Translation and functional rules of circular RNAs in human cancer

Abstract

Circular RNAs are a new class of non -coding RNAs that play important role in various biological function. Recent methodologies have enabled the characterization of circRNAs for identifications and potential function.

Introduction

Circular RNAs are a new type of endogenous RNAs produced by non -canonical back-splicing events.

The first circRNAs was discovered in RNA virus in 1976, and were observed in eukaryotic cell lines by electron microscopy in 1991.genomic and transcriptomic that are generated by next generations sequencing projects and bioinformatics algorithms have identified amount of circRNAs in eukaryotic clearly demon-strating .high throughput technologies have enabled in depth charactization. Recent studies interested in biological function of circRNAs in human cancer. functions of circular RNAs:

* Acts as transcriptional regulators to control expression of genes
* Service the prognostic biomarker because of there stable charasteristics
* The knowledge of hidden peptides through encoding circular RNAs

The translation of RNAs is used to provide new perspective for cancer treatment

**Related Works**

1. Circular RNA transcripts were first identified in the early 1990s but knowledge of these species has remained limited, as their study through traditional methods of RNA analysis has been difficult. Now, novel bioinformatic approaches coupled with biochemical enrichment strategies and deep sequencing have allowed comprehensive studies of circular RNA species.Recent studies have revealed thousands of endogenous circular RNAs in mammalian cells,some of which are highly abundant and evolutionarily conserved. Evidence is emerging that some circRNAs might regulate microRNA (miRNA) function, and roles in transcriptional control have also been suggested. Therefore, study of this class of noncoding RNAs has potential implications for therapeutic and research applications. We believe the key future challenge for the field will be to understand the regulation and function of these unusual molecules. (eck WR, Sharpless NE. Detecting and characterizing circular RNAs. Nat Biotechnol.)
2. Noncoding RNAs (ncRNAs) play increasingly appreciated gene-regulatory roles. Here, we describe a regulatory network centered on four ncRNAs-a long ncRNA, a circular RNA, and two microRNAs-using gene editing in mice to probe the molecular consequences of disrupting key components of this network. The long ncRNA Cyrano uses an extensively paired site to miR-7 to trigger destruction of this microRNA. Cyrano-directed miR-7 degradation is much more effective than previously described examples of target-directed microRNA degradation, which come primarily from studies of artificial and viral RNAs. By reducing miR-7 levels, Cyrano prevents repression of miR-7-targeted mRNAs and enables accumulation of Cdr1as, a circular RNA known to regulate neuronal activity. Without Cyrano, excess miR-7 causes cytoplasmic destruction of Cdr1as in neurons, in part through enhanced slicing of Cdr1as by a second miRNA, miR-671. Thus, several types of ncRNAs can collaborate to establish a sophisticated regulatory network.( Kleaveland B, Shi CY, Stefano J, Bartel DP. A network of noncoding regulatory RNAs acts in the mammalian brain. Cell.)