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Structural symphony of diverse metal coordination in soluble methane monooxygenase (sMMO) through auxiliary components

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The soluble methane monooxygenase (sMMO), bacterial multicomponent monooxygenase (BMM) superfamily, requires hydroxylase (MMOH), a regulatory component (MMOB), and reductase (MMOR) for methane hydroxylation for the O_2 and C-H activation of substrates. The analysis of a gene map of sMMO from type II and X methanotrophs indicates that *mmoR* (MMOR) and *orfY* (MMOD) are positioned upstream of *mmoX*, which expresses MMOH α-subunit. Prior approaches proposed that MMOD regulates copper coordination for the expression of sMMO and particulate MMO (pMMO). The functions of MmoR are not yet clearly understood due to the lack of biochemical studies, although its functions are proposed through sequencing studies. In this presentation, the biophysical aspects of MMOD and MmoR are elucidated by the over-expressed and purified proteins.

X-ray crystallography of MMOH-MMOD indicates that MMOD replaces the binding site of MMOB and controls the diiron active site in MMOH. The four-helix bundle controls the coordination of four-Glu and two-His for the hydroxylation of substrates, but MMOD rearranges the coordination as an inhibitory enzyme for the resting state of MMOH. MmoR, a transcriptional activator, interacts with specific sequences in upstream activating sequences (UAS) for interaction with sigma-54, a transcriptional regulator, in the absence of copper ions.

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