

EP06.40: Driver Mutations and Co-Mutation Profiles in Bangladeshi NSCLC: Insights from a Multicenter NGS Cohort

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INTRODUCTION

Next-generation sequencing (NGS) can simultaneously detect multiple genomic alterations, helping to identify actionable driver mutations and thus guide targeted therapy.

While the genomic landscape of NSCLC is well documented in high-income countries, data from low and middle-income countries, like Bangladesh, are unexplored.

Our objective is to define the driver mutation and co-mutation profile of Bangladeshi NSCLC population using real-world multicenter NGS data.

METHODS

Design: Retrospective, multicenter cohort study.

Participants: 3 tertiary oncology centers in Bangladesh.

Population: NSCLC patients tested with NGS from January 2020 till July 2025.

Testing: Multi-gene NGS panel (FFPE tissue or liquid biopsy) to screen for pathogenic/likely pathogenic somatic alterations.

Analysis: Descriptive statistics were used to evaluate mutation frequency and co-mutation patterns and were reported as counts and percentages.

DISCUSSION AND CONCLUSION

Actionable Take Away Message

- This is one of the earliest real-world NGS dataset to characterize the driver mutation and co-mutation landscape of NSCLC in Bangladesh.
- The most frequent actionable driver mutation was EGFR (43.11%), making it the preferred target for targeted therapy in this population.
- Almost half of the mutation positive patients had co-mutations, of which TP53 was the most common co-alteration.
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Future Direction for Research

- Access to multigene NGS testing in Bangladesh should be expanded as it could improve treatment selection and outcomes for NSCLC patients.
- Future outcome-driven research is needed to determine how this mutation profile affects the actual treatment response and survival in this population

REFERENCES & ACKNOWLEDGEMENTS

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Disclosures

No pharmaceutical/biotech funding. Not a clinical trial; however, it is a feasibility study. There was no medical writing done by industry sponsors.

RESULTS

270 NSCLC Patients from 3 centers were analyzed from Jan 2020 to Jul 2025:

- 70.4% male and Adenocarcinoma was the most common histology (67.0%).
- PD-L1 tested in 50% (n=135) with 54.8% positive result.
- 218 cases (80.7%) had a pathogenic genomic alteration.
- Of these, 52.75% had a single alteration and 47.25% showed co-mutations.
- EGFR was the most frequently altered gene (43.1%), followed by TP53 (27.5%) and KRAS (14.2%).
- TP53 was the most common co-mutated gene.
- The most common EGFR subtype (54.3% of all EGFR altered cases) was exon 19 deletion.

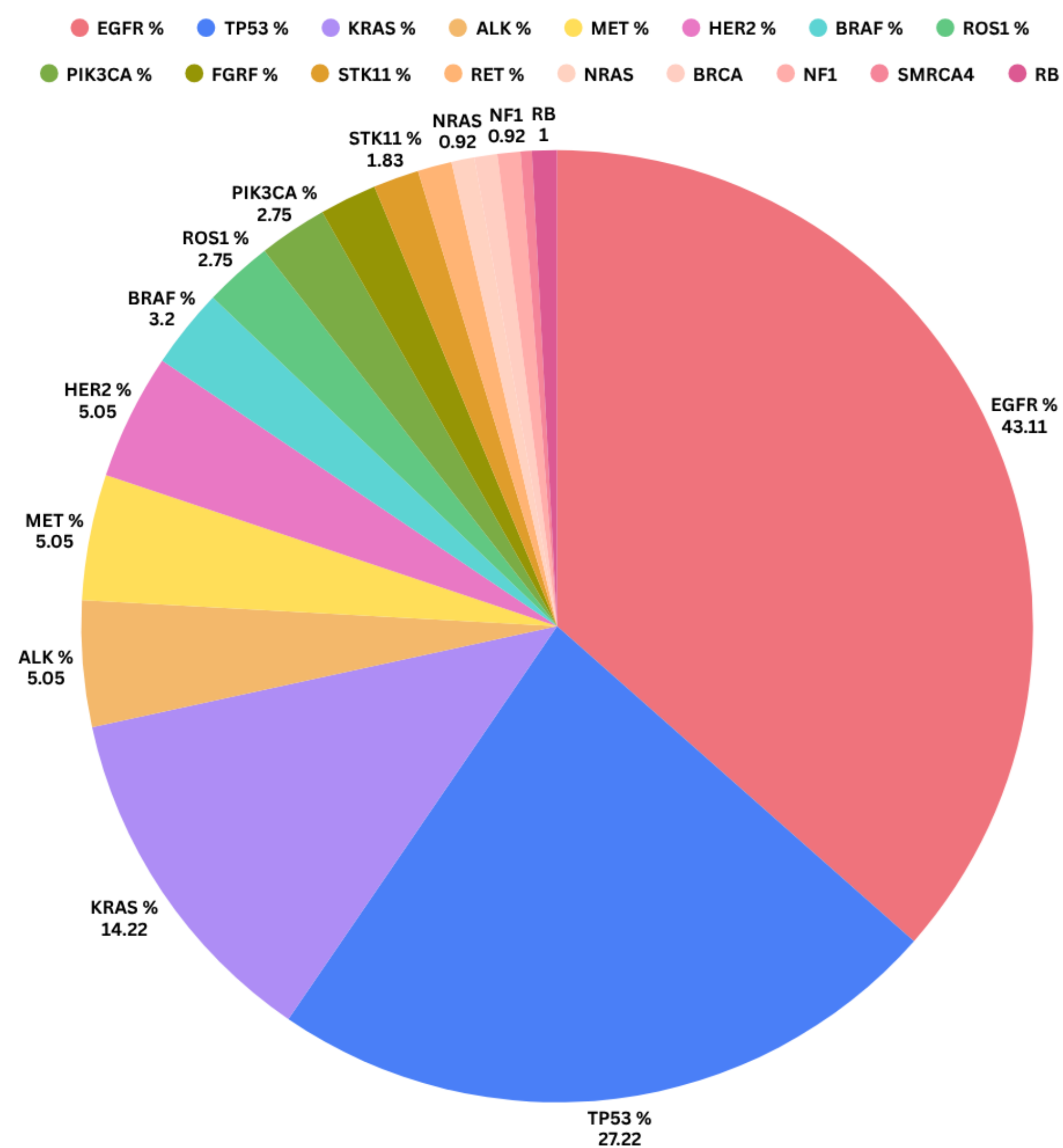


Figure 1. Distribution of genomic alterations in NSCLC patients with detectable mutations (n=218).

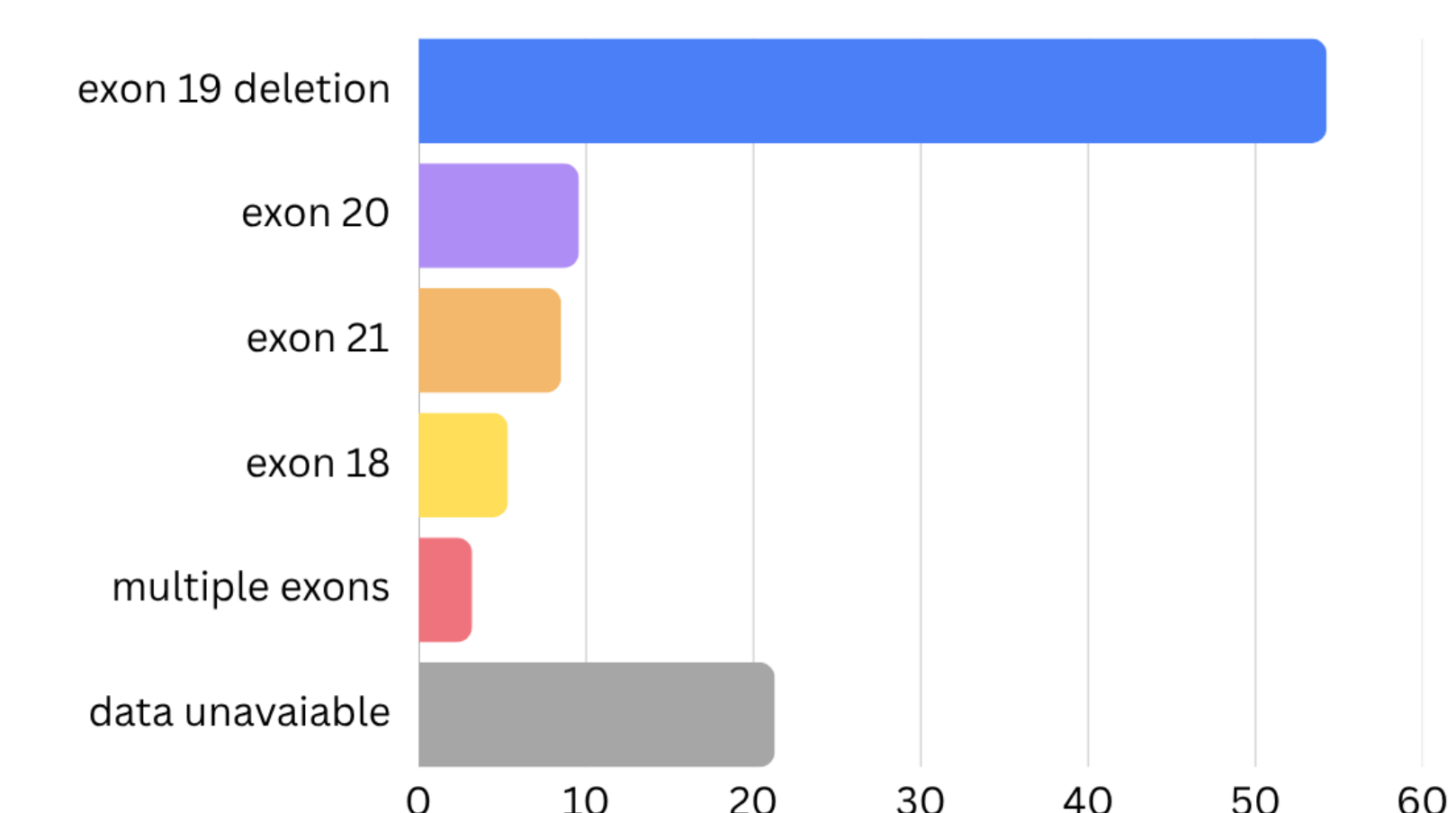


Figure 2. EGFR mutation subtypes among EGFR-altered cases (n=94).

