

Histone Methyltransferase Assay *in vitro*

Pengfei Sui, Yu Yu and Aiwu Dong*

Department of Biochemistry, Fudan University, Shanghai, China

*For correspondence: aiwudong@fudan.edu.cn

[Abstract] Histone methylation is an important epigenetic modification that plays important roles in plant development and growth. Histone methyltransferases are the enzymes to establish histone methylation and here we describe a simple and effective protocol for detecting methyltransferase activity and specificity *in vitro*.

Materials and Reagents

1. ¹⁴C labeled-methyl-adenosyl-L-methionine (SAMS) (Sigma-Aldrich)
2. Purified recombinant histones (from *E. coli*)
3. Histone H3 (Roche Diagnostics, catalog number: 1034758)
4. Core histones (Sigma-Aldrich, catalog number: H9250)
5. Mononucleosomes and Oligonucleosomes (see procedure)
6. Coomassie brilliant blue R-250
7. MiliQ water
8. SDS-PAGE
9. KCl
10. MgCl₂
11. Sucrose
12. ZnCl₂
13. β-mercaptoethanol
14. MAB buffer (see Recipes)

Equipment

1. Water bath

Procedure

A. Substrate:

Purified recombinant Histones (Ding *et al.*, 2007), histone H3, core histones, mononucleosome

and oligonucleosome (from HeLa cells or recombinant ones from *E.coli*).

Note: The mononucleosomes and oligonucleosomes prepared from HeLa cells were gifts from Yi Zhang (UNC Chapel Hill, USA). The recombinant oligonucleosomes from E. coli were gifts from Bing Zhu (NIBS, Beijing, China).

B. Reaction

A mixture containing 1-5 μ l enzyme (such as SDG725), 5 μ l 4x MAB buffer, 250 nCi 14 C labeled SAM and 1 μ g substrates to 20 μ l volume, is kept at 37 °C for 1-2 h. The reaction is stopped by adding 5 μ l 5x SDS-PAGE loading buffer and boiling at 100 °C for 5 min, and 5 μ l samples will be analyzed by 15% SDS-PAGE gel electrophoresis and visualized by Coomassie brilliant blue R-250. The SDS-PAGE gel is dried and exposed to X-ray films or scanned by Typhoon (GE) (15% refers to the concentration of Acr/Bis. Different histones can be separated more clearly by 15% SDS-PAGE).

Recipes

1. MAB buffer

1x MAB buffer
50 mM Tris-Cl (pH 8.5)
20 mM KCl
10 mM MgCl₂
250 mM Sucrose
100 μ M ZnCl₂
10 mM β -mercaptoethanol

Acknowledgments

The protocol was adapted from previously published papers (Rea *et al.*, 2000; Ding *et al.*, 2007).

References

1. Ding, B., Zhu, Y., Gao J., Yu, Y., Cao, K. M., Shen W. H., Dong, A. (2007) [Molecular characterization of three rice SET-domain proteins](#). *Plant Sci* 172:1072-1078.
2. Rea, S., Eisenhaber, F., O'Carroll, D., Strahl, B. D., Sun, Z. W., Schmid, M., Opravil, S., Mechtler, K., Ponting, C. P., Allis, C. D. and Jenuwein, T. (2000). [Regulation of chromatin structure by site-specific histone H3 methyltransferases](#). *Nature* 406(6796): 593-599.

-
3. Sui, P., Jin, J., Ye, S., Mu, C., Gao, J., Feng, H., Shen, W. H., Yu, Y. and Dong, A. (2012). [H3K36 methylation is critical for brassinosteroid-regulated plant growth and development in rice.](#) *Plant J* 70(2): 340-347.