

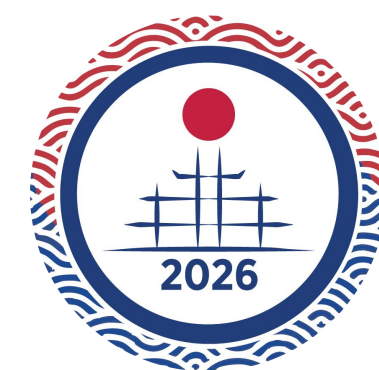


EP03.13: Network Pharmacology and Experimental Validation Reveal the Multi-Target Anti-Lung Cancer Mechanisms of Rutaecarpine

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IASLC 2026 World
Conference on Lung Cancer

SEPTEMBER 12 - 15, 2026
SEOUL, REPUBLIC OF KOREA

INTRODUCTION

Lung cancer remains the leading cause of cancer-related mortality worldwide, and novel therapeutic strategies are urgently needed. Rutaecarpine, a natural indoloquinazoline alkaloid derived from *Evodia rutaecarpa*, has been reported to possess anti-inflammatory and anti_x0002_tumor activities, but its mechanisms in lung cancer are not fully understood.

METHODS

A network pharmacology strategy was applied to identify potential targets of Rutaecarpine against lung cancer. PPI networks and topological algorithms were used to identify hub genes. Expression patterns of hub genes were validated using TCGA data and the Human Protein Atlas (HPA). Molecular docking was performed to evaluate the binding affinity between Rutaecarpine and hub proteins. Finally, in vitro experiments were conducted in A549 lung cancer cells to validate the expression of hub genes by qPCR and Western blot.

DISCUSSION AND CONCLUSION

Our integrative study combining network pharmacology, molecular docking, and experimental validation demonstrates that Rutaecarpine exerts anti-lung cancer effects through multi-target and multi-pathway regulation, particularly by suppressing MMP9, CCNA2, PARP1, and TERT. These findings provide new mechanistic insights and support Rutaecarpine as a potential therapeutic candidate for lung cancer treatment.

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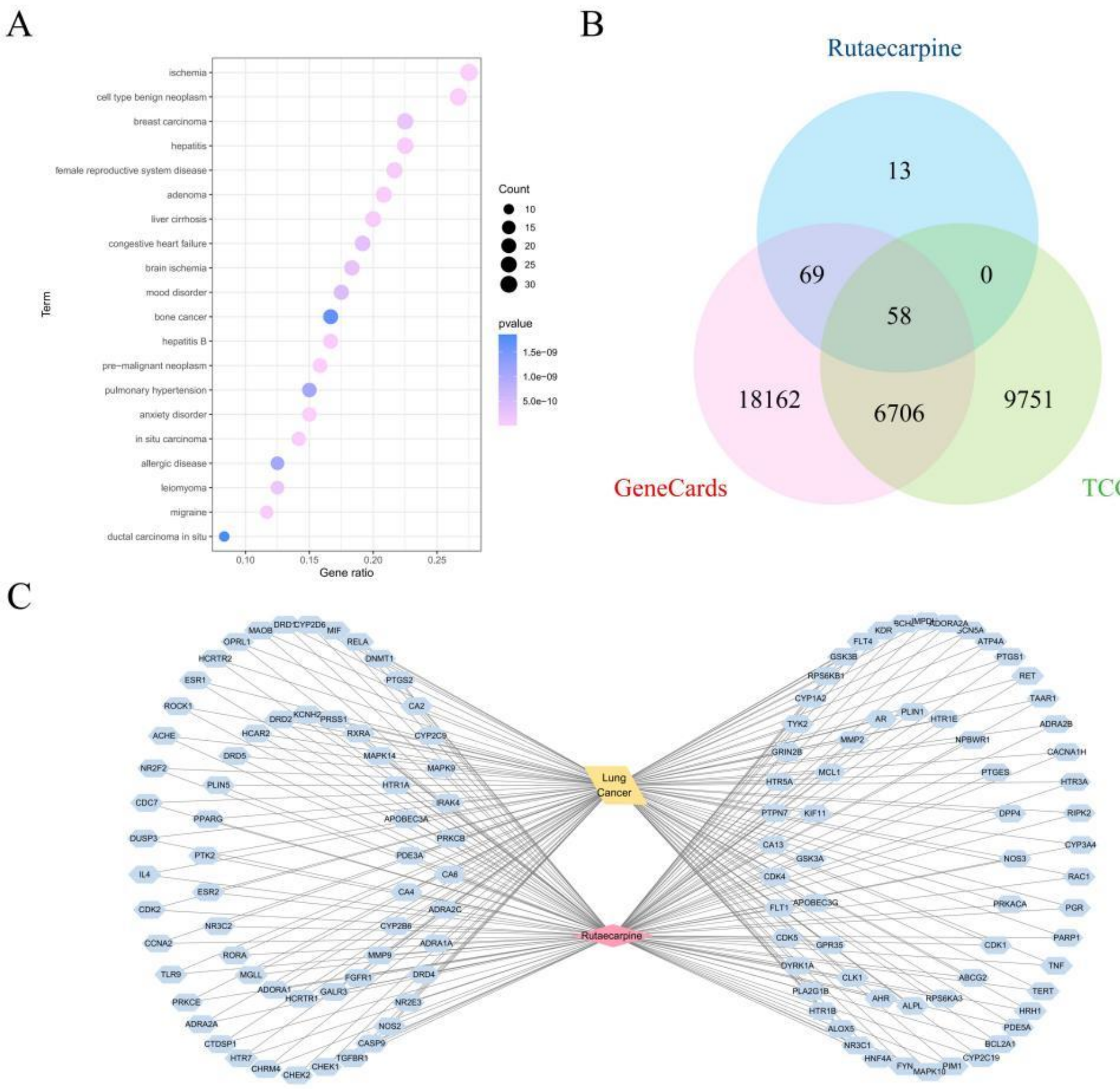
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In accordance with the standards and guidance set forth by the Accreditation Council for Continuing Medical Education (ACCME), we hereby disclose that artificial intelligence (AI) tools were not utilized in the development of this educational material.

Acknowledgements

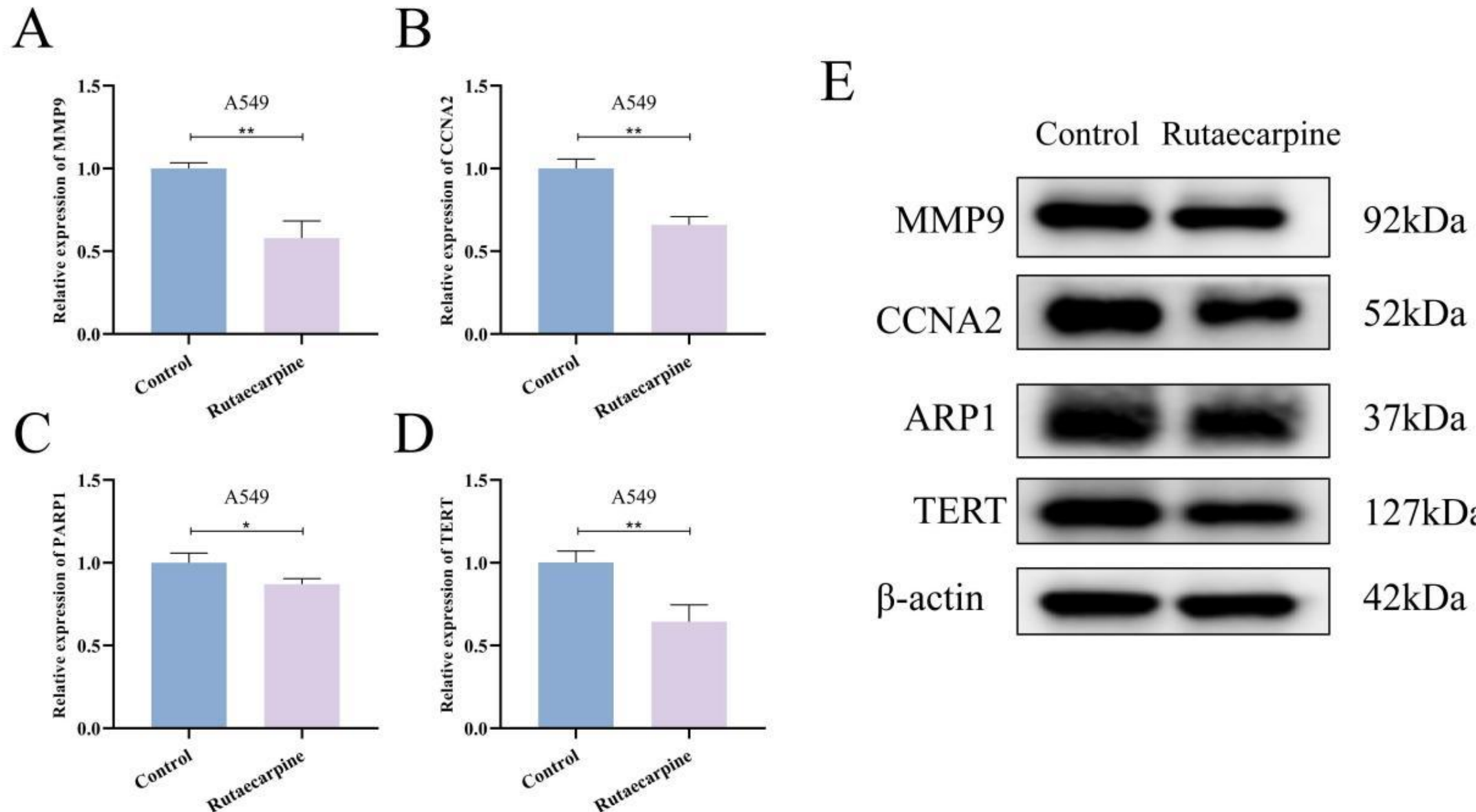
Our study was supported by the supported by the Gaoxin Branch of The First Affiliated Hospital of Nanchang University (KYZZ202407).

RESULTS



A total of 58 overlapping genes were identified as potential targets of Rutaecarpine in lung cancer. PPI network analysis identified four hub genes (MMP9, CCNA2, PARP1, and TERT).

Molecular docking revealed favorable binding energies, particularly between Rutaecarpine and MMP9 (-13.3 kcal/mol).



Consistently, Rutaecarpine treatment significantly reduced the mRNA and protein expression of the four hub genes in A549 cells.