Interactome of radiation-induced microRNA predicted target genes

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Abstract:

The progress in microRNA research has prompted the need to reexamine the complexity of the genomic regulatory network. These ~22-nt non-coding RNAs function as global negative regulators of gene expression and have been associated with a multitude of biological process such as cell differentiation, proliferation, metabolic regulation and apoptosis. The dysfunction of the microRNA-ome has been linked to various diseases including cancers. Our laboratory recently reported modulation in the expression of miRNA in a variety of cell types exposed to ionzing radiation (IR). To further understand microRNAs' role in IR induced stress pathways, we catalogued a set of common microRNAs modulated in various irradiated cell lines and generated a list of predicted target genes. Using advanced bioinformatics tools, we identified cellular pathways where miRNA predicted target genes function. The miRNA targeted genes were found to play key roles in previously identified IR stress pathways such as cell cycle, p53 pathway, TGF-beta pathway, ubiquitin mediated proteolysis, focal adhesion pathway, MAPK signaling, thyroid cancer pathway, adherens junction, insulin signaling pathway, oocyte meiosis, regulation of actin cytoskeleton and renal cell carcinoma pathway. Interestingly, we were able to identify novel targeted pathways that have not been identified in cellular radiation response, such as aldosterone-regulated sodium reabsorption pathway and long-term potentiation pathway. Our analysis indicates that the microRNA interactome in irradiated cells provide a platform for comprehensive modeling of the cellular stress response to IR exposure.