

Integrating disulfidptosis-related long noncoding RNAs in colorectal cancer prognosis: A path to precision medicine

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Abstract

This commentary explores the burgeoning field of disulfidptosis-related long noncoding RNAs (lncRNAs) in the prognosis and therapeutic targeting of colorectal cancer (CRC). By evaluating recent research, including the pivotal study "Predicting colorectal cancer prognosis based on long noncoding RNAs of disulfidptosis genes" by Wang *et al*, this analysis underscores the critical role of lncRNAs in deciphering the molecular complexities of CRC. Highlighting the innovative methodologies and significant findings, I discuss the implications for patient survival, therapeutic response, and the potential of lncRNAs as biomarkers for precision medicine. The integration of bioinformatics, clinical databases, and molecular biology in these studies offers a promising avenue for advancing CRC treatment strategies and improving patient outcomes.

Key Words: Colorectal cancer; Disulfidptosis; Long noncoding RNAs; Prognosis; Precision medicine

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Core Tip: This commentary emphasizes the novel role of disulfidptosis-related long noncoding RNAs (lncRNAs) in colorectal cancer prognosis. Focusing on the intersection of genetic research and clinical practice, it highlights how the study of lncRNAs can facilitate the development of targeted therapies and prognostic models. The critical evaluation of recent research underscores the potential of lncRNAs as biomarkers and therapeutic targets, marking a significant step towards personalized medicine in colorectal cancer treatment.

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TO THE EDITOR

I recently read the insightful study titled "Predicting colorectal cancer prognosis based on long noncoding RNAs of disulfidptosis genes" by Wang *et al*[1] published in *World Journal of Clinical Oncology*. The study pioneers the exploration into the prognostic value of disulfidptosis-related lncRNAs (DRLs) in colorectal cancer (CRC). Through meticulous analysis and innovative approaches, the research uncovers eight significant lncRNAs associated with disulfidptosis, shedding light on their potential as prognostic markers and therapeutic targets.

Key methodologies like leveraging The Cancer Genome Atlas for data collection and the development of a prognostic model through bioinformatics techniques, showcasing the integration of clinical and genetic data for precision medicine. The findings suggest a profound connection between lncRNAs, immune response, and CRC prognosis, offering a novel perspective on cancer treatment strategies. Furthermore, drug sensitivity analysis indicated that Epirubicin, bortezomib, teniposide, and BMS-754807 exhibit the least sensitivity among the assessed immunotherapy drugs, underscoring the necessity for customized therapeutic approaches to augment cancer treatment efficacy.

The relevance of this study is further underscored by related literature, such as the validation of lncRNA prognostic models in CRC, the prognostic significance of disulfidptosis-associated lncRNA signatures, and their implications for the tumor microenvironment and therapeutic options[2-4]. These complementary studies highlight the potential of lncRNAs in understanding CRC's molecular mechanisms and in developing targeted therapies.

The study's findings are pivotal, offering a novel perspective on CRC treatment strategies through DRL utilization. This advancement could revolutionize precision medicine by enabling more personalized and effective treatments. Future research is essential to understand DRLs' impact on CRC progression and treatment response, and their viability as therapeutic targets, potentially leading to innovative treatments that significantly improve patient outcomes[5]. Validating the functions of disulfidptosis-related lncRNAs and immune checkpoints' anti-cancer mechanisms through comprehensive animal and cell studies is imperative.

FOOTNOTES

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