EP06.07-Co-Mutation Burden as a Determinant of Outcome in EGFR-Mutated Metastatic NSCLC — Real-World Evidence From India

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INTRODUCTION

• EGFR-mutated mNSCLC is targetable, yet clinical outcomes remain heterogeneous.

• Co-occurring genomic alterations may modify treatment response, but a simple present/absent framework may miss the effect of genomic complexity.

• Objective: characterize the co-mutation landscape and explore whether co-mutation burden (0, 1, ≥2) better explains outcome variability.

METHODS

RETROSPECTIVE CLINICOGENOMIC ANALYSIS

43 — **EGFR-mutated mNSCLC**

Jan 2024-Mar 2026 — **Study period**

CGP — **Clinical + genomic review**

0 • 1 • ≥2 — **Co-mutation burden groups**

Endpoints: PFS and OS
Statistics: Kaplan-Meier + log-rank test
Censoring: last follow-up if no event
Median follow-up: 9.9 months (reverse Kaplan-Meier)

DISCUSSION AND CONCLUSION

ACTIONABLE TAKE-AWAY

• Any co-mutation: 45.5% (20/44).

• TP53 was dominant (~70% of co-mutated cases), but neither TP53 nor any co-mutation significantly separated survival.

• Burden showed a directional signal: ≥2 co-mutations had shorter disease control; one co-mutation showed the most favorable outcomes.

• The signal is exploratory: all comparisons p > 0.05.

FUTURE DIRECTION

Validate complexity-based genomic stratification in larger prospective cohorts with longer follow-up and treatment-specific analyses, and determine whether burden adds information beyond individual genes such as TP53.

REFERENCES & ACKNOWLEDGEMENTS

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References
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Kim Y, et al. *J Thorac Oncol.* 2019;14:193-202.
Offin M, et al. *J Thorac Oncol.* 2019;14:1784-1793.

RESULTS

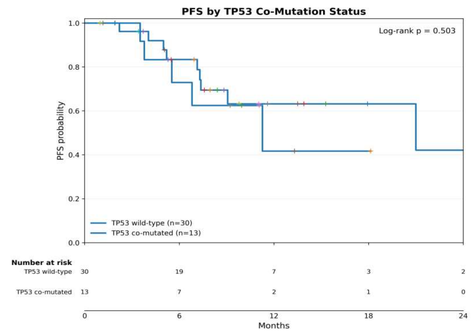
43 patients • median age 62.5 years • 63.6% female • median follow-up 9.9 months

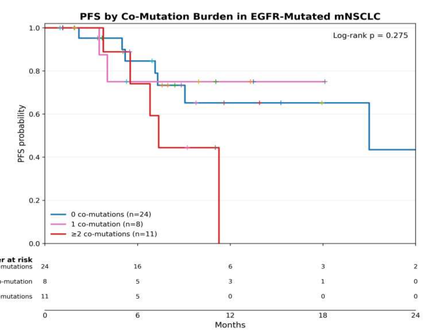
45.5% — **WITH ≥1 CO-MUTATION**

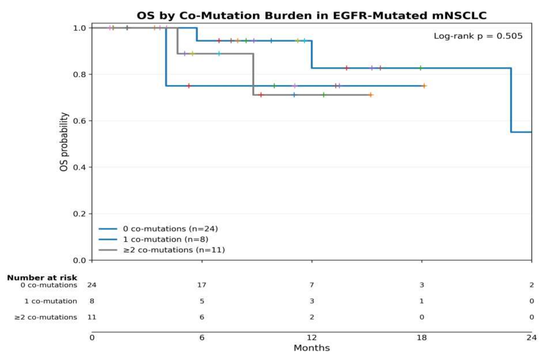
~70% — **TP53 AMONG CO-MUTATED CASES**

8–9 mo — **MEDIAN PFS OVERALL COHORT**

SURVIVAL FINDINGS







FROM MUTATION-CENTRIC → COMPLEXITY-BASED STRATIFICATION

The presence of a single named co-alteration did not explain outcome heterogeneity. The number of co-occurring alterations showed a more consistent directional relationship with disease behavior, supporting genomic complexity as a hypothesis-generating biomarker.