Title:	Investigating post-translational regulation by glutathionylation of glycolytic pathway enzymes of Saccharomyces cerevisiae
Authors:	Mishra, Vibhu (/jspui/browse?type=author&value=Mishra%2C+Vibhu)
Issue Date:	22-Oct-2019
Publisher:	IISERM

Abstract:	Glycolysis is the pathway that consumes glucose to produce energy. It is present in all organisms, from bacteria in the deep oceans to complex life forms present on the earth. During oxidative stress, the cell shifts the glycolytic pathway flux into Pentose Phosphate pathway to generate NADPH to be used by glutaredoxins and thioredoxins to deal with oxidative stress. For this to happen, the flux through the glycolytic pathway has to be shut off by regulation of enzymes of the glycolysis. This has to happen quickly to deal with damaging oxidative stress, since the enzymes' thiols may get permanently oxidised and degraded. So, the cell needs a mechanism that can regulate as well as protect the protein cysteine thiol from permanent oxidation.Glutathionylation is such a mechanism. Several reports have shown that many glycolytic proteins undergo glutathionylation under cellular oxidative stress. Glutathionylation prevents irreversible oxidation of cysteine residues present in proteins by formation of mixed disulphides. However, the mechanistic role of glutathionylation of these glycolytic proteins has not been well studied. In the current study, we tried to investigate this process in detail under stress and non-stress conditions.From the literature there are six enzymes known to be glutathionylated in yeast. These enzymes are Glyceraldehyde-3-phosphate dehydrogenase (TDH3), Fructose-bisphosphate aldolase (FBA1), 3-Phosphoglycerate Kinase (PGK1), Enolase (ENO2), Pyruvate Kinase (CDC19) and Triose Phosphate Isomerase (TPI1). To initiate investigations on the project, all six genes were cloned and expressed downstream of a strong yeast promoter. The expression of three of these enzymes Fba1p, Pgk1p, Eno2p could be confirmed. We then evaluated glutathionylation of these enzymes under stressed and non-stressed conditions. To investigate the enzyme involved in the glutathionylation and deglutathionylation process, we examined glutathionylation or deglutathionylation in genetic backgrounds deleted for the different thioredoxins and glutaredoxins that are known to be involved in these pathways. Preliminary results indicate a role of Grx3p in the glutathionylation of Fba1p, Grx1p in the glutathionylation of Pgk1p and Trx2p in the deglutathionylation of Pgk1p. However, more detailed studies are required to confirm these initial findings and determine the mechanisms involved.
URI:	http://hdl.handle.net/123456789/3662 (http://hdl.handle.net/123456789/3662)
Appears in Collections:	MS Dissertation by MP-2016 (/jspui/handle/123456789/4311)

Files in This Item:

File	Size	Format	
MP16019.pdf (/jspui/bitstream/123456789/3662/1/MP16019.pdf)	2.52 MB	Adobe PDF	View/Open (/jspui/bitstream/123456789/3662/1/MP160

Show full item record (/jspui/handle/123456789/3662?mode=full)

(/jspui/handle/123456789/3662/statistics)