

P039 Global gene expression profiling reveals widespread, yet distinctive, translational responses to different eIF2B-targeting stress pathways
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Dramatic inhibition of protein synthesis is a common feature of many cellular stresses. Although specific mRNAs remain translated (e.g. yeast *GCN4*), the extent and variation of such resistance is unclear. We have combined polysomal and Affymetrix microarray analyses to identify yeast mRNAs which are regulated at the translational step in response to two related stresses: amino acid depletion and fusel alcohol addition. Both stresses target the eukaryotic translation initiation factor 2B (eIF2B) via distinct mechanisms.

The microarray data highlight the widespread but very divergent reprogramming of translation in response to these stresses. These data suggest that translational control is a key component of proteome remodelling during the adaptation to stress. More specifically, there is a biphasic response to amino acid starvation, with an early 'scavenging' phase preceding the classical Gcn4p-dependent 'biosynthetic' phase. Additionally, specific functional classes of mRNA are co-regulated at both transcript level and translation.

Moreover, computational analysis of upstream regions of translationally regulated mRNAs following amino acid depletion and butanol addition reveals a possible link between frequencies of AUG triplets and translational regulation.