



P2.186: Minimal Residual Disease Dynamic Monitoring in First-Line Serplulimab Plus Chemotherapy in Treatment of Extensive-Stage Small Cell Lung Cancer

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INTRODUCTION

Chemo-immunotherapy has improved ES-SCLC outcomes, but durable benefit remains limited and established tissue biomarkers have inconsistent predictive value.

Circulating tumor DNA (ctDNA) enables non-invasive, longitudinal assessment of molecular residual disease and may reveal response or relapse earlier than imaging.

Objective: Evaluate the prognostic value of longitudinal ctDNA-based MRD monitoring in ES-SCLC patients treated with first-line Chemo-immunotherapy

METHODS

Design:

Prospective, single-center exploratory study (NCT05873790). Treatment-naïve ES-SCLC patients received serplulimab plus platinum-etoposide for up to 6 cycles, followed by serplulimab maintenance.

Plasma samples were collected at baseline (T0), after 2 cycles (T1), after 6 cycles (T2), at 6 months post-chemotherapy cessation, and upon tumor progression.

Genomic DNA from tumor tissue and plasma ctDNA were analyzed by targeted NGS. Tumor samples were sequenced using a 437-gene lung cancer panel (~850× depth), and ctDNA was analyzed with an ultra-deep NGS panel targeting 2,365 cancer-relevant genes (~30,000×).

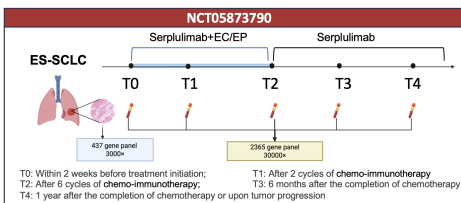


Figure 1. Study schema.

DISCUSSION AND CONCLUSION

Actionable Take-Away Message

- On-treatment ctDNA dynamics were more informative than baseline ctDNA.
- ctDNA clearance was associated with longer PFS.
- ctDNA monitoring is more sensitive than conventional imaging for detecting progression, identifying molecular signs of disease progression months earlier.

Patients achieving MRD clearance during treatment showed significantly prolonged PFS: 11.51 vs 6.63 months (P=0.009).

Future Direction for Research

- Validate in larger multicenter cohorts with longer OS follow-up.
- Test ctDNA-guided treatment adaptation.
- Standardize optimal sampling time-points and quantitative clearance thresholds

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Artificial Intelligence (AI) Use Disclaimer:

The authors confirm that no generative AI or AI-assisted technologies were used in the preparation of this poster or the analysis of the presented data.

RESULTS



Baseline genomic landscape

- Twenty-three of the top 30 tissue mutations were detectable in baseline plasma.
- TMEM132D, MTAP, FTM1, and NAV3 mutations were associated with shorter PFS (P<0.001 to P=0.014).

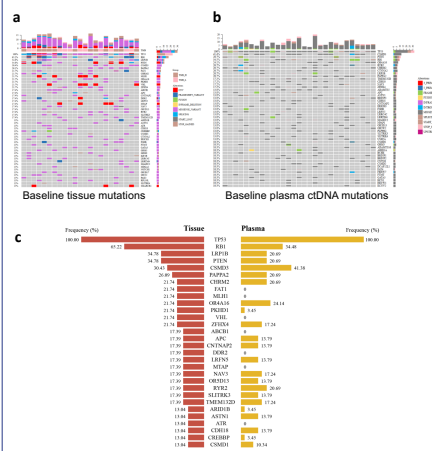


Figure 4. Tissue/plasma profiles and PFS by baseline mutation status.

Early ctDNA clearance stratified prognosis

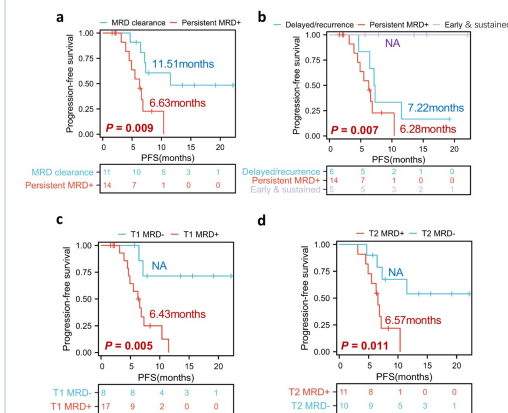


Figure 5. Impact of ctDNA dynamics on PFS. a, b Longitudinal ctDNA Dynamics: Kaplan-Meier curves comparing PFS according to (a) ctDNA status during treatment (MRD clearance vs. persistent MRD+) and (b) kinetic clearance patterns (early-sustained, delayed or recurrence, and persistent MRD+). c, d Landmark Analyses: PFS stratified by ctDNA status at specific timepoints: (c) T1 (after 2 cycles) and (d) T2 (after 6 cycles).