Lactococcus lactis TrxD represents a subgroup of thioredoxins prevalent in Gram-positive bacteria containing WCXDC active site motifs - DTU Orbit (12/05/2019)

Lactococcus lactis TrxD represents a subgroup of thioredoxins prevalent in Gram-positive bacteria containing WCXDC active site motifs.

Three protein disulfide reductases of the thioredoxin superfamily from the industrially important Gram-positive Lactococcus lactis (LlTrxA, LlTrxD and LlNrdH) are compared to the "classical" thioredoxin from Escherichia coli (EcTrx1). LlTrxA resembles EcTrx1 with a WCQPC active site motif and other key residues conserved. By contrast, LlTrxD is more distantly related and contains a WCQDC motif. Bioinformatics analysis suggests that LlTrxD represents a subgroup of thioredoxins from Gram-positive bacteria. LlNrdH is a glutaredoxin-like electron donor for ribonucleotide reductase class Ib. Based on protein-protein equilibria LlTrxA ($E^0_1 = \text{-259 mV}$) and LlNrdH ($E^0_1 = \text{-238 mV}$) show approximately 10 mV higher standard state redox potentials than the corresponding E. coli homologues, while $E^0_1$ of LlTrxD is -243 mV, more similar to glutaredoxin than "classical" thioredoxin. EcTrx1 and LlTrxA have high capacity to reduce insulin disulfides and their exposed active site thiol is alkylated at a similar rate at pH 7.0. LlTrxD on the other hand, is alkylated by iodoacetamide at almost 100 fold higher rate and shows no activity towards insulin disulfides. LlTrxA, LlTrxD and LlNrdH are all efficiently reduced by NADPH dependent thioredoxin reductase (TrxR) from L lactis and good cross-reactivity towards E. coil TrxR was observed with LlTrxD as the notable exception.