Methane utilization by Methylobacterium species: new evidence but still no proof for an old controversy

Recently, Van Aken et al. (2004) reported on the isolation of a novel species of the genus Methylobacterium, Methylobacterium populi, from internal tissues of poplar trees and claimed that representatives of this species can use methane as the sole source of carbon and energy. The methanotrophic potential of representatives of the genus Methylobacterium is the subject of an old and murky debate, and we think that any new evidence on this topic needs to be proven and verified to the strictest scientific standards.

The genus Methylobacterium is composed of a variety of pink-pigmented facultatively methylotrophic (PPFM) bacteria, which can grow on one-carbon compounds such as formate, formaldehyde and methanol as the sole source of carbon and energy, as well as on a wide range of multi-carbon growth substrates (Green, 1999). Currently, this genus encompasses 15 recognized species that are represented by a few hundred strains. The type species of this genus, Methylobacterium organophilum, was originally described as a facultative methane-utilizing bacterium (Patt et al., 1974, 1976). However, until recently, a single strain of this species, M. organophilum strain XX, remained the only PPFM bacterium that has been reported to be capable of growth on methane. Unfortunately, this unique ability of strain XX could never be independently verified. Either the ability has been lost or the original report was in error. Later examination showed that neither the culture stored in the National Collection of Industrial Bacteria nor that in the American Type Culture Collection was able to grow on methane (Green & Bousfield, 1983). Numerous other, unpublished efforts were also unsuccessful. It has been suggested that the genetic ability of this organism to assimilate methane might have been plasmid-borne and became lost because cultures were not maintained on inorganic medium under a methane-containing atmosphere (R. S. Hanson, personal communication cited by Green, 1999). As a consequence, methane assimilation has been omitted as an essential feature in an emended description of the genus Methylobacterium (Green & Bousfield, 1983).

Since that time our knowledge of both the genetic and metabolic basis for methanotrophy has expanded significantly. However, neither the key enzyme of methanotrophic metabolism, i.e. methane monoxygenase (MMO), nor the genes encoding different forms of MMO have ever been detected in the PPFM bacteria. The genus Methylobacterium is not included in the list of currently known methanotrophic bacteria. Thus, the description of a novel methane-utilizing species of this genus by Van Aken et al. (2004) represents an extraordinary claim. In light of this, a reader should expect to see a sound data set that demonstrates without question two things: that the culture is pure, and that growth definitely occurs on methane as the sole energy source (i.e. cryptic growth or growth on contaminating substances is not occurring). Unfortunately, both points are lacking in the manuscript, and growth is simply reported as positive. In addition, the routine procedure used for the description of novel methanotrophic organisms, which has been carefully maintained in methanotroph systematics for years, has not been followed in this article. This procedure should include (i) tests for culture purity, (ii) identification of the pathway used for formaldehyde assimilation, (iii) observation of intracytoplasmic membrane structures, (iv) MMO activity measurements and (v) detection of genes encoding MMO.

We strongly encourage the authors to do this work. M. populi may provide a unique chance to confirm the capability of some representatives of the genus Methylobacterium to grow on methane, since M. organophilum strain XX is no longer suitable for this purpose. More careful examination of M. populi could therefore help to resolve an old debate. However, until this is done, the claim that this organism is able to grow on methane must be treated with considerable scepticism.

Svetlana N. Dedyshev,1 Peter F. Dunfield2 and Yuri A. Trotsenko3

1Winogradski Institute of Microbiology, Russian Academy of Sciences, Moscow 117312, Russia
2Max-Planck-Institut für Terrestrische Mikrobiologie, D-35043 Marburg, Germany
3Institute of Biochemistry and Physiology of Microorganisms, Russian Academy of Sciences, Pushchino, Moscow region, 142292, Russia

Correspondence: Svetlana N. Dedyshev (dedyshev@mail.ru)


