

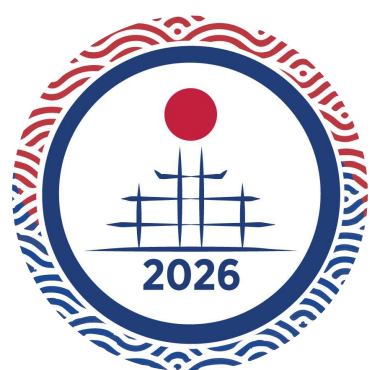


EP03.20: Investigate the Prognostic Value of Radiation-Associated RNA-binding Protein-Coding Genes in Lung Adenocarcinoma

J.B. Xu¹, J. Deng¹, F. Yu^{1,2}, F. Qiu^{1,2}

¹ Gaoxin Branch of The First Affiliated Hospital of Nanchang University, Nanchang/CN ,² The First Affiliated Hospital of Nanchang University, Nanchang/CN

Correspondence: 2718710461@qq.com



IASLC 2026 World
Conference on Lung Cancer

SEPTEMBER 12 – 15, 2026
SEOUL, REPUBLIC OF KOREA

INTRODUCTION

Studies have shown that cancer cells can use RNA binding proteins (RBPs) dysfunction to regulate various cancer-associated transcripts to promote tumourigenesis, but the mechanism of action of RBPs-related genes (RBP-RGs) in radiation-associated lung adenocarcinoma (LUAD) is unknown.

METHODS

This study used LUAD datasets (TCGA-LUAD, GSE72094) and 1542 RBP-related genes. Candidate genes were obtained by intersecting differentially expressed genes from LUAD-control, radiosensitive-radioresistant, and DE-RBP-RG high/low-score groups. Univariate COX, LASSO and multivariate COX regressions were applied to select prognostic genes for the risk model. Risk scores and clinical features were used to identify independent prognostic factors for nomogram construction. Functional enrichment and immune-related analyses were further conducted on these prognostic genes.

DISCUSSION AND CONCLUSION

Four genes, NTSR1, RHCG, OR1F1, and C1orf141, were identified as prognostic genes to construct risk model, which provided a basis for understanding LUAD pathogenesis.

Our analysis is mainly based on database-derived data, the mechanistic investigation is not sufficiently in-depth, and further clinical trials are required to validate our findings.

REFERENCES & ACKNOWLEDGEMENTS

References

- Leiter A, Veluswamy RR, Wisnivesky JP. The global burden of lung cancer: current status and future trends[J]. Nat Rev Clin Oncol, 2023, 20(9): 624-639. DOI: 10.1038/ s41571-023-00798-3.
- BRAY F, LAVERSANNE M, SUNG H, et al. Global cancer statistics 2022: GLOBOCAN estimates of incidence and mortality world-wide for 36 cancers in 185 countries[J]. CA Cancer J Clin, 2024, 74(3): 229 - 263.
- Hill W, Lim EL, Weeden CE, et al. Lung adenocarcinoma promotion by air pollutants. Nature. 2023 Apr;616(7955):159-167. doi: 10.1038/s41586-023-05874-3. Epub 2023 Apr 5. PMID: 37020004; PMCID: PMC7614604.
- Cai L, Zhu CX, Zhang XL, et al. [Interpretation of global lung cancer statistics]. Zhonghua Liu Xing Bing Xue Za Zhi. 2024 Apr 10;45(4):585-590. Chinese. doi: 10.3760/cma.j.cn112338-20230920-00172. PMID: 38678357.
- Chen P, Liu Y, Wen Y, et al. Non-small cell lung cancer in China[J]. Cancer Commun (Lond). 2022, 42(10): 937-970.

Artificial Intelligence (AI) Use Disclaimer

In accordance with the standards and guidance set forth by the Accreditation Council for Continuing Medical Education (ACCME), we hereby disclose that artificial intelligence (AI) tools were not utilized in the development of this educational material.

Acknowledgements

Our study was supported by the supported by the Gaoxin Branch of The First Affiliated Hospital of Nanchang University (2022-KJZC-029).

RESULTS

In this study, a total of 181 candidate genes were identified by overlapping 9,549 DEGs¹, 1,129 DEGs², and 4860 DEGs³, of which NTSR1, RHCG, OR1F1, and C1orf141 were prognostic genes through a series of analyses.

Furthermore, a risk model for LUAD was created using prognosis genes to classify LUAD patients into high/low-risk groups. Then, the risk score and T3/4 at T stage were included nomogram to predict the survival rate of LUAD patients.

Subsequently, functional enrichment results showed that the signaling pathways of significant enrichment of prognostic genes included cerebrospinal fluid circulation, asthma and so on. In immune infiltration analysis, Monocytes and resting memory T cells CD4 were significantly associated with prognostic genes.

