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ctDNA analysis of *EGFR*-mutant NSCLC patients receiving osimertinib following previous tyrosine kinase inhibitor treatment

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Aim

Explore the feasibility of ctDNA testing in a clinical setting for NSCLC patients receiving osimertinib as a second or third line EGFR-TKI

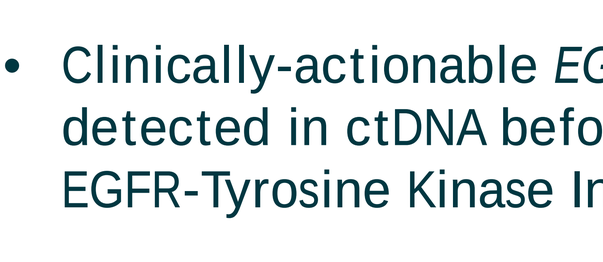
Background

- Circulating tumor (ct)DNA analysis is increasingly used to guide clinical management of advanced non-small cell lung cancer (NSCLC)
- Clinically-actionable *EGFR* mutations can be detected in ctDNA before or after first-line EGFR-Tyrosine Kinase Inhibitor (TKI) treatment
- Data concerning ctDNA detection are limited for patients with a complex treatment history

Materials and Methods

Twenty NSCLC patients who had received osimertinib as a second or third line EGFR-TKI. Pathological and clinical data were acquired.

Tumor-tissue



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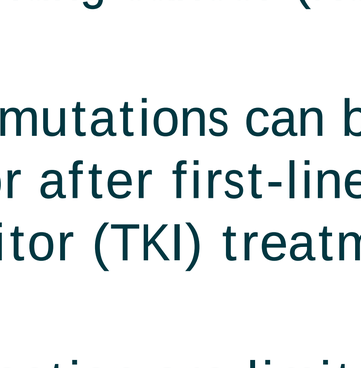
Illumina TruSeq Amplicon Cancer Panel (48 genes)

Plasma cfDNA



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EGFR mutations by Droplet digital PCR (ddPCR)

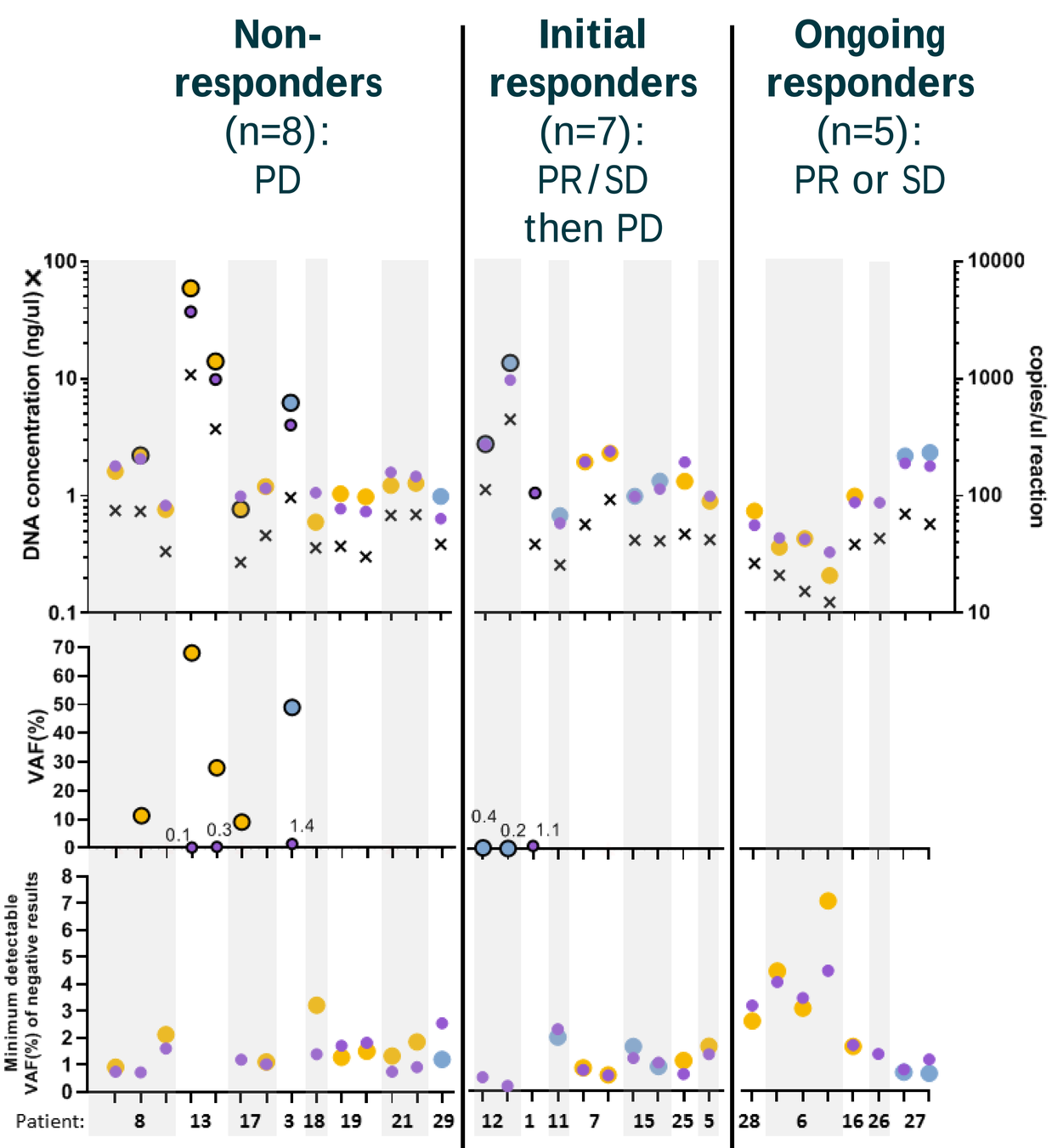
Results

Patients classified based on osimertinib response

Key:

- PD: Progressive Disease
- PR: Partial Response
- SD: Stable Disease
- Exon 19 del
- L858R
- T790M

wt mutant



	Non-responders (n=8): PD	Initial responders (n=7): PR/SD then PD	Ongoing responders (n=5): PR or SD
ctDNA detected:	4/8 (50%) patients	2/7 (29%) patients	0/5 (0%) patients

The fraction of *EGFR*-mutant ctDNA tended to be higher in non-responders (0.1 - 68%) than initial responders (0.2 – 1.1%).

No significant difference in overall cfDNA concentration between response groups or the number of metastatic sites.

Conclusion

These results support a potential role for ctDNA analysis in response monitoring of NSCLC patients with a complex EGFR-TKI treatment history.

Poster

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