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Analysis of Correlation Between Rab1A Expression and its Prognosis in cancers: a meta-analyses

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ADMINISTRATIVE INFORMATION

Support - No.

Review Stage at time of this submission - Completed but not published.

Conflicts of interest - None declared.

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Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 17 June 2023 and was last updated on 17 June 2023.

INTRODUCTION

Review question / Objective Rab1A not only regulated eukaryotic secretion, autophagy and intracellular traffic, but also extensively participated in the development of cancer. Thus, we collected data to investigate the clinical value of Rab1A in cancers.

Rationale Rab protein was a member of the GTPase superfamily, with about 70 human members. It regulated eukaryotic secretion and autophagy and intracellular traffic, and was the manager protein of intracellular membrane dynamics . Among them, Rab1A (Member RAS Oncogene Family) played an important role in vesicular transport from endoplasmic reticulum to Golgi apparatus, and was involved in signal transduction, cell migration and autophagy. With the development of research, Rab1A not only acted on intracellular traffic, but also could be abnormally expressed in some clinical diseases, including Parkinson's disease , immune disease, primary cardiomyopathy and a variety of malignancies.

Condition being studied Cancers, manifested by unfavorable clinical manifestation and poor prognosis, have long plagued people's lives and health, and have always been one of the main causes of death and obstacles to extending life expectancy for people around the world.

METHODS

Search strategy The search strategy was as follows: ("Rab1A") AND ("carcinoma" OR "neoplasm" OR "tumour" OR "cancer") AND ("survival" OR "prognostic" OR "outcome" OR"prognosis").

Participant or population Participants received a pathological diagnosis of cancer and received reasonable and effective therapeutic measures will be included.

Intervention All participants were separated into cohorts, based on their Rab1A levels, and survival analysis was completed on both cohorts.

Comparator We will analyze clinicopathologic and survival differences in cancer patients with different Rab1A expressions.

Study designs to be included Case-control studiesls will be included.

Eligibility criteria 1) All subjects were clinical cancer patients undergoing surgical treatment; 2) The expression of Rab1A in cancer patients was detected, and cancer patients were divided into two groups according to the expression level of Rab1A; 3) Overall survival (OS) of patients in both groups was assessed and survival data could be provided; 4) The study design was scientific and reasonable.

Information sources The applicable English article was obtained through online search of PUBMED, Web Of Science, PMC and other databases (up to May 2023).

Main outcome(s) The results showed that up-regulated Rab1A led to poor prognosis in cancer patients($P < 0.001$). We further analyzed and confirmed that high expression of Rab1A was associated with a number of adverse clinicopathological parameters ($P < 0.05$).

Quality assessment / Risk of bias analysis Newcastle-Ottawa Scale (NOS) (including selection, comparability, and exposure) was also used in this analysis to obtain objective scores of the quality of the included article, of which no less than 6 were classified as high-quality articles, and Begg's and Egger's tests were statistical methods to check whether there was publication bias in this meta-analyses.

Strategy of data synthesis We evaluated the prognostic value of Rab1A in cancer patients by combining the hazard ratio (HR) and 95% confidence intervals (CI) included in the articles. It should be pointed out that the HR and corresponding 95% CI were obtained directly from the article or estimated from the Kaplan-Meier curve, and the HR obtained through multivariate analysis was preferred in the actual calculation. In addition, we formed a 2*2 contingency table for the relationship between Rab1A expression and clinicopathological parameters in each available article, and further identified the relationship between Rab1A expression and clinical characteristics by combining odds ratios (ORs).

Subgroup analysis We further evaluated the prognostic value of Rab1A in different cancer types and sample sizes and analysis methods by subgroup analysis.

Sensitivity analysis Sensitivity analysis was used to assess the stability of this analysis.

Language restriction English.

Country(ies) involved China.

Keywords Rab1A; prognosis; oncogenicity; biomarker; cancer; meta-analyses.

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