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Different glycolytic pathways for glucose and fructose in the halophilic archaeon *Halococcus saccharolyticus*

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We found out that all experiments described for Halococcus saccharolyticus in this paper were actually performed with Haloarcula marismortui. The incorrect assignment became obvious after purification and characterization of acetate/acetyl-CoA-converting enzymes from this organism. Using N-terminal amino acid sequences of the purified enzymes, we identified open reading frames (ORFs) in the partially sequenced genome of *Haloarcula marismor*tui. We amplified these ORFs by PCR using template DNA from the organism used in our experiments and obtained sequences identical to those of the Haloarcular marismotui ORFs, thus identifying the organism as Haloarcula marismortui. In accordance, a partial 16S rRNA sequence of the strain was determined; the sequence corresponded to that of Haloarcula marismortui rather than to that of Halococcus saccharolyticus.

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