

# Star Circular RNAs In Human Cancer: Progress And Perspectives

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**Abstract:** Circular RNAs (circRNAs) are a recently discovered subclass of non-coding RNAs (ncRNAs) characterized by a covalently closed loop structure created by reverse splicing. Because they do not have a 5' cap structure and a 3' poly A tail, circRNAs have higher stability, abundance and evolutionary conservation than linear RNA between species. These features produce various potential biological functions of circRNAs, such as miRNA sponges, RNA-binding proteins that form RNA protein complexes. In recent years, more and more studies have shown that circRNAs play a vital role in the occurrence and development of human diseases. At the same time, their enormous potential as a biomarker and therapeutic target is also evolving. The purpose of this review is to summarize existing cancer-associated circRNAs and to try to find circRNAs that are abnormally expressed in many cancers. Therefore, we reviewed previous circRNAs studies related to cancer and selected them by statistics. The eight circRNAs that have the highest frequency in different cancers or involve key pathways are called star circRNAs. Here, we review the classification, features, and functions of emerging star circRNAs, with particular attention to the role of circRNAs in various cancers.

**Keywords:** circular RNA, cancer, targeted therapy, diagnosis

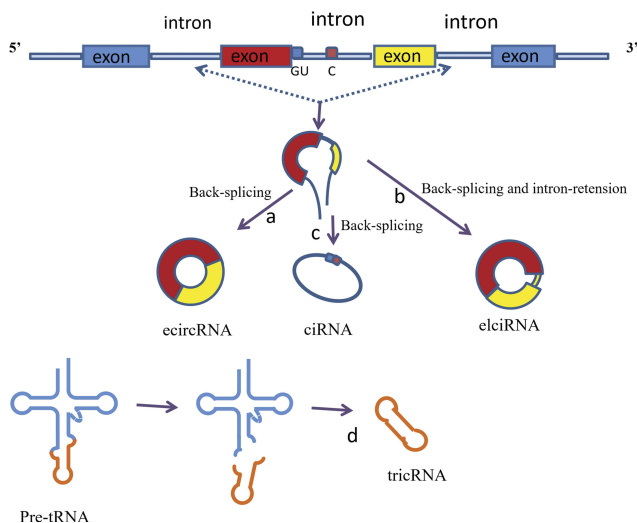
## Introduction

In 1976, Sanger et al first proposed the concept of circular RNAs (circRNAs), and they found that some higher plant viruses are single-strand, covalently closed circRNA molecules.<sup>1</sup> CircRNAs were first observed in humans in 1986 after infection with hepatitis D virus.<sup>2</sup> Soon after, a group of researchers used the sensitivity analysis of RNA expression to find four circRNAs from the DCC gene in normal and tumor cells in rodents and humans.

CircRNAs are an endogenous RNA that can be formed between a downstream 3' splice site and an upstream 5' splice site in linear precursor mRNA (pre-mRNA).<sup>3,4</sup> Due to technical deficiencies, these covalently closed circular RNA molecules are considered to be viroid-like, hepatitis virus molecule and splicing error results.<sup>5,6</sup> With the advancement of bioinformatics tools, the identification of many circular RNAs has been revealed, and their important roles have been studied, such as Xu et al reviewed.<sup>7</sup> In this review, we briefly describe the current understanding of the role of emerging star circRNAs and highlight their potential impact on cancer-targeted therapies.

## Classification Of CircRNAs

CircRNAs are produced by splice-mediated pre-sequence discontinuous splicing.<sup>8</sup> This splicing process is completely different from traditional linear RNA splicing. According

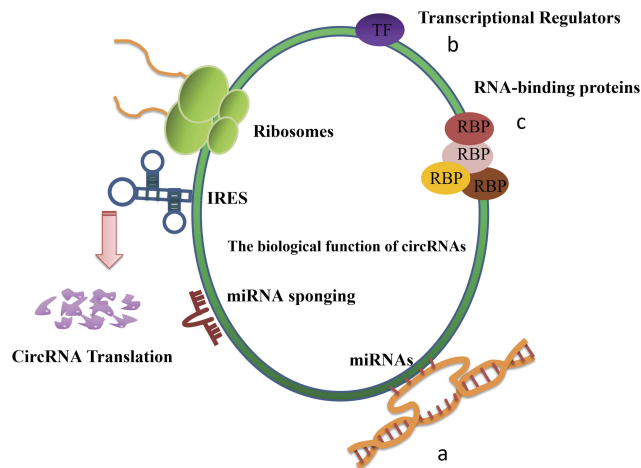


**Figure 1** Classification of circRNAs. Exon skipping occurs in pre-mRNA, and an exon-containing lariat intermediate is formed. The introns in the lariat are then removed and back-splicing occurs to produce circRNA. (a) EcircRNA. If the introns are spliced out completely, ecircRNA will be produced. (b) EIciRNA. If the introns are spliced out partially, EIciRNA will be produced. (c) CiRNA. The production of ciRNAs by back-splicing and mainly depends on a 7-nt GU-rich element near the 5' splice site and an 11-nt C-rich element near the branch-point site. (d) TricRNA. Introns that are removed during pre-tRNA splicing and then produce tricRNA by back-splicing.

to the selection of splice sites, a single locus can splicing multiple circRNAs.<sup>9</sup> According to the source sequence, circRNAs can be divided into four categories (Figure 1): a) exon circular RNAs (ecircRNAs), circRNAs originate from the exons of a linear transcript on the strand,<sup>10,11</sup> b) exon-intron circular RNAs (EIciRNAs), circRNAs, circRNAs transcribe from the same gene positions of linear transcripts of adjacent genes;<sup>11</sup> circular intron RNAs (ciRNAs), circRNAs originate from the intron of a linear transcript; c) circular intron RNAs (ciRNAs), circRNAs originate from the intron of a linear transcript;<sup>10,12</sup> exon-intron circular RNAs (EIciRNAs), circRNAs, circRNAs transcribe from the same gene positions of linear transcripts of adjacent genes; and d) tRNA intronic circRNA(tricRNAs). tricRNAs derive from introns that are removed during pre-tRNA splicing,<sup>13,14</sup> as Wu et al and Zhang et al reviewed.<sup>15,16</sup> For these circRNAs, ecircRNAs account for approximately 85% of all identified circRNAs and are the most abundant type, and most of them are predominantly localized in the cytoplasm.<sup>10</sup> In contrast, ciRNAs and EIciRNAs mainly locate in the nucleus indicate that these circRNAs have roughly different biological functions.

## Biological Functions Of CircRNAs

CircRNAs are considered to be a splicing by-product of long-term biological function, so past researchers have



**Figure 2** The biological function of circRNAs. CircRNAs with more miRNA-binding sites are more potent miRNA sponges and therefore play more significant roles in cancer development. (a) MiRNA sponge. MiRNA-binding sites and miRNA sponge. (b) Transcriptional regulators. EIciRNAs and ciRNAs, which are predominantly located in the nucleus, work as regulators of transcription. (c) Interaction with RBPs. CircRNAs with RBP-binding sites can regulate other RBPs in a way that resembles their impact on miRNA activities, namely as RBP sponges.

paid little attention to this nonlinear RNA. In recent years, more and more research has focused on circRNAs. Based on this, people have come to realize that circRNA might have many biological functions (Figure 2).<sup>17</sup>

## CircRNAs Can Act As miRNA Sponges

Most circRNAs are primarily localized in the cytoplasm,<sup>10,18</sup> and the results prompted researchers to study circRNA function in post-transcriptional regulation. MiRNAs can bind to their respective targets by bases paired with the 3'-untranslated region (3'-UTR) and act as a negative regulator of gene expression at the post-transcriptional level, thereby inhibiting protein translation.<sup>19</sup>

CircRNAs can bind miRNAs through a miRNA response element (MRE), which can act as a causative gene or a disease-promoting gene.<sup>10</sup> The first identified human circRNA acts as a miRNA sponge, and the most powerful evidence for sponge activity is the antisense cerebellar degeneration-associated protein 1 transcript (CDR1as). CDR1as was first identified as a sponge of miR-7 in zebrafish neuron tissue, leading to midbrain developmental damage.<sup>20</sup> Recent studies have shown that miR-7 plays an important role in the development and progression of cancer, respectively, and CDR1as as miR-7 sponge is important for all types of cancer. For example, the CDR1as/miR-7 signal axis may be a molecular target for the treatment of osteosarcoma.<sup>21</sup>

CDR1as may be a promising biomarker for hepatic microvascular invasion and a novel therapeutic target for inhibition of hepatocellular carcinoma (HCC) microvascular invasion.<sup>22</sup>

## CircRNAs Can Function As Transcription Modulators

Recent studies have shown that circRNAs can act as a transcriptional regulator.<sup>23,24</sup> For example, the intron circRNA ci-Ankyrin repeat domain 52 (ci-ankrd52) has been found to be enriched at its transcriptional site. Ci-ankrd52 may regulate its parental gene expression by modulating the prolonged activity of RNA polymerase II.<sup>21</sup> The mechanism of action indicates that the circular intron transcripts exerts a new cis-regulatory effect on the expression of its parental coding gene. Further studies have shown that the EIciRNA-U1 small nuclear ribonucleoprotein (snRNP) complex is a special kind of circRNA, which may accelerate the expression of parental genes through RNA-RNA interaction, and complex with Pol II transcription on the parental gene promoter,<sup>24</sup> as Ng, W. L et al reviewed.<sup>25</sup>

## CircRNAs Can Interact With RBPs

RNA-binding proteins (RBPs) are a rich class of proteins involved in gene transcription and translation, and the basic elemental functions of circRNA, including occurrence, translation, target gene transcriptional regulation, and extracellular transport function through interaction with RBP.<sup>26</sup> In addition, RBP can interact with circRNA and participate in splicing, processing, folding, stabilization, and localization of circRNA.<sup>27</sup> For example, Dudekula et al uses a network tool called CircInteractome to identify has\_circ\_0000020 with multiple RBPs in the flanking sequence.<sup>28</sup> The binding sites are on either side of the body sequence at a much higher frequency than the body sequences used to target the circRNA. This finding suggests that RBP tends to bind to the has\_circ\_0000020 intersection. Recent studies have shown that circRNAs can focus on specific components via RBP sponges, RBP assembly platforms and supertransporters, thereby competitively binding RBP, regulating RBP function and interacting with RBP.<sup>29,30</sup>

## The Associations Between Star circRNAs And A Wide Range Of Diseases

By reference to previous circRNA-related literature, we have found that some circRNAs are involved in the development and progression of many diseases, and we call these circRNAs often appear in the literature as star circRNAs. We believe that by studying and analyzing star circRNA in cancer, we can explore the complete mechanism of circRNA-mediated cancer and use this mechanism to study whether circRNAs can develop into a clinically directed new tumor marker or tumor therapeutic target. Therefore, this article lists the eight most widely involved circRNA molecules in recent studies and briefly describes their function and related mechanisms in disease progression and progression, as well as the corresponding circRNAs as biomarkers or therapeutic targets. There are two broad categories between circRNAs and cancers: identifying potential biomarkers for cancer diagnosis by detecting circRNAs expression patterns and demonstrating the regulatory role of circRNAs in cancer development (Table 1).

It is worth mentioning that there are many reasons for circRNA disorders in cancer, such as abnormal cis-elements, abnormal chromosomes and genomes, abnormal transcription, abnormal splice machinery and abnormal trans-acting factors. In addition, there are two hypothetical mechanisms for epigenetic aberrations involving circulator dysregulation: chromatin remodeling factors and post-translational modifications of histones affect transcription rate,<sup>31</sup> and chromatin remodeling affects alternative splicing involving circRNAs biogenesis,<sup>4</sup> as Wu et al previously commented on.<sup>15</sup>

## Cerebellar Degeneration-Related Protein I Transcript Antisense RNA (CDR1as)

Hsa\_circ\_0001946, also known as CDR1as, is located at chrX: 139865339–139866824 with a total length of 1485. This gene represents naturally occurring RNA transcribed antisense with CDR1 (cerebellar degeneration associated protein 1, 34 kDa; GeneID: 1038), some of which may be circular rather than linear. Antisense circRNAs bind to miRNAs such as miR-7, acting as a sponge for these molecules and preventing them from interacting with target transcripts. The circRNA produced by this locus is down-regulated by miR-671, which also reduces the level of CDR1 transcript.

CDR1as is a circRNA molecule associated with the occurrence of various cancers and diseases. For instance, Xu B et al found that the CDR1as acting as miR-7 sponge could be the

**Table 1** A Summary Of Cancer Related circRNAs

| Cancer Type And Symbol          | Expression In Tumors | Function                | Related Mechanisms  | References |
|---------------------------------|----------------------|-------------------------|---|------------|
| <b>Osteosarcoma</b>             |                      |                         |   |            |
| circ-TADA2A                     | Up                   | Tumor promoter          | Promoting osteosarcoma progression and metastasis by sponging miR-203a-3p   | 73         |
| hsa_circ_0000502                | Up                   | Tumor promoter          | Oncogenic functions of circ_0000502 is partially dependent on its regulation of miR-1238.   | 74         |
| CDR1as                          | Up                   | Tumor promoter          | Promoting tumor growth of osteosarcoma by sponging miR-7  | 21         |
| circ-HIPK3                      | Down                 | Tumor suppressor        | –   | 41         |
| hsa_circ_0103801                | Up                   | Tumor promoter          | Promoting the incidence and development of osteocarcoma by suppressing miR-338-3p activity  | 61         |
| hsa_circ_0104980                | Down                 | –                       | –   | 61         |
| hsa_circ_0007534                | Up                   | Tumor promoter          | Affecting AKT/GSK-3 $\beta$ signaling pathway   | 66         |
| circ-UBAP2                      | Up                   | Tumor promoter          | Acting as a sponge of miR-143 to promote osteosarcoma progression   | 70         |
| <b>Cholangiocarcinoma</b>       |                      |                         |   |            |
| CDR1as                          | Up                   | –                       | –   | 32         |
| hsa_circ_0001649                | Down                 | Tumor suppressor        | hsa_circ_0001649 overexpression caused tumor suppressive effects via inhibiting cell proliferation, migration and invasion; inducing cell apoptosis in KMBC and Huh-28 cells  | 49         |
| hsa_circ_0005230                | Up                   | tumor promoter          | Directly sponging miR-1238 and miR-1299 to exert its oncogenic functions.   | 75         |
| <b>Hepatocellular carcinoma</b> |                      |                         |   |            |
| CDR1as                          | Up                   | Tumor promoter          | Exerting function by sponging miR-7   | 33         |
| hsa_circ_0001649                | Down                 | Tumor suppressor        | –   | 48         |
| hsa_circ_0067934                | Up                   | Tumor promoter          | circ_0067934/miR-1324/FZD5/ $\beta$ -catenin signaling axis   | 57         |
| hsa_circ_0103809                | Down                 | Tumor suppressor        | Suppressing HCC proliferation and invasion by sponging miR-620  | 62         |
|                                 | Up                   | Tumor promoter          | miR-490-5p/SOX2 signaling pathway   | 63         |
| hsa_circ_0000567                | Down                 | Tumor suppressor        | Exerting function by sponging miR-421   | 76         |
| <b>Nasopharyngeal carcinoma</b> |                      |                         |   |            |
| hsa_circ_0000285                | Up                   | Tumor promoter          | Sponging miR-124 further target STAT3   | 38         |
| hsa_circ_0000543                | Up                   | Sensitization knockdown | Knockdown sensitized NPC cells by targeting miR-9/platelet-derived growth factor receptor B (PDGFRB) axis.  | 77         |
| <b>Glioma</b>                   |                      |                         |   |            |
| circ-HIPK3                      | Up                   | Tumor promoter          | Promoting glioma progression by regulating miR-654/IGF2BP3 signaling  | 39         |
| circ-ITCH                       | Down                 | Tumor suppressor        | circ-ITCH plays an anti-oncogenic role through sponging miR-214 and regulating ITCH-Wnt/ $\beta$ -catenin pathway   | 44         |
| hsa_circ_0007534                | Up                   | Tumor promoter          | Serveing as an oncogene in glioma via promoting ZIC5 expression by repressing miR-761 availability  | 67         |
| Circ-SHPRH                      | Down                 | Tumor suppressor        | SHPRH-146aa generated from overlapping genetic codes of circ-SHPRH, SHPRH-146aa protects full-length SHPRH from degradation by the ubiquitin proteasome. Stabilized SHPRH sequentially ubiquitinates proliferating cell nuclear antigen (PCNA) as an E3 ligase, leading to inhibited cell proliferation and tumorigenicity. | 47         |
| hsa_circ_0008344                | Up                   | Tumor promoter          | hsa_circ_0008344 can sponge tumor suppressor miRNAs like miR-433-3p   | 69         |

(Continued)

Table 1 (Continued).

| Cancer Type And Symbol                       | Expression In Tumors | Function           | Related Mechanisms  | References |
|--|----------------------|--------------------|---|------------|
| hsa_circ_0014359                             | Up                   | Tumor promoter     | hsa_circ-0014359 promotes glioma progression via targeting miR-153/PI3K signaling pathway   | 79         |
| hsa_circ_0001946                             | Down                 | Tumor suppressor   | hsa_circ_0001946 inhibited GBM growth through circ_0001946/miR-671-5p/CDR1 pathway  | 80         |
| hsa_circ_0034642                             | Up                   | Tumor promoter     | The oncogenic function of hsa_circ_0034642 is partly attributed to its modulation on miR-1205/BATF3 axis.   | 81         |
| hsa_circ_0076248                             | up                   | tumor promoter     | hsa_circ_0076248 promote glioma growth and invasion via sponging miR-181a, which downregulates the SIRT1 expression.                                    | 82         |
| <b>Gallbladder Cancer</b><br>circ-HIPK3      | Up                   | Tumor promoter     | circHIPK3 promotes gallbladder cancer cell growth possibly by sponging miR-124.   | 40         |
| <b>Gastric cancer</b><br>hsa_circ_0000199    | Up                   | Promote resistance | Promoting PIK3R1 expression by sponging miR-198, thus enhance cisplatin resistance.   | 83         |
| Circ-DONSON                                  | Up                   | Tumor promoter     | Promoting GC progression through recruiting the NURF complex to initiate SOX4 expression.   | 84         |
| hsa_circ_0001368                             | Down                 | Tumor suppressor   | Playing a tumor-suppression role in GC via the miR-6506-5p/FOXO3 axis.  | 85         |
| circ-PSMC3                                   | Down                 | Tumor suppressor   | Acting as a competitive endogenous RNA through sponging miR-296-5p to suppresses the proliferation and metastasis of gastric cancer.                    | 86         |
| circ-NRIP1                                   | Up                   | Tumor promoter     | Acting as a miR-149-5p sponge to promote gastric cancer progression via the AKT1/mTOR pathway.  | 87         |
| hsa_circ_0067997                             | Up                   | Oncogene           | An oncogene in GC by regulating miR-515-5p/XIAP axis.   | 88         |
| <b>Breast Cancer</b><br>circ-ITCH            | Down                 | Tumor suppressor   | Acting as a sponge for miR-214 and miR-17 to increase expression of its ITCH linear isoform, thereby inactivating Wnt/ $\beta$ -catenin signaling.      | 42         |
| circ-UABP2                                   | Up                   | Tumor promoter     | Playing a vital regulatory role in TNBC via the miR-661/MTA1 axis   | 71         |
| hsa_circ_0007534                             | Up                   | Oncogene           | Acting as a miR-593 sponge to promote MUC19 expression  | 64         |
| circ-TADA2As                                 | down                 | tumor suppressor   | preferentially acting as a miR-203a-3p sponge to restore the expression of miRNA target gene SOCS3, resulting in a less aggressive oncogenic phenotype. | 89         |
| circ-KIF4A                                   | Up                   | Tumor promoter     | The circKIF4A-miR-375-KIF4A axis regulates TNBC progression via the competitive endogenous RNA (ceRNA) mechanism.                                       | 90         |
| circ-AGFG1                                   | Up                   | Tumor promoter     | circAGFG1 promotes TNBC progression through circAGFG1/miR-195-5p/CCNE1 axis.  | 91         |
| <b>Papillary thyroid cancer</b><br>circ-ITCH | down                 | tumor suppressor   | circ-ITCH/miR-22-3p/CBL/ $\beta$ -catenin signaling pathway   | 43         |
| circ-RAPGEF5                                 | Up                   | Tumor promoter     | circRAPGEF5 acts as a tumor promoter via a novel circRAPGEF5/miR-198/FGFR1 axis.  | 92         |
| hsa_circ_0067934                             | Up                   | Tumor promoter     | hsa_circ_0067934 could improve the development of thyroid carcinoma by promoting EMT and PI3K/AKT signaling pathways.                                   | 53         |

(Continued)

Table 1 (Continued).

| Cancer Type And Symbol             | Expression In Tumors | Function         | Related Mechanisms  | References |
|------------------------------------|----------------------|------------------|---|------------|
| hsa_circ_0025033                   | Up                   | Oncogene         | hsa_circ_0025033/miR-1231/miR-1304 axis involved in PTC initiation and progression.   | 93         |
| <b>Bladder Cancer</b>              |                      |                  |   |            |
| circ-ITCH                          | Down                 | Tumor suppressor | Acting as a tumor suppressor by a novel circ-ITCH/miR-17, miR-224/p21, PTEN axis.   | 45         |
| hsa_circ_0001429                   | Up                   | Tumor promoter   | Targeting at miR-205-5p to regulate VEGFA and promote the development of bladder cancer.  | 94         |
| hsa_circ_0087960                   | Down                 | Tumor suppressor | Binding to miR-762 and inhibit its activity as a miRNA sponge.  | 95         |
| circ-cTFRC                         | up                   | tumor promoter   | acting as a competing endogenous RNA (ceRNA) for miR-107 to regulate TFRC expression.   | 96         |
| circ-MTO1                          | Down                 | Tumor suppressor | Sponging miR-221 and overexpression of circMTO1 negatively regulated the E-cadherin/N-cadherin pathway to inhibit bladder cancer cells' EMT by competing for miR-221. | 97         |
| <b>Ovarian Cancer</b>              |                      |                  |   |            |
| circ-ITCH                          | Down                 | Tumor suppressor | Acting as a ceRNA to sponge miR-145, increases the level of RASA1, and inhibits the malignant progression of OC cells via the circ-ITCH-miR-145-RASA1 axis            | 46         |
| <b>Retinoblastoma</b>              |                      |                  |   |            |
| hsa_circ_0001649                   | Down                 | Tumor suppressor | Regulating cell proliferation and apoptosis via AKT/mTOR signaling pathway.   | 50         |
| Esophageal squamous cell carcinoma |                      |                  |   |            |
| circ-PRKCI                         | Up                   | Tumor promoter   | Playing an important role in esophageal squamous cell carcinoma thorough circ-PRKCI/miR-3680- 3p/AKT3 regulatory network.   | 51         |
| hsa_circ_0067934                   | Up                   | Tumor promoter   | –   | 52         |
| hsa_circ_0000337                   | Up                   | Tumor promoter   | Binding to miR-670-5p, a ncRNA involved in carcinogenesis.  | 98         |
| <b>Cervical Cancer</b>             |                      |                  |   |            |
| hsa_circ_0067934                   | Up                   | Tumor promoter   | Promoteing CC progression via miR-545/EIF3C axis.   | 54         |
| circ-EIF4G2                        | Up                   | Tumor promoter   | Promoting cell proliferation and migration via the miR-218/HOXA1 pathway.   | 99         |
| hsa_circ_0101996                   | Up                   | Tumor promoter   | hsa_circRNA_101996-miR-8075-TPX2 network promoted cervical cancer progression.  | 100        |
| hsa_circ_0000263                   | Up                   | Tumor promoter   | hsa_circ_0000263/miR-150-5p/MDM4/p53 regulatory network   | 101        |
| circ-RNA8924                       | Up                   | Tumor promoter   | regulating CBX8 by competitively binding to miR-518d-5p/519-5p.   | 102        |
| <b>Lung Cancer</b>                 |                      |                  |   |            |
| hsa_circ_0067934                   | Up                   | Oncogene         | Exhibiting its anti-cancer role by modulating EMT progression.  | 55         |
| hsa_circ_0103809                   | Up                   | Tumor promoter   | hsa_circRNA_103809/miR-4302/ZNF121/MYC regulatory signaling pathway promote lung cancer cell proliferation and invasion.  | 56         |
| circ-UBAP2                         | Up                   | Oncogene         | inhibiting the growth and invasion of lung cancer cells in vitro and induce cell cycle arrest and apoptosis.  | 58         |
|                                    |                      |                  |   | 72         |

(Continued)



Table 1 (Continued).

| Cancer Type And Symbol   | Expression In Tumors | Function         | Related Mechanisms   | References |
|--------------------------|----------------------|------------------|--|------------|
| circ-FOXMI               | Up                   | Tumor promoter   | circ-FOXMI upregulated the level of pancreatic progenitor cell differentiation and proliferation factor (PPDPF) and metastasis-associated in colon cancer 1 (MACC1) by sponging miR-1304-5p, increasing the proliferation and invasion of NSCLC cells. | 103        |
| hsa_circ_0003645         | Up                   | Tumor promoter   | hsa_circ_0003645 acted as a ceRNA to sponge miR-1179, which resulted in the elevation of TMEM14A expression and facilitated cell progression.  | 104        |
| <b>Colorectal Cancer</b> |                      |                  |  |            |
| hsa_circ_0103809         | Down                 | Tumor suppressor | Participating in the regulation of biological functions through the miR-532e3P/FOXO4 axis in the CRC.  | 59         |
| hsa_circ_0007534         | Down                 | Tumor suppressor | –  | 60         |
| hsa_circ_0104916         | Up                   | Tumor promoter   | –  | 65         |
| hsa_circ_0104916         | Down                 | Tumor suppressor | Suppressing migration and invasion of tumor cells by inhibiting the epithelial-mesenchymal transition.   | 105        |
| hsa_circ_0006990         | Up                   | Tumor promoter   | Potentially binding to hsa-miR-101-3p (miR-101) associated with the colorectal cancer pathway.   | 106        |
| <b>Pancreatic Cancer</b> |                      |                  |  |            |
| hsa_circ_0007534         | Up                   | Tumor promoter   | Oncogenic functions of circ_0007534 is partly dependent on its regulation of miR-625 and miR-892b.   | 68         |
| CDR1as                   | Up                   | Tumor promoter   | Playing an oncogene role in PDAC, partly by targeting miR-7 and regulating the EGFR/STAT3 signaling pathway.   | 107        |
| hsa_circ_0030235         | Up                   | Tumor promoter   | Oncogenic properties of circ_0030235 was partly dependent on its suppression on miR-1253 and miR-1294.   | 108        |
| circ-RHOT1               | Up                   | Tumor promoter   | Playing a role in pancreatic cancer through binding miR-26b, miR-125a, miR-330 and miR-382 to regulate multiple tumor-associated pathways.   | 109        |

molecular target for the treatment of osteosarcoma;<sup>21</sup> Jiang XM et al suggested that cCDR1as may serve as a potential vicious molecular biomarker to predict the aggressive tumor progression and worse prognosis for Cholangiocarcinoma (CCA) patients;<sup>32</sup> Xu LL et al reported that CDR1as may be a promising biomarker of hepatic microvascular invasion and a novel therapy target for restraining microvascular invasion in HCC.<sup>33</sup> In addition, the interaction between CDR1as and miR-7 has also been investigated in many non-tumor diseases. Xu HY et al revealed the effects of the strongly interacting pair of Cdr1as/miR-7 on insulin secretion;<sup>34</sup> Li XB et al demonstrated that CDR1as acts as a miR-7 inhibitor, triggering the upregulation of GDF5 and subsequent Smad1/5/8 and p38 MAPK phosphorylation to promote osteogenic differentiation of periodontal ligament stem cells;<sup>35</sup> and Yao WX et al indicated that the interaction between miR-7 and circRNA CDR1as may exert important functions and provide potential therapeutic

targets in lung fibrotic diseases.<sup>36</sup> Recent studies have shown that CDR1as can exert anti-oncogenic functions in bladder cancer by sponging miR-135a.<sup>37</sup>

### Homeodomain Interacting Protein Kinase 3 (HIPK3)

The parental gene of circHIPK3 is located at 11p13 and contains a total of 19 exons. The gene HIPK3 is ubiquitous in fat (RPKM 29.7), gallbladder (RPKM 21.4) and 25 other tissues. HIPK3 is a protein-coding gene. Gene ontology (GO) annotations associated with this gene include transferase activity, transfer of phosphorus-containing groups, and protein tyrosine kinase activity.

Circ-HIPK3 is transcribed by the gene HIPK3 and is involved in tumorigenesis, invasion or metastasis of many cancers. At the same time, circ-HIPK3 may be a biomarker or therapeutic target for many cancers. Shuai MX et al

indicated that circRNA\_0000285(circ-HIPK3) may be a novel biomarker for nasopharyngeal carcinoma(NPC) and is involved in NPC radiosensitivity;<sup>38</sup> Jin PC et al demonstrated that circ-HIPK3 contributes to glioma progression through targeting miR-654 from IGF2BP3 and implied circ-HIPK3 might be a potential target for glioma therapy;<sup>39</sup> Kai D et al concluded that circHIPK3 promotes gallbladder cancer cell growth possibly by sponging miR-124 and the over-expressed circ-HIPK3 could be a novel therapeutic target and diagnosis marker of human gallbladder cancer;<sup>40</sup> Ma XL et al suggested that circ-HIPK3 may become a novel potential biomarker for diagnosis and treatment target of osteosarcoma.<sup>41</sup>

### Itchy E3 Ubiquitin Protein Ligase (ITCH)

The coding gene for circ-ITCH is located at 20q11.22 and contains 31 exons. Gene ICTH is ubiquitously expressed in testis (RPKM 12.7), esophagus (RPKM 11.6) and 25 other tissues. The gene encodes a member of the Nedd4 family of the HECT structural domain E3 ubiquitin ligase. HECT domain E3 times in protein ligase transfers the ubiquitin from E2 times in protein conjugate to protein substrate, so as to target specific proteins for lysosomal degradation. Mutations in this gene are the cause of multiple autoimmune syndromes. A variety of spliced transcripts of the same type encoding this gene have been observed.

Circ-ITCH acts primarily as a miRNA sponge that affects the Wnt/ $\beta$ -catenin signaling pathway and may also affect other signaling pathways. Wang ST et al found that circ-ITCH acts as a sponge of miR-214 and miR-17, increasing the expression of its ITCH linear isoform, thereby inactivating the Wnt/ $\beta$ -catenin signal, thereby showed that circ-ITCH is a tumor suppressor, a promising prognostic biomarker in triple-negative breast cancer (TNBC) and that its restoration could well be a successful strategy in TNBC;<sup>42</sup> Wang MN et al revealed a novel signaling pathway of circ-ITCH/miR-22-3p/CBL/ $\beta$ -catenin involved in papillary thyroid cancer (PTC) development and progression;<sup>43</sup> Li F et al suggested that circ-ITCH is a tumor-suppressor gene in glioma and may serve as a promising prognostic biomarker for glioma patients by sponging miR-214 and regulating ITCH-Wnt/ $\beta$ -catenin pathway;<sup>44</sup> Yang CD et al concluded that circ-ITCH acts as a tumor suppressor by a novel circ-ITCH/miR-17, miR-224/p21, PTEN axis, which may provide a potential biomarker and therapeutic target for the management of bladder cancer.<sup>45</sup> Hu JH et al provided a novel

tumor suppressive role regarding circ-ITCH function in the malignant progression of ovarian cancer through targeting miR-145/RASA1 signaling.<sup>46</sup>

### SNF2 Histone Linker PHD RING Helicase (SHPRH)

The coding gene for circ-SHPRH is located at 6q24.3 and contains a total of 37 exons. The SHPRH gene is present in the ovary (RPKM 1.7), thyroid (RPKM 1.5) and 25 other tissues. SHPRH is a ubiquitously expressed protein containing motifs of several DNA repair proteins, transcription factors and helicases. SHPRH is a functional homolog of Rad5.<sup>78</sup>

Recent studies indicated that circ-SHPRH could be seen as biomarkers and therapeutic targets in many cancers. Zhang ML et al discovered that a novel protein SHPRH-146aa generated from overlapping genetic codes of circ-SHPRH is a tumor suppressor in human glioblastoma;<sup>47</sup> Qin ML et al indicated that hsa\_circ\_0001649 (circ-SHPRH) might serve as a novel potential biomarker for HCC and may function in tumorigenesis and metastasis of HCC;<sup>48</sup> Xu Y et al suggested that hsa\_circ\_0001649 might be a rational CCA-related therapeutic target based on its overexpression caused tumor suppressive effects via inhibiting cell proliferation, migration and invasion, inducing cell apoptosis in KMBC and Huh-28 cells;<sup>49</sup> Xing LC et al reported that circ-SHPRH might be a potentially useful prognostic biomarker and therapeutic target for Retinoblastoma via affect AKT/mTOR signaling pathway.<sup>50</sup>

### Protein Kinase C Iota (PRKCI)

The coding gene for circPRKCI is located at 3q26.2 and contains 18 exons. The gene PRKCI is ubiquitously expressed in the stomach (RPKM 19.1), thyroid (RPKM 17.9) and other 24 tissues. This gene encodes serine/threonine protein kinase as a member of the protein kinase C (PKC) family. The PKC family contains at least 8 members that are differentially expressed and involved in various cellular processes. This kinase can be recruited into vesicular tubular clusters (VTC) through direct interaction with small gtpase RAB2, which plays a role in tubular kinetics by phosphorylating glyceraldehyde 3-phosphodehydrogenase (GAPD/GAPDH) and microRNA in the early secretory pathway.

Shi NM et al and Xia WJ et al revealed that circ-PRKCI plays an important role in esophageal squamous



cell carcinoma (ESCC) by affecting miR-3680-3p thus regulated AKT3 expression and that provide new insights into the pathogenesis of ESCC;<sup>21,52</sup> Wang HH et al concluded that circ\_0067934(circ-PRKCI) could improve the development of thyroid carcinoma by promoting epithelial-mesenchymal-transition (EMT) and PI3K/AKT signaling pathways;<sup>53</sup> Hu CJ et al revealed that circ-PRKCI promotes cervical cancer progression via miR-545/EIF3C axis;<sup>54</sup> Zou Q et al and Wang J et al indicated that circ-PRKCI may be a predictive marker for the prognosis of non-small cell lung cancer (NSCLC) and a target for the treatment of the disease;<sup>55,56</sup> Zhu Q et al summarized that the circ-PRKCI/miR-1324/FZD5/ $\beta$ -catenin signaling axis might serve as a promising therapeutic target for HCC intervention.<sup>57</sup>

### Adaptor Related Protein Complex 4 Subunit Epsilon I (AP4EI)

The coding gene for circAP4EI is located at 15q21.2 and contains a total of 23 exons. The gene AP4EI is present in lymph nodes (RPKM 2.9), testes (RPKM 2.9) and 25 other tissues. The gene encodes members of the large subunit protein family of the linker complex. These proteins are components of the cohesive protein complex and play an important role in the secretory and endocytic pathways by mediating vesicular formation and the sorting of integrative membrane proteins.

Liu W et al illustrated a novel hsa\_circRNA\_103809 (circ-AP4EI/miR-4302/ZNF121/MYC regulatory signaling pathway promotes lung cancer progression;<sup>58</sup> Bian LJ et al and Zhang PL et al indicated that circ-AP4EI may be a potential novel gene target for the diagnosis and treatment of colorectal cancer (CRC) by participating in the regulation of biological functions through the miR-532-3P/FOXO4 axis;<sup>59,60</sup> Liu WH et al indicated that circRNAs may serve as biomarkers of osteosarcoma diagnosis and treatment;<sup>61</sup> Li X et al and Cai HJ et al concluded that circ-AP4EI may serve as a potential biomarker and novel therapeutic target of HCC by binding to miR-620 and inhibiting the tumorigenicity of HCC,<sup>62</sup> and facilitating HCC malignant progression by regulating miR-490-5p/SOX2 signaling pathway.<sup>63</sup>

### DEAD-Box Helicase 42 (DDX42)

The coding gene for circ-DDX42 is located at 17q23.3 and contains a total of 20 exons. The gene DDX42 is ubiquitously expressed in testis (RPKM 27.4), ovary (RPKM

25.5) and 25 other tissues. The gene encodes a member of the Asp-Glu-Ala-Asp (DEAD) casein family. Members of this protein family are presumed RNA helicases and are involved in cellular processes involved in RNA secondary structural changes.

Song LL et al suggested an oncogenic role for hsa\_circ\_0007534 (circ-DDX42) in breast cancer by acting as a miR-593 sponge to promote MUC19 expression;<sup>64</sup> Zhang R et al concluded that circ-DDX42 plays a crucial role in the initiation and progression of CRC and may be a potential therapeutic target of CRC;<sup>65</sup> Li BQ et al summarized that circ-DDX42 may be a rational predictive marker and therapeutic target for osteosarcoma by affecting AKT/GSK-3 $\beta$  signaling pathway;<sup>66</sup> Li GF et al suggested that circ-DDX42/miR-761/ZIC5 axis might be a target for glioma treatment;<sup>67</sup> Hao LG et al illuminated a novel circRNA (circ-DDX42) that confers an oncogenic function in pancreatic ductal adenocarcinoma (PDAC) by sponging miR-625 and miR-892b.<sup>68</sup>

### Ubiquitin Associated Protein 2 (UBAP2)

The coding gene for circUBAP2 is located at 9q13.3 and contains a total of 30 exons. The gene UBAP2 is widely expressed in testis (RPKM 18.9), adrenal gland (RPKM 7.6) and other 25 tissues. The protein encoded by this gene contains a UBA (ubiquitin-associated) domain, which is characteristic of proteins that play a role in the ubiquitination pathway. This gene may be expressed in adrenal and lymphoid tissues.

Zhou JX et al concluded that hsa\_circ\_0008344(circ-UBAP2) is upregulated in glioblastoma and may contribute to the progression of this malignancy;<sup>69</sup> Zhang H et al suggested that circ-UBAP2 sponging miR-143 to promote osteosarcoma progression and implicate its potential in prognosis prediction and cancer therapy;<sup>70</sup> Wang ST et al revealed that circ-UBAP2 plays a vital regulatory role in TNBC via the miR-661/MTA1 axis and may serve as a promising therapeutic target for TNBC patients;<sup>71</sup> Yin YJ et al concluded that circ-UBAP2 exerts an important role in the proliferation and invasion of human lung cancer. Silencing of circUBAP2 might be a novel target for molecular targeted therapy of patients with lung cancer.<sup>72</sup>

### Conclusion And Perspective

In the past, researchers generally believed that circRNAs were splicing errors and that the intermediates were detached from the intron sleeve, so circRNAs were not considered to have important functions. In recent years,

with the rapid development of high-throughput sequencing, it has been found that circRNAs play an indispensable role in the occurrence and development of many diseases through biological functions such as miRNA sponge, protein binding molecules and transcriptional regulators. Due to the large number of circRNAs in blood and tissue samples, many scholars have pointed out that circRNAs are biomarkers for cancer screening, prognosis assessment, clinical diagnosis and cancer treatment goals. In the future, circRNAs have great potential in these areas.

However, studies on circRNAs in cancer recurrence and metastasis are still incomplete and require further exploration. Based on this state, rapid development of multiple displacement amplification (MDA), multiple annealing and cycle-based amplification cycles, MALBAC, single-cell sequencing and next-generation sequencing can greatly improve sequencing efficiency during the development phase. Accuracy helps identify new circRNAs and also helps researchers perform small sequence variation detection, individual cytogenetic differences, gene rearrangements, etc., which can help explain cancer recurrence, metastasis, and progression. At the same time, it opens up new ideas for studying various complex diseases and physiological processes from the single nucleotide level. Although many functions of circRNAs have been discovered and the number of circRNAs has some function, there are still thousands of circRNAs with unknown functions. Further studies of the biogenesis of circRNAs may be needed to discover more functions of circRNAs. Due to its classicity and high research maturity, most existing circRNA studies focus on the mechanism by which miRNAs adsorb miRNAs. In fact, although research in this area is not thorough enough, the ability of circRNAs to work by binding to DNA or proteins is also promising. In addition, circRNAs are different from linear RNA cleavage and deserves further study. For example, circus splicing abnormalities are a very good research direction under physiological and pathological conditions.

The ultimate goal of medical research is to provide services for clinical diagnosis and treatment. How to apply the research results of circRNAs to clinical practice requires more relevant research to support it, such as the design of molecularly targeted drugs for specific regions of circRNAs. Drug delivery and the discovery of circRNAs involved in the development of most cancers. The work of this review is to try to discover circRNAs that are involved in a variety of cancers. We hope that with the development

of biotechnology and basic research, we will be able to discover more circRNAs and more physiological and pathological circRNA functions, so that circRNAs can better serve clinical diagnosis and treatment.

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## Disclosure

The authors report no conflicts of interest in this work.

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