



Carbon isotope fractionation and the acetyl-CoA pathway

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Homoacetogenic bacteria can catalyze the reductive synthesis of acetate from CO_2 via the acetyl-CoA pathway. Besides this unifying property homoacetogenic bacteria constitute a metabolically and phylogenetically diverse bacteriological group. Therefore their environmental role is difficult to address. It has been recognized that in methanogenic environments homoacetogenic bacteria contribute to the degradation of organic matter. The natural abundance of ^{13}C may be used to understand the functional impact of homoacetogenic bacteria in the soil environment. To distinguish the acetyl-CoA pathway from other dominant processes, the isotopic composition of acetate and CO_2 can be determined and the fractionation factors of the individual processes may be used to discriminate between the dominant pathways. To characterize the fractionation factor associated with the acetyl-CoA pathway the phylogenetic and metabolic diversity needs to be considered. Therefore the fractionation factor of substrate utilization and product formation of different homoacetogens (*Acetobacterium woodii*, *Sporomusa ovata*, *Thermoanaerobacter kivui*, *Morella thermoautotrophica*) has been studied under pure culture conditions in two defined minimal medium with H_2/CO_2 as sole source of carbon and energy. It became obvious that the cultivation conditions have a major impact on the obtained fractionation factors.