of SiO₂ microspheres is very smooth. By comparison, when the dendritic DNA structure is formed on the SiO₂ microspheres by HB-HCR (Fig. 3c), the surface of the SiO₂ sphere became rougher. Furthermore, Fig. 3d shows the assembled DNA products by HB-HCR, and the dendritic DNA structure with an average length of 200 ± 40 nm was obviously observed, indicating that the branched DNA structure was successfully prepared by HB-HCR process.

Atomic force microscopy characterization of the HB-HCR products

To further confirm the assembled DNA products by HB-HCR, we directly visualized the morphology of the dendritic DNA structure with atomic force microscopy (AFM) imaging.



Fig. 5 UV-vis absorption spectra of (A) (a) SiO₂ microspheres, (b) H1, (c) SiO₂-H1. (B) (a) H1-S3-H2-SH-H3, (b) Dox, (c) H1-S3-H2-SH-H3-Dox



Fig. 6 (A) Feasibility of the HB-HCR-Cy5-BHQ2 fluorescence sensing system. (a) blank, (b) with 10 fM Cu^{2+} . (B) Feasibility of the HB-HCR-Dox fluorescence sensing system. (a) 10 μ M free Dox, (b) blank, (c) 10 fM ATP (before centrifuge), and (d) 10 fM ATP (after centrifuge)



Fig. 7 a FL responses of the proposed strategy corresponding to different concentrations of Cu^{2+} (a to j corresponding to 0, from 10 aM to 1 nM). **b** The relationship between fluorescence signal and Cu^{2+} concentration. Inset: The linear relationship between FL intensity and logarithmic value of Cu^{2+}

Table 1Comparison of the application performances for Cu^{2+} in ourproposed FL assay with that in some previous references

Methods	Linear range, nM	Detection limit, nM	Refs
FL	$10^{-7} \sim 0.01$	10 ⁻⁷	This work
FL	30~600	0.15	[31]
FL	0.01~200	10^{-3}	[32]
ECL	0.005~900	10^{-3}	[33]
Colorimetric	3~430	1.3	[34]
SERS	0.5~1000	0.18	[35]

Table 2	Comparison of different methods for assay of ATP			
Methods	Linear range, nM	Detection limit, nM	Refs	
FL	$10^{-9} \sim 0.01$	10 ⁻⁹	This work	
FL	0.1~125	0.081	[36]	
ECL	$2 \times 10^{-5} \sim 0.2$	$6.7 imes 10^{-6}$	[37]	
ECL	$5 \times 10^{-3} \sim 5$	1.5×10^{-3}	[38]	
PEC	$5 \times 10^{-4} \sim 5$	1.8×10^{-4}	[39]	
PEC	$10^{-5} \sim 100$	3.3×10^{-6}	[40]	

Figure 4a displays the dendritic DNA nanostructures of different lengths, and the height is approximately 4.35 nm (Fig. 4b). In contrast, Fig. 4c displays the dendritic DNA nanostructures in the presence of ATP, some small spots instead of assembled products were observed, and the thickness was about 0.6 nm (Fig. 4d); this indicates that the specific interaction of ATP with its aptamer result in the dissociation of the DNA dendritic nanostructure. Therefore, the assembled dendritic DNA fluorescence system by HB-HCR can be used for ATP detection.



Fig. 8 a Fluorescence spectra of the HB-HCR-Dox system to various concentrations of ATP (a to k corresponding to 0, 0.1 $aM\sim100$ pM). **b** The relationship between the fluorescence intensity and the concentration

of ATP. Inset: Linear relationship between fluorescence intensity and logarithm of ATP concentration



Fig. 9 a Selectivity of the FL strategy for detecting different metal ions (concentrations of metal ions, 10 fM). b Selectivity of the proposed strategy to ATP analysis (ATP concentrations, 10 fM)

Characterization of SiO₂-H1 and H1-S3-H2-SH-H3-Dox by UV-vis absorption spectra

As illustrated in Fig. 5A, curve a shows that SiO₂ microspheres have no absorbance peak, and curve b shows that H1 has an absorption peak at 260 nm. When H1 was bound to the SiO₂ microspheres, obvious absorption peak (curve c) indicated the successful conjugation of them.

In order to investigate the application of the assembled DNA nanostructure (H1-S3-H2-SH-H3) for Dox delivery to cancer cells, the assembly process of dox in H1-S3-H2-SH-H3 was characterized using absorption spectra. As illustrated in Fig. 5B, H1-S3-H2-SH-H3 showed a distinct absorption peak at 260 nm (curve a), and the anticancer drug Dox has a distinct absorption peak at 480 nm (curve b). When Dox is inserted into the dsDNA, two peaks of both DNA and Dox appeared, the peak intensity of Dox increases, and the peak

cubation with (a) 10 µM

with SiO₂-HB-HCR-Dox

position shifts red (curve c); this indicates that Dox was successfully embedded into double-stranded DNA.

Feasibility of the HB-HCR fluorescence platform for detection of target Cu²⁺

The feasibility of the fluorescence sensing system for Cu²⁺ assay was studied. The excitation wavelength of Cy5-BHQ2 is 635 nm, and the emission peak of Cy5-BHQ2 is 668 nm. In the absence of target Cu^{2+} , the signal probes (H3) are not opened up, and there is a very low fluorescence signal (Fig. 6A, curve a, blank). When the target Cu^{2+} was present, abundant signal probes (H3) were introduced to the sensing system and opened up by HB-HCR process; therefore, obviously higher fluorescence signal was observed (curve b), indicating that the HB-HCR fluorescence sensing system can be used for target Cu^{2+} assay.



Feasibility of the HB-HCR fluorescence platform for assay of ATP

The feasibility of the fluorescence system with Dox for ATP detection was investigated. As shown in Fig. 6B, when the excitation wavelength of Dox is 480 nm, the free Dox showed very high fluorescence signal at the emission peak of 555 nm (curve a), while the HB-HCR-Dox displayed a low fluorescence signal (curve a, blank) without target ATP. The fluorescence signal of the Dox-SiO₂-HB-HCR chimera without centrifugation is shown in the curve c; therefore, obviously higher fluorescence signal was observed. When ATP was present, the interaction of ATP with its aptamer results in destruction of HB-HCR-Dox structure and release of Dox was observed that the centrifuged Dox-SiO₂-HB-HCR chimera showed obvious high fluorescence signal (curve d), indicating that the HB-HCR fluorescence sensing system can be used for ATP assay.

Analytical performance of the HB-HCR amplified fluorescence system

The performance of the proposed HB-HCR amplified fluorescence system for Cu²⁺ detection was examined. The fluorescence signal of the Cy5-based sensing system increased gradually with increasing Cu2+ concentration from 10 aM to 1.0 nM (Fig. 7a). Figure 7b shows that the fluorescence intensity is linearly related to the logarithmic value of Cu²⁺ concentration in the range of 0.1 fM to 100 pM, and the regression equation is Y =1423.13 + 250.05 lgc. The calculated detection limit for Cu^{2+} is 0.1 fM (LOD = 3SB/m, where m is the slope of the corresponding calibration curve and SB is the standard deviation of the blank), indicating that the method is more sensitive than other reported strategy (Table 1). In addition, to verify the accuracy of this method, the relative standard deviation (RSD) was calculated to be 2.3% by parallel detection of 10 pM target for three times. These results indicate that the proposed strategy has well analytical performance.

Table 3 Determination of Cu^{2+} added in real water samples (n = 3) with the proposed strategy

Sample	Added/ fM	Obtain/ fM	Recovery/ %	RSD/ %
1	1	1.04	103.57	3.14
2	5	4.95	96.43	2.79
3	10	10.29	102.48	4.85
4	100	99.08	99.63	3.63

Table 4Determination of ATP added in human serum samples (n = 3)with the proposed strategy

Sample	Added/ fM	Obtain/ fM	Recovery/ %	RSD/ %
1	1	0.94	94.72	5.11
2	5	5.04	104.45	3.25
3	10	10.08	100.07	4.03
4	100	99.04	99.31	3.48

Under the optimized conditions, the proposed strategy was used for quantitative determination of target ATP. Figure 8a shows that the FL signal of the HB-HCR-Dox increased gradually with increase of ATP concentration from 0.1 aM to 100 pM. Figure 8b shows the linear relationship between the FL signal and the logarithm of ATP concentration from 1.0 aM to 10 pM, and the linear equation is Y = 2484.98 + 334.78 lgc. The detection limit is 1.0 aM (LOD = 3SB/m, where m is the slope of the corresponding calibration curve and SB is the standard deviation of the blank), which is lower than that of other reported methods (Table 2). The relative standard deviation (RSD) was calculated to be 3.1% by three parallel detection of 10 pM target, demonstrating that the proposed method has good analytical performance.

Selectivity of the fluorescence strategy

The selectivity of the fluorescence strategy for Cu^{2+} was demonstrated by using Hg²⁺, Ag⁺, Pb²⁺, Fe²⁺, and Ca²⁺ as interferences. As shown in Fig. 9a, it is clear that other metal ions have no apparent fluorescence responses, while the target Cu^{2+} even at low concentration led to a significant enhanced FL signal. The results prove that the proposed strategy exhibited well selectivity.

The selectivity of the FL strategy for ATP assay was demonstrated by thymidine triphosphate analogues of GTP, UTP, and CTP. As illustrated in Fig. 9b, only ATP caused a marked fluorescence increase. It was found that no significant fluorescence signal change was obtained for CTP, GTP, and UTP in comparison with that of ATP, so the interferences were negligible for ATP analysis. The proposed strategy possesses excellent selectivity for detection of ATP.

ATP-induced drug release of the SiO₂-HB-HCR-Dox in cancer cells

We investigated ATP-triggered drug release from SiO_2 -HB-HCR-Dox to MCF-7 cells. Oligomycin is a well-known inhibitor of ATP, when the cells were preincubated with oligomycin, followed by incubation with SiO_2 -HB-HCR- Dox, weak fluorescence signals were obtained (Fig. 10a). While MCF-7 cells in medium were incubated with SiO₂-HB-HCR-Dox, brighter red fluorescence signal of Dox was observed (Fig. 10b), and the Dox signal is distributed in the nucleus [41, 42], while the dispersed white small particles are SiO₂ microspheres. These results proved that the SiO₂-HB-HCR-Dox is an effective drug loading and delivery system [43, 44], and ATP can induce drug release in cancer cells. The Dox in the nucleus mainly binds with chromosomes to exert an anticancer function. These results demonstrated that the SiO₂-HB-HCR-Dox was an efficient drug Dox loading and delivery system, and the ATP in the MCF-7 cells could induce an intracellular drug release.

Application of the strategy in real samples

To further evaluate the applicability of the developed method, Cu^{2+} in water samples and ATP in human serum were detected. Cu^{2+} was not found in real water samples by our proposed method [45, 46], and 1 µL of water sample was firstly used to detect the fluorescence signal, then 1 µL of different concentrations of Cu^{2+} was added, and the fluorescence signals of the mixed solution were detected to obtain recovery rate. As can be seen from Table 3, the data from 1 to 4 showed recoveries from 96.43 to 103.57% and RSD from 2.79 to 4.85% of Cu^{2+} , confirming that the sensing platform can be used for Cu^{2+} assay in water samples.

The ATP level in human serum is about 0.94 μ M [47], which is detected by our method. After the diluted human serum samples (10 μ L) were spiked with different ATP samples (10 μ L), the fluorescence signals of the mixture solution were measured. The data from 1 to 4 (Table 4) display the recovery of ATP in the range of 94.72–104.45% and the RSD of 3.25–5.11%, indicating that the proposed method shows good reliability and reproducibility for quantification of ATP.

Conclusions

We have developed a versatile amplified fluorescence system based on click chemistry reaction and HB-HCR for ultrasensitive detection of Cu^{2+} and ATP as well as drug delivery to cancer cells. Target Cu^{2+} firstly triggered click chemistry reaction and DNA walking amplification process to produce a lot of DNA S3. S3 then initiated HB-HCR to assemble a novel dendritic DNA nanostructure on SiO₂ microsphere, which was used to conjugate a large amount of signal probe H3 for detection of target Cu^{2+} . Furthermore, plentiful Dox is loaded into the dendritic DNA nanostructure with ATP aptamer for amplified detection of ATP and drug delivery in cancer cells. The SiO₂-HB-HCR-Dox dendritic DNA structure with abundant Dox display much high amplification efficiency, and only the released free Dox in the presence of ATP can show obvious higher fluorescence signal and effective drug effects. Based on the dual amplification strategy of the HB-HCR and DNA walker, the dendritically amplified fluorescence system enabled versatile detection of diverse targets with ultralow detection limit. Furthermore, this strategy can be used as a universal platform to detect multiple biomolecules in basic research and clinical application of drug delivery, even if a lot of DNA was used and the size of signal probe should be controlled for entering into cells.

Funding This work was supported by the National Natural Science Foundation of China (No. 21575072).

Compliance with ethical standards

Conflict of interest The authors declare that they have no competing interests.

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