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Bisulfite-free and base-resolution analysis of 5-methylcytidine and 5-hydroxymethylcytidine in RNA with peroxotungstate†

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5-Methylcytosine (5mC) and 5-hydroxymethylcytosine (5hmC), two of the best-studied DNA modifications, play crucial roles in normal development and disease in mammals. Although 5-methylcytidine (m⁵C) and 5-hydroxymethylcytidine (hm⁵C) have also been identified in RNA, their distribution and biological function in RNA remain largely unexplored, due to the lack of suitable sequencing methods. Here, we report a base-resolution sequencing method for hm⁵C in RNA. We applied the selective oxidation of hm⁵C to trihydroxylated-thymine (thT) mediated by peroxotungstate. thT was subsequently converted to T during cDNA synthesis using a thermostable group II intron reverse transcriptase (TGIRT). Base-resolution analysis of the hm⁵C sites in RNA was performed using Sanger sequencing. Furthermore, in combination with the TET enzyme oxidation of m⁵C to hm⁵C in RNA, we expand the use of peroxotungstate oxidation to detect m⁵C in RNA at base-resolution. By using this method, we confirmed three known m⁵C sites in human tRNA, demonstrating the applicability of our method in analyzing real RNA samples.

Epitranscriptome, which refers to the multitude of RNA chemical modifications, has vital roles in post-transcriptional gene regulation.^{1–3} 5-Methylcytidine (m⁵C) and 5-hydroxymethylcytidine (hm⁵C) are two of the major RNA modifications in eukaryotic cells, however, our understanding of them is still in its infancy. M⁵C is abundant in noncoding RNA, and has the ability to stabilize tRNA secondary structure,^{4–6} but the knowledge about its distribution and function in mRNA are still very limited due to the inconsistent results obtained from the current sequencing methods.^{7–9} Hm⁵C has been shown to be enriched in *Drosophila melanogaster* mRNA, increase mRNA translation and play a central

role in *Drosophila* brain development.¹⁰ Hm⁵C also exists in mammalian RNA, albeit at low levels,¹¹ and the TET proteins that oxidize 5-methylcytosine (5mC) to 5-hydroxymethylcytosine (5hmC) in DNA can also do so in RNA.^{10,12} However, the distribution and regulation roles of hm⁵C in the mammalian transcriptome remain unknown due to the lack of sensitive and robust sequencing methods.

The most common way to sequence m⁵C in RNA is to adopt bisulfite sequencing, which is widely used to sequence 5mC in DNA. Bisulfite treatment deaminates unmethylated cytosine to uracil in single-strand RNA, while leaving m⁵C unconverted. Therefore, bisulfite sequencing provides base-resolution information of m⁵C. Using bisulfite sequencing, widespread m⁵C sites were identified in both coding and non-coding RNAs.^{7,8} However, bisulfite treatment employs sequential thermal acidic and alkaline conditions that severely damage the RNA. Further analysis also revealed potential false positives from RNA bisulfite sequencing due to incomplete conversion of unmethylated cytosine in the double-stranded RNA regions and other modifications resistant to bisulfite treatment.^{13–15} Other methods to sequence m⁵C in RNA are immunoprecipitation-based that use m⁵C-specific antibodies or methyltransferases to pull down m⁵C-containing RNA.^{16–18} These methods, however, do not have base-resolution and lose the quantitative levels of m⁵C. Mapping hm⁵C in RNA is even more challenging. To date, there is no base-resolution sequencing method for hm⁵C. The only reported method is the antibody-based immunoprecipitation approach.¹⁰ This method has been applied to the *Drosophila* transcriptome, but has yet to be successful in the mammalian transcriptome. Clearly, new RNA-friendly and high-resolution sequencing methods are highly desirable to further study the elusive distribution, localization and biological roles of these two modifications in RNA. Here, we report bisulfite-free and base-resolution sequencing methods for hm⁵C and m⁵C based on peroxotungstate oxidation.

Peroxotungstate oxidation was first developed by the Okamoto group^{19,20} for selective oxidation of 5hmC in DNA to trihydroxylated-thymine (thT). thT is a thymine derivative, and will induce C-to-T

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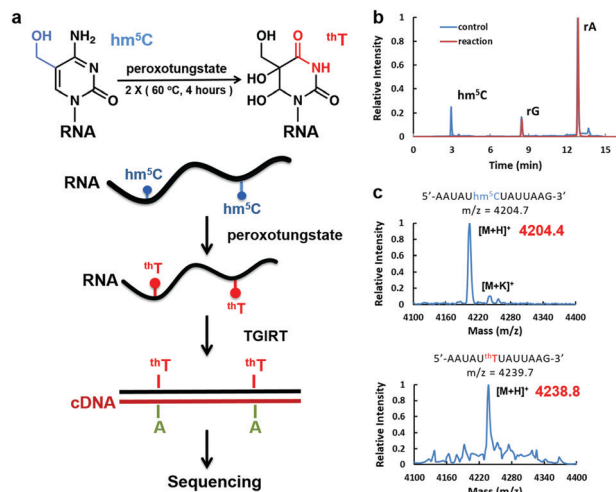


Fig. 1 Peroxotungstate reaction on hm⁵C-containing RNA. (a) Illustration of the peroxotungstate reaction and workflow of WO-Seq. Hm⁵C-containing RNA is specifically oxidized by peroxotungstate, and then reverse transcribed by thermostable group II intron reverse transcriptase (TGIRT). The oxidation product of hm⁵C (thT) is converted to T during cDNA synthesis, thus can be used for base-resolution sequencing of hm⁵C in RNA. (b) HPLC-MS/MS results of the hydrolysed product of synthesized hm⁵C-containing RNA1 before and after the peroxotungstate reaction. Peaks of adenosine (rA), guanosine (rG) and hm⁵C are labelled in the figure. (c) MALDI-MS characterization of an hm⁵C-containing RNA fragment of RNA1 treated with peroxotungstate. Calculated *m/z* is shown in black, observed *m/z* is shown in red.

transition in DNA after PCR. However, the peroxotungstate oxidation reaction requires single-strand DNA. The reaction is strongly inhibited in double-strand DNA with a conversion rate of less than 10%, which severely limits its application.²⁰ Although this reaction is not suitable for DNA samples, we hypothesized that it could be ideal to detect hm⁵C in RNA, which is mostly single-strand (Fig. 1a). We termed this approach peroxotungstate oxidation sequencing (WO-Seq).

We started with optimizing the oxidation conditions of the peroxotungstate against in vitro-transcribed hm⁵C-containing RNA1. MALDI-TOF MS and HPLC-MS/MS were used to monitor the reaction rate. After two rounds of 4 hours incubation at 60 °C, the hm⁵C peak in HPLC-MS/MS was undetectable (Fig. 1b), and the MALDI peak of RNA fragments containing one hm⁵C changed from *m/z* = 4204.4 to *m/z* = 4238.8. This is consistent with the calculated *m/z* change from hm⁵C-containing RNA to thT-containing RNA (Fig. 1c). Sensitivity of the peroxotungstate treatment for hm⁵C was also tested (Fig. S1, ESI[†]). Samples of different combination of hm⁵C modified RNA and unmodified RNA were treated by peroxotungstate, and then analysed by HPLC-MS/MS. The conversion rates of hm⁵C were similar in all samples, indicating that the peroxotungstate treatment is suitable for real biological samples which has low hm⁵C content.

Next, we investigated the potential of the hm⁵C-to-T transition during cDNA synthesis using the peroxotungstate-oxidized RNA template. We designed and synthesized a 73mer RNA that contained three hm⁵C sites (RNA2). To enable us to monitor the efficiency of the hm⁵C-to-T conversion, one hm⁵C was positioned

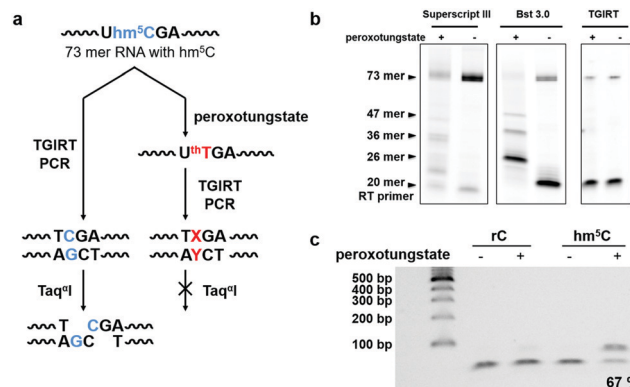


Fig. 2 Restriction enzyme digestion assay showed effective base change during cDNA synthesis using the peroxotungstate-oxidized RNA template. (a) Illustration of the restriction enzyme digestion assay for the investigation of the base change mediated by peroxotungstate. X represent T or A or G, while Y is the complementary base of it. (b) Reverse transcription products of hm⁵C-containing RNA2 before and after peroxotungstate treatment using different reverse transcriptases. Hm⁵C-containing RNA2 has three hm⁵C sites at position 26, 36 and 47. The full length is 73 mer. (c) RT-PCR product of the 73-mer model RNA2 containing a Taq^qI cut site. Samples without peroxotungstate treatment and control normal cytidine (rC) containing RNA2 treated with peroxotungstate were cleaved completely. About 67% of the reacted hm⁵C-RNA amplified product stayed intact, indicating the loss of the restriction enzyme cut site and the successful base change.

so that, upon successful hm⁵C-to-T conversion, a Taq^qI restriction enzyme recognition site in the resulting RT-PCR product was destroyed (Fig. 2a). Since thT is not a natural occurring base, we first sought to investigate its behavior during cDNA synthesis. Several commercially available reverse transcriptases were tested on this RNA template. Interestingly, only the thermostable group II intron reverse transcriptase (TGIRT)^{21,22} could read though all reacted hm⁵C sites, while Superscript III and Bst 3.0 DNA polymerase induced truncations at the reacted hm⁵C sites (Fig. 2b). The reaction conditions of TGIRT were further optimized to get the best reverse transcription efficiency, and after subsequent PCR, the DNA products were digested with Taq^qI. As shown in Fig. 2c, 67% of the PCR products from the oxidized hm⁵C-containing RNA2 sample stayed intact after the Taq^qI treatment, indicating loss of restriction enzyme cut site and the successful base change induced by the peroxotungstate-oxidized RNA during cDNA synthesis.

We then performed Sanger sequencing of the PCR product from the oxidized RNA samples (Fig. 3). At each hm⁵C site, a new peak of thymine signal appears, confirming the base change is indeed C-to-T. In order to accurately quantify the C-to-T conversion rate, the PCR product was cloned and sequenced individually. A 62.1% conversion rate was observed from a total of 66 hm⁵C sites sequenced (Fig. S2, ESI[†]), consistent with the restriction enzyme digestion result. As a control, PCR products of peroxotungstate-treated normal cytosine (rC)-containing RNA2 and m⁵C-containing RNA2 were also cloned and sequenced (Fig. S3, ESI[†]). Results showed that both rC and m⁵C sites did not change after the treatment, indicating an excellent selectivity of peroxotungstate oxidation on hm⁵C.



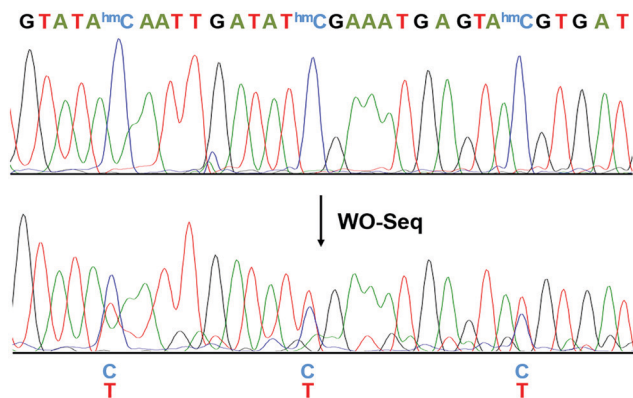


Fig. 3 Electropherograms of Sanger sequencing results before and after WO-Seq. The conversion of C-to-T happened at each hm⁵C site.

Notably, peroxotungstate oxidation is a mild reaction, which showed less damage on RNA compared with bisulfite reaction (Fig. S4, ESI[†]).

After demonstrating WO-Seq for hm⁵C sequencing, we next sought to expand its use for m⁵C sequencing in RNA. In DNA, 5hmC is generated by the oxidation of 5mC mediated by the TET enzyme. Recently, the mammalian TET enzyme was reported to have the ability of oxidizing m⁵C to hm⁵C in RNA.¹² We tested *Naegleria* Tet-like oxygenase (NgTET1)²³ and showed it can also oxidize m⁵C to hm⁵C on m⁵C-containing RNA1 by both MALDI-MS and HPLC-MS/MS (Fig. S5, ESI[†]). Based on this, we further aimed to combine the peroxotungstate oxidation with NgTET1 oxidation to detect m⁵C in a procedure we termed TET-Assisted WO-Seq (TAWO-Seq) (Fig. 4a). The results of both oxidation reactions were verified by HPLC-MS/MS (Fig. S6, ESI[†]). Restriction enzyme digestion assays and Sanger sequencing were performed (Fig. 4b and c). Sanger sequencing results showed the C-to-T transition at each m⁵C site. The m⁵C-to-T conversion rate was 50% estimated by restriction enzyme analysis, lower than that of hm⁵C, due to incomplete m⁵C to hm⁵C oxidation by NgTET1 (Fig. S6, ESI[†]). We also cloned and sequenced individual PCR product for the m⁵C sample. As shown in Fig. S7 (ESI[†]), 33.3% of the total m⁵C sites were successfully detected. Commercially available mouse Tet1 (mTet1) was also tested for the TAWO-Seq, which gives similar results with NgTET1 (Fig. S8a, ESI[†]). We further demonstrated that β -glucosyltransferase (β GT) can label hm⁵C with glucose and thereby protect it from peroxotungstate oxidation (Fig. S9, ESI[†]). Combining β GT protection with TAWO-Seq could therefore enable it to detect m⁵C specifically.

To further demonstrate the utility of TAWO-Seq on real RNA sample, we applied it to the endogenous tRNA^{Asp(GUC)} in 293T cells. The tRNA^{Asp(GUC)} contains three known m⁵C sites at structural positions 38, 47 and 48 (Fig. S10a, ESI[†]).^{24–26} Both NgTET1 and mTet1 were used to oxidize the tRNA and the products were then treated with peroxotungstate. The RT-PCR product of treated tRNA^{Asp(GUC)} was cloned and sequenced. As shown in Fig. S10b and c (ESI[†]), 35.2% of the m⁵C sites were successfully detected with NgTET1 assisted WO-Seq, and 37.5% of the m⁵C sites were detected using mTet1 assisted WO-Seq,

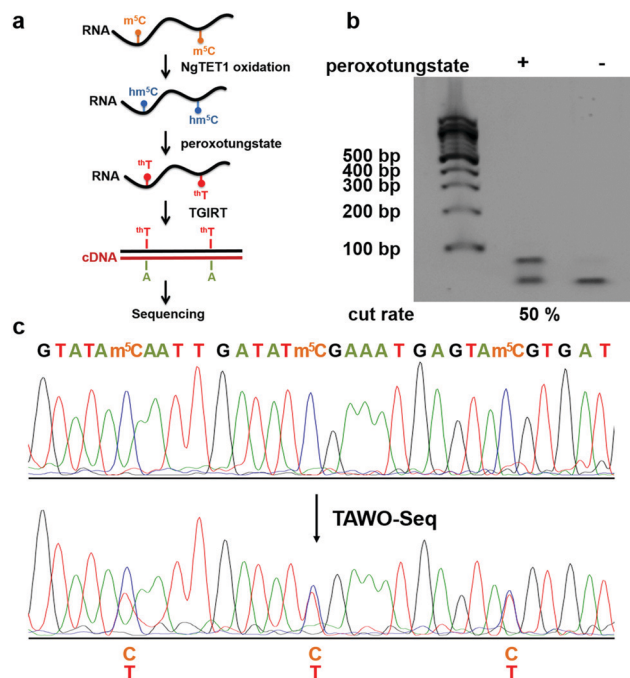


Fig. 4 The combination of NgTET1 oxidation and peroxotungstate reaction in detecting m⁵C in RNA in TAWO-Seq. (a) Illustration of TAWO-Seq strategy for the identification of m⁵C in RNA at single-nucleotide resolution. (b) Restriction enzyme digestion assay of (+) and (–) NgTET1-assisted peroxotungstate-treated samples. About 50% of the m⁵C sites were detected. (c) Sanger-sequencing results before and after TAWO-Seq.

which demonstrated the applicability of TAWO-Seq to real RNA samples. Among the three m⁵C sites in tRNA^{Asp(GUC)}, we found that m⁵C at position 48 has the highest C-to-T conversion rate (68.4% by NgTET1 assisted WO-Seq, 77.8% by mTet1 assisted WO-Seq). According to the tRNA^{Asp(GUC)} structure, this site is in a double-stranded CpG context, which is an ideal substrate of TET enzyme.²³ It is likely that the different m⁵C-to-T conversion rates of three m⁵C sites are caused by the sequence preference of the TET proteins.

In conclusion, we have described WO-Seq as an RNA friendly, chemical oxidation-based, base-resolution method to sequence hm⁵C in RNA. We demonstrate the specific hm⁵C-to-T transition using peroxotungstate to oxidize the RNA followed by cDNA synthesis with the TGIRT enzyme, and Sanger sequencing results have proved the base-resolution sequencing ability of this method. We further demonstrate the ability of TAWO-Seq to detect m⁵C by combining WO-Seq with the prior NgTET1 or mTet1 oxidation of m⁵C to hm⁵C. The successful detection of m⁵C sites in human tRNA demonstrates our method is applicable for real RNA samples. Both WO-Seq and TAWO-Seq could potentially solve the false positive issue of bisulfite sequencing since they directly detect modified cytosine without affecting unmodified cytosine. Further improvement of both methods to increase the conversion rate and apply to mRNA samples using next-generation sequencing technology are underway in the lab. We believe this method could be highly useful for the identification of unexplored m⁵C/hm⁵C distribution and function in the transcriptome.



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Conflicts of interest

There are no conflicts to declare.

Notes and references

- 1 Y. Saletore, K. Meyer, J. Korfach, I. D. Vilfan, S. Jaffrey and C. E. Mason, *Genome Biol.*, 2012, **13**, 175.
- 2 M. A. Machnicka, K. Milanowska, O. Osman Oglou, E. Purta, M. Kurkowska, A. Olchowik, W. Januszewski, S. Kalinowski, S. Dunin-Horkawicz, K. M. Rother, M. Helm, J. M. Bujnicki and H. Grosjean, *Nucleic Acids Res.*, 2013, **41**, D262–D267.
- 3 M. Frye, S. R. Jaffrey, T. Pan, G. Rechavi and T. Suzuki, *Nat. Rev. Genet.*, 2016, **17**, 365.
- 4 J. E. S. a. B. S. Cooperman, *Biochemistry*, 1992, **31**, 10825–10834.
- 5 H. S.-G. Y. Chen, R. Guenther, K. Everett and P. F. Agris, *Biochemistry*, 1993, **32**, 10249–10253.
- 6 Y. Motorin and M. Helm, *Biochemistry*, 2010, **49**, 4934–4944.
- 7 M. Schaefer, T. Pollex, K. Hanna and F. Lyko, *Nucleic Acids Res.*, 2009, **37**, e12.
- 8 J. E. Squires, H. R. Patel, M. Nusch, T. Sibbritt, D. T. Humphreys, B. J. Parker, C. M. Suter and T. Preiss, *Nucleic Acids Res.*, 2012, **40**, 5023–5033.
- 9 X. Yang, Y. Yang, B.-F. Sun, Y.-S. Chen, J.-W. Xu, W.-Y. Lai, A. Li, X. Wang, D. P. Bhattarai, W. Xiao, H.-Y. Sun, Q. Zhu, H.-L. Ma, S. Adhikari, M. Sun, Y.-J. Hao, B. Zhang, C.-M. Huang, N. Huang, G.-B. Jiang, Y.-L. Zhao, H.-L. Wang, Y.-P. Sun and Y.-G. Yang, *Cell Res.*, 2017, **27**, 606.
- 10 F. W. Benjamin Delatte, L. V. Ngoc, E. Collignon, E. Bonvin, R. Deplus, E. Calonne, B. Hassabi, P. Putmans, S. Awe, C. Wetzel, J. Kreher, R. Soin, C. Creppe, P. A. Limbach, C. Gueydan, V. Kruijs, A. Brehm, S. Minakhina, M. Defrance, R. Steward and F. Fuks, *Science*, 2016, **351**, 282–285.
- 11 H. Y. Zhang, J. Xiong, B. L. Qi, Y. Q. Feng and B. F. Yuan, *Chem. Commun.*, 2016, **52**, 737–740.
- 12 L. Fu, C. R. Guerrero, N. Zhong, N. J. Amato, Y. Liu, S. Liu, Q. Cai, D. Ji, S. G. Jin, L. J. Niedernhofer, G. P. Pfeifer, G. L. Xu and Y. Wang, *J. Am. Chem. Soc.*, 2014, **136**, 11582–11585.
- 13 S. Hussain, J. Aleksic, S. Blanco, S. Dietmann and M. Frye, *Genome Biol.*, 2013, **14**, 215.
- 14 W. V. Gilbert, T. A. Bell and C. Schaening, *Science*, 2016, **352**, 1408–1412.
- 15 A. Shafik, U. Schumann, M. Evers, T. Sibbritt and T. Preiss, *Biochim. Biophys. Acta, Gene Regul. Mech.*, 2016, **1859**, 59–70.
- 16 S. Edelheit, S. Schwartz, M. R. Mumbach, O. Wurtzel and R. Sorek, *PLoS Genet.*, 2013, **9**, e1003602.
- 17 V. Khoddami and B. R. Cairns, *Nat. Biotechnol.*, 2013, **31**, 458–464.
- 18 S. Hussain, A. A. Sajini, S. Blanco, S. Dietmann, P. Lombard, Y. Sugimoto, M. Paramor, J. G. Gleeson, D. T. Odom, J. Ule and M. Frye, *Cell Rep.*, 2013, **4**, 255–261.
- 19 A. Okamoto, K. Sugizaki, A. Nakamura, H. Yanagisawa and S. Ikeda, *Chem. Commun.*, 2011, **47**, 11231–11233.
- 20 G. Hayashi, K. Koyama, H. Shiota, A. Kamio, T. Umeda, G. Nagae, H. Aburatani and A. Okamoto, *J. Am. Chem. Soc.*, 2016, **138**, 14178–14181.
- 21 S. Mohr, E. Ghanem, W. Smith, D. Sheeter, Y. Qin, O. King, D. Polioudakis, V. R. Iyer, S. Hunicke-Smith, S. Swamy, S. Kuersten and A. M. Lambowitz, *RNA*, 2013, **19**, 958–970.
- 22 S. T. Carrell, Z. Tang, S. Mohr, A. M. Lambowitz and C. A. Thornton, *Nucleic Acids Res.*, 2018, **46**, e1–e1.
- 23 J. E. Pais, N. Dai, E. Tamanaha, R. Vaisvila, A. I. Fomenkov, J. Bitinaite, Z. Sun, S. Guan, I. R. Corrêa, C. J. Noren, X. Cheng, R. J. Roberts, Y. Zheng and L. Saleh, *Proc. Natl. Acad. Sci. U. S. A.*, 2015, **112**, 4316–4321.
- 24 M. G. Goll, F. Kirpekar, K. A. Maggert, J. A. Yoder, C.-L. Hsieh, X. Zhang, K. G. Golig, S. E. Jacobsen and T. H. Bestor, *Science*, 2006, **311**, 395–398.
- 25 M. Schaefer, T. Pollex, K. Hanna and F. Lyko, *Nucleic Acids Res.*, 2009, **37**, e12–e12.
- 26 W. A. Cantara, P. F. Crain, J. Rozenski, J. A. McCloskey, K. A. Harris, X. Zhang, F. A. P. Vendeix, D. Fabris and P. F. Agris, *Nucleic Acids Res.*, 2011, **39**, D195–D201.

