Role of miRNAs in amino acid metabolism: Model of ER stress in human dermal fibroblasts

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Endoplasmic reticulum (ER) stress is a key cellular event that disrupts protein folding and homeostasis and is implicated in the pathogenesis of various metabolic and degenerative diseases. Despite extensive research on ER stress, the precise mechanisms linking ER stress-induced metabolic alterations and post-transcriptional regulation by microRNAs remain inadequately understood. Given the central role of amino acid metabolism in stress adaptation and the emerging importance of miRNAs in fine-tuning gene expression under stress conditions, this study was undertaken to explore the interplay between ER stress, amino acid metabolism, and microRNA regulation. In this study, ER stress was induced in human dermal fibroblast cell line CCD-1135Sk using tunicamycin, a potent inhibitor of N-linked glycosylation. Amino acid profiles were analyzed using liquid chromatography-mass spectrometry, and differentially expressed miRNAs associated with metabolic shifts were identified through real-time PCR. Our findings demonstrate that ER stress significantly alters amino acid metabolism, and these changes correlate with differential expression of specific miRNAs that may orchestrate cellular stress responses and metabolic adaptations. This integrated analysis provides novel insights into how cells modulate metabolic networks and gene regulation under ER stress conditions, which could have implications for understanding disease mechanisms and developing targeted interventions.

Keywords: Unfolded protein response, Tunicamycin, Metabolic adaptation, Non-coding RNA, Human skin cells