

COBALAMIN DEPENDENT METHYLATION AND DEMETHYLATION BY VERATROL O-DEMETHYLASE

Christopher Grimm, University of Graz
grimm-christopher@web.de
Judith Farnberger, University of Graz
Simona Pompei, University of Graz
Wolfgang Kroutil, University of Graz

Key Words: methyl transferases, cobalamin, methylation, demethylation

The formation and breakage of C-O ether bonds are valuable synthetic transformations contributing to the structural diversification of natural products and pharmaceuticals [1-3]. Moreover, O-methylated phenol derivatives are useful building blocks for the manufacture of antioxidants, flavoring agents, fragrances, dyes, agrochemicals and fine chemicals [4,5]. Despite the large variety of chemical reactions for methylation and demethylation, none reaction is reversible and sustainable. They often lack chemo-, regio- and stereoselectivity and rely on harsh reaction conditions [6]. Thus, the development of milder alternatives such as biocatalytic methylation and demethylation reactions is of high interest [7].

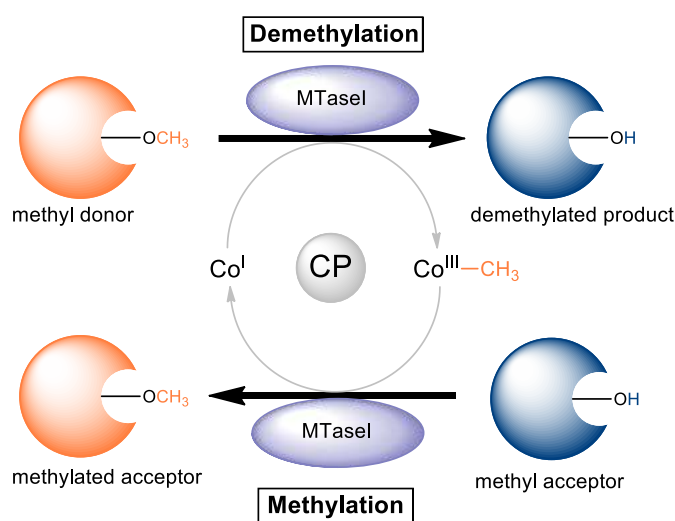


Figure 1: The cobalamin dependent methyltransferase (MTase) catalyzes the demethylation of a methyl donor and the methylation of a methyl acceptor alongside with the corrinoid protein (CP) acting as a methyl shuttle.

We present an enzymatic system utilizing cobalamin (vitamin B12) dependent methyl transferases (MTases) derived from the anaerobic bacteria which enable both methylation and demethylation of heteroatoms [8,9]. Naturally, the bacterial system involves four proteins for these reactions whilst our concept requires only two proteins (see Figure 1): the veratrol O-demethylase (MTase) from *Acetobacterium dehalogenans* and the corrinoid protein (CP) derived from another origin. The CP incorporates a cobalamin prosthetic group functioning as methyl carrier. Along with the CP the MTase catalyzes both, the demethylation of a donor and the methylation of an acceptor substrate in a reversible manner. The activity of the MTase relies on the amount of CP and zinc, because it incorporates a zinc binding motif [10]. The approach represents a substrate promiscuous alternative to common chemical and enzymatic methyl transfer methodologies and a valuable extension for the toolbox of available biocatalysts for ether bond formation as well as cleavage.

- 1 Law, B. J. C., Bennett, M. R., Thompson, M. L., Levy, C., Shepherd, S. A., Leys, D., Micklefield, J. (2016), *Angew. Chem. Int. Ed.*, 55: 2683-2687.
- 2 Zhang, M.-X., Hu, X.-H., Xu, Y.-H., Loh, T.-P. (2015), *Asian J. Org. Chem*, 4: 1047-1049.
- 3 Lee, D., Park, H. L., Lee, S.-W., Bhoo, S. H., Cho, M.-H. (2017), *J. Nat. Prod.*, 80: 1467-1474.
- 4 Bjørsvik, H.-R.; Liguori, L.; Minisci, F (2000), *Org. Process Res. Dev.*, 4: 534-543.
- 5 Zhang, H.; Tsao, R (2016), *Curr. Opin. Food Sci.*, 8: 33-42.
- 6 Farnberger, J. E.; Richter, N.; Hiebler, K.; Bierbaumer, S.; Pickl, M.; Skibar, W.; Zepeck, F.; Kroutil, W. (2018), *Commun. Chem.*, 1: 82.
- 7 Richter, N.; Farnberger, J. E.; Pompei, S.; Grimm, C.; Skibar, W.; Zepeck, F.; Kroutil, W. (2019), *Adv. Synth. Catal.*, 361:1-9.
- 8 Matthews, R. G.; Koutmos, M.; Datta, S. (2008), *Curr. Opin. Struct. Biol.*, 18: 658-666.
- 9 Richter, N.; Zepeck, F.; Kroutil, W. (2015), *Trends Biotechnol.*, 33: 371-373.
- 10 Studenik, S.; Kreher, S.; Diekert, G. (2011), *FEMS Microbiol. Lett.*, 318: 131-136.