

INTRODUCTION

Comprehensive molecular testing is essential for precision oncology in non-small cell lung cancer (NSCLC), enabling the identification of actionable alterations and personalized treatment strategies. The prevalence of somatic mutations varies according to population ancestry and regional differences. Comprehensive molecular testing is essential for precision oncology in non-small cell lung cancer (NSCLC), enabling the identification of actionable alterations and the design of personalized treatment strategies. The prevalence of somatic driver mutations varies according to population ancestry and regional/ethnic background, underscoring the need for molecular epidemiology data from underrepresented populations. In Brazil, previously reported frequencies of driver alterations in NSCLC include EGFR mutations in 23.6% of cases, EGFR exon 20 insertions in 2.9%, ERBB2 (HER2) mutations in 3.4%, ALK fusions in 4.4%, and KRAS mutations in 28.4%¹. The Brazilian Amazon represents a unique setting, hosting the largest indigenous population in the country (~490,900 individuals), with Manaus accounting for the largest urban Indigenous population (~71,700), according to the 2022 national census (IBGE)², providing a distinct context for genomic investigation.

METHODS

Design:

This was a retrospective observational study using secondary data from medical records of patients with histopathologically confirmed NSCLC who underwent molecular testing between 2019 and 2024. The study was conducted at three institutions in Manaus, Brazil: two private oncology centers (SENSUMED Oncologia - Oncoclínicas and Instituto do Câncer de Manaus - Oncoclínicas) and one public cancer center (Fundação Centro de Controle de Oncologia do Estado do Amazonas - FCECON). Genomic profiling was performed using next-generation sequencing (NGS) with commercially available platforms (FoundationOne and GS Infinity) through the Lung Mapping program. The study was approved by the local ethics committee (CAAE 81245524.0.0000.0004).

DISCUSSION AND CONCLUSION

Take Away Message

These findings demonstrate a high prevalence of actionable mutations, particularly in EGFR and ERBB2, along with a low frequency of KRAS G12C, suggesting a distinct genomic profile in the Amazonas population. These results highlight the need for region-specific precision oncology strategies and expanded access to molecular testing in underrepresented populations.

Clinical Impact: Empowers oncologists to base therapeutic decisions on real-world regional evidence, sparing patients from generic systemic treatments and optimizing the use of targeted therapies.

Future Directions: Subsequent research must investigate the etiology of these mutational divergences and promote clinical trials specifically designed for the prevalent molecular subgroups in the Amazonas population.

REFERENCES & ACKNOWLEDGEMENTS

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Artificial Intelligence (AI) Use Disclaimer

Artificial intelligence tools were used in the preparation of this poster. Data visualization (pie chart) was generated using Google Gemini, and English translation and editing were assisted by ChatGPT (OpenAI). The authors reviewed all content and take full responsibility for its accuracy.

RESULTS

A total of **612 patients** with NSCLC were identified between 2019 and 2024. Smoking history was unknown in 42.6% of cases, while 37.3% were former smokers, 10.3% never smokers, 7.8% current smokers, and 1.9% had passive exposure. Among these patients, **61 underwent molecular analysis by NGS**, comprising the genomic cohort. There were a predominance of **females (55.7%)** and a **high proportion of metastatic disease at diagnosis (68.8%)**. **EGFR mutations were identified in 45.9% of cases (n=28)**, including **exon 19 deletions (53.5%)**, L858R (n=6), L861Q (n=2), exon 18 alteration (n=2), and exon 20 insertions (n=1). **ERBB2 (HER2) mutations were observed in 11.5% of patients (n=7)**, while **ALK fusions and MET alterations were detected in 8.2% of cases each (n=5)**. KRAS mutations were identified in 16.4% (n=10), with only 3.3% (n=2) corresponding to the G12C variant. BRAF mutations were observed in 3.3% of patients (n=2).

NGS Molecular Findings in NSCLC Cohort

