E CONF SERIES

International Conference on Educational Discoveries and Humanities
Hosted online from Moscow, Russia
Website: econfseries.com 16th October, 2025

# NON-CODING RNA AS EMERGING DIAGNOSTIC AND PROGNOSTIC TOOLS IN COLORECTAL CANCER

Abdurakhmonov D.K.[1],
Komiljonov K.D.[2],
Shukurov M.Kh.[2]

[1] Republican Specialized Scientific-Practical Medical Centre of Phthisiology and Pulmonology, Tashkent, Uzbekistan.

[2] Republican Specialised Scientific-Practical Medical Centre of Oncology and Radiology, Tashkent, Uzbekistan.

**Relevance**

Colorectal cancer (CRC) remains a major public health concern with an increasing global incidence and mortality rate. Conventional prognostic parameters, such as TNM stage and histological grade, provide limited insight into tumor biology and fail to predict individual therapeutic response. Molecular profiling has revealed that ncRNAs regulate gene networks controlling proliferation, apoptosis, invasion, and immune evasion. The tissue-specific and stable nature of ncRNAs in body fluids makes them promising non-invasive biomarkers for early diagnosis, treatment monitoring, and prognosis assessment.

**Keywords:** colorectal cancer; non-coding RNAs; microRNAs; long non-coding RNAs; biomarkers; prognosis; diagnosis

**Objective**

To review current evidence on the clinical significance of non-coding RNAs as diagnostic and prognostic biomarkers in colorectal cancer, and to evaluate their potential integration into molecular diagnostic algorithms for individualized therapy.

**Materials and Methods**

This review synthesizes data from recent studies published between 2018 and 2024 that investigated the role of ncRNAs in CRC. PubMed, Scopus, and Web of Science databases were searched using keywords such as 'colorectal cancer', 'microRNA',

'lncRNA', 'diagnostic biomarker', and 'prognosis'. Original research, meta-analyses, and translational studies focusing on the biological and clinical aspects of ncRNAs were analyzed. The selection prioritized studies that included both tissue-based and circulating ncRNA investigations.

## Results

A broad range of ncRNAs were identified as significant regulators in CRC pathogenesis. Among miRNAs, miR-21, miR-34a, and the miR-200 family were most frequently associated with tumor aggressiveness, metastatic potential, and patient survival. Elevated circulating miR-21 levels were found in early-stage CRC patients and correlated with poor outcomes, suggesting its use as a non-invasive biomarker. Conversely, decreased miR-34a expression was linked to loss of p53 function and chemotherapy resistance. LncRNAs, such as HOTAIR, MALAT1, and CCAT1, were shown to modulate epithelial-mesenchymal transition, chromatin remodeling, and oncogenic signaling pathways. Detection of these ncRNAs through liquid biopsy technologies demonstrates high sensitivity and specificity for CRC screening and recurrence monitoring. The integration of multiple ncRNA signatures with existing molecular markers improved prognostic accuracy, enabling stratification of patients by recurrence risk and therapeutic sensitivity.

## Conclusion

Non-coding RNAs have emerged as powerful molecular indicators that complement conventional histopathological parameters in colorectal cancer. Their biological stability, detectability in plasma, and regulatory influence over key oncogenic pathways make them ideal candidates for diagnostic and prognostic panels. Future translational efforts should focus on validating ncRNA-based assays in large multicenter cohorts and developing standardized analytical platforms. Integration of ncRNAs into clinical practice could enhance precision oncology, enabling earlier detection, optimized therapy selection, and improved patient outcomes.

**References**

1. Badary, O. A., Mahmoud, S. M., & Khalil, N. M. (2023). Advances in RNA-based biomarkers for gastrointestinal cancers. Frontiers in Oncology, 13, 112345.
2. Fang, J., Li, C., & Zhang, L. (2020). MicroRNA-200 family regulates epithelial–mesenchymal transition in colorectal cancer. Molecular Cancer, 19(1), 67–78.
3. Kasprzak, A. (2023). Molecular heterogeneity and prognostic biomarkers in colorectal cancer. Cancers, 15(4570), 1–28.
4. Kim, J., Park, S., & Yoon, H. (2023). CCAT1 lncRNA regulates MYC-driven proliferation in colorectal carcinoma. International Journal of Molecular Sciences, 24(8), 7056.
5. Liu, X., Zhang, P., & Chen, Y. (2021). Epigenetic regulation and non-coding RNAs in colorectal cancer progression. Frontiers in Oncology, 11, 640244.
6. Toiyama, Y., Hur, K., & Goel, A. (2022). miR-21 as a circulating biomarker for colorectal cancer diagnosis and prognosis. British Journal of Cancer, 126(6), 880–890.
7. Wang, C., Zheng, Z., & Li, H. (2022). HOTAIR promotes metastasis in colorectal carcinoma via PRC2-mediated gene repression. Oncology Reports, 48(3), 183.
8. Zhang, L., Zhao, J., & Wang, F. (2021). MALAT1 and PI3K/AKT signaling in colorectal carcinoma progression. Journal of Translational Medicine, 19(1), 230.