

## Liquid Biopsy: Current and Future Applications

Valsamo Anagnostou, MD, PhD Associate Professor, Johns Hopkins School of Medicine Co-director, Upper Aerodigestive Malignancies Program Leader, Precision Oncology Analytics, Molecular Tumor Board & Lung Cancer Precision Medicine Center of Excellence

@ValsamoA | @HopkinsThoracic | @MolecularOncLab | https://anagnostoulab.org





## **Disclosure information**

### Valsamo Anagnostou

I have the following financial relationships to disclose:

Current/within the past 5 years: Grant/Research support (to Johns Hopkins) from: Astra Zeneca, Bristol-Myers Squibb, Personal Genome Diagnostics/Labcorp and Delfi Diagnostics; advisory board member for: Astra Zeneca and Neogenomics, honoraria: Foundation Medicine, Personal Genome Diagnostics

My additional financial relationship disclosures are:

I am an inventor on patent applications (63/276,525, 17/779,936, 16/312,152, 16/341,862, 17/047,006 and 17/598,690) submitted by Johns Hopkins University related to cancer genomic analyses, ctDNA therapeutic response monitoring and immunogenomic features of response to immunotherapy that have been licensed to one or more entities. Under the terms of these license agreements, the University and inventors are entitled to fees and royalty distributions.

#### -and-

I will not discuss off label use and/or investigational use in my presentation.

## Comprehensive genomic profiling (CGP)

- Single NGS assay that assesses a variety of genomic alterations
- Single nucleotide variants, indels, splice variants, copy number variation, fusions
- Genomic signatures, tumor mutation burden, microsatellite instability, homologous recombination deficiency

#### ctDNA CGP **Tumor tissue CGP** Minimally invasive Gold standard for tumor Fast turn around time genotyping Higher false negative rate Invasive Higher false positive rate (CH, Longer turnaround time Higher rate of failed or missing aging) Varying LOD based on alteration tumor tissue sequencing • Higher false negative rate when Captures tumor heterogeneity Captures tumor evolution and tumor purity is low Does not capture tumor new targets May alleviate health disparities heterogeneity or evolution Disparities in tumor CPG in genomic testing

# Liquid biopsy approaches for sensitive and specific detection of cancer



Bruhm et al., Nat Genet, 2023, Mattox et al., Cancer Discov, 2023, Wang et al., PNAS, 2023, Sivapalan et al., Clin Can Res, 2023, Foda et al., Cancer Discov, 2023 Cohen et al., Nat Biotechnol, 2021, Cristiano et al., Nature, 2019, Anagnostou et al., Can Res, 2019, 2020, Cohen et al., Science, 2018, Phallen et al., Science TM, 2017

## Liquid biopsy methods for ctDNA detection



Landon et al., International Review of Cell and Molecular Biology, in press

# The confounding effect of clonal hematopoiesis variants in clinical outcome prediction



Sivapalan et al., presented at AACR24

# ctDNA CGP may overcome challenges with tissue CGP



Patients With Therapeutically Targetable Mutations

## Capturing residual disease through liquid biopsies



Tumor arises.



Tumor cells shed ctDNA in the blood stream.



ctDNA is isolated from serial blood draws.



Mutations in ctDNA are detected by NGS.

Interventional ctDNA Trials

#### Detection of Residual Disease



Liquid biopsies allow for minimal residual disease detection after surgery.



Detection of ctDNA early after definitive therapy may be a robust biomarker for minimal residual disease.

#### Monitoring Therapeutic Response



Imaging is inadequate to capture clinical response in the setting of immunotherapy.

Liquid biopsies allow for minimally invasive, real time tracking of circulating tumor burden during therapy. 

Interventional ctDNA trials rely on molecular response assessments during therapy.

Patients are stratified by ctDNA response, followed by treatment escalation or de-escalation.

## Landmark ctDNA MRD predicts outcomes for NSCLC

ctDNA MRD+ Recurrence + (n=25)

#### **Clinical sensitivity 49%**

ctDNA MRD-Recurrence + (n=26)

#### 51% discordance

ctDNA in-evaluable Recurrence + (n=19)



- Tumor-informed anchored multiplex PCR enrichment
- Assay sensitivity using a 50-variant panel at 0.01% VAF was > 90% at DNA input > 20 ng
- LOD 95 VAF 0.008% (80 PPM)
- Landmark ctDNA MRD assessed within 120 days of surgery: 25% ctDNA MRD+
- Clinical sensitivity 49% (fraction of ctDNA MRD+ among those who recurred)
- Landmark ctDNA MRD+ patients had a hazard ratio of 5.3 for OS and a hazard ratio of 6.8 for freedom from relapse relative to MRD- (P<0.001)
- Landmark-positive patients had the longest lead times (228 days)
- Patients relapsing in the first year of surgery are more likely to be MRD positive

# What is the role of ctDNA MRD in navigating the evolving therapeutic landscape of early-stage NSCLC?

- Numerous treatment options are currently available to reduce the risk of recurrence in patients with earlystage resectable non-small-cell lung cancer (NSCLC), including neoadjuvant and adjuvant immunotherapy, which have been shown to improve outcomes in patients undergoing surgery.
- Major pathological response (MPR; ≤10% viable tumor cells remain after surgery) or pathological complete response (pCR; no viable tumor cells remaining after surgery) have been shown to predict disease-free survival post neoadjuvant immune checkpoint blockade and are commonly used as surrogate endpoints.
- Despite the expanding field, we are limited in our ability to **risk-stratify** patients for neoadjuvant immunotherapy or **personalize adjuvant therapy** following neoadjuvant immunotherapy.
- It is imperative to employ ultra-sensitive ctDNA approaches to define the subset of patients who will benefit
  most from additional therapy in the neoadjuvant/adjuvant space that is the pre-requisite stepping stone for the
  design of ctDNA interventional clinical trials for patients with resectable NSCLC.

Felip E et al., Lancet, 2021, O'Brien M et al., Lancet Oncol, 2022, Cascone T et al., N Engl J Med, 2024, Heymach JV et al., N Engl J Med, 2023, Forde PM et al., N Engl J Med, 2022, Lu S et al., JAMA, 2024, Wakelee H et al., N Engl J Med, 2023

## IMpower-010: Adjuvant immunotherapy may delay ctDNA MRD emergence

#### DFS by treatment arm and post-chemo ctDNA clearance status

Time to ctDNA+ by treatment arm



ctDNA cleared	Atezo (n=36)	BSC (n=28)
mDFS, mo	31.3	13.3
HR (95% CI)	<b>0.7</b> (0.37, 1.34)	

ctDNA not cleared	Atezo (n=19)	BSC (n=20)
mDFS, mo	4.2	3.9
HR (95% CI)	<b>0.67</b> (0.34, 1.32)	



## Pre-op ctDNA clearance predicts pCR and EFS with neoadjuvant chemo-immunotherapy



## Post-op ctDNA clearance predicts DFS (AEGEAN trial)



 In the AEGEAN clinical trial, patients with ctDNA detected at adjuvant C1D1 had the poorest disease-free survival outcomes compared to ctDNA-negative patients in both treatment arms.

### ctDNA assessment may help refine the heterogeneity of non pCR



Kelly, Landon et al., Nat Med, 2024

## ctDNA dynamics during immune checkpoint blockade







Anagnostou, Forde et al., Cancer Res, 2019, Huang et al., J Immunother Cancer, 2022, Sivapalan et al., Clin Can Res, 2023, Murray, Sivapalan et al., Clin Can Res, 2024

## BR.36: A ctDNA-directed phase II/III study of molecular response adaptive immunotherapy in NSCLC



Individuals with ctDNA progression on pembrolizumab can be rapidly and accurately identified followed by treatment escalation





ctDNA response



• Liquid biopsies better predict overall survival.

CCTG BR.36, NCT04093167, Anagnostou et al., Nat Med, 2023

### ctDNA-RECIST response concordance



- BR.36 stage 1 met its primary endpoint.
- The sensitivity of molecular response for RECIST best overall response was 82%, (90% CI: 52% - 97%), specificity was 75% (90% CI: 56.5% -88.5%).
- Median time to ctDNA response 2.1 months
- Patients with mR attained longer PFS and OS.

Anagnostou et al., Nat Med, 2023

BR.36 stage 2-A Biomarker-Directed, Open Label, Multi-Center Phase II/III Study of Molecular Response Adaptive Immuno-Chemotherapy in Patients with NSCLC



NCT04093167, sponsored by the Cancer Research Institute, the Mark Foundation for Cancer Research and Labcorp/Personal Genome Diagnostics

## Bridging scientific discovery with clinical cancer care through ctDNA-adaptive trials



Adapted from Sivapalan et al., Clin Cancer Res, 2023, Sivapalan et al., J Immunother Cancer, 2023



- Liquid biopsy approaches can be implemented in clinical diagnostic applications in precision-oncology.
- ctDNA CGP complements tissue CGP and has advantages in capturing tumor evolution and emerging therapeutic targets.
- Technical performance and biologic noise in ctDNA CPG represent challenges.
- Serial ctDNA measurements and molecular response are promising early endpoints.
- ctDNA molecular response adaptive clinical trials will establish the role of ctDNA as an early endpoint of immunotherapy response.
- ctDNA MRD can be informative in navigating the expanding therapeutic options for patients with early stage NSCLC





## Acknowledgements

Molecular Oncology Lab @Hopkins Thoracic





Lavanya Sivapalan Noushin Niknafs











Jaime Wehr

Blair Landon

K Velliangiri

Danny Rabizadeh

James White









@ValsamoA

Mimi Naiiar

Thoracic Oncology Julie Brahmer **Christine Hann Kristen Marrone Ben Levy** Amna Jamali Joy Feliciano Vincent Lam Joe Murray

**Susie Scott** Aliya Pabani

**Hopkins BME Rachel Karchin** 

**Cancer Genetics** & Epigenetics Victor Velculescu **Steve Baylin** Nilo Azad Hari Easwaran

Cancer Immunology **Drew Pardoll Kellie Smith** 

#### Pathology

Peter Illei Janis Taube Kay Li

**Quantitative Sciences Rob Scharpf** 

**Thoracic Surgery Richard Battafarano Stephen Yang** Jinny Ha **Stephen Broderick** Malcolm Brock

CCTG and BR.36 investigators Janet Dancey Cheryl Ho **Penelope Bradbury Pierre-Olivier Gaudreau** Keyue Ding **Garth Nicholas Rosalyn Anne Juergens Adrian Sacher Andrea Fung Paul Wheatley-Price** Scott Laurie Sara Moore **Egor Avrutin** Liting Zhu Lisa Callahan

**Cancer Research** Institute

ECOG-ACRIN, PrECOG Charu Aggarwal Zhuoxin Sun **Karen Padilla** 



LUNG CANCER SYMPOSIUM

@ValsamoA | @HopkinsThoracic | @MolecularOncLab https://anagnostoulab.org



