Influence of mistranslation stress on oxidative stress response in bacteria Escherichia coli

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Mistakes during translation can occur due to inaccurate amino acid selection by aminoacyl-tRNA synthetases (aaRSs). Some aaRSs possess editing domain and hydrolyze incorrect aa-tRNA product. Although mistranslation is usually toxic due to production of functionally aberrant proteins, there are few examples of its adaptive effect on cellular responses to subsequent stresses. Research on organisms with editing-deficient aaRS and their response to oxidative stress is scarce. In our experiments, we used *Escherichia coli* strain expressing isoleucyl-tRNA synthetase with inactivated editing domain which produces mistranslated proteins if amino acids structurally similar to isoleucine, such as proteinogenic amino acid valine (Val) or nonproteinogenic amino acid norvaline (Nva), are added to the media. To observe the effect of mistranslation and subsequent oxidative stress on cell morphology, proliferation and viability, cells were observed under microscope, growth curves were determined, and survival assays were performed. Mistranslation was induced by overnight incubation of bacteria with various concentrations of Val or Nva (0.25, 0.5, 0.75 and 1 mM), and cells were then exposed to oxidative stress by adding 1 mM H_2O_2. Prominent filamentation of the cells was observed with cell size increasing in Val or Nva concentration-dependent manner. Survival assays indicated increased survival of bacteria grown with 0.75 and 1 mM Val or Nva in the presence of H_2O_2. Growth curve measurements showed that after induction of oxidative stress, lag phase was shorter for cultures grown with 1 mM Val or 0.75 mM Nva. The results indicate that there is mistranslation-induced preadaptation to oxidative stress, albeit only in a narrow range of Val and Nva concentrations. Further work will be focused on identification of cellular mechanisms that allow better survival under oxidative stress due to misincorporation of valine or norvaline at isoleucine positions in proteins.