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Bioinformatics comparison of cofactor independent and dependent phosphoglycerate mutase

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Background and Aims: Phosphoglycerate mutase(PGM, EC 5.4.2.1) is an enzyme of the glycolytic and gluconeogenic pathway. There are two isoforms of PGM, cofactor- dependent(dPGM) and cofactor-independent(iPGM). Helicobacter pylori(strain ATCC 700392/26695) contains only iPGM. Bioinformatics analysis of H.pylori PGM and comparison with human PGM2 can help to design selective inhibitors for iPGM.
Methods: The data have been obtained using the following sites: PubMed/NCBI, Protein Data Bank (PDB), Expasy, Clustal W, Prot param, Compute PI/Mw, Uniprot, BRENDA, Swiss PDB Wiever.
Results: The gene sequence of H.Pylori iPGM(NC_000915.1) contains 1475 bp and PGM2 coding gene contains 9861 bp(NG_013016.1) located on chromosome 7p13-p12. It has 3 variants that encode the same protein. Alignment of their DNA sequences showed no significant similarity. iPGM is a monomeric, contains 491 amino acid, MW 54788 Da, PI 6.44. Human PGM2 is dimeric protein with 253 amino acids, MW 28766.17 Da, and PI is 6.8. In iPGM, Ser 61 is active site of enzyme that forms phosphoserin intermediate in its catalytic process. Intramolecular transfer of phospho groups are occurred in iPGM. In PGM2 His 11 and His 186 are the active sites that phosphorylated during the reaction. Intermolecular transfer of phospho groups occurred during catalysis, PGM2 requires 2,3 bisphosphoglycerate as cofactor and Arg 62 interacted to carboxyl group of phosphoglycerate. iPGM requires Manganese ion for its activity. Its protein similarity with PGM2 is 55%.
Conclusions: In contrast to H.Pylori, glycolysis in human mediated by dPGM. consider to the presence of different active sites in iPGM(Ser61) and PGM2(His 11,His 186), also cofactor dependence on PGM2(no in iPGM), it seems that iPGM may be used as differential target against H.pylori.

Keywords: iPGM; PGM 2; *H. Pylori*