Microbe processes carbon via new metabolic pathway

January 21 2011, by Lin Edwards

(PhysOrg.com) -- A Dead Sea microbe has been found to use a previously unknown metabolic pathway to metabolize fats as a source of carbon to synthesize carbohydrates. This suggests there may be other undiscovered pathways and more ways to live in extreme habitats than previously believed.

Every organism known metabolizes carbon compounds to produce energy and the basic cellular building blocks. Humans and other vertebrates do this via the Krebs cycle, in which acetyl coenzyme A (acetyl-CoA) plays an important role.

Vertebrates are unable to convert acetyl-CoA into malate, a precursor of other molecules such as sugars, but many plants and microorganisms can, via either the glyoxylate cycle or the ethylmalonyl-CoA pathway, which was discovered in 2007 by a team of scientists led by Dr. Ivan A. Berg of the University of Freiburg in Germany. The new microbe, a single-celled microorganism of the domain Archaea, was discovered by the same research team to use a third pathway that was previously unknown.

The researchers realized the microbe could not use the glyoxylate cycle because an essential enzyme in the cycle, isocitrate lyase, was missing. It could not use the ethylmalonyl-CoA pathway either because it lacks some of the genes necessary to synthesize the enzymes used in the cycle.

Over a period of two years the researchers analyzed the enzymes *H. marismortui* used when it was grown on a medium containing acetate and determined it was using the methylaspartate cycle (named after an intermediate in the cycle to convert acetyl-CoA to malate. This cycle is longer and more complex than the other two pathways but it does have advantages for a microbe living in such salty conditions, since one of the intermediates in the cycle limits osmosis, which would draw water out of the cell in attempt to balance the salinity across the cell membrane.

Dr. Berg said the discovery of the third metabolic pathway means there could be others, and added that "the diversity of life is bigger than we know now."

The discovery also sheds some light on evolutionary processes since the enzymes in the cycle are similar to those found in ancient bacteria, but are not present in other Archaea, which suggests *H. marismortui's* ancestors obtained the genes by lateral gene transfer rather than evolving through a lengthy series of random mutations. Berg said there were few such examples where it is so clear how the metabolic pathway evolved, which he said makes the pathway "a kind of a wonder."

More information: A Methylaspartate Cycle in Haloarchaea, *Science* 21 January 2011: Vol. 331 no. 6015 pp. 334-337. DOI:10.1126/science.1196544