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Exploring the Diagnostic Potential of hsa-circRNA-001587 and hsa-circ-0004872 in Colorectal Cancer: A Population-Based Diagnostic Approach

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ABSTRACT

Background & Objective: Colorectal cancer contributes substantially to global cancer mortality, ranking among the leading causes of cancer-related deaths. Studies have linked its development to diminished expression of the SLC4A4 gene alongside elevated levels of the microRNAs hsa-miR-223-3p and hsa-miR-106a-5p. This study examines hsa-circRNA-001587 and hsa-circ-0004872 to determine their utility as population-based markers for colorectal cancer detection. By focusing on these circRNAs, the investigation aimed to contribute valuable insights into CRC diagnostics.

Materials & Methods: This investigation leveraged population-based data by retrieving thirty matched pairs of colorectal carcinomas and adjacent non-tumoral tissues from patients at Shahid Beheshti University of Medical Sciences and Valiasr Hospital in Birjand, Iran. Systematic patient recruitment, comprehensive data collection, and rigorous tissue sample procedures were employed. RNA extraction and analysis focused on hsa-circRNA-001587 and hsa-circ-0004872, with validation carried out through reverse transcription qPCR and Sanger sequencing.

Results: Our findings indicated that hsa-circRNA-001587 and hsa-circ-0004872 were reduced by 1.34-fold and 2.19-fold, respectively, in CRC specimens compared with matched adjacent non-tumorous tissues, although these differences did not reach statistical significance ($p > 0.05$). Furthermore, our statistical analysis demonstrated a robust and significant link between hsa-circ-0004872 and hsa-circRNA-001587, suggesting that an increase in one corresponds consistently with an increase in the other (p-value ≤ 0.001, $r = 0.81$).

Conclusion: Although the non-significant downregulation—likely reflecting our small sample size—suggests caution, hsa-circ-0004872 and hsa-circRNA-001587 probably act as tumor suppressors via the hsa-circ-0004872/hsa-circRNA-001587/hsa-miR-223-3p/hsa-miR-106a-5p/SLC4A4 axis, warranting further evaluation in serum and plasma as CRC diagnostic markers and therapeutic targets.

Keywords: Colorectal Cancer, Biomarker, hsa-circRNA-001587, hsa-circ-0004872

1. Introduction

Colorectal cancer (CRC) ranks as the third most frequently diagnosed malignancy and the third leading cause of cancer-related death worldwide (1, 2). Although prompt, multimodal treatment-encompassing radiotherapy and systemic chemotherapy-yields favorable initial responses, many patients still face substantial risks from tumor recurrence and the development of distant metastases (3). While extensive work has characterized key signaling networks and coding and non-coding RNAs in CRC, deeper insights into the molecular drivers of disease progression and the discovery of robust diagnostic and prognostic biomarkers remain essential (4, 5).

Non-coding RNAs(ncRNAs) account for a large share of the human transcriptome and span a spectrum of non-protein-coding molecules—from short microRNAs (miRNA) and extended noncoding transcripts (lncRNA) to covalently closed circular RNAs (CircRNA) (6). Recent estimates indicate that human cells harbor on the order of 1×10^5 unique circular RNA species (2, 7). CircRNAs are increasingly recognized as valuable diagnostic and prognostic markers across various cancers, correlating with tumor progression and patient outcomes. For example, CDR1as (commonly called CiRS-7) and a circular transcript derived from the ERBB2 locus have been implicated in distinct tumor types owing to their specific subcellular localization and roles in metastatic processes (8, 9). For instance, circLARP4 correlates with improved survival, whereas circUBAP2 predicts poorer outcomes, underscoring the varied functions of circRNAs (10, 11). Integrating circRNA patterns enhances predictive accuracy, as seen in risk stratification for patients with colon cancer and mantle-cell lymphoma, leading to more targeted therapeutic strategies (12).

CircRNAs are formed through a dynamic process involving different genomic regions, resulting in various lengths. Their formation involves circularizing elements such as exons, introns, and untranslated regions (13). CircRNAs may also derive from hybrid exon–intron transcripts. Their biogenesis can proceed via exon lariat back-splicing, complementary pairing of flanking introns, or mediation by specific RNA-binding proteins, giving rise to a diverse array of circular isoforms (Figure 1) (14). They exhibit a covalently closed topology that provides enhanced protection against exonuclease-mediated decay and extends their intracellular half-life compared with linear transcripts, thereby supporting sustained functional activity in cells (15).

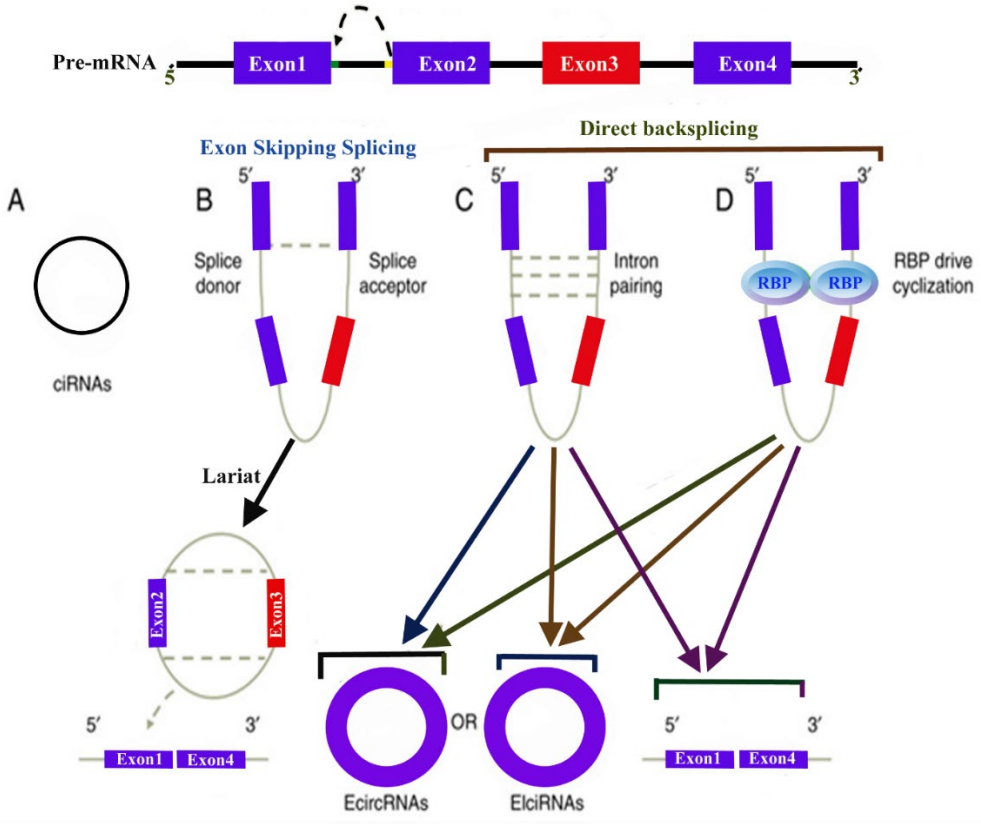

Figure 1. CircRNAs' mechanism for creating loops. CircRNA is also known as ciRNA, exon circRNAs, exon intron circRNAs, and RNA binding protein (RBP) (**Designed by Authors, 2025**).

CircRNAs also serve as specific biomarkers, significantly in disease detection and differentiation in cancers with tissue-specific characteristics (2, 16). circRNA expression profiles have been leveraged both to detect aggressive prostate tumors and to stratify distinct forms of mammary carcinoma and non–small-cell

pulmonary carcinoma (2, 16-18). Additionally, plasma-based assays can effectively distinguish hepatocellular carcinoma patients from healthy individuals, while the potential of exosomal circRNAs for early colorectal cancer detection is promising. Remarkably, circ0001785 has been reported to outperform standard biomarkers in both prognostic and diagnostic contexts for breast cancer. Likewise, circLDLRAD3 shows considerable potential for guiding diagnosis and prognosis in pancreatic neoplasms (19-21). Accumulating evidence underscores the central role of circRNAs in tumorigenesis—including colorectal cancer—where they influence gene expression via miRNA sponging, as seen with hsa-miR-224 in gastric malignancy and hsa-miR-223 in pancreatic tumors, thereby highlighting their value as markers of cancer development and clinical outcome.

By integrating computational predictions with laboratory validation, our earlier work revealed that downregulation of SLC4A4 may be instrumental in colorectal cancer development (22). Moreover, CRC tumor samples exhibited elevated expression of hsa-miR-223-3p and hsa-miR-106a-5p, which inversely corresponded to the reduced abundance of SLC4A4 mRNA (23).

We assessed hsa-circRNA-001587 and hsa-circ-0004872 as candidate biomarkers in colorectal cancer by quantifying their levels in paired tumor and adjacent non-tumorous tissues, guided by earlier evidence implicating SLC4A4 and hsa-miR-223 in CRC pathogenesis (23). Recent evidence indicates that hsa-circ-0004872 modulates miR-224 in gastric cancer (GC), whereas hsa-circRNA-001587 interacts with miR-223 in pancreatic cancer (PC), underscoring their roles in oncogenic signaling pathways (24, 25). This investigation characterizes these circRNAs to illuminate mechanisms underlying colorectal tumorigenesis and to explore their suitability for early disease screening and as candidates for precision therapy.

2. Materials and Methods

2.1 Patients and Clinical Tissue Samples

We obtained thirty paired colorectal tumor and adjacent non-tumorous specimens from patients sampled at the Gastroenterology and Liver Research Center of Shahid Beheshti University of Medical Sciences and Valiasr Hospital in Birjand. The study enrolled male and female patients with CRC who met the inclusion criteria of clinical confirmation by a physician and pathological and genetic assessments. Patients with underlying conditions such as autoimmune diseases, diabetes, cardiovascular diseases, and a history of chemotherapy or radiation therapy were excluded from sampling. Before inclusion, all participants provided signed consent following a full explanation of the study. Ethical clearance was obtained from the Birjand University of Medical Sciences Ethics Committee (approval no. IR.BUMS.REC.1400.319).

2.2 Isolation of Total RNA and Quantitative Reverse Transcription PCR (qRT-PCR)

Total RNA was isolated from tissue samples using TRIzol® Reagent (Invitrogen, Carlsbad, CA, USA) by the manufacturer's protocol. Subsequently, 1 µl of RNase R was added to 1 µg of each RNA sample (to separate circRNAs from linear RNAs) and incubated for 2 minutes at 37°C. The products were then identified by RT-qPCR. The isolated RNAs were converted into cDNA using the Yekta Tajhiz Azma kit (lot no: YT4500) according to the manufacturer's protocol, and qRT-PCR was conducted with the 2x Real-Time PCR Master Mix Green-high Rox (Amplicon). Beta-actin (B-actin) was an internal control, and the gene-relative expression levels were determined using the $2^{-\Delta\Delta Ct}$ formula. The primer sequences utilized in this research were:

For hsa-circ-0004872: Forward primer 5' GTTGGTACAGGGCTCCAGAA 3', Reverse primer 5' CAGGGTTCTCTGGCAGTAGG 3'.

- For hsa-circRNA-001587: Forward primer 5' CATTTATTGAAAACATGCGTGGC 3', Reverse primer 5' CACCAAGGCCGTTACCAAGTA 3'.
- For B-actin: Forward primer 5' CATGTACGTTGCTATCCAGGC 3', Reverse primer 5' CTCCTTAATGTCACGCACGAT 3'.

2.3 Statistical Analysis

All statistical analyses were carried out in SPSS version 16.0. Data distribution was first checked using the Shapiro–Wilk test. Because each CRC specimen was paired with its adjacent normal tissue, expression differences for hsa-circ-0004872 and hsa-circRNA-001587 were evaluated using a marginal model fitted by generalized estimating equations (GEE). Continuous variables are reported as mean ± standard deviation or median (interquartile range), and categorical variables are reported as counts (percentages). A two-sided p-value below 0.05 was considered indicative of statistical significance.

3. Results

3.1 Participant Demographics and GEE Assessment of circRNA Expression

Participants averaged 61.45 ± 11.48 years of age; 70 % were male, and 30 % had a family history of cancer. All tumors were adenocarcinomas, most frequently located in the rectum and cecum (55 %) and least in the transverse colon (20 %) (Table 1). Applying a marginal model with generalized estimating equations to paired samples, CRC tissues exhibited lower hsa-circ-0004872 expression ($\beta = -0.158$) and reduced hsa-circ-001587 expression ($\beta = -0.070$) compared with adjacent non-tumorous tissues.

3.2 Association of circRNA Levels with Patient Demographics

Chi-square analysis revealed no link between a family history of cancer and the abundance of hsa-circ-0004872 or hsa-circRNA-001587 (P = 0.78). By Mann–Whitney U test, male patients showed marginally higher levels of hsa-circ-0004872 (P = 0.78) and hsa-circRNA-001587 (P = 0.14) than females, but neither difference reached significance. Similarly, Kruskal–Wallis comparisons across tumor sites uncovered no meaningful variation in transcript levels. Pearson correlation indicated a non-significant inverse trend between age and the two circRNAs—hsa-circ-0004872 (r = –0.29, P = 0.39) and hsa-circRNA-001587 (r = –0.14, P = 0.56)—implying a slight decline with advancing age (Table 2). Notably, the two circRNAs were tightly co-regulated (r = 0.81, P ≤ 0.001), such that increases in one mirrored increase in the other (Figure 2A).

3.3 CircRNAs Expression Status by RT-qPCR

To evaluate the expression profiles of hsa-circ-0004872 and hsa-circRNA-001587 in CRC, RNA extracted from CRC tissues and adjacent normal tissues (considered as controls) was assessed using RT-qPCR. As demonstrated in Figure 2B, the expression level of hsa-circRNA-001587 decreased in tumor samples compared to control samples (1.34-fold down, p-value = 0.45). Additionally, a decrease in hsa-circ-0004872 expression was identified in tumor samples versus control samples (Figure 2C) (2.19-fold down, p-value = 0.54). Nonetheless, more extensive research involving larger sample sizes is necessary to confirm these findings (Table 3).

Table 1. Demographic information of patients.

Variable		n	%
Sex	Male	21	70
	Female	9	30
Family history CRC	Yes	6	30
Biopsy sample	Ascending colon	1	0.05
	Rectum and Cecum	11	0.55
	Descending colon	4	0.2
	Transverse colon	4	0.2

Table 2. The relationship between the expression of has-circ-0004872 and has-circ-001587 with demographic characteristics of patients.

Groups		has-circ-001587			has-circ-0004872		
		Mean ± SD	Median (IQR)	p-value	Mean ± SD	Median (IQR)	p-value
Family history	Yes	0.46 ± 0.3	0.38 (0.58)	0.78	0.83± 1.03	0.48(1.66)	0.78
	No	0.99 ±1.42	0.46(0.98)		0.86±1.17	0.41(0.78)	
Sex	Female	0.43 ±0.24	0.38 (0.5)	0.14	0.66 ± 0.8	0.39(0.56)	0.78
	Male	1.16 ±1.57	0.74(1.21)		0.99 ± 1.3	0.48(1.12)	
Location	Descending colon	0.2±0.28	0.2(0)	0.74	0.13±0.1	0.13(0)	0.53
	Rectum and Cecum	0.85± 1.24	0.26(0.95)		0.75± 1	0.41(0.84)	
	Transverse colon	0.72±0.38	0.66(0.74)		0.68±0.39	0.61(0.74)	

Table 3. Coefficient's estimation of marginal model of the effect of the disease on the expression of the has-circ-0004872 and has-circ-001587 genes.

Dependent variable	Parameter	Coefficients	Std. Error	Test statistics	*p*-value
has-circ-0004872	CRC (base line = control)	-0.158	0.1922	0.68	0.410
has-circ-001587	CRC (base line = control)	-0.070	0.2027	0.12	0.731

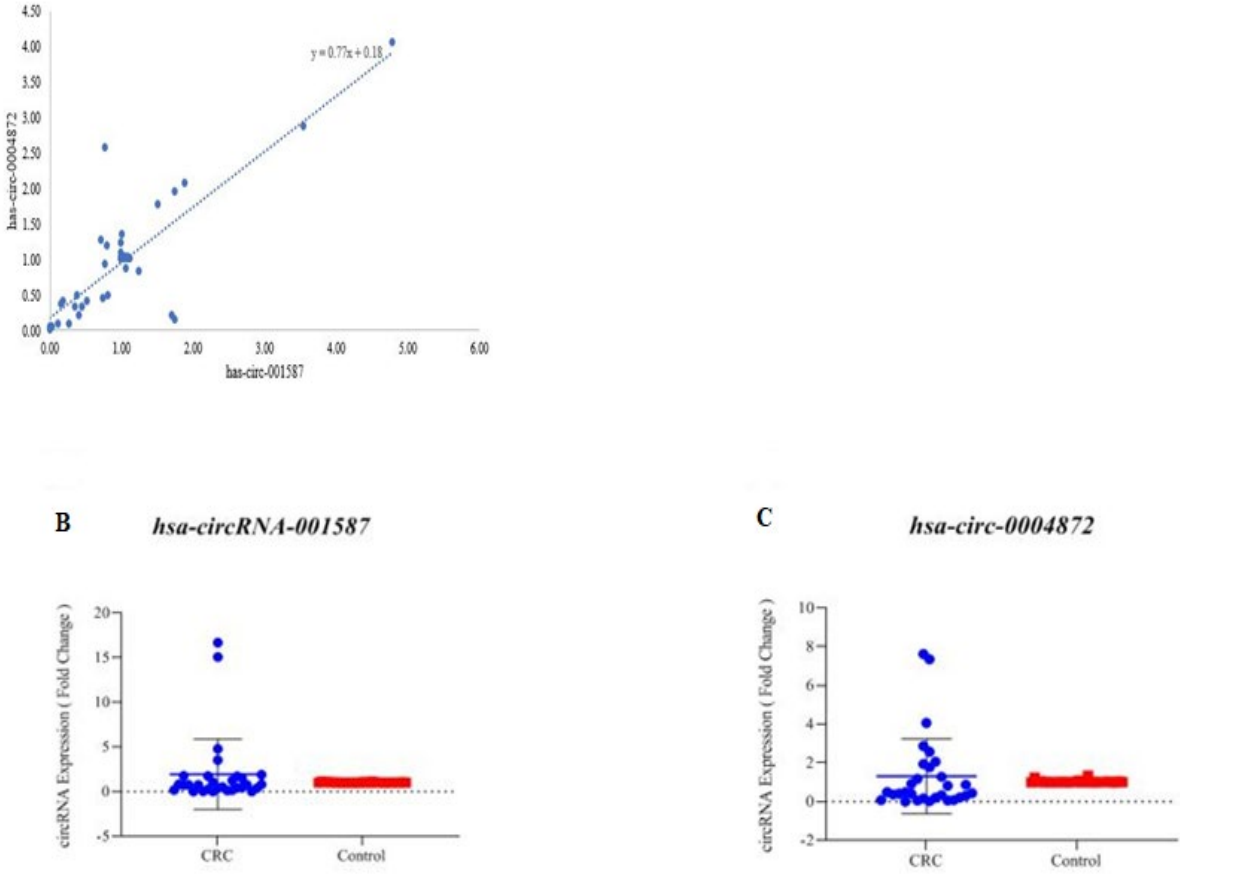

Figure 2. **(A)** a strong and statistically significant association between hsa-circ-0004872 and has-circ-001587 (P-value ≤ 0.001, r = 0.81). The data clearly illustrates that an increase in one of these factors consistently corresponds to an increase in the other, highlighting a robust relationship between the two. **(B & C)** RT-qPCR analysis of hsa-circ-0004872 and hsa-circRNA-001587 **(B & C)** expressions status. hsa-circRNA-001587 was downregulated in CRC tissues compared to normal adjacent tissues. hsa-circ-0004872 expression decreased in CRC tissues compared to normal adjacent tissues.

4. Discussion

Each year, approximately 700,000 people die from CRC, making it the fourth most lethal cancer globally (26). Moreover, recent epidemiological projections indicate that, within the next two decades, the annual global incidence of colorectal cancer may approach 3.2 million (27). Early detection of CRC enables effective treatment and significantly reduces the mortality rate (28). CircRNAs feature prominently across diverse human cancers, and accumulating evidence highlights their utility in CRC detection and outcome prediction (24). Comparative analyses in osteosarcoma, OSCC, lung cancer, hepatocellular carcinoma, glioma, gastric cancer, colorectal cancer, breast cancer, and bladder cancer have uncovered pronounced disparities in circRNA abundance between malignant lesions and their adjacent non-cancerous tissues (29-37).

Motivated by growing evidence that circRNAs act as biomarkers and drivers of colorectal cancer, this study profiles their abundance in paired tumor specimens and corresponding adjacent non-tumorous tissues.

In their 2020 study, Zhang and co-workers performed qRT-PCR to evaluate microRNA-223 and hsa-circRNA-001587 expression in pancreatic carcinoma specimens and corresponding cell culture models. Their results demonstrated that hsa-circRNA-

001587 curtailed pancreatic cancer cell motility, invasiveness, angiogenic capacity, and tumor-forming ability by disrupting the miR-223–mediated suppression of SLC4A4 (24). Recent work has shown that hsa-miR-223-3p functions as an oncogenic microRNA in renal cell carcinoma by downregulating the SLC4A4/KRAS signaling axis, thereby driving malignant progression (38). Barbagallo et al (39) reported that pancreatic cancer patients exhibited significantly elevated miR-223 levels in blood, plasma, and serum compared with healthy controls, with a marked decline following tumor resection. These observations support miR-223 as a tumor-associated biomarker and suggest it may play a similar diagnostic and functional role in colorectal cancer, warranting further investigation (39).

In Iranian patients with CRC, our previous research has shown an upregulation of hsa-miR-223-3p expression and a decrease in SLC4A4 gene expression (23). Our findings on the regulatory interplay between hsa-circRNA-001587, miR-223, and SLC4A4 closely mirror the patterns described by Zhang et al (24). The present study investigated how much hsa-circRNA-001587 was expressed in CRC tissues and adjacent normal tissues. Our findings revealed that CRC tissues had lower levels of hsa-circRNA-001587 expression than normal adjacent tissues. Our findings imply that hsa-circRNA-001587, an upstream regulatory factor of hsa-miR-223-3p and the SLC4A4 gene, is down-regulated in CRC tissues, which causes hsa-miR-223-3p to be up-regulated. This, in turn, results in the downregulation of its target gene, SLC4A4, which is associated with malignancy and a decrease in overall patient survival (23).

On the other hand, we revealed a negative link between the two based on our statistical analysis of hsa-circ-0004872 expression in CRC tissues. Mirroring our findings, Dai et al (40) demonstrated that circ-0004872 is substantially reduced in OSCC specimens and cell lines. Restoring circ-0004872—thereby acting as a decoy for miR-424-5p-led to lower miR-424-5p levels, attenuated tumor cell growth, and glucose uptake, restricted invasive behavior, and promoted apoptotic cell death (40). Ma et al (25) found that hsa-circ-0004872 abundance was markedly lower in gastric carcinoma specimens than in the surrounding non-malignant mucosa. Both in vitro and in vivo, its expression prevented GC from proliferating, invading, and spreading. This circular RNA acted as a miR-224 sponge, increasing the expression of downstream targets of miR-224, including Smad4 and p21 (25). Moreover, Zhang et al (41) reported a pronounced upregulation of miR-224 in both colorectal tumor specimens and cell lines, a change associated with accelerated cell cycle progression, heightened invasive capacity, facilitation of distant spread, and simultaneous suppression of Smad4. These findings indicate that miR-224 reflects CRC cell behavior and serves as a prognostic indicator for patient relapse (41).

5. Conclusion

Our findings indicate a trend toward downregulating hsa-circRNA-001587 and hsa-circ-0004872 in CRC tissues compared to normal tissues; nevertheless, these differences fell short of statistical significance. While circRNAs appear to be involved in CRC pathogenesis, further studies with larger cohorts are necessary to establish their clinical relevance as biomarkers.

6. Declarations

6.1 Acknowledgments

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6.2 Ethical Considerations

The Birjand University of Medical Sciences Research Ethics Committee approved this study (IR.BUMS.REC.1400.319). Before any procedures, participants were fully informed of the study aims and methods and provided written agreement. All research activities were conducted by the ethical principles outlined in the Declaration of Helsinki.

6.3 Authors' Contributions

M. Siami-Aliabad: conceptualization, methodology, writing (original draft), editing, sample collection; N. Moradi: methodology, conceptualization; T. Tavakoli: patient care, clinical data, sample collection; F. Salmani: data management, interpretation, statistical analysis; J. Ranjbaran: sample collection, clinical data acquisition; H. Safarpour: methodology, clinical data acquisition; E. Chamani: project administration, writing (original draft), editing, materials provision. All authors approved the final manuscript.

6.4 Conflict of Interest

The authors have no conflict of interest.

6.5 Fund or Financial Support

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6.6 Using Artificial Intelligence Tools (AI Tools)

The authors were not utilized AI Tools.

6.7 Availability of Data and Material

All datasets generated and analyzed during the current study are included in this published article.

Additional supporting data can be obtained from the corresponding author upon reasonable request.

References

1. Siegel RL, Wagle NS, Cercek A, Smith RA, Jemal A. Colorectal cancer statistics, 2023. CA Cancer J Clin. 2023;73(3):233-54. [DOI:10.3322/caac.21772] [PMID]
2. Pisignano G, Michael DC, Visal TH, Pirlog R, Ladomery M, Calin GA. Going circular: history, present, and future of circRNAs in cancer. Oncogene. 2023;42(38):2783-800. [PMCID] [DOI:10.1038/s41388-023-02780-w] [PMID]
3. Aljama S, Lago EP, Zafra O, Sierra J, Simón D, Santos C, et al. Dichotomous colorectal cancer behaviour. Crit Rev Oncol Hematol. 2023;189: 104067. [PMID] [DOI:10.1016/j.critrevonc.2023.104067]
4. Farc O, Budisan L, Berindan-Neagoe I, Braicu C, Zanoaga O, Zaharie F, et al. A Group of Tumor-Suppressive micro-RNAs Changes Expression Coordinately in Colon Cancer. Curr Issues Mol Biol. 2023;45(2):975-89. [DOI:10.3390/cimb45020063] [PMID] [PMCID]
5. Zhu X, Jin X, Li Z, Chen X, Zhao J. miR-152-3p facilitates cell adhesion and hepatic metastases in colorectal cancer via targeting AQP11. Pathol Res Pract. 2023;244:154389. [DOI:10.1016/j.prp.2023.154389] [PMID]
6. Zhang X, Xie K, Zhou H, Wu Y, Li C, Liu Y, et al. Role of non-coding RNAs and RNA modifiers in cancer therapy resistance. Mol Cancer. 2020; 19(1):47. [DOI:10.1186/s12943-020-01171-z] [PMID] [PMCID]
7. Babin L, Andraos E, Fuchs S, Pyronnet S, Brunet E, Meggetto F. From circRNAs to fusion circRNAs in hematological malignancies. JCI Insight. 2021;6(21):e151513. [PMCID] [PMID] [DOI:10.1172/jci.insight.151513]
8. Dawoud A, Ihab Zakaria Z, Hisham Rashwan H, Braoudaki M, Youness RA. Circular RNAs: New layer of complexity evading breast cancer heterogeneity. Noncoding RNA Res. 2023;8(1): 60-74. [DOI:10.1016/j.ncrna.2022.09.011] [PMID] [PMCID]
9. Zhou W-Y, Cai Z-R, Liu J, Wang D-S, Ju H-Q, Xu R-H. Circular RNA: metabolism, functions and interactions with proteins. Mol Cancer. 2020; 19:1-19. [DOI:10.1186/s12943-020-01286-3] [PMID] [PMCID]
10. Brown JR, Chinnaiyan AM. The Potential of Circular RNAs as Cancer Biomarkers. Cancer Epidemiol Biomarkers Prev. 2020;29(12):2541-55. [DOI:10.1158/1055-9965.EPI-20-0796] [PMID]
11. Lyu L, Zhang S, Deng Y, Wang M, Deng X, Yang S, et al. Regulatory mechanisms, functions, and clinical significance of CircRNAs in triple-negative breast cancer. J Hematol Oncol. 2021; 14(1):41. [DOI:10.1186/s13045-021-01052-y] [PMID] [PMCID]
12. Hue SS, Jin Y, Cheng H, Bin Masroni MS, Tang LWT, Ho YH, et al. Tissue-Specific microRNA Expression Profiling to Derive Novel Biomarkers for the Diagnosis and Subtyping of Small B-Cell Lymphomas. Cancers (Basel). 2023;15(2):453. [DOI:10.3390/cancers15020453] [PMID] [PMCID]
13. He Z, Zhu Q. Circular RNAs: Emerging roles and new insights in human cancers. Biomed Pharmacother. 2023;165:115217. [DOI:10.1016/j.biopha.2023.115217] [PMID]
14. Zhang Y, Luo J, Yang W, Ye WC. CircRNAs in colorectal cancer: potential biomarkers and therapeutic targets. Cell Death Dis. 2023;14(6): 353. [DOI:10.1038/s41419-023-05881-2] [PMID] [PMCID]
15. Hashemi M, Khosroshahi EM, Daneii P, Hassanpoor A, Eslami M, Koohpar ZK, et al. Emerging roles of CircRNA-miRNA networks in cancer development and therapeutic response. Noncoding RNA Res. 2025;10:98-115. [PMID] [DOI:10.1016/j.ncrna.2024.09.006] [PMCID]
16. He YD, Tao W, He T, Wang BY, Tang XM, Zhang LM, et al. A urine extracellular vesicle circRNA classifier for detection of high-grade prostate cancer in patients with prostate-specific antigen 2-10 ng/mL at initial biopsy. Mol Cancer. 2021;20(1):96. [PMID] [PMCID] [DOI:10.1186/s12943-021-01388-6]
17. Wang Z, Deng H, Jin Y, Luo M, Huang J, Wang J, et al. Circular RNAs: biology and clinical significance of breast cancer. RNA Biol. 2023; 20(1):859-74. [PMID] [PMCID] [DOI:10.1080/15476286.2023.2272468]
18. Yang J, Chen Z, He J, Zhao Y, Zhou C, Zhao X, et al. A circRNA-based ceRNA network shows its diagnostic value in non-small-cell lung cancer. Clin Biochem. 2023;121-122:110657. [PMID] [DOI:10.1016/j.clinbiochem.2023.110657]
19. Yi Q, Yue J, Liu Y, Shi H, Sun W, Feng J, et al. Recent advances of exosomal circRNAs in cancer and their potential clinical applications. J Transl

Med. 2023;21(1):516. [PMID] [PMCID] [DOI:10.1186/s12967-023-04348-4]

20. Afzal S, Hassan M, Ullah S, Abbas H, Tawakkal F, Khan MA. Breast Cancer; Discovery of Novel Diagnostic Biomarkers, Drug Resistance, and Therapeutic Implications. Front Mol Biosci. 2022;9:783450. [PMID] [PMCID] [DOI:10.3389/fmolb.2022.783450]
21. Lim MCJ, Baird AM, Aird J, Greene J, Kapoor D, Gray SG, et al. RNAs as Candidate Diagnostic and Prognostic Markers of Prostate Cancer-From Cell Line Models to Liquid Biopsies. Diagnostics (Basel). 2018;8(3):60. [PMID] [PMCID] [DOI:10.3390/diagnostics8030060]
22. Nomiri S, Hoshyar R, Chamani E, Rezaei Z, Salmani F, Larki P, et al. Prediction and validation of GUCA2B as the hub-gene in colorectal cancer based on co-expression network analysis: In-silico and in-vivo study. Biomed Pharmacother. 2022;147:112691. [DOI:10.1016/j.biopha.2022.112691] [PMID]
23. Ranjbaran J, Safarpour H, Nomiri S, Tavakoli T, Rezaei Z, Salmani F, et al. Experimental validation of in silico analysis estimated the reverse effect of upregulated hsa-miR-106a-5p and hsa-miR-223-3p on SLC4A4 gene expression in Iranian patients with colorectal adenocarcinoma by RT-qPCR. Cancer Med. 2023;12(6):7005-18. [DOI:10.1002/cam4.5499] [PMID] [PMCID]
24. Zhang X, Tan P, Zhuang Y, Du L. hsa_circRNA_001587 upregulates SLC4A4 expression to inhibit migration, invasion, and angiogenesis of pancreatic cancer cells via binding to microRNA-223. Am J Physiol Gastrointest Liver Physiol. 2020;319(6):G703-G17. [DOI:10.1152/ajpgi.00118.2020] [PMID]
25. Ma C, Wang X, Yang F, Zang Y, Liu J, Wang X, et al. Circular RNA hsa_circ_0004872 inhibits gastric cancer progression via the miR-224/Smad4/ADAR1 successive regulatory circuit. Mol Cancer. 2020;19(1):157. [PMCID] [DOI:10.1186/s12943-020-01268-5] [PMID]
26. Xi L, Liu Q, Zhang W, Luo L, Song J, Liu R, et al. Circular RNA circCSPP1 knockdown attenuates doxorubicin resistance and suppresses tumor progression of colorectal cancer via miR-944/FZD7 axis. Cancer Cell Int. 2021;21(1):153. [DOI:10.1186/s12935-021-01855-6] [PMID] [PMCID]
27. Xi Y, Xu P. Global colorectal cancer burden in 2020 and projections to 2040. Transl Oncol. 2021;14(10):101174. [PMID] [PMCID] [DOI:10.1016/j.tranon.2021.101174]
28. Mo S, Dai W, Wang H, Lan X, Ma C, Su Z, et al. Early detection and prognosis prediction for colorectal cancer by circulating tumour DNA methylation haplotypes: A multicentre cohort study. EClinicalMedicine. 2023;55:101717. [DOI:10.1016/j.eclinm.2022.101717][PMID] [PMCID]
29. Viralippurath Ashraf J, Sasidharan Nair V, Saleh R, Elkord E. Role of circular RNAs in colorectal tumor microenvironment. Biomed Pharmacother. 2021;137:111351. [DOI:10.1016/j.biopha.2021.111351] [PMID]
30. Li Z, Li X, Xu D, Chen X, Li S, Zhang L, et al. An update on the roles of circular RNAs in osteosarcoma. Cell Prolif. 2021;54(1):e12936. [DOI:10.1111/cpr.12936] [PMID] [PMCID]
31. Li Y, Gong L, Qin N, Wei X, Miao L, Yuan H, et al. Comprehensive analysis of circRNA expression pattern and circRNA-miRNA-mRNA network in oral squamous cell carcinoma. Oral Oncol. 2021;121:105437. [PMID] [DOI:10.1016/j.oraloncology.2021.105437]
32. Ning J, Luo Y, Chen L, Xiao G, Tanzhu G, Zhou R. CircRNAs and lung cancer: Insight into their roles in metastasis. Biomed Pharmacother. 2023; 166:115260. [DOI:10.1016/j.biopha.2023.115260] [PMID]
33. Huang G, Liang M, Liu H, Huang J, Li P, Wang C, et al. CircRNA hsa_circRNA_104348 promotes hepatocellular carcinoma progression through modulating miR-187-3p/RTKN2 axis and activating Wnt/β-catenin pathway. Cell Death Dis. 2020;11(12):1065. [PMID] [PMCID] [DOI:10.1038/s41419-020-03276-1]
34. Tang C, He X, Jia L, Zhang X. Circular RNAs in glioma: molecular functions and pathological implications. Non-Coding Rna Res. 2024;9(1): 105-15. [DOI:10.1016/j.ncrna.2023.10.007] [PMID] [PMCID]
35. Song X, Zhang G, Niu J, Liu H, Li C, Ning W, et al. Circular RNA circPFKP suppress gastric cancer progression through targeting miR-346/CAMD3 axis. Exp Cell Res. 2025;445(1): 114390. [DOI:10.1016/j.yexcr.2024.114390] [PMID]
36. Zhang F, Li L, Fan Z. circRNAs and their relationship with breast cancer: a review. World J Surg Oncol. 2022;20(1):373. [PMCID] [DOI:10.1186/s12957-022-02842-5] [PMID]
37. Cheng F, Zheng B, Si S, Wang J, Zhao G, Yao Z, et al. The Roles of CircRNAs in Bladder Cancer: Biomarkers, Tumorigenesis Drivers, and Therapeutic Targets. Front Cell Dev Biol. 2021;9: 666863. [DOI:10.3389/fcell.2021.666863] [PMID] [PMCID]
38. Xiao W, Wang X, Wang T, Xing J. MiR-223-3p promotes cell proliferation and metastasis by downregulating SLC4A4 in clear cell renal cell

carcinoma. Aging (Albany NY). 2019;11(2):615-33. [DOI:10.18632/aging.101763] [PMID] [PMCID]

39. Barbagallo D, Ponti D, Bassani B, Bruno A, Pulze L, Akkihal SA, et al. MiR-223-3p in Cancer Development and Cancer Drug Resistance: Same Coin, Different Faces. Int J Mol Sci. 2024;25(15): 8191. [DOI:10.3390/ijms25158191] [PMID] [PMCID]
40. Dai Y, Zhu Y, Xu H. circ_0004872 inhibits proliferation, invasion, and glycolysis of oral squamous cell carcinoma by sponged miR-424-5p. J Clin Lab Anal. 2022;36(7):e24486. [DOI:10.1002/jcla.24486] [PMID] [PMCID]
41. Zhang GJ, Zhou H, Xiao HX, Li Y, Zhou T. Up-regulation of miR-224 promotes cancer cell proliferation and invasion and predicts relapse of colorectal cancer. Cancer Cell Int. 2013;13(1): 104. [DOI:10.1186/1475-2867-13-104] [PMID] [PMCID]

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