**The role of lncRNA CERS6-AS1 in cancer and its molecular mechanisms: A systematic review and meta-analysis**

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**Abstract**

**Background**

LncRNAs have the potential to play a regulatory role in different processes of cancer development and progression. We conducted a [systematic review](https://www.sciencedirect.com/topics/medicine-and-dentistry/systematic-review) and meta-analysis of evidence on the [clinical significance](https://www.sciencedirect.com/topics/medicine-and-dentistry/clinical-significance) and prognostic value of [lncRNA](https://www.sciencedirect.com/topics/medicine-and-dentistry/long-untranslated-rna) *CERS6-AS1* in cancer.

**Methods**

This [systematic review](https://www.sciencedirect.com/topics/medicine-and-dentistry/systematic-review) was conducted following PRISMA guidelines. [Medline](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/medline) and [Embase](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/embase) databases were searched using the relevant key terms covering [lncRNA](https://www.sciencedirect.com/topics/pharmacology-toxicology-and-pharmaceutical-science/long-untranslated-rna) *CERS6-AS1* and cancer. We pooled the estimated effect sizes and their 95 % confidence interval (CI) using random-effects models in STATA 16.0 (StataCorp, College Station, TX, USA).

**Results**

Eleven articles on pancreatic, colorectal, gastric, papillary [thyroid](https://www.sciencedirect.com/topics/medicine-and-dentistry/thyroid-gland), breast, and hepatocellular cancers fulfilled our eligibility criteria. Studies consistently found that [lncRNA](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/long-non-coding-rna) *CERS6-AS1* expression is upregulated in all assessed cancers. Based on our meta-analysis, its aberrant expression was directly associated with unfavorable clinical outcomes, including higher stage (pooled Odds ratios (95 % CI): 3.15 (2.01–4.93; I2 = 0.0 %), tumor size (1.97 (1.27–3.05; I2 = 37.8 %), [lymph node metastasis](https://www.sciencedirect.com/topics/medicine-and-dentistry/lymph-node-metastasis) (6.48 (4.01–10.45; I2 = 0.40 %), and poor survival (Pooled log-rank test P-value < 0.001) in patients. Regarding potential mechanisms, functional studies revealed that *LncRNA CERS6-AS1* is involved in cancer growth mainly by sponging [miRNAs](https://www.sciencedirect.com/topics/medicine-and-dentistry/microrna) and regulating their downstream targets.

**Conclusion**

Available evidence suggests that LncRNA CERS6-AS1 is upregulated in different cancers and has an oncogenic role. *LncRNA CERS6-AS1* expression level might predict [cancer prognosis](https://www.sciencedirect.com/topics/medicine-and-dentistry/cancer-prognosis), highlighting its potential application as a prognostic biomarker for cancer.

**Introduction**

In recent years, discovering cancer-related genes has been one of the main goals of preclinical cancer research. The development of small molecules and antibodies targeting the protein products of these genes was a breakthrough in cancer treatment [22], [41], [42]. Besides protein-coding genes, non-coding RNAs, including long non-coding RNAs (lncRNAs), have been recognized to play a critical role in cancer progression and development [28], [32], [35], [37], [53] by regulating cancer-related genes' expression. Hence, they have the potential to be used as a diagnostic/prognostic biomarker or novel therapeutic target in cancer.[10], [30], [43].

Some lncRNAs drive different cancer phenotypes via various molecular mechanisms [9], [14], [21], [38]. However, the role of most lncRNAs in cancer is still unknown.

*CERS6 antisense RNA 1 (CERS6-AS1)* is one of the recently studied lncRNAs in cancer. [5], [11], [13], [15], [26], [39], [48], [49], [51], [52], [54] *lncRNA CERS6-AS1* is the transcript of the *CERS6* gene located at chromosome region 2q24.3. We aimed to summarize the main findings of the studies on the expression changes, clinical significance, and potential molecular mechanisms of *lncRNA CERS6-AS1* in different types of cancer.

**Section snippets**

**Material and methods**

We conducted this systematic review and meta-analysis following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. This study was exempt from institutional ethics committee approval as a systematic review and meta-analysis of published studies.

All studies assessing the functional roles, molecular mechanisms, and clinical significance of lncRNA *CERS6-AS1* in cancer meeting our eligibility criteria were included in this study.

**Study selection process**

We identified 51 items by the initial search from three databases, of which 15 were duplicates. A further 25 were excluded after screening by title/abstract (n = 23) or full-text reviews (n = 2). Finally, eleven eligible studies were included, including ten studies on both human and in-vitro (animal experiments examined in five) and one on human samples. The selection process is summarized in suppl Fig. 1.

Included studies were conducted in pancreatic (n = 4), breast (n = 2), colorectal (n = 1),

**Discussion**

Based on our systematic review and meta-analysis, *lncRNA CERS6-AS1* acts as an oncogene in cancer. Its high expression level is associated with poor prognosis (Pooled log-rank test P-value < 0.001), tumor stage (Pooled Crude OR (95 % CI): 3.15 (2.01–4.93)), tumor size (1.97 (1.27–3.05)), and lymph node metastasis (6.48 (4.01, 10.45)). Functional studies revealed that upregulation of *lncRNA CERS6-AS1* promotes tumor cell proliferation, growth, invasion, and metastasis.

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**Ethics Statement**

N/A

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