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Prognostic value of PEG10 in Asian solid tumors: A meta-analysis

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ABSTRACT

Background: The involvement of paternally expressed gene 10 (PEG10) in the development of solid tumors has been demonstrated. However, the available data have not yet been fully analyzed. We conducted this meta-analysis to evaluate the correlations between PEG10 and the clinicopathological characteristics in patients with solid tumors.

Methods: An electronic search for relevant articles was conducted in PubMed, Web of Science, Cochrane Library, EMBASE, Chinese CNKI, and Wan Fang. The relationships between PEG10 and the clinicopathological features and prognosis of patients with cancer were determined using pooled odds ratios and hazard ratios with 95% confidence interval (CI).

Results: Ten studies comprising 1014 patients were included. The pooled analyses indicated the significant association of PEG10 overexpression with the risk of cancer, differentiation, lymph node metastasis and advanced TNM stage, but not with gender in cancer patients. Moreover, a high level of PEG10 expression correlated with poor prognosis and could be used as an independent prognostic biomarker for patients with solid tumors.

Conclusions: PEG10 expression is associated with advanced clinicopathological characteristics and can be used as a prognostic biomarker in patients with solid tumors.

1. Background

Cancer is the leading cause of death in economically developed countries and the second leading cause of death in developing countries, which constitutes an enormous burden all over the world [1]. Curative surgical resection is still established as the optimal treatment for primary solid tumors. However, clinical outcomes may vary in patients with the same type of tumor following surgery. Clinicopathologic features, such as pathological grade and clinical stage, are the main prognostic factors currently being used. However, these parameters often do not effectively predict individual outcomes. Although various biomarkers have been identified in malignancies and advances have been made in therapeutic technologies, prognosis remains poor because of the high incidence of recurrence, lymph node invasion, and distant metastasis. Therefore, it is crucial to identify novel tumor biomarkers with improved sensitivity and specificity to determine the optimal therapeutic strategies and predict the prognosis of solid tumors.

Paternally expressed gene (PEG) 10 is a paternally expressed imprinted gene which was first reported in 2001 [2]. The human PEG10 gene is located on chromosome band 7q21 and functions as a transcriptional factor. PEG10 can be detected in a variety of normal tissues, including brain, kidney, ovary, spleen, thymus, testis, lymphoblasts, endothelial cells, and placenta [3]. However, aberrant expression of PEG10 has been documented in multiple human cancers, such as leukemia, breast cancer, prostate cancer, pancreas cancer, gallbladder cancer, and hepatocellular carcinoma (HCC), indicating that PEG10 plays an important role in the development and progression of cancer [4–7]. Recent studies have indicated that the expression of PEG10 is closely associated with the prognosis of cancer patients. Accordingly, we performed a comprehensive meta-analysis to assess the correlation of the high expression of PEG10 with clinicopathologic characteristics in malignancies and to explore the clinical value of PEG10 as a potential therapeutic target and prognostic indicator for solid tumors.

2. Materials and methods

2.1. Search strategy

PubMed, Web of Science, Cochrane Library, EMBASE, Chinese

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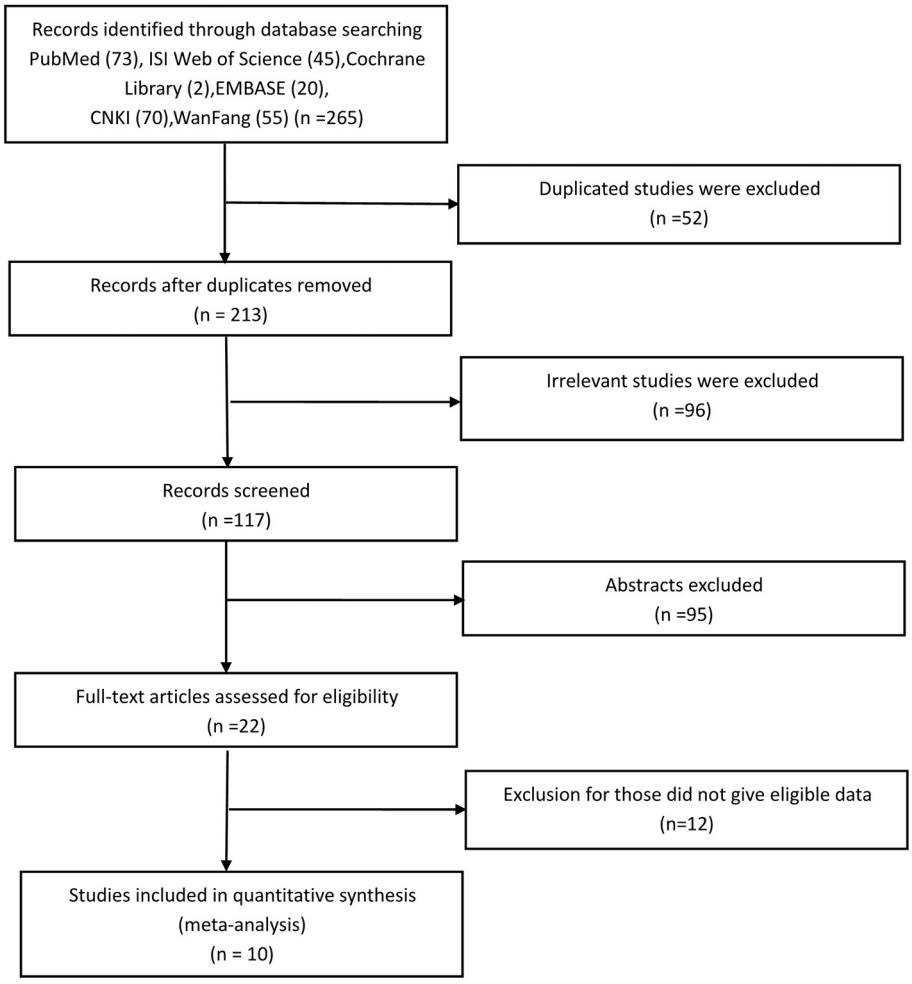

Fig. 1. Flow diagram study selection.

Table 1
Characteristics of studies included in the meta-analysis.

Author	Year	Country	Cancer type	Sample type	Detection method	No. of patients	Cancer (+/−) Control (+/−)	Lymph node metastasis Positive (+/−) Negative (+/−)	Male (+/−) Female (+/−)	High & moderate (+/−) Low (+/−)	III/IV (+/−) I/II (+/−)	Outcomes	Score
Bang H[8]	2015	Korea	HCC	tissue	IHC	218	148/70 NA	NA	116/63 32/7	109/60 39/10	NA	OS	8
Sharan Singh S[9]	2017	India	OSCC	tissue	RT-PCR	118	83/35 NA	62/16 21/19	NA	NA	78/28 5/7	OS	8
Liu DC[10]	2011	China	GBC	tissue	IHC	108	52/56 9/37	35/24 17/32	15/16 53/24	26/41 26/15	NA	OS	7
Peng YP[11]	2017	China	PC	tissue	RT-PCR	85	58/27 NA	25/11 33/16	NA	NA	30/13 28/14	OS	7
Zhang H[12]	2015	China	HCC	tissue	IHC	58	44/14 NA	NA	28/13 16/1	27/13 17/1	25/2 19/12	OS	8
Wu SM[13]	2007	China	HCC	tissue	RT-PCR	43	34/9 0/43	24/2 10/7	28/5 6/4	4/5 30/4	23/1 11/8	NA	6
Zhu ZH[14]	2016	China	LC	tissue	IHC	101	73/28 NA	47/5 26/23	37/19 36/9	35/23 38/5	40/5 33/23	NA	8
Liu Z[15]	2014	China	GBC	tissue	IHC	126	62/64 NA	47/32 15/32	20/25 42/39	38/54 24/10	54/39 8/25	OS	9
Peng W[16]	2016	China	DLBCL	tissue	RT-PCR	107	54/53 NA	NA	30/24 24/29	NA	35/26 19/27	OS	7
Liu Y[17]	2012	China	HCC	tissue	IHC	50	42/8 5/45	NA	36/6 6/2	NA	32/2 10/6	NA	7

Abbreviations: HCC = Hepatocellular carcinoma; OSCC = Oral squamous cell carcinoma; GBC = Gallbladder carcinoma; PC = Pancreatic cancer; LC = Lung cancer; DLBCL = Diffuse large B cell lymphoma; IHC = Immunohistochemistry; RT-PCR = Real-time polymerase chain reaction; OS = Overall survival; NA = not available.