RNAs enable dynamic responses to stresses caused by changes in environmental conditions. We are investigating potential changes in transcriptional networks upon exposure to various oxidative-prone environmental conditions. These networks enable responses to diverse and rapidly changing environmental stimuli by affecting a vast number of gene targets at, frequently, multiple biological levels. Given their relevance to pathogenesis, and extremophilic phenotypes, and their potential biotechnological relevance, understanding their functions is a broad scientific goal. In this talk, we will describe our recent advances in developing high throughput approaches that allow for characterization of changes in RNA modifications and RNA transcriptional levels in specific RNAs. Given increasing findings that RNA modifications play a key regulatory role in gene transcription under cellular stress conditions and disease, two fundamental questions are: (1) what biochemical mechanisms lead to the breakdown of normal (healthy) expression levels of these RNAs in their respective pathways? And, (2) how is the breakdown of biological function at the molecular level caused by environmentally-induced chemical modifications? We will focus on RNAs that are more susceptible to oxidative species and on the impact of changes in their levels and chemistries on overall cell function.