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Chemoenzymatic Synthesis and Utilization of a SAM Analog with an Isomorphous Nucleobase

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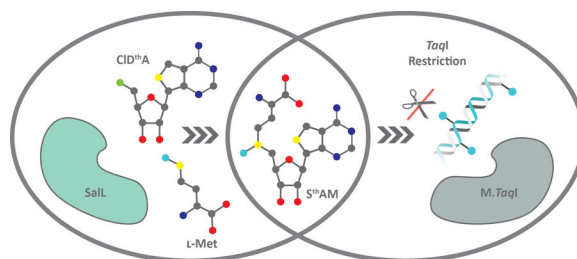
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Abstract

SalL, an enzyme that catalyzes the synthesis of SAM from L-methionine and 5'-chloro-5'-deoxyadenosine, is shown to accept 5'-chloro-5'-deoxythienoadenosine as a substrate and facilitate the synthesis of a synthetic SAM analog with an unnatural nucleobase. This synthetic cofactor is demonstrated to replace SAM in DNA methylation reaction with *M. TaqI*.

Graphical abstract



A synthetic SAM analog with an unnatural isomorphous nucleobase is enzymatically synthesized and shown to serve as a methyl donor

Following ATP, S-adenosyl-L-methionine (SAM, also known as AdoMet) is the most ubiquitous and utilized adenosine-containing cofactor. SAM serves as the methyl donor in numerous methyltransferase (MTase)-catalyzed reactions, which are responsible for methylating both large biopolymers (e.g., DNA, RNA, proteins) and low molecular weight metabolites (e.g., catecholamines, polyketides). It has also been discovered to bind riboswitches, highlighting its regulatory roles in transcription and translation. As such, defects in SAM metabolism and its associated reactions are intimately linked to human health.

Due to its universal role as the source of methyl groups, modified SAM analogs have been gaining utility in a variety of chemical biological applications. Modified analogs where the sulfonium center has been replaced by an aziridinyll⁻ or a (2-haloethyl)amino-group (*N*-

mustard)⁻, have been used to conjugate or crosslink biomolecules involved in SAM-mediated transformations. In another class of SAM analogs, the methyl group has been replaced by a larger chemical entity that could directly be transferred to a substrate by methyl transferases, diverse SAM-dependent enzymes.⁻ Such modified SAM analogs can be used to further functionalize biomolecules through bioorthogonal conjugations, such as Click reactions. Clickable groups have been used, for example, to biotinylated biomolecules or to conjugate diverse fluorophores to DNA for super-resolution optical DNA mapping.[·]

SAM analogs with isomorphous nucleobases have been minimally studied, and the tolerance of the enzymes involved in their biosynthesis and methylation reactions has not been broadly assessed. Such analogs can shed light on the fidelity of enzymes involved in metabolic processes and can potentially be used as mechanistic and biophysical probes. Furthermore, due to their distinct heterocyclic nucleus, conferring unique photophysical features, they can facilitate the fabrication of biophysical and inhibitor-discovery assays. Before advancing such applications, a viable enzymatic approach to such molecules is needed, and their biochemical performance needs to be assessed.

SAM can be enzymatically synthesized by SAM synthetases using L-methionine and ATP.[·] This reaction has been utilized to prepare a library of non-native S/Se-containing modified SAM analogs and to alkylate small molecules *in situ*. Alternatively, chemoenzymatic synthesis of several SAM analogs has been demonstrated using SalL, a chlorinase from *Salinaspota tropica*. This halogenase is known to naturally catalyze the breakdown of SAM to L-methionine and 5'-chloro-5'-deoxyadenosine (CIDA), but the reaction can be reversed *in vitro*, at low chloride and high L-methionine concentrations. Using this enzyme, different SAM analogs were synthesized and *in situ* utilized to enzymatically alkylate a small molecule, a peptide and DNA.[·]

To explore whether or not such metabolic partners tolerate SAM analogs with unnatural heterocycles, which are not derived from adenosine, we have investigated the ability of SalL to synthesize SthAM, a SAM analog where adenosine has been replaced by a thieno[3,4-d]pyrimidine-based adenosine surrogate (Fig. 1). This heterocycle is a member of a modified RNA alphabet we previously fabricated as a mechanistic and biophysical tool kit for exploring transformations of nucleosides, nucleotides and oligonucleotides.[·] Here we demonstrate the successful SalL-mediated synthesis of SthAM from L-methionine and 5'-chloro-5'-deoxythienoadenosine (CIDthA). We then subsequently illustrate the applicability of SthAM as the methyl donor in methyl transferase-mediated DNA methylation. These results illustrate the broad tolerance of enzymes involved in the biosynthesis of SAM and its methyl transfer reactions to alterations of the adenosine moiety.

The synthesis pathway to SthAM commences with the conversion of the nucleoside thA to its 5'-chloro-5'-deoxy derivative CIDthA (Fig. 2A), following established procedures.[·] Incubating this halogenated non-native nucleoside with SalL and a large excess of L-methionine ($\times 75$) at 37°C, generates SthAM, the modified analog. The formation of the desired product during the enzymatic reaction was monitored by HPLC and confirmed by HR-MS (Fig. 2. B and C, Fig. S3[†] and S7[†]). The production of SthAM could be scaled up and optimized by increasing reaction volumes and using higher concentrations of the

enzyme. The best conversion we observed, as reflected by the highest ratio of product (SthAM) to starting material (CIDthA) was 1.38, reflecting consumption of about 60% of the chlorinated nucleoside (Fig. S4[†]). Control experiments show no formation of SthAM in the absence of the enzyme excluding any direct substitution reaction between L-methionine and CIDthA (Fig. S6[†]).

To study its capability as a methylating agent, SthAM was used in a DNA methylation-restriction assay with a common DNA substrate (a pUC19 plasmid linearized by *SacI*) and an *M. TaqI* methyl transferase (MTase). This enzyme naturally catalyzes the methylation of the exocyclic amino group of adenine within the 5'-TCGA-3' sequence in double stranded DNA. The methylation reaction can then be followed by incubation with the Endonuclease *TaqI*. This enzyme has the same recognition sequence as *M. TaqI*, but is unable to cleave the methylated DNA sequences. Finally, the reactions are analyzed by agarose gel electrophoresis using ethidium bromide staining (Fig. 1). A control reaction with SAM, the natural cofactor, can be executed in parallel to compare the two methyl donors. As seen in Figure 3, after an hour long reaction, a nearly complete protection was observed with SthAM (Fig. 3, lane 1), compared to a complete reaction with SAM, the native cofactor (lane 2). Control reactions (lanes 3–6) confirm the need for all components for a successful DNA protection.

To semi-qualitatively compare the reaction rates of *M. TaqI* with SAM and SthAM, the DNA methylation reaction was followed over a 2 hour time course (Fig. 4). Five time points were taken for each cofactor after 10, 30, 45, 105 and 120 min exposure to the MTase, followed by incubation with *TaqI*. While the reaction with SAM was virtually quantitative after 10 min (lanes 6–10), the reaction with SthAM was slower but essentially reached completion after 2 h (lanes 1–5).

To test whether SthAM can be formed *in situ* and used directly in a methylation reaction, SalL and *M. TaqI* were combined in a one-pot reaction (Fig. 5). This combined synthesis/methylation reaction and the subsequent cleavage were done for both CIDA (lane 1) and CIDthA (lane 2). Positive controls in which SAM was added in the absence of SalL (lane 3 and 4) were also performed. Negative controls in which either SalL (lane 5 and 6), L-Met (lane 7 and 8), CIDA/CIDthA (lane 9) or *M. TaqI* (lane 10 and 11) were omitted and one control with only DNA (lane 12 and 13) were performed under the same conditions. The reaction with CIDA (lane 1) showed full protection. The one where CIDthA was used (lane 2) shows partial protection and the negative controls show no protection as expected, with the exception of lane 9, where one extra band with a higher molecular weight compared to the largest possible fragment is present. This extra band, indicating partial DNA protection, could result from small amounts of *in situ* generated SAM. The latter is formed from traces on CIDA bound to SalL, which has been reported to co-purify with A and CIDA when expressed in chloride-containing media. As exogenous CIDA/CIDthA is absent in Lane 9, traces of SAM facilitate a small, yet observable, protection and therefore leads to a partly “false positive” result. Nevertheless, as the full length DNA is not present in this control

[†]Electronic Supplementary Information (ESI) available: Synthesis and characterization of new compounds, Expression of SalL enzyme, enzymatic procedures and control experiments. See DOI: 10.1039/x0xx00000x

lane, but is present in lane 2, the protection seen in the latter must be due to the formation of SthAM.

Although SthAM appears to be somewhat inferior to SAM in its enzymatic synthesis and methyl transfer reactions, it is rather remarkable that the enzymes involved in its synthesis and utilization show such tolerance for nucleobase modifications. In particular, while the halogenated adenosine has been crystallographically shown to be buried within the SalL active site, with the Asn188's amide side chain forming two H bonds to the Hoogsteen face of adenine, the enzyme tolerates the replacement of the imidazole unit in adenine with a thiophene. In contrast, *M. TaqI* does not appear to form specific contacts with the adenine's imidazole moiety, which may explain its higher tolerance and ability to effectively utilize SthAM in DNA methylation reactions. (Fig. S8†)

Conclusions

A chemoenzymatic synthesis of SthAM, a new functional SAM analog, has been accomplished by combining L-methionine and CIDthA in a reaction catalyzed by SalL, an enzyme known to perform a similar reaction with CIDA. The new synthetic cofactor could be used for DNA methylation reactions in a methylation-restriction assay using a pUC19 vector and *M. TaqI* MTase. These results highlight the isomorphism of thA, a new adenosine isoster, and the tolerance level of enzymes involved in the biosynthesis and utilization of SAM. The availability of functional analogs with altered nucleobases can also facilitate future biophysical analyses and mechanistic studies of biochemical processes involving this abundant cofactor. Our observations suggest that thA, a highly isomorphic adenosine surrogate, may be able to substitute the native nucleoside in other cofactors and second messengers.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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Notes and references

1. Schubert HL, Blumenthal RM, Cheng X. Trends Biochem Sci. 2003; 28:329–335. [PubMed: 12826405]
2. Zhang J, Zheng YG. ACS Chemical Biology. 2016; 11:583–597. [PubMed: 26540123]
3. Struck AW, Thompson ML, Wong LS, Micklefield J. Chembiochem. 2012; 13:2642–2655. [PubMed: 23180741]
4. Winkler WC, Breaker RR. Annu Rev Microbiol. 2005; 59:487–517. [PubMed: 16153177]
5. McDaniel BA, Grundy FJ, Henkin TM. Mol Microbiol. 2005; 57:1008–1021. [PubMed: 16091040]
6. Trausch JJ, Xu Z, Edwards AL, Reyes FE, Ross PE, Knight R, Batey RT. Proc Natl Acad Sci U S A. 2014; 111:6624–6629. [PubMed: 24753586]

7. Anstee QM, Day CP. *J Hepatol.* 2012; 57:1097–1109. [PubMed: 22659519]
8. Mischoulon D, Fava M. *Am J Clin Nutr.* 2002; 76:1158S–1161S. [PubMed: 12420702]
9. Zhang J, Zheng YG. *ACS Chemical Biology.* 2015
10. Comstock LR, Rajskei SR. *J Am Chem Soc.* 2005; 127:14136–14137. [PubMed: 16218579]
11. Comstock LR, Rajskei SR. *Nucleic Acids Res.* 2005; 33:1644–1652. [PubMed: 15778434]
12. Pignot M, Siethoff C, Linscheid M, Weinhold E. *Angew Chem Int Ed Engl.* 1998; 37:2888–2891.
13. Pljevaljcic G, Pignot M, Weinhold E. *Journal of the American Chemical Society.* 2003; 125:3486–3492. [PubMed: 12643710]
14. Pljevaljcic G, Schmidt F, Peschlow A, Weinhold E. *Methods Mol Biol.* 2004; 283:145–161. [PubMed: 15197308]
15. Pljevaljcic G, Schmidt F, Weinhold E. *Chembiochem.* 2004; 5:265–269. [PubMed: 14997517]
16. Weller RL, Rajskei SR. *Org Lett.* 2005; 7:2141–2144. [PubMed: 15901154]
17. Weller RL, Rajskei SR. *Chembiochem.* 2006; 7:243–245. [PubMed: 16365907]
18. Hymbaugh Bergman SJ, Comstock LR. *Bioorganic & Medicinal Chemistry.* 2015; 23:5050–5055. [PubMed: 26037613]
19. Du Y, Hendrick CE, Frye KS, Comstock LR. *Chembiochem.* 2012; 13:2225–2233. [PubMed: 22961989]
20. Dalhoff C, Lukinavicius G, Klimasauskas S, Weinhold E. *Nat Protoc.* 2006; 1:1879–1886. [PubMed: 17487172]
21. Klimasauskas S, Weinhold E. *Trends Biotechnol.* 2007; 25:99–104. [PubMed: 17254657]
22. Parks LW. *J Biol Chem.* 1958; 232:169–176. [PubMed: 13549407]
23. Schlenk F, Dainko JL. *Biochim Biophys Acta.* 1975; 385:312–323. [PubMed: 1092359]
24. Vranken C, Deen J, Dirix L, Stakenborg T, Dehaen W, Leen V, Hofkens J, Neely RK. *Nucleic Acids Res.* 2014; 42:e50. [PubMed: 24452797]
25. Neely RK, Dedecker P, Hotta J-i, Urbanaviciute G, Klimasauskas S, Hofkens J. *Chemical Science.* 2010; 1:453–460.
26. Ottink OM, Nelissen FHT, Derks Y, Wijmenga SS, Heus HA. *Analytical Biochemistry.* 2010; 396:280–283. [PubMed: 19748477]
27. Leonard NJ. *CRC Crit Rev Biochem.* 1984; 15:125–199. [PubMed: 6365449]
28. Sinkeldam RW, McCoy LS, Shin D, Tor Y. *Angew Chem Int Ed Engl.* 2013; 52:14026–14030. [PubMed: 24288262]
29. McGee DPC, Martin JC. *Canadian Journal of Chemistry.* 1986; 64:1885–1889.
30. Micoli A, Turco A, Araujo-Palomo E, Encinas A, Quintana M, Prato M. *Chemistry.* 2014; 20:5397–5402. [PubMed: 24648250]
31. Cantoni GL. *Journal of the American Chemical Society.* 1952; 74:2942–2943.
32. Gross A, Geresh S, Whitesides GM. *Appl Biochem Biotechnol.* 1983; 8:415–422. [PubMed: 6679195]
33. Singh S, Zhang J, Huber TD, Sunkara M, Hurley K, Goff RD, Wang G, Zhang W, Liu C, Rohr J, Van Lanen SG, Morris AJ, Thorson JS. *Angew Chem Int Ed Engl.* 2014; 53:3965–3969. [PubMed: 24616228]
34. Eustaquio AS, Pojer F, Noel JP, Moore BS. *Nat Chem Biol.* 2008; 4:69–74. [PubMed: 18059261]
35. Lipson JM, Thomsen M, Moore BS, Clausen RP, La Clair JJ, Burkart MD. *Chembiochem.* 2013; 14:950–953. [PubMed: 23650044]
36. Thomsen M, Vogensen SB, Buchardt J, Burkart MD, Clausen RP. *Org Biomol Chem.* 2013; 11:7606–7610. [PubMed: 24100405]
37. Shin D, Sinkeldam RW, Tor Y. *Journal of the American Chemical Society.* 2011; 133:14912–14915. [PubMed: 21866967]
38. Mizrahi RA, Shin D, Sinkeldam RW, Phelps KJ, Fin A, Tantillo DJ, Tor Y, Beal PA. *Angew Chem Int Ed Engl.* 2015; 54:8713–8716. [PubMed: 26095193]
39. Shin D, Lonn P, Dowdy SF, Tor Y. *Chem Commun (Camb).* 2015; 51:1662–1665. [PubMed: 25500944]

40. Ottink OM, Nelissen FH, Derks Y, Wijmenga SS, Heus HA. *Anal Biochem.* 2010; 396:280–283. [PubMed: 19748477]
41. Labahn J, Granzin J, Schluckebier G, Robinson DP, Jack WE, Schildkraut I, Saenger W. *Proc Natl Acad Sci U S A.* 1994; 91:10957–10961. [PubMed: 7971991]

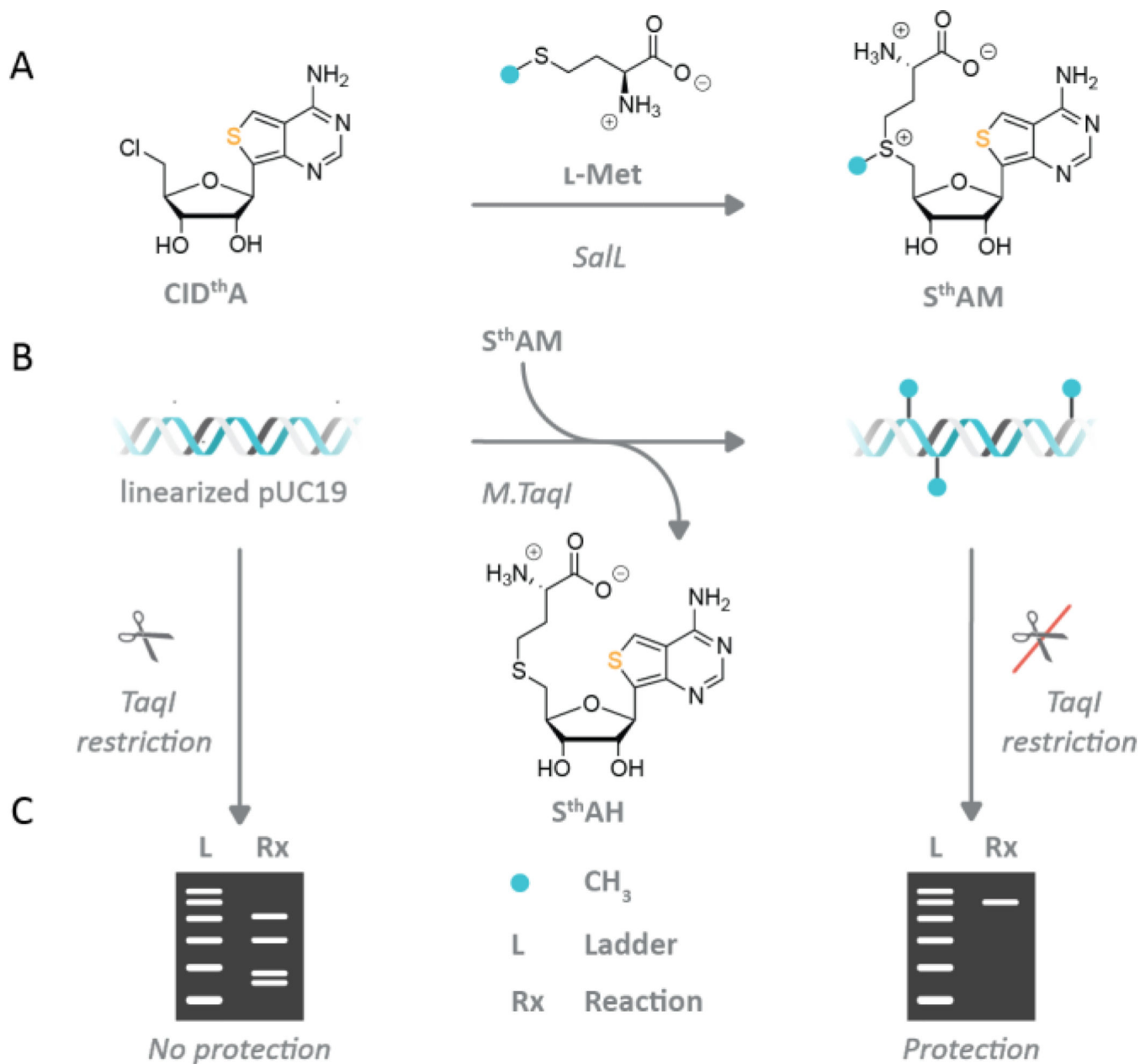
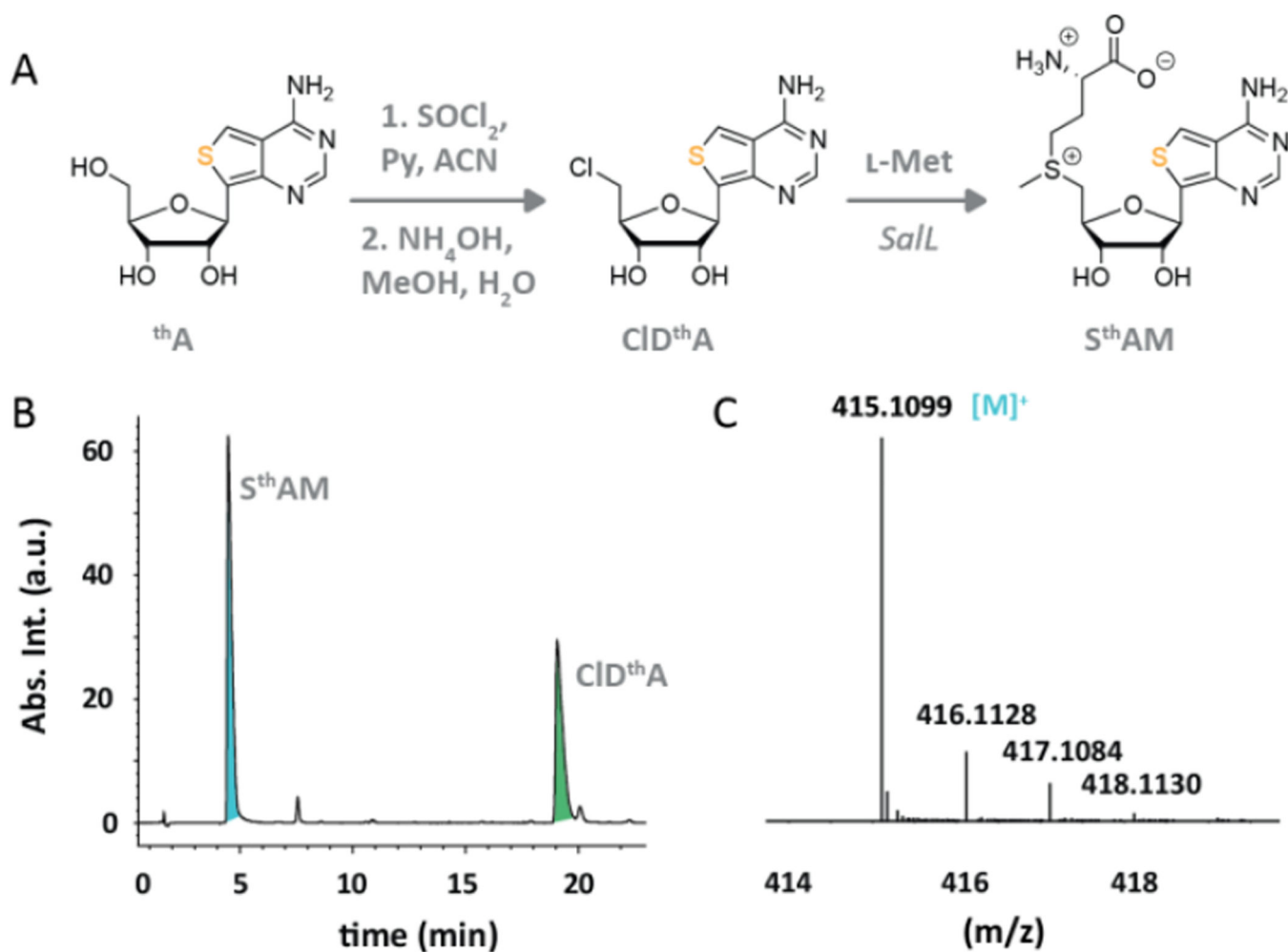


Fig. 1.

A. SthAM is enzymatically prepared from CIDthA and L-methionine using Sall. B. Methylation of linearized pUC19 DNA with *M. TaqI* and SthAM is followed by a strand cleavage step with *TaqI* (a restriction enzyme). C. Reactions are then analyzed by agarose gel electrophoresis. Methylation (protection) prevents any digestion and shows full length DNA. Unmethylated DNA shows full digestion after the exposure to a restriction enzyme.

**Fig. 2.**

A. Synthesis of SthAM. CIDthA is synthesized from the modified nucleoside thA using an established chlorination method, which is then converted to SthAM using L-methionine and SalL. B. HPLC trace of a typical enzymatic SthAM synthesis reaction, containing 0.2 mM CIDthA, 15 mM L-Met and 9 μM SalL for 2 hours at 37°C. C. HR-MS trace of SthAM, purified using HPLC.

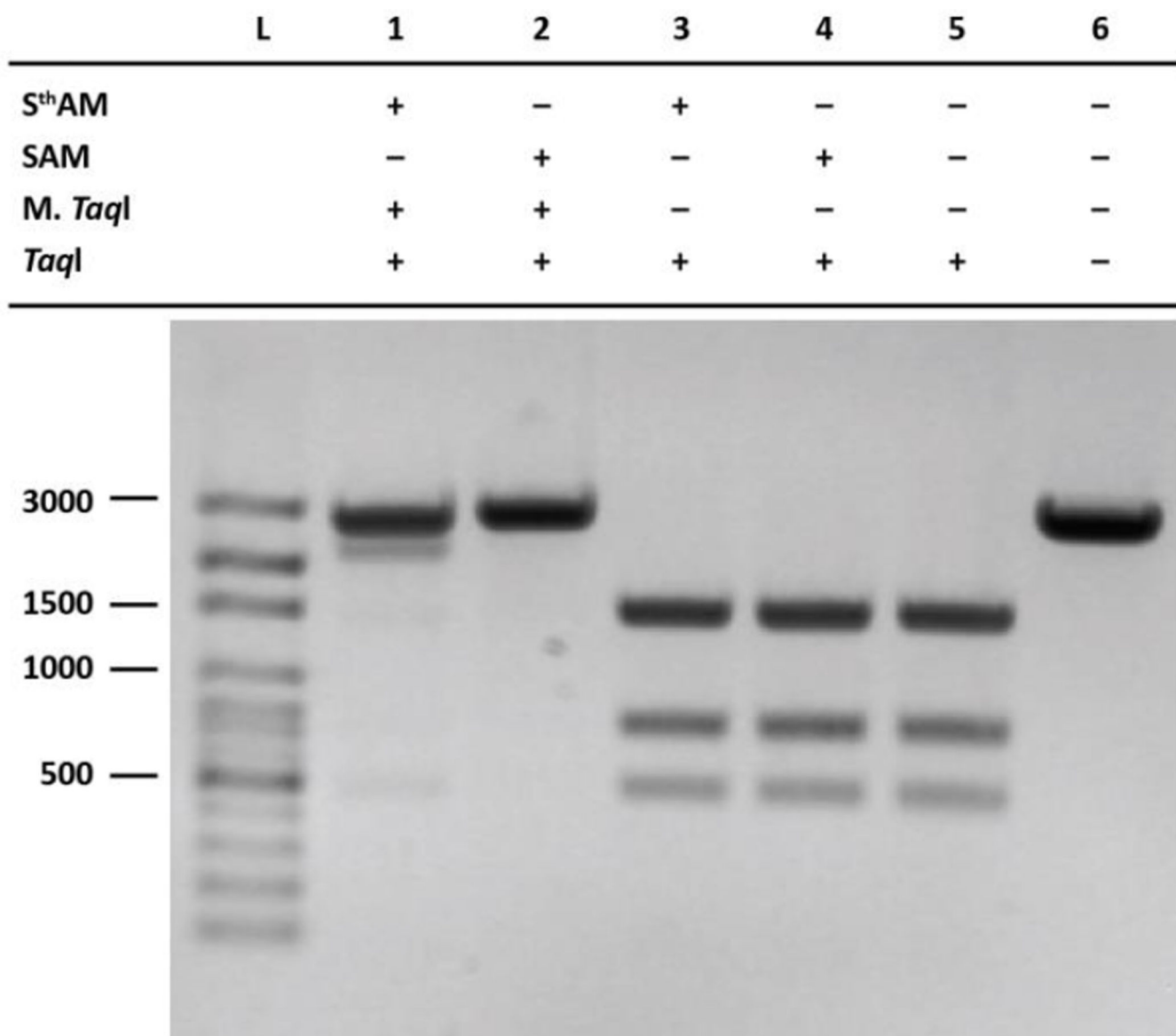


Fig. 3. Methylation of linearized pUC19 DNA by *M. TaqI* MTase. A DNA marker (100–3000 bp) was used as a reference (lane L). Lane 1 and 2 show the result after the reaction using SthAM and SAM respectively. Negative controls in the absence of *M. TaqI* for the reaction with SthAM (lane 3), SAM (lane 4) or no cofactor (lane 5) are shown. Lane 6 shows a control reaction in absence of any cofactor or enzyme.

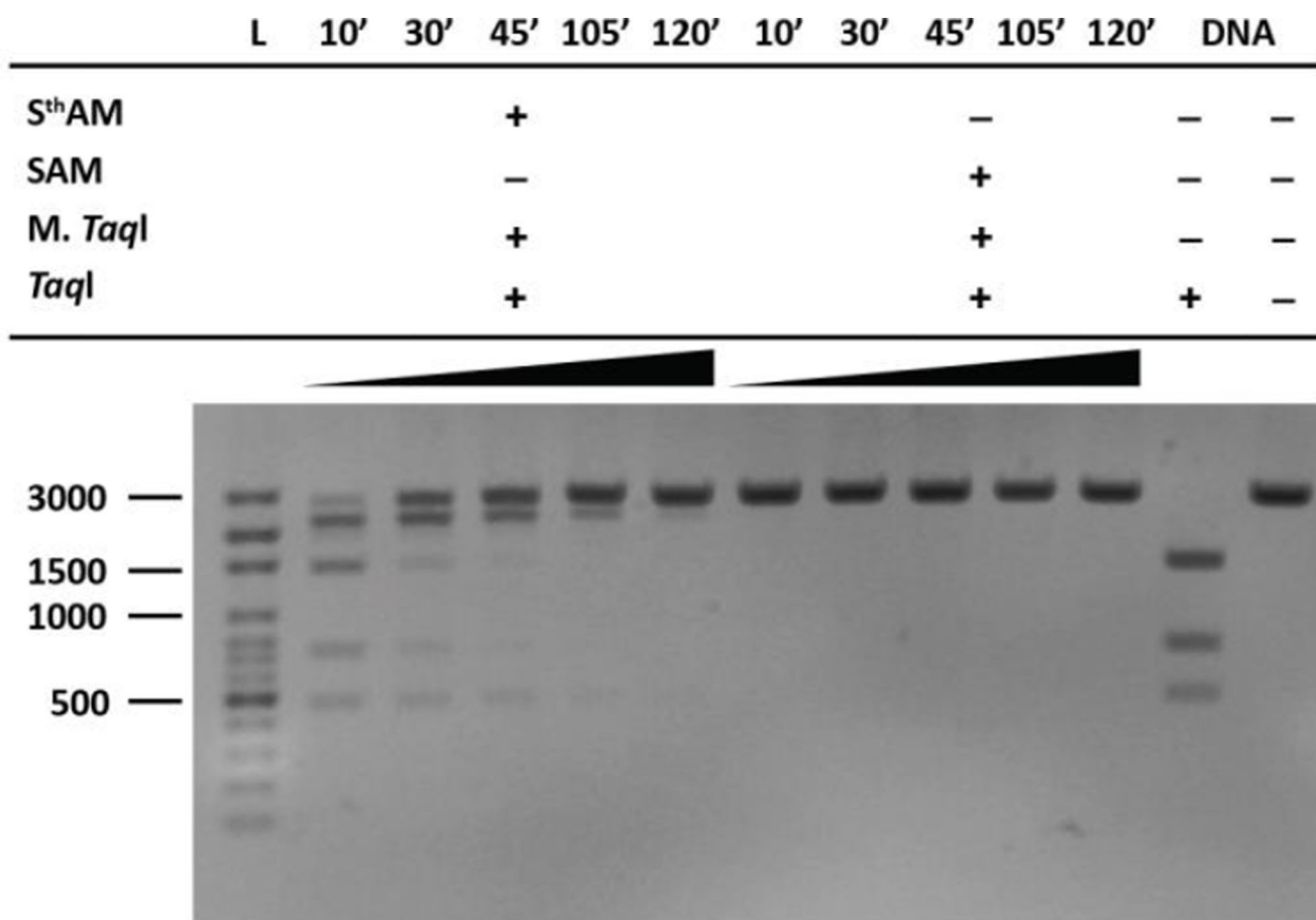
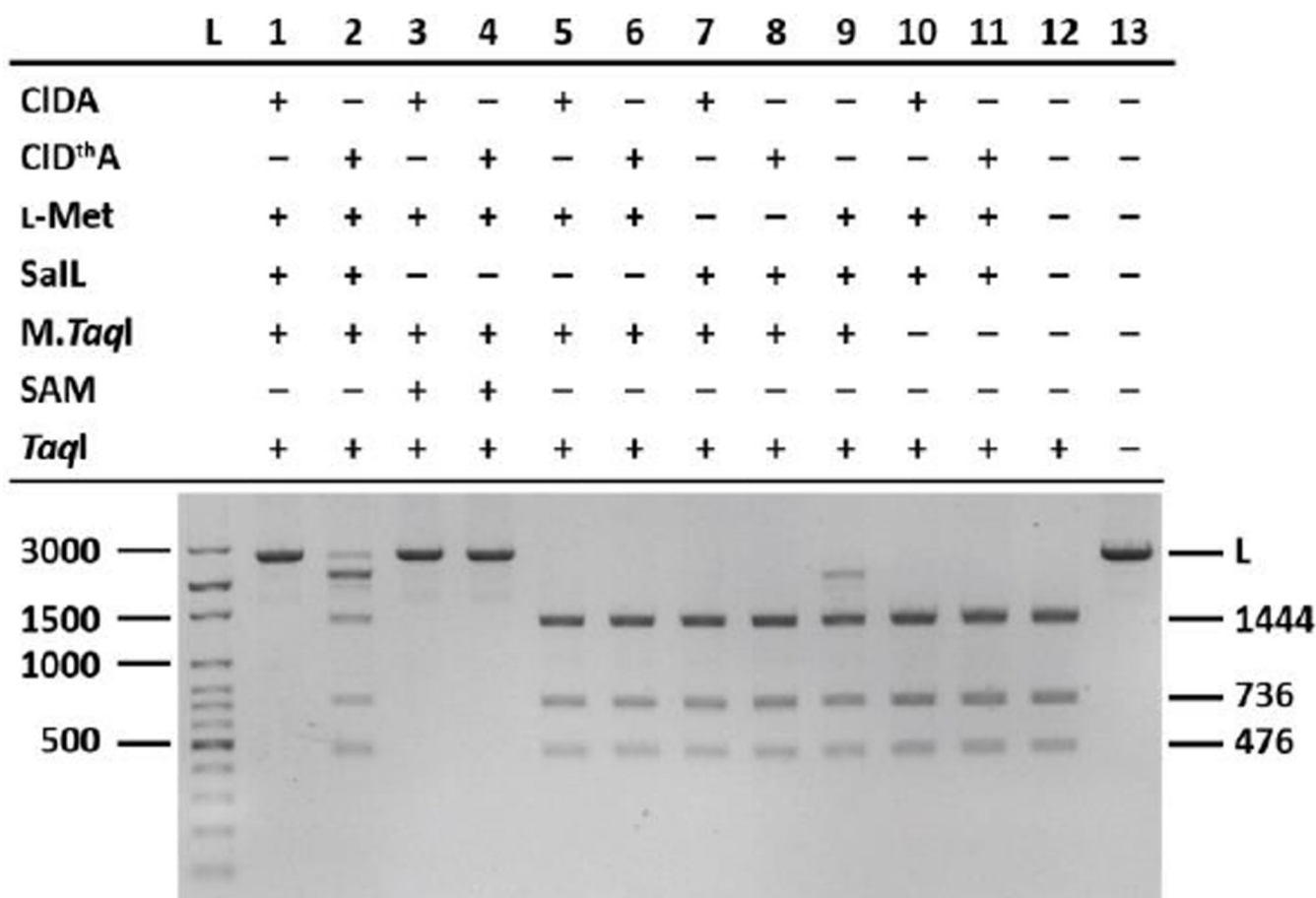


Fig. 4. Time course methylation-restriction assay of linearized pUC19 DNA by *M. TaqI* methyltransferase. A 100bp ladder DNA marker (100–3000 bp) was used as a reference (lane L). During the methylation reaction, five time points were taken for both SthAM (first group of time points) and SAM (second group of time points). After treatment with *TaqI*, the reactions were analyzed on a 1% agarose gel. The DNA lane shows the control in the absence of *M. TaqI* and cofactor, in the presence and absence of *TaqI*.

**Fig. 5.**

Combination synthesis-methylation-restriction assay using linearized pUC19 DNA, SalI and *M. TaqI*. Lane L is a 100bp ladder DNA marker (100–3000 bp). Lane 1 and 2 are the combination reactions with respectively CIDA and CIDthA. Lane 3 and 4 are positive controls in the presence of SAM, but absence of SalI. Negative controls with respectively CIDA and CIDthA were performed in the absence of SalI (lane 5 and 6), of L-Met (lane 7 and 8) and of *M. TaqI* (lane 10 and 11). Controls without CIDthA (lane 9) and only DNA (lane 13) are shown.