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Metabolite profiling and dynamic ^{13}C metabolomics of methane assimilation pathways in methanotrophic bacteria

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Methane is recognized as one of the most powerful greenhouse gases, emitted at approximately 600 Tg y^{-1}. Aerobic methane oxidation conducted by a group of bacteria, known as methanotrophs, represents the major biological barrier that limits gas emission from natural ecosystems. The current knowledge of metabolic pathways involved in methane oxidation and assimilation is mostly based on enzymatic studies. We used metabolomics to refine C1-pathways in the strains of Type I and Type II methanotrophs. The metabolite profiles were studied using a combination of liquid chromatography-mass spectrometry and gas chromatography MS. To elucidate the major metabolic flux for methane assimilation, the ^{13}C methane assimilated into downstream intermediates was tracked. Around 60 metabolites including amino acids, carboxylic acids, sugar phosphates and CoA derivatives were quantified by LC-MS/MS and GC-MS. The methanotrophic type I strains displayed significantly increased levels of sugar phosphates and their precursors that are involved in ribulose monophosphate pathway (RuMP pathway). Some primary metabolites involved in the TCA cycle, serine cycle and ethylmalonyl-CoA pathway were found to have significant increases in type II cultures. The ^{13}C labeling pattern in pyruvate obtained by both analytical techniques was analyzed to distinguish how methane was assimilated through two variants of the RuMP pathway in type I strains. Similarly, the analysis of serine labeling patterns (singly, doubly and triply labeled Ser) and tracking of the CoA derivatives labeling were used to reveal the role of the serine cycle and ethylmalonyl-CoA pathways in methane assimilation by type I and II methanotrophic bacteria.

Biography

Dr. Yang completed his doctorate in school of chemical engineering at the Tianjin University in 2007. After that, he is working as a research scientist at the Mary E. Lidstrom Lab in the University of Washington. Dr. Yang is currently applying the metabolomic methods to identify metabolic changes related to different bacterial phenotypes and growth behavior on different substrates. He is also working on the metabolic flux analysis to optimize the yield of biosynthetic compounds.