

The Role of Circular RNAs as Prognostic Factors in Lung Cancer: A Meta Analysis

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Aim: The study aimed to systematically evaluate the prognostic value of circular RNAs (circRNAs) in lung cancer.

Methods: A comprehensive search was conducted in PubMed, Embase, and MEDLINE databases for studies examining the association between circRNAs and overall survival (OS) or disease-free survival (DFS) in lung cancer patients. Pooled hazard ratios (HRs) and 95% confidence intervals (CIs) were calculated to assess the prognostic significance of circRNAs. Statistical analyses were performed using RevMan 5.4 software, employing a random effects model due to heterogeneity across studies.

Results: A total of 43 studies met the inclusion criteria, predominantly focusing on non-small cell lung cancer (NSCLC), with only one study addressing small cell lung cancer (SCLC). High expression of upregulated circRNAs was significantly correlated with poorer prognosis and worse OS (HR 1.93, 95% CI [1.61-2.33], $p < 0.00001$). Conversely, high expression of downregulated circRNAs was associated with better prognosis and improved OS (HR 0.73, 95% CI [0.58-0.94], $p = 0.01$). However, no significant association was found between circRNA expression levels and DFS (HR 1.44, 95% CI [0.92-2.24], $p = 0.11$).

Conclusion: This meta-analysis supports the significant role of circRNAs as prognostic biomarkers in lung cancer, especially NSCLC. Elevated expression of upregulated circRNAs is linked to poorer outcomes, while downregulated circRNAs are associated with better survival, highlighting their potential as therapeutic targets in lung cancer management.

