Abstract

The unceasing progress in sequencing technologies and analytical methods in recent years has resulted in the rise in attention to epitranscriptomics – a form of which is RNA editing, the most common form being A-to-I RNA editing. ADAR-mediated A-to-I RNA editing is well-studied in cancers but is relatively uncharted in the human heart. In this study, two datasets were analyzed for A-to-I RNA editing activity, representing cardiac differentiation and ischemic heart disease (IHD). Identification of editing sites was done through a pipeline mainly utilizing GATK's variant calling suite as the core. A total of 35,948 and 24,797 unique editing sites were identified in the differentiation and IHD datasets, respectively, mainly affecting Alu repeats located in 3'UTR and intronic regions. *LIN28A* was significantly differently edited across the cardiac differentiation time course, though this might not be exclusive to cardiomyocytes. In IHD, *RYR2* and *FKBP5* were among the genes corresponding to the top editing sites. A-to-I RNA editing activity was also found to induce protein recoding in both datasets, corresponding to transcripts known to be edited in cancers such as *SRP9*, *COG3*, *KANSL1*, and *COPA*. The exact functional implications remain to be determined, though this study provides a baseline of the landscape of A-to-I RNA editing in cardiomyocyte differentiation and disease state.

Keywords: RNA editing, ADAR, transcriptomics, epitranscriptomics, cardiovascular diseases, cardiomyocytes.