Bacillus halodurans Strain C125 Encodes and Synthesizes Enzymes from Both Known Pathways To Form dUMP Directly from Cytosine Deoxyribonucleotides

Analysis of the genome of Bacillus halodurans strain C125 indicated that two pathways leading from a cytosine deoxyribonucleotide to dUMP, used for dTMP synthesis, were encoded by the genome of the bacterium. The genes that were responsible, the comEB gene and the dcdB gene, encoding dCMP deaminase and the bifunctional dCTP deaminase:dUTPase (DCD:DUT), respectively, were both shown to be expressed in B. halodurans, and both genes were subject to repression by the nucleosides thymidine and deoxycytidine. The latter nucleoside presumably exerts its repression after deamination by cytidine deaminase. Both comEB and dcdB were cloned, overexpressed in Escherichia coli, and purified to homogeneity. Both enzymes were active and displayed the expected regulatory properties: activation by dCTP for dCMP deaminase and dTTP inhibition for both enzymes. Structurally, the B. halodurans enzyme resembled the Mycobacterium tuberculosis enzyme the most. An investigation of sequenced genomes from other species of the genus Bacillus revealed that not only the genome of B. halodurans but also the genomes of Bacillus pseudofirmus, Bacillus thuringiensis, Bacillus hemicellulosilyticus, Bacillus marmarensis, Bacillus cereus, and Bacillus megaterium encode both the dCMP deaminase and the DCD:DUT enzymes. In addition, eight dcdB homologs from Bacillus species within the genus for which the whole genome has not yet been sequenced were registered in the NCBI Entrez database.