



P2.195: Prognostic Significance of CSF ctDNA Profiling in EGFR-Mutant NSCLC With Leptomeningeal Metastasis: A Multi-Center Real-World Analysis

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INTRODUCTION

Leptomeningeal metastasis (LM) is a severe complication in EGFR-mutant non-small cell lung cancer (NSCLC), with limited biomarkers to guide prognosis and treatment. We evaluated the prognostic value of cerebrospinal fluid (CSF)-derived circulating tumor DNA (ctDNA) profiling in a real-world, multi-center cohort.

METHODS

Design: This retrospective study included patients with EGFR-mutant NSCLC who developed LM and underwent CSF ctDNA profiling using a 118-gene targeted next-generation sequencing (NGS) panel between May 2022 and December 2024 at three hospitals in Taiwan.

Clinical data and molecular alterations were analyzed for their association with overall survival (OS) from the time of CSF sampling.

DISCUSSION AND CONCLUSION

Actionable Take Away Message

- CSF ctDNA NGS captures actionable resistance mutations
- Three independent risk factors shorten OS
- Osimertinib Pretreatment: Median OS 9.5 vs. 29.9 months (HR 4.22)
- Smoking History: HR 4.62
- CSF EGFR L858R: HR 2.43
- Profiling revealed high-frequency targets including EGFR amplification and TP53 mutation.

Future Direction for Research

- Biomarker-guided clinical trials to match to CSF ctDNA profiles.
- Track longitudinal CSF ctDNA kinetics to detect early progression and measure CNS response.
- Evaluate genotype-directed regimens based on CSF mutations.

REFERENCES & ACKNOWLEDGEMENTS

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RESULTS

