



Rapid sequential detection of Hg²⁺ and biothiols by a probe DNA—MOF hybrid sensory system

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ABSTRACT

A one-dimensional (1D) metal–organic framework (MOF) of [Cu(Cdcbp)(H₂O)₂·2H₂O]_n (**1**, H₃CdcbpBr = 3-carboxyl-(3,5-dicarboxybenzyl)-pyridinium bromide) has been synthesized and characterized. MOF **1** features a cationic Cu²⁺ center, conjugated tricarboxylate ligand bearing positively charged pyridinium and uncoordinated carboxylate groups within its skeleton. These features enable MOF **1** to tightly adsorb thymine rich (T-rich) single-stranded DNA (ss-DNA) probe labeled with carboxyfluorescein (FAM) (denote as P-DNA) through π -stacking, electrostatic interactions and/or hydrogen bonding to give a hybrid complex (denote as P-DNA@**1**), and quenches its fluorescence via a photo-induced electron transfer (PET) process. The formed P-DNA@**1** hybrid can thus function as a sensing platform for the detection of Hg²⁺, driven by the formation of hairpin-like double-stranded DNA (ds-DNA@Hg²⁺) with a T-Hg-T coordination motif, and subsequently dissociated into the solution due to its more rigid nature than ss-DNA, leading to the recovery of FAM fluorescence. In the presence of biothiols, including cysteine (Cys), homocysteine (Hcy) and glutathione (GSH), the strong coordination interaction between Hg²⁺ and the mercapto function serves to sequester the Hg²⁺ from the ds-DNA@Hg²⁺ duplex. The released ss-DNA, in turn, are re-adsorbed by MOF **1**, leading to the formation of the initial P-DNA@**1** state with fluorescence quenching. As such, P-DNA@**1** detects Hg²⁺ and biothiols Cys/Hcy/GSH in sequence with detection limits of (2.3 ± 0.8) nM and (29.6 ± 0.1) nM/(19.8 ± 0.5) nM/(10.2 ± 0.1) nM. The sensing process is efficient and selective with instantaneous response time. The detection mechanism was further validated by circular dichroism (CD), and simulation studies using Molecular Operating Environment (MOE) package.

1. Introduction

Biological thiols (biothiols), including cysteine (Cys), homocysteine (Hcy) and glutathione (GSH), contain a mercapto group and play important roles in a variety of physiological processes [1]. For example, GSH and Cys are often involved in the reversible redox reactions and cellular functions including metabolism and detoxification [2–6]. Abnormal levels of these biothiols in human serum and urine are associated with many diseases [7,8]. Similarly, Hg²⁺ is one of the most impactful heavy-metal pollutants, and its overdose is causative of brain damage [9], kidney failure, various cognition and motion disorders, and etc. [10]. Importantly, Hg²⁺ has a strong binding affinity toward the mercapto group [11], with the potential to disturb the biothiol level in the physiological system. In addition, the biothiol reaction with Hg²⁺ may cause the inactivation of their enzymes [12]. And the

activity of many biothiol-containing enzymes, such as amino-transferases [13,14] and dehydrogenases [15,16], when modified, significantly alter their activities [12]. Therefore, it is of great significance to develop rapid, cost-effective, and reliable methods to sequentially monitor the Hg²⁺ and biothiol levels.

Among various detection assays, fluorescence assay has been promising because of its advantages of high sensitivity, high selectivity, less sample consumption and operational convenience [17]. Thus, many fluorescence sensors based on functional materials, such as gold nanoparticles [5,18], silver nanoclusters [19,20], carbon nanomaterials [21,22], silica nanoparticles [23,24], semiconductor quantum dots [25], graphene oxide (GO) [26,27] have been developed. Among them, the hybrid sensors from these materials with the specific native or artificial DNA bases for the detection of metal ions has aroused increasing interests due to their higher specificity [28,29]. Specifically for Hg²⁺

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sensing, the formation of a hairpin-like thymine–Hg²⁺–thymine (T–Hg–T) motif is ideal [30,31], and a number of DNA-conjugated nanoparticles, nanorods or nanoclusters [32–35] are established as fluorescence biosensors using this concept.

Metal–organic frameworks (MOFs) have also emerged as a new class of functional materials for the detection of detect metal ions and/or biothiols. The widely practiced principle of metal ion detection by a MOF is through decoration of functionalities on the MOF pore surface [36,37]. These functionalities include thiol [38], pyridyl [39], benzimidazolyl [40], methionine [41], and melamine [42], which can specifically interact with metal ions, especially for Hg²⁺ due to its larger ionic radius than many other metal ions [43–48]. The interaction between functional group and Hg²⁺ hinders the energy transfer from organic ligands to metals ions in MOFs, thus cause the alternation of luminescence emission of the MOFs [49]. The biothiol detection by MOFs is operated via the similar way by incorporating functional groups such as maleimide [50,51], malonitrile [52], aldehyde [53], silver nanoparticles [54] etc. in the MOFs. In addition, some inherent catalytic properties of MOFs were also used for biothiol detection [55–57].

More recently, Zhang et al. used the UiO-66-NH₂ MOF to construct a MOF/DNA hybrid for the efficient fluorescent sensing of Hg²⁺ with high sensitivity and selectivity [58]. However, MOF-based hybrid sensing systems that than perform multiple tasks associated with Hg²⁺ and bio-related molecules, either synchronously or successively, is still limited [59]. This is primarily to due to the inherent stability of MOFs in aqueous phase, in addition to a variety of other factors, such as the competitive binding of Hg²⁺ to the carboxylate ligands, and the binding of phosphate from the DNA backbone or the simulated body fluid to the metals from the MOF, both serve to decompose the MOF connectivity [60–62].

We report a one-dimensional (1D) MOF of [Cu(Cdcbp)(H₂O)₂(2H₂O)]_n (**1**, H₃CdcbpBr = 3-carboxyl-(3,5-dicarboxybenzyl)-pyridinium bromide), which can strongly absorb T-rich single-stranded DNA (ss-DNA) probe labeled with carboxyfluorescein (FAM) (the formed MOF-ss DNA hybrid denotes as P-DNA@**1**) through π -stacking, electrostatic interactions and/or hydrogen bonding interactions, and quenches its fluorescence via a photo-induced electron transfer (PET) process [63–68]. The formed P-DNA@**1** sensing platform can be used for Hg²⁺ detection due to the formation of double-stranded DNA (ds-DNA@Hg²⁺) through the formation of rigid hairpin-like T–Hg–T motif, which was ejected from MOF **1**, leading to fluorescence recovery. Upon subsequent sequestration of Hg²⁺ by biothiols, including cysteine (Cys), homocysteine (Hcy), and glutathione (GSH), the released P-DNAs are re-adsorbed by MOF **1**, leading to fluorescence quenching again, thus further realized the biothiols detection (Scheme 1).

2. Experimental

2.1. General

IR spectra were recorded on a Nicolet MagNa-IR 550 infrared spectrometer. Elemental analyses for C, H, and N were performed on an EA1110 CHNS elemental analyzer. Powder X-ray diffraction (PXRD) spectra were recorded with a Rigaku D/max-2200/PC. The X-ray generated from a sealed Cu tube was monochromated by a graphite crystal and collimated by a 0.5 mm MONOCAP (λ Cu-K α = 1.54178 Å). The tube voltage and current were 40 kV and 40 mA, respectively. Fluorescence spectra were measured on an LS55 spectrofluorimeter. Circular dichroism was measured on Applied Photophysics Ltd. (UK) Chirascan plus ACD type circular dichroism spectrometer. The P-DNA, ds-DNA@Hg²⁺ and MOF **1** structures were constructed using Molecular Operating Environment (MOE) package [69]. The initial P-DNA@**1** or **1** + ds-DNA@Hg²⁺ structures were first optimized in MOE using MMFF94x force field and then re-optimized in UFF of Gaussian 09 [70], where Gibbs free energy calculations were simplified by calculating

single point energies. Finally, Python molecule (PyMOL) [71] was employed for visual analysis of binding modes.

The DNA sequences (P-DNA: 5'-TTCCTTCTCCCTTGTGTT-FAM-3') were purchased from Sangon Inc. (Shanghai, China) and were dissolved in 10 mM Hepes buffer (pH 7.4, Hepes = 2-(2-hydroxyethyl)-1-piperazinyl ethane sulfonic acid) and stored at 4 °C for use. The other reagents and solvents were obtained from commercial sources and used without further purification.

2.2. Synthesis of [Cu(Cdcbp)(H₂O)₂(2H₂O)]_n (**1**)

Powder of H₃CdcbpBr (38.1 mg, 0.1 mmol) was suspended in H₂O (20 mL) and the pH adjusted to 7.0 with 0.1 M NaOH to give a clear solution, a solution of CuSO₄·5H₂O (24.9 mg, 0.1 mmol) in H₂O (20 mL) was subsequently introduced. The resulting mixture was stirred for 15 min to give a clear light-blue solution. After filtration, the filtrate was allowed to stand at ambient temperature for about one week to produce crystals of MOF **1**, which were collected by filtration, washed with ether, and dried under vacuum. Yield: 40.0 mg (92%). Anal. Calcd. for C₁₅H₁₇NO₁₀Cu·2H₂O: C 38.26, H 4.50, N 2.97. Found: C 38.16, H 4.31, N, 2.86. IR (KBr disc, cm⁻¹) ν 3418 (s), 3036 (s), 1551 (s), 1437 (s), 1369 (s), 1213 (m), 1156 (m), 1019 (w), 768 (s), 713 (s), 642 (m), 540 (m), 486 (m), 441 (m).

3. Results and discussion

3.1. Characterization of MOF **1**

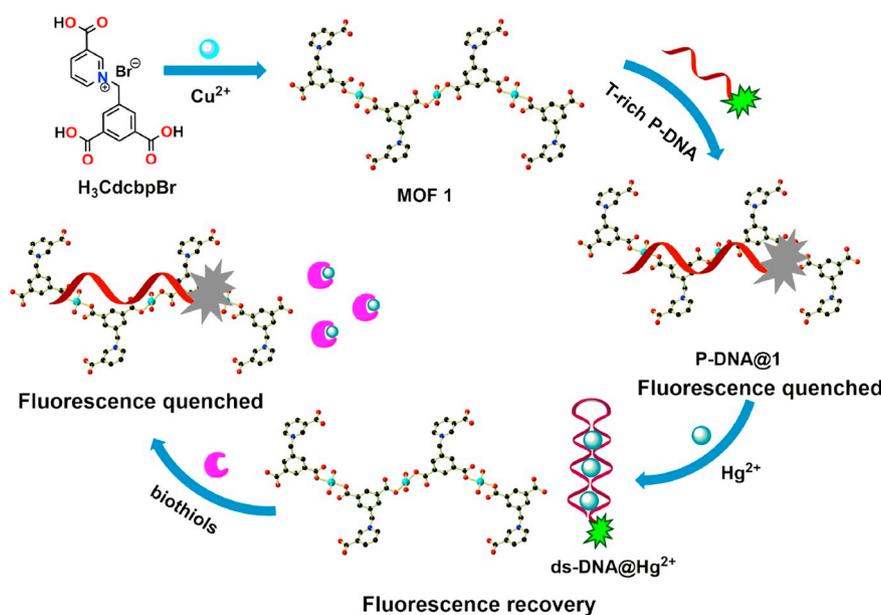
MOF **1** is moisture and water stable with the powder X-ray diffraction (PXRD) pattern of the as-synthesized sample, that immersed in H₂O or Hepes buffer, in good agreement with that of the simulated, indicating its bulky phase purity and water stability (Fig. 1a). MOF **1** crystallizes in the triclinic space group P-1 and each asymmetric unit contains one [Cu(Cdcbp)(H₂O)₂] molecule and two dissociated H₂O molecules. As shown in Fig. 1b, each Cu(II) is coordinated with two carboxylates from two Cdcbp ligands, both in monodentate fashion, and two additional water molecules, thus forming a quadrilateral geometry. Two carboxylate groups of each ligand connect to two Cu(H₂O)₂ units to form a 1D chain structure. The third free and uncoordinated carboxylate each carry a negative charge, thus maintaining the overall charge neutrality of MOF **1**. The detailed crystallographic parameters and the selected bond lengths and angles of MOF **1** (CCDC number 1888000) are listed in Tables 1 and 2, respectively.

3.2. Hg²⁺ detection using the P-DNA@**1** hybrid

MOF **1** exhibits a 1D structure with cationic Cu(II) center, conjugated tricarboxylate ligand of Cdcbp bearing positively charged pyridinium and uncoordinated carboxylates, allowing a maximum exposure of these functionalities [72,73]. These features are advantageous in forming π -stacking, electrostatic interactions and/or hydrogen bonding with negatively charged P-DNA sequences.

The fluorescence quenching experiments of P-DNA by MOF **1** were performed by keeping the concentrations of P-DNA constant, while gradually increasing the concentrations of MOF **1** at room temperature. Specifically, aliquots of a solution of MOF **1** containing P-DNA (50 nM) in 10 mM Hepes buffer was added to a solution of P-DNA (50 nM) in the same buffer and stirred to form stable P-DNA@**1** system. As shown in Fig. 2a, the fluorescence intensity of P-DNA decreases gradually with the increase of MOF **1** concentration. When the concentration of MOF **1** reaches 4.0 μ M, the fluorescence quenching efficiency (Q_E, %) of P-DNA is (88.0 \pm 3.3)%, as calculated according to the equation Q_E = (F₀ - F_M)/F₀ \times 100%, wherein F_M and F₀ are the fluorescence intensity at 518 nm in the presence and absence of MOF **1**, respectively.

In order to investigate the detection time for Hg²⁺, a solution of HgCl₂ was added into the solution of P-DNA@**1** with a concentration of



Scheme 1. The proposed Hg^{2+} and biothiols detection mechanism based on the P-DNA@1 hybrid.

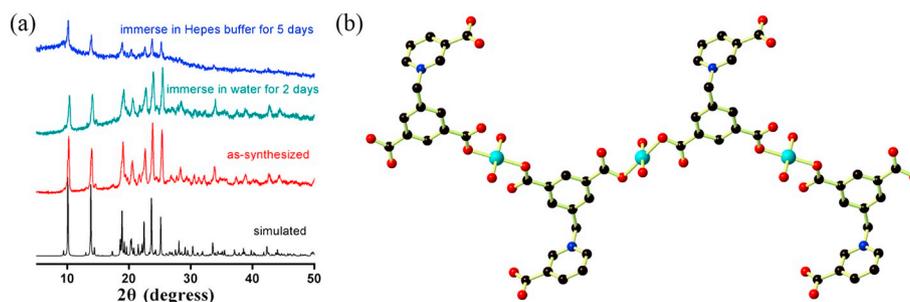


Fig. 1. (a) PXRD patterns of MOF 1 showing agreement among the simulated, as-synthesized, the fresh powder immersed in water for 2 days, and in Hepes buffer for 5 days. (b) The 1D structure of MOF 1. Color codes: Cu (cyan), O (red), N (blue), C (black).

Table 1
Crystallographic data for MOF 1.

Molecular formula	$\text{C}_{15}\text{H}_{17}\text{NO}_{10}\text{Cu}$		
Crystal system	Triclinic	D_{calc} (g cm^{-3})	1.677
Formula weight	434.84	λ (Mo K α) (\AA)	0.71073
Space group	$P\bar{1}$	μ (cm^{-1})	1.326
a (\AA)	8.7858(18)	Total reflections	8829
b (\AA)	10.289(2)	Unique reflections	3903
c (\AA)	10.517(2)	No. observations	3402
α ($^\circ$)	65.69(3)	No. parameters	247
β ($^\circ$)	83.62(3)	R^a	0.0404
γ ($^\circ$)	87.48(3)	wR^b	0.1028
V (\AA^3)	861.0(3)	GOF ^c	1.054
Z	2	$\Delta\rho_{\text{max}}$ (e \AA^{-3})	0.800
T/K	293(2)	$\Delta\rho_{\text{min}}$ (e \AA^{-3})	-0.523

$$^a R_1 = \frac{\sum ||F_o| - |F_c||}{\sum |F_o|}$$

$$^b wR_2 = \left\{ \frac{\sum [w(F_o^2 - F_c^2)^2]}{\sum w(F_o^2)^2} \right\}^{1/2}$$

^c GOF = $\left\{ \frac{\sum [w(F_o^2 - F_c^2)^2]}{(n-p)} \right\}^{1/2}$, where n is the number of reflections and p is total number of parameters refined.

0.05 μM and the fluorescence intensity recorded at different time intervals (Fig. 2b). When the time reached 2 min, the fluorescence was completely recovered. The short detection time may due to the 1D chain structure of MOF 1. Comparing to the 2D and 3D MOFs, MOF 1 with 1D chain structure shows small steric hindrance, and Hg^{2+} can readily induce P-DNA from MOF 1 to form ds-DNA@ Hg^{2+} through T-Hg-T base pairs to detach from MOF 1.

Based on the previous experiment, the fluorescence recovery

Table 2
Selected bond lengths (\AA) and angles ($^\circ$) for MOF 1.

Bond lengths (\AA)			
Cu(1)-O(5)	1.9485(18)	Cu(1)-O(5)#1	1.9485(18)
Cu(1)-O(1W)#1	1.943(2)	Cu(1)-O(1W)	1.943(2)
Cu(2)-O(2W)#2	1.943(2)	Cu(2)-O(2W)	1.943(2)
Cu(2)-O(3)	1.9588(18)	Cu(2)-O(3)#2	1.9588(18)
Bond angles ($^\circ$)			
O(5)-Cu(1)-O(5)#1	180.00(11)	O(5)-Cu(1)-O(1W)#1	89.95(9)
O(5)#1-Cu(1)-O(1W)#1	90.05(9)	O(5)-Cu(1)-O(1W)	90.05(9)
O(5)#1-Cu(1)-O(1W)	89.95(9)	O(1W)#1-Cu(1)-O(1W)	180.00(12)
O(2W)#2-Cu(2)-O(2W)	180.000(1)	O(2W)#2-Cu(2)-O(3)	89.42(9)
O(2W)-Cu(2)-O(3)	90.58(9)	O(2W)#2-Cu(2)-O(3)#2	90.58(9)
O(2W)-Cu(2)-O(3)#2	89.42(9)	O(3)-Cu(2)-O(3)#2	180.00(8)
Cu(1)-O(1W)-H(1W1)	120.5	Cu(1)-O(1W)-H(1W2)	125.0
Cu(2)-O(2W)-H(2W1)	104.0	Cu(2)-O(2W)-H(2W2)	116.8

Symmetry transformations used to generate equivalent atoms:

#1: $-x + 1, -y, -z$; #2: $-x + 1, -y + 2, -z - 1$.

experiments (R_E , %) were conducted by adding Hg^{2+} of varying concentrations to the P-DNA@1 sensing platform and maintained for 2 min to give a 1 + ds-DNA@ Hg^{2+} mixture. As shown in Fig. 2c, with the increase of Hg^{2+} concentration, the fluorescence intensity of P-DNA rapidly increased. When the Hg^{2+} concentration reaches 0.55 μM , the fluorescence recovery of P-DNA was completed with R_E value being

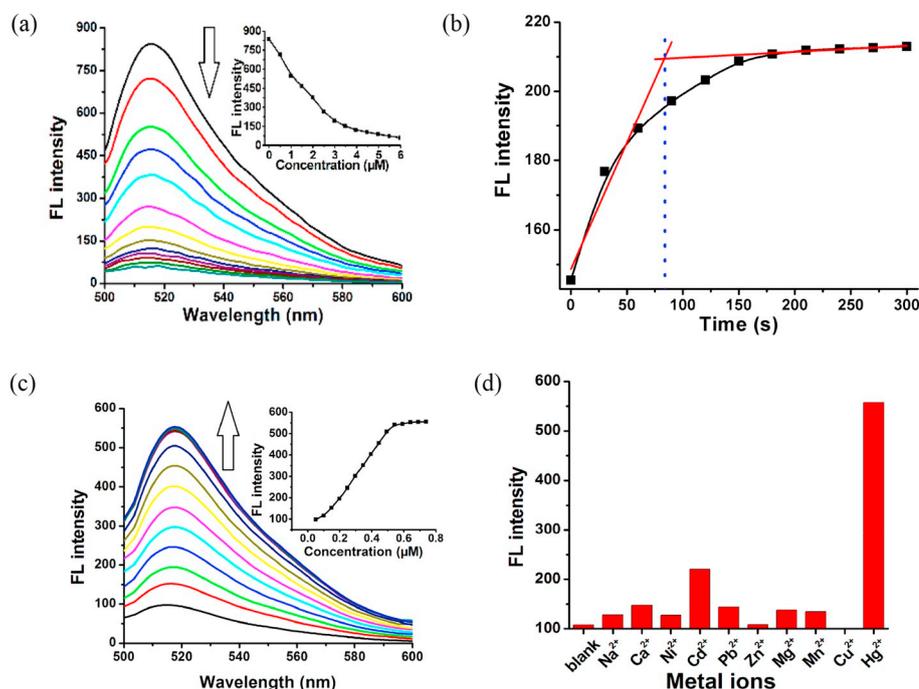


Fig. 2. (a) The fluorescence quenching of the P-DNA (50 nM) incubated with MOF 1 of varying concentrations at room temperature ($\lambda_{\text{ex}} = 480$ nm, $\lambda_{\text{em}} = 518$ nm). Inset: plot of fluorescence intensity versus the concentration of MOF 1. (b) The fluorescence intensity of the P-DNA@1 (50 nM/4.0 μM) at a function of time for the Hg^{2+} (0.05 μM) detection. (c) The fluorescence spectra of the P-DNA@1 sensing system (P-DNA@1, 50 nM/4.0 μM) incubated with different concentrations of Hg^{2+} in HEPES buffer (pH = 7.4, 10 mM). Inset: plot of the fluorescence intensity versus the concentrations of Hg^{2+} . (d) The selectivity of P-DNA@1 sensing system toward Hg^{2+} and the other metal ions (Hg^{2+} , 0.6 μM ; the other metal ions, 6 μM).

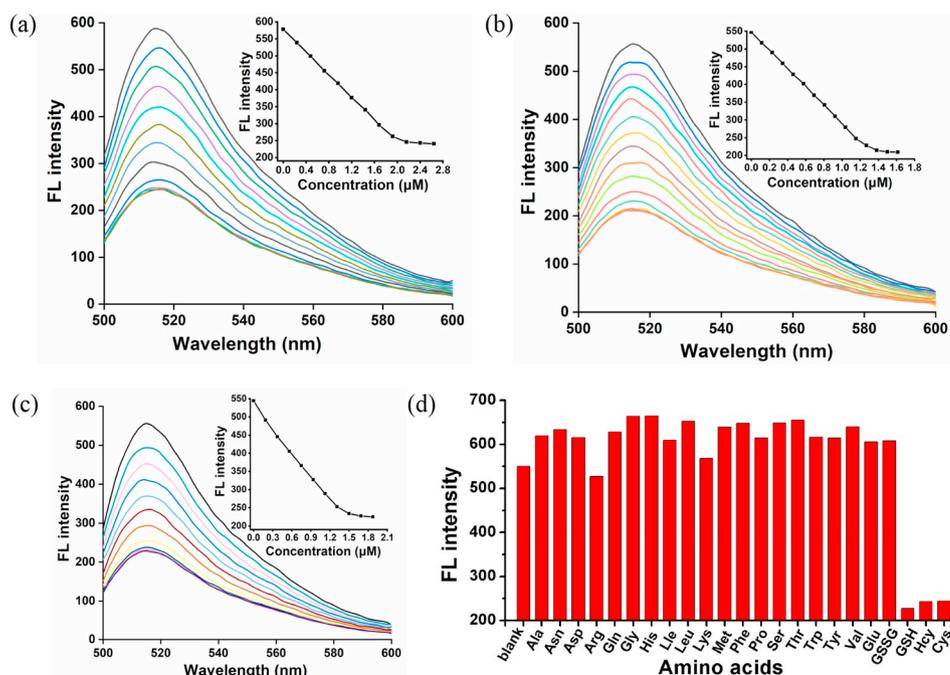


Fig. 3. The fluorescence intensity of the 1 + ds-DNA@ Hg^{2+} (4.0 μM /50 nM/0.55 μM) versus biothiols at different concentrations: Cys (a), GSH (b), and Hcy (c) in HEPES buffer (pH = 7.4, 10 mM) at room temperature. Inset: the fluorescence intensity as a function of concentration of Cys (a), GSH (b), and Hcy (c). (d) The selectivity of the 1 + ds-DNA@ Hg^{2+} system toward biothiols and the other amino acids (biothiols, 2.0 μM ; the other amino acids, 20.0 μM).

(4.5 ± 0.2), as calculated using the formula $R_E = (F_T - F_M)/F_M$, wherein F_T and F_M are the fluorescence intensities at 518 nm in the presence and the absence of Hg^{2+} , respectively. There is a good linear relationship between the fluorescence intensity and Hg^{2+} concentration from 0.10 to 0.55 μM . According to the $3\delta_b/\text{slope}$ (δ_b = standard deviation of five blank measurements), the limit of detection (LOD) is calculated to be (2.3 ± 0.8) nM with $R^2 = 0.9980$ and $\delta_b = 0.7679$, which is lower than the Environmental Protection Agency (EPA) limit of acceptable Hg^{2+} concentration in drinkable water (10 nM) and the toxicity level of Hg^{2+} in drinking water (30 nM) defined by the World Health Organization (WHO) [22,74].

In order to verify whether the P-DNA@1 sensing platform is selective toward Hg^{2+} , we investigated the fluorescence response of P-DNA@1 sensing platform to other metal ions, including Na^+ , Ca^{2+} ,

Ni^{2+} , Cd^{2+} , Pb^{2+} , Zn^{2+} , Mg^{2+} , Mn^{2+} , Cu^{2+} , whose concentrations are 10-fold higher than Hg^{2+} using the above method. As shown in Fig. 2d, the fluorescence intensity increased markedly in the presence of Hg^{2+} , while with other metal ions, only very limited changes of the fluorescence intensity are observed, indicating that the P-DNA@1 sensing platform is capable of specifically recognizing Hg^{2+} .

3.3. Biothiols detection using 1 + ds-DNA@ Hg^{2+} system

Upon addition of different concentrations of biothiols to the above formed 1 + ds-DNA@ Hg^{2+} system, the fluorescence intensity decreased until saturation was observed with the concentration of 2.2 μM for Cys (Fig. 3a), 1.4 μM for GSH (Fig. 3b), 1.8 μM for Hcy (Fig. 3c). The Q_E values are (58.3 ± 1.5)%, (61.6 ± 1.4)% and (58.7 ± 0.4)% for

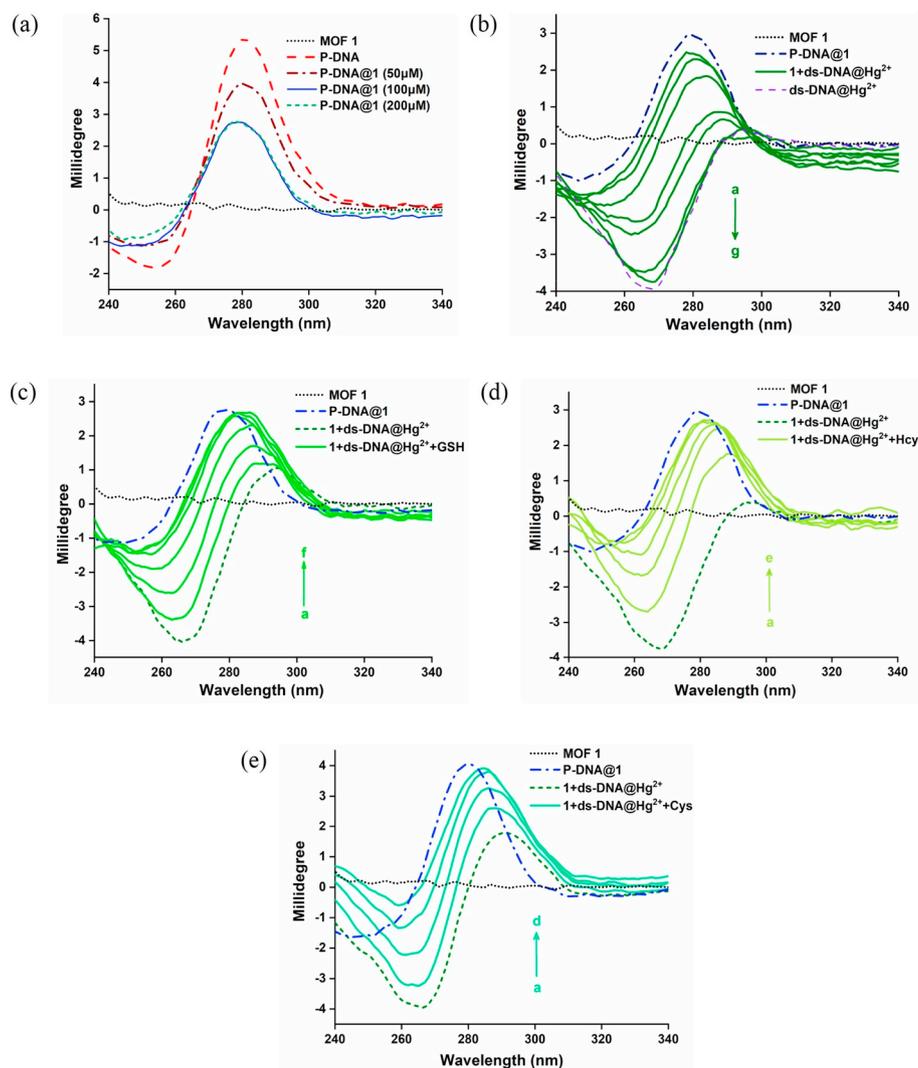


Fig. 4. (a) The CD spectra of P-DNA (10 μM) with different concentrations of MOF 1 (0, 50, 100, 200 μM), (b) the CD spectra of P-DNA@1 (10 μM /200 μM) with different concentrations of Hg^{2+} (10, 20, 40, 60, 80, 100, 120 μM , a–g) and ds-DNA@ Hg^{2+} (10 μM /120 μM), (c) the CD spectra of 1 + ds-DNA@ Hg^{2+} (200 μM /10 μM /120 μM) with different concentrations of GSH (30, 60, 90, 120, 150, 180 μM , a–f), as well as (d) Hcy (30, 60, 90, 120, 150 μM , a–e), and (e) Cys (30, 60, 90, 120 μM , a–d).

Cys, GSH and Hcy, respectively. With the good linear relationship between the concentration of biothiols and the fluorescence intensity (from 0 to 1.92 μM with $R^2 = 0.9996$ and $\delta_b = 1.6370$ for Cys, from 0 to 1.27 μM with $R^2 = 0.9999$ and $\delta_b = 0.8674$ for GSH, and from 0 to 1.31 μM with $R^2 = 0.9965$ and $\delta_b = 1.4438$ for Hcy). The LOD are accordingly (29.6 ± 0.1) nM, (10.2 ± 0.1) nM, and (19.8 ± 0.5) nM for Cys, GSH and Hcy.

In order to verify the specificity of the 1 + ds-DNA@ Hg^{2+} sensing platform toward biothiols, we further used other amino acids, namely, Ala, Asn, Asp, Arg, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Val, Glu, and GSSG, without thiol group as a control. The concentrations of other amino acids are also 10-fold higher than biothiols. It can be concluded from Fig. 3d that the fluorescence exhibits an obvious decay only with the addition of biothiols, suggesting that the 1 + ds-DNA@ Hg^{2+} sensing platform can detect biothiols selectively.

To further validate the alternate formation of P-DNA and ds-DNA@ Hg^{2+} , we performed a circular dichroism (CD) test during the detection process. At a concentration of 10 μM , the P-DNA has a strong positive peak at 280 nm, while MOF 1 has no CD signal. When increased concentration of MOF 1 was added into the P-DNA solution, the peak intensity gradually decreases, indicating that P-DNA is adsorbed by MOF 1 to form P-DNA@1. MOF 1 with highest concentration of 200 μM

partially adsorbed P-DNA (10 μM), resulting in partial disappearance of its CD peak (Fig. 4a).

When increased concentration of Hg^{2+} was added to the system of P-DNA@1, a new negative peak appeared with slight red shift, coinciding with the peak position of ds-DNA@ Hg^{2+} (Fig. 4b). With the ultimate introduction of biothiols, the negative peak of ds-DNA@ Hg^{2+} disappeared and the positive peak of P-DNA re-appeared, indicating that biothiols captures Hg^{2+} from the ds-DNA@ Hg^{2+} and release P-DNA (Fig. 4c–e).

3.4. Simulation studies of the sensing mechanism

In order to elucidate the detection mechanism, the binding free energy difference ($\Delta\Delta G$) between reactions of MOF 1 with P-DNA ($\Delta G_{\text{P-DNA@MOF}}$) or with ds-DNA@ Hg^{2+} ($\Delta G_{\text{MOF+ds-DNA@Hg}^{2+}}$) is calculated. When $\Delta\Delta G < 0$ ($\Delta\Delta G = \Delta G_{\text{P-DNA@MOF}} - \Delta G_{\text{MOF+ds-DNA@Hg}^{2+}}$), meaning that $\Delta G_{\text{P-DNA@MOF}} < \Delta G_{\text{MOF+ds-DNA@Hg}^{2+}}$ and the binding of P-DNA to MOF 1 is stronger than that of ds-DNA@ Hg^{2+} , and vice versa. The result showed that $\Delta\Delta G = -28.22 \text{ kcal/mol} < 0$, suggesting that P-DNA binds to MOF 1 more tightly than that of ds-DNA@ Hg^{2+} , in accordance with the experimental observation.

The electrostatic surface showed that the surface of MOF 1 was

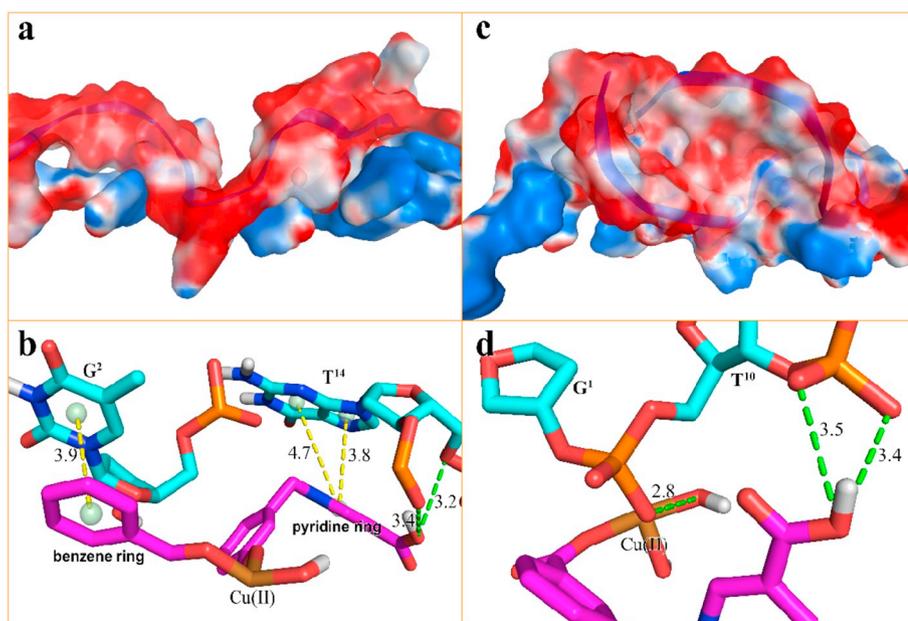


Fig. 5. The interactions between MOF 1 and P-DNA and ds-DNA@Hg²⁺: (a) and (c) showed the charge distributions where red area represented negative charges, blue positive, and white neutral; (b) and (d) showed the partial local binding modes where MOF 1 was displayed by magenta sticks, while P-DNA or ds-DNA@Hg²⁺ by cyan sticks. Charge centers and aromatic ring centers were denoted by pale green spheres, π - π stacking interactions by yellow dashes, and hydrogen bonding by green dashes.

largely positive and P-DNA was covered by a negative and neutral surface with the scattered positive area, which led to good electronic complement between MOF 1 and P-DNA. Single chain P-DNA exhibits a higher contact area with MOF 1 due to its structural flexibility (Fig. 5a), while double chain ds-DNA@Hg²⁺ only has a small interface (Fig. 5c). MOF 1 bound to P-DNA mainly through ten π - π stacking between the aromatic rings in MOF 1 and heterocycle in P-DNA with the ring centroid distances in the range of 3.8–4.7 Å. This is in addition to six hydrogen bonding between the heterocycle in P-DNA and the carboxylate groups in MOF 1, with the donor-acceptor distances in the range of 3.2–3.4 Å. In sharp contrast, there are only six hydrogen bonding between oxygen atoms of the phosphate group in ds-DNA@Hg²⁺ and H₂O or carboxylate groups in MOF 1, with donor-acceptor distances in the range of 2.8–3.5 Å. The partial local binding modes between MOF 1 and P-DNA or ds-DNA@Hg²⁺ was displayed in Fig. 5b and d.

4. Conclusion

In summary, a 1D water-stable Cu(II)-zwitterionic carboxylate MOF 1 has been synthesized and characterized. MOF 1 was subsequently used in the sensitive and specific detection of Hg²⁺ and biothiols in a sequential manner. Such sensing sequence is first enabled by the formation of hairpin-like ds-DNA@Hg²⁺ featuring the T-Hg-T motif (for the sensing of Hg²⁺, fluorescence on). The established 1 + ds-DNA@Hg²⁺, in turn, functions as a sensor for Cys, Hcy and GSH, driven by the stronger coordination of mercapto with Hg²⁺ that serves to sequester Hg²⁺, accompanied by the unfolding of ds-DNA into ss-DNA to reach the initial P-DNA@1 state (fluorescence off). The detection is highly efficient, featuring Hg²⁺ and Cys/Hcy/GSH in sequence with detection limits of (2.3 ± 0.8) nM and (29.6 ± 0.1)/(19.8 ± 0.5)/(10.2 ± 0.1) nM. Our future work involves the development of MOF systems for the synergistic sensing of biologically relevant metal ions and organic species, such as Fe³⁺/GSH, Fe³⁺/ascorbic acid, using the simple redox reaction.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.jinorgbio.2019.04.004>.

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