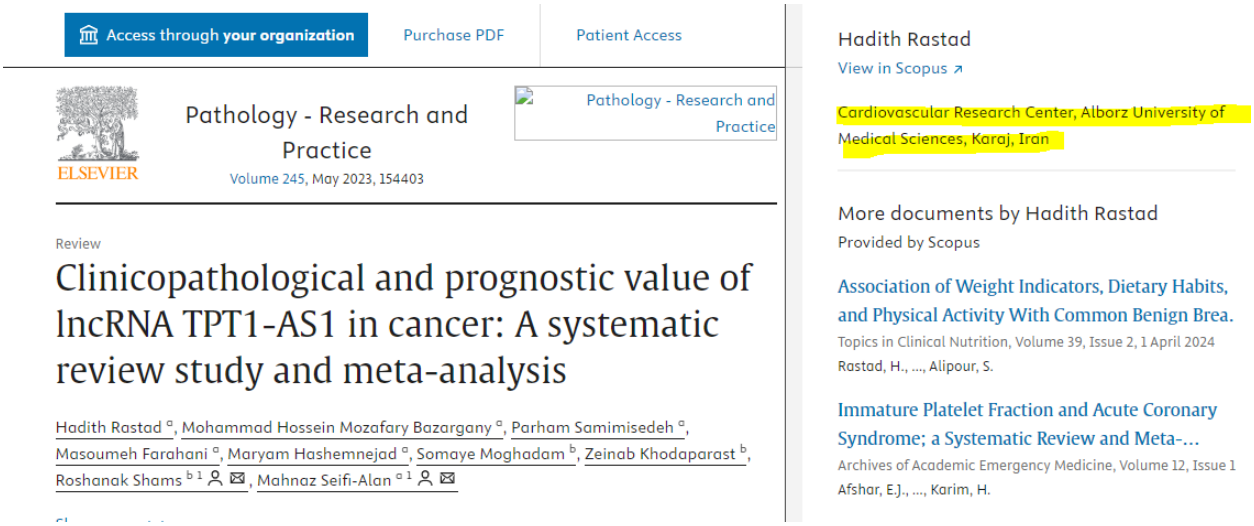

Conflict of interests

Authors declare no conflict of interest....

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Patient consent statement

NA....

Clinicopathological and prognostic value of lncRNA TPT1-AS1 in cancer: A systematic review study and meta-analysis

Author links open overlay panelHadith Rastad [a], Mohammad Hossein Mozafary Bazargany [a], Parham Samimisedeh [a], Masoumeh Farahani [a], Maryam Hashemnejad [a], Somaye Moghadam [b], Zeinab Khodaparast [b], Roshanak Shams [b 1]
, Mahnaz Seifi-Alan [a 1]
a

Cardiovascular Research Center, Alborz University of Medical Sciences, Karaj, Iran

b

Bone and Joint Reconstruction Research Center, Department of Orthopedics, School of Medicine, Iran University of Medical Sciences, Tehran, Iran

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Abstract

Introduction

Aberrant expression of lncRNAs in cancer cells can impact their key phenotypes. We aimed to summarize available evidence on clinicopathological and prognostic value of lncRNA TPT1-AS1 in cancer.

Methods

A systematic search was performed on Medline and Embase databases using relevant key terms covering lncRNA TPT1-AS1, cancer, and clinical outcomes. The effect size estimates and their 95 % confidence interval (CI) were pooled using random-effects models. Meta- analyses were conducted using STATA 16.0 software.

Results

Seventeen articles met our eligibility criteria. Tumor tissue compared to normal tissue showed increased level of lncRNA TPT1-AS1 expression (pooled standardized mean difference (95 % CI): 0.65 (0.52–0.79)). Overexpression of this lncRNA was a significant predictor for poor prognosis (Pooled log-rank test P-value < 0.001); in patients with high-level of lncRNA TPT1-AS1, the risk of death at five years was 1.40 times greater than their counterparts. The pooled Odds ratios for association lncRNA TPT1-AS1 with tumor stage, tumor size, and lymph node metastasis were 1.94 (95 % CI: 0.90–4.19, 8 studies, I^2 = 79.6 %), 2.33 (95 % CI: 1.31–4.14, 5 studies, I^2 = 40.0 %), and 1.89 (95 % CI: 1.08–3.36, 5 studies, I^2 = 61.7 %), respectively. Regarding the identified potential mechanisms, lncRNA TPT1-AS1 plays a role in cancer growth mainly by sponging miRNAs and regulating their downstream targets or controlling the expression of key cell cycle regulators.

Conclusion

In cancer patients, elevated expression of lncRNA TPT1-AS1 might be associated with a shorter Overall Survival, advanced stages, larger tumor size, and lymph node metastasis.

Introduction

Cancer is primarily caused by genetic and epigenetic alterations leading to the aberrant expression of genes [1]. Cancer has remained a leading cause of mortality and morbidity worldwide despite the great advancement in therapeutic approaches [2], [3]. Understanding the molecular mechanisms underlying cancer development is vital to identify novel diagnostic/prognostic biomarkers and therapeutic targets for more efficient interventions in the fight against cancer [4].

The development of targeted therapy focusing on the regulation of cancer-related protein-coding genes was a breakthrough in cancer diagnosis, prognosis, and treatment [5], [6], [7]. Besides protein-coding genes, non-coding RNAs, such as microRNAs (miRNAs) and long non-coding RNAs (lncRNAs), have been recognized to play a critical role in cancer biological processes, including cellular differentiation, proliferation, apoptosis, migration, and invasion [8], [9], [10], [11], [12]. Hence, they have the potential to be used as diagnostic and prognostic biomarkers and novel therapeutic targets in multiple cancers [13], [14], [15].

LncRNAs are exquisitely regulated. Based on growing evidence, the aberrant expression of certain lncRNAs drives various important phenotypes of cancer through regulating the expression of protein-coding genes in different ways, including transcriptional, posttranscriptional, post-translational, and epigenetic regulation [16], [17], [18], [19]. However, the specific functions and clinical value of most lncRNAs have remained largely unknown in cancer.

Tumor protein translationally controlled 1 - antisense RNA 1 (TPT1-AS1) is the transcript of the TPT1 gene located at chromosome region 13q14.13. In recent years, increasing studies have attempted to identify the expression changes, clinical significance, and potential molecular mechanisms of lncRNA TPT1-AS1 in different cancers [20], [21], [22], [23], [24], [25], [26], [27], [28], [29], [30], [31], [32], [33], [34], [35], [36]. We aimed to summarize the main findings reported in original studies on the clinical significance and functional roles of lncRNA TPT1-AS1 in different types of cancer.

Section snippets

Materials and methods

The present systematic review was undertaken under the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. As a systematic review of published studies, it required no ethical approval.

All eligible studies assessing the functional roles, molecular mechanisms, and/or the clinical significance of lncRNA TPT1-AS1 in cancer were included in this systematic review.

Study selection process

A total of 67 items were identified on the initial search from two databases, of which 23 were duplicates. A further 27 were excluded after screening by title/abstract (n = 21) or full text (n = 6) reviews. Hence, we included 17 studies meeting our eligibility criteria of which, including 11 studies on both human and in-vitro [20], [21], [22], [24], [25], [26], [27], [28], [29], [30], [31] (animal experiments examined in 5 of them), 5 only on human [32], [33], [34], [35], [36], and one on

Discussion

Based on our meta-analysis results, the expression of TPT1-AS1 lncRNA is deregulated in cancer.

Its overexpression was a significant predictor for poor prognosis (Pooled log-rank test P-value < 0.001); high-level of lncRNA TPT1-AS1 was directly associated with tumor stage (Pooled Crude OR (95 % CI): 1.94 (0.90–4.19)), tumor size (2.33 (1.31–4.14)), and lymph node metastasis (1.89 (1.08, 3.36)). According to available evidence, aberrant expression of TPT1-AS1 lncRNA promotes tumor cell growth,

Conclusion

Studies have found that lncRNA TPT1-AS1 expression may be aberrantly expressed in different cancers. Misexpressed lncRNA TPT1-AS1 is involved in tumor cell growth, invasion, and metastasis by transcriptional and posttranscriptional regulation. Our included studies suggest that lncRNA TPT1-AS1 may be a promising therapeutic target. However, research on lncRNA TPT1-AS1 remains in the experimental phases.

Ethics approval statements

As our study is a systematic review of available litterateurs, thus there is no need for ethical approval.

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CRediT authorship contribution statement

MS and HR had the idea, designed the study, and prepared the manuscript. MM, HR, PS, and ZKH developed the search strategy and selection process. SHS, MHM, PS and MS extracted the data. All authors critically revised the manuscript for important intellectual content and gave final approval to publish the version.

Conflict of interests

Authors declare no conflict of interest.

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Cited by (1)

- **Conduction and validation of a novel prognostic signature in cervical cancer based on the necroptosis characteristic genes via integrating of multiomics data**