

# 2018年度 ストラスブール大学派遣研究者講演会

2019年2月22日（金）16時–17時30分

理学部2号館405室

## Genomics and metabolism of chloromethane-degrading methylophilic bacteria

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Chloromethane ( $\text{CH}_3\text{Cl}$ ) is a halogenated carbon compound abundantly present in the atmosphere, and is responsible for significant chlorine-dependent ozone destruction. Although chloromethane is produced industrially, larger amounts are emitted naturally in terrestrial ecosystems through specific biological activities of plants and the degradation of plant organic matter in soils. Nonetheless, the magnitudes of chloromethane production and of its microbial degradation are still poorly characterized. To evaluate chloromethane biodegradation in the environment, we have been studying the key enzymes and regulation elements involved in halogenated methane microbial degradation.

Under laboratory conditions, chloromethane-degrading bacteria isolated from leaves and soils harbor the *cmu* pathway (for chloromethane utilization), the only known microbial pathway for utilization of chloromethane. Among the methylophilic microorganisms able to utilize  $\text{C}_1$  compounds, only a few are able to grow with chloromethane provided as the sole source of carbon and energy. The *cmu* pathway involves tetrahydrofolate and vitamin  $\text{B}_{12}$  as essential cofactors of chloromethane dehalogenase and has been characterized in detail for *Methylobacterium extorquens* CM4. Key players of the bacterial response to growth with chloromethane were identified using random mini-transposon Tn5 mutagenesis, comparative genomics, proteomics, and transcriptomics, as well as experimental evolution approaches.

Bacteria associated with chloromethane degradation in soils and plant leaves were identified by stable isotope probing (SIP) using incubation with  $^{13}\text{C}$ -labelled  $\text{CH}_3\text{Cl}$ . High throughput sequencing of the heavy DNA targeted taxonomical and *cmu* genes, as well as metagenomes. In most experiments, detected taxa did not correspond to bacteria known to contain *cmu*.

Future research is needed to grasp the diversity of chloromethane-degrading-associated metabolisms and taxa of the microbial chloromethane sink. High variations in chloromethane flux emissions have been reported which suggests that low and high affinity chloromethane-degrading populations may be found in the environment, as is the case for methane.

学生・教職員の多数の来場を歓迎いたします。

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