

PATIENT-CENTERED CARE
May 8
From Bench to Bedside: Molecular Oncology's Role in Personalized Cancer Diagnosis and Treatment

Sound Check
11:55

Start Time
12:00

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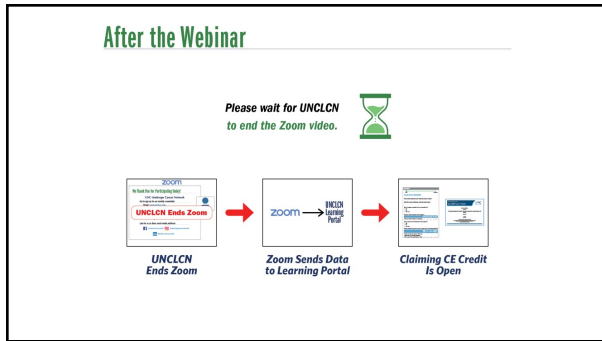
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May 21 - May 22

unclineberger.org/symposium


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Our Presenter



Lori Ramkissoon, PhD

Lori Ramkissoon, Ph.D., is a Clinical Assistant Professor of Pathology and Laboratory Medicine at the University of North Carolina Medical Center, where she leads the Cytogenetics Laboratory. This laboratory specializes in advanced genetic testing methodologies, including karyotyping, chromosome microarrays, and fluorescence in situ hybridization, to detect structural genetic variations in a broad spectrum of specimens ranging from prenatal and constitutional to oncological. These diagnostic services are crucial for identifying genetic disorders and pinpointing specific genetic markers that help classify various tumor types, thereby enhancing patient care through precise diagnoses.

Dr. Ramkissoon received a BA in Biochemistry from Baylor University and a Ph.D. from Weill Cornell Graduate School of Medical Sciences. Her postdoctoral tenure at the Dana-Farber Cancer Institute, under the mentorship of Dr. Keith Ligon, was pivotal in shaping her research focus on the genomic underpinnings of pediatric brain tumors. This experience motivated her to complete a clinical fellowship in Molecular and Clinical Cytogenetics at UNC, culminating in her board certification in Laboratory Genetics and Genomics. Additionally, Dr. Ramkissoon contributes her expertise to the UNC Precision Oncology Program, facilitating the incorporation of genomic insights into personalized treatment strategies for oncology patients.

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Our Presenter _____

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Our Presenter _____

- Lori Ramkissoon, PhD is Director of the Cytogenetics laboratory at the University of North Carolina Medical Center

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Our Presenter _____

- Lori Ramkissoon, PhD is Director of the Cytogenetics laboratory at the University of North Carolina Medical Center
- She earned her PhD from Weill Cornell Graduate School of Medical Sciences and did a postdoctoral fellowship at Dana-Farber Cancer Institute

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Our Presenter

4. Lori Ramkissoon, PhD is Director of the Cytogenetics laboratory at the University of North Carolina Medical Center
3. She earned her PhD from Weill Cornell Graduate School of Medical Sciences and did a postdoctoral fellowship at Dana-Farber Cancer Institute
2. Prior to graduate school, she was a pre-doctoral fellow in the laboratory of Dr. Neal Young at the National Heart, Lung and Blood Institute in Bethesda, MD

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Our Presenter

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2. Prior to graduate school, she was a pre-doctoral fellow in the laboratory of Dr. Neal Young at the National Heart, Lung and Blood Institute in Bethesda, MD
1. She worked for a year as a staff assistant in the United States Senate.

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ACCME Disclosure

This activity has been planned and implemented under the sole supervision of the Course Director, Stephanie Wheeler, M.D. MPH, in association with the UNC Office of Continuing Professional Development (CPD). The course director received research support from AstraZeneca (ended June 2023) and Pfizer Medical Foundation (ended December 2023). These financial relationships have been mitigated. CPD staff have no relevant financial relationships with ineligible companies as defined by the ACCME.

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The presenter has no relevant financial relationships with ineligible companies as defined by the ACCME.

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1.0 Contact Hours Provided

Relevant Financial Relationship:
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Criteria for Activity Completion:
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Approved Provider Statement:
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Cancer is fundamentally a disease caused by changes to the "normal" sequence of a patient's genome, and the goal of molecular oncology is to define and understand these changes to benefit the diagnosis and treatment of cancer.

True


False

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From Bench to Bedside: Molecular Oncology's Role in Personalized Cancer Diagnosis and Treatment

Lori Ramkissoon, PhD
Lori.Ramkissoon@unchealth.unc.edu
May 8, 2024



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Molecular biomarkers are only used in the research setting and are not part of current standard of care clinical paradigms?

True 0%

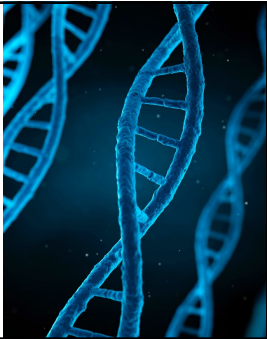
False 0%

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Learning Objectives


- Review advancements in the laboratory methods used to detect molecular biomarkers in oncology specimens
- Illustrate how molecular biomarkers have been integrated into diagnostic algorithms for certain cancer types
- Discuss the contributions of molecular oncology in treatment strategies



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Conventional treatment options for cancer patients





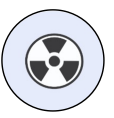
Surgery

- Resection
- Biopsy
- Fine needle aspirations



Chemotherapy

- Cytotoxic
- Neo-adjuvant or Adjuvant
- Maintenance regimens




Radiation

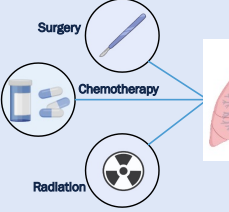
- External
- Internal

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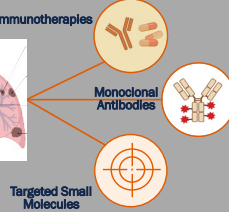
Advancement in treatment options



Conventional Treatments




Precision Medicine



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Biomarkers guiding cancer care



Prior to Cancer	Diagnosis	After Cancer Diagnosis				Post Treatment
Am I at increased risk for cancer?	Do I have cancer? What type of cancer?	What is the expected course of my cancer?	Will my cancer respond to this drug?	Should I receive a normal or lower dose?	How's my cancer responding to this treatment?	Will my cancer come back?
Risk Assessment	Diagnosis	Prognosis	Predicting Treatment Response	Pharmacokinetics	Monitoring Treatment Response	Recurrence

Natl Compr Canc Netw, 2019

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Molecular biomarkers in cancer

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What are biomarkers?

Biomarker: "cellular, biochemical or molecular alterations that are measurable in human tissues, cells, or fluids"

Biomarker	Example
Physiological biomarker	Blood pressure
Inflammatory biomarker	C-reactive protein
Prostate cancer biomarker	PSA
Molecular biomarker	EGFR
Somatic mutational biomarker	KRAS G12D
Germline mutational biomarker	BRCA1
Tumor agnostic biomarker	TMB, MSI, NTRK
Immune biomarker	PDL1

Biomarker Applications:

- Screen of diseases
- Assess risk of developing diseases
- Monitor diseases status before and after therapy
- Determine prognosis independent of therapy
- Predict response to therapy
- Distinguish between benign versus malignant process

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How are molecular biomarkers used in oncology?

Diagnostic

- Assist with establishing diagnosis or classification
- Example: *BCR::ABL1* gene fusion in chronic myeloid leukemia (CML)

Prognostic

- Assist with determining the likely aggressiveness or course of disease
- Example: *TP53* mutations are an adverse prognostic factor in chronic lymphocytic leukemia (CLL)

Therapeutic

- Assist with prediction of response or resistance to a given drug, biologic, or regimen
- Example: *EGFR* activating mutations are associated with response to EGFR tyrosine kinase inhibitor (TKI) therapy in Non-Small Cell Lung Cancer

Clinical Trial Eligibility

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NCCN Guidelines and biomarkers

- Currently more than 800 biomarker recommendations are included in NCCN Guidelines
 - Determine risk of disease (BRCA-1/BRCA-2)
 - Screening (PSA for prostate)
 - Diagnostic (BCR/ABL in CML)
 - Prognostic (CA 19-9 in pancreas)
 - Predictive (ER/PR status in breast)
 - Risk of toxicity (UGT1A1*28 allele for irinotecan)
 - Response/disease monitoring (AFP; HCG in testicular)

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NCCN recommendations for biomarker testing in non-small cell lung cancer

Adapted from genetechnology.com and NCCN guidelines.

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NCCN biomarkers in colorectal cancer

© 2019 by ASCO.org

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Biomarker landscape in solid & hematologic cancers

Brain: NOTCH1, IDH1/2, pTERT, 1p/19q co-deletion

Thyroid: ALK, HRAS, NRAS, BRAF, TERT, RET

Lung: EGFR, ALK, ROS1, RET, BRAF, KRAS, HER2

Melanoma: BRAF, KIT, NRAS, ROS1, ALA

Hematologic: ABL, FLT3, IDH1/2, KRAS, PDGFRA, WT1, KIT

Breast: PI3KCA, ERBB2, BRCA1, BRCA2, MLH1, MSH2, MSH6, PMS2, CDK4/6

Colorectal: BRAF, NRAS, NRAS, ERBB2, MLH1, MSH2, MSH6, PMS2

Prostate: BRCA1, BRCA2, PTEN, AR, MLH1, MSH2, MSH6, PMS2

Ovarian/Cervical: BRCA1, BRCA2, MLH1, MSH2, MSH6, PMS2

Tumor agnostic biomarkers in solid tumors: Fusions (NTRK), TMB, MSI

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ASCO Guidelines SOMATIC GENOMIC TESTING IN PATIENTS WITH METASTATIC OR ADVANCED CANCER
PROVISIONAL CLINICAL OPINION

WHICH METASTATIC OR ADVANCED SOLID TUMORS SHOULD UNDERGO GENOMIC SEQUENCING?

- Patients with metastatic or advanced solid tumors if there are genomic biomarker-linked therapies for that disease approved by the relevant regulatory agency (FDA)
- Patients with metastatic or advanced solid tumors if there are clearly defined resistance markers for a treatment being considered.

Chakraverty D et al. J Clin Oncol (2022); 40:1231-1298


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Detecting molecular biomarkers in cancer

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Types of genomic alterations that define cancer biomarkers



Base Pair Substitutions

- Limited to a single base pair/region within a single gene
- Examples: EGFR L858R, T790M; BRAF V600E, IDH1 R132H

Insertions/deletions

- Limited to single genes and small changes in DNA sequence
- Examples: EGFR exon 19 deletions, MET exon 14

Copy Number Alterations


- Overexpression/amplification
- Examples: HER2 amplification, PDGFRA amplification

Gene Rearrangements (Fusions)

- Detected via DNA and RNA (ASCO recommends RNA)
- Examples: ALK fusions, NTRK fusions


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Driver versus passenger alterations



Driver mutations (driving the bus)

- Mutations that give a cancer cell a competitive advantage
 - Increased rate of proliferation
 - Decreased apoptosis
 - Resistance to therapy
 - Etc.
- Contribute to oncogenesis ("oncogenic")




Passenger mutations (along for the ride)

- Mutations that arise in cancer cells but don't improve the "fitness" of the cancer cell
- Do not contribute to cancer development/progression

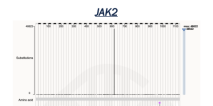
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Gain-of-function versus Loss-of-function alterations

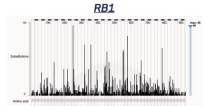


- Targetable mutations are typically GAIN OF FUNCTION mutations in oncogenes that encode for SIGNALING MOLECULES
 - GAIN OF FUNCTION mutations are frequently heterozygous (only one copy needs activated to drive the pathway)
 - There is generally a very limited number of mutations that can activate a protein
 - GAIN OF FUNCTION mutations tend to be recurrent among individuals

- LOSS OF FUNCTION mutations typically occur in TUMOR SUPPRESSOR GENES
 - Mutations tend to be LOSS OF FUNCTION, which requires BIALLELIC mutation
 - You need to lose BOTH copies to eliminate normal protein function
 - Because many different mutations can result in loss of function, there is typically a much broader spectrum of clinically significant mutations in tumor suppressor gene




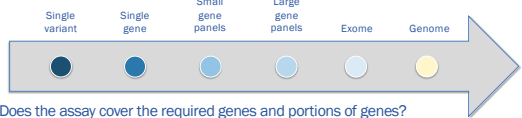
JAK2



RB1

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Finding the right assay





- Does the assay cover the required genes and portions of genes?
- What variant types can the assay detect?
 - Does the assay detect variant types required given the clinical indication for testing (single nucleotide variants, insertion-deletion, copy number gain/loss, gene rearrangements)?
- What are sample requirements?
- What is the expected turnaround time and cost?


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Methodologies to detect cancer biomarkers







Fluorescence in situ hybridization (FISH)
Detect specific genomic translocations, copy number deletions/gains



Chromosome Analysis
Detects changes in chromosome number, translocations, large deletions/insertions




SNP microarrays
Used for genotyping and copy number determination




Gene expression arrays
Can provide subtype classification for certain tumors and/or prognostic information


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Methodologies to detect cancer biomarkers

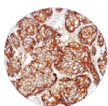




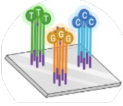
Single Gene Assays
Evaluate alterations in a single gene



Hotspot Panels
Sequencing of select hotspot codons, and not the entire coding region, of the genes included on the panel.



Immunohistochemistry
Determines protein expression within tissue sample



Broad Panel (Comprehensive Genomic Profiling)
An NGS test that sequences a defined list of genes with at least 50 genes in total. May also include RNA testing

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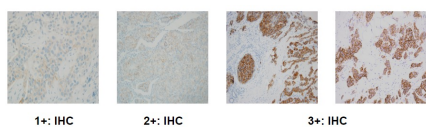
Methodologies are often combined to identify biomarkers

HER2 biomarker testing in invasive breast cancers

HER2 testing by validated immunohistochemistry (IHC) assay^{2,6}

- IHC 0,1⁺ → HER2 (-)
- IHC 2⁺ → Equivocal result
- IHC 3⁺ → HER2 (+)

Must reflex test with ISH (if same specimen), or order new test with IHC or dual probe ISH (if new specimen available).



1+ IHC 2+ IHC 3+ IHC

40

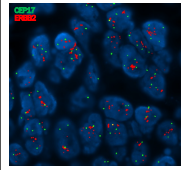
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- IHC 2⁺ → Equivocal result
- IHC 3⁺ → HER2 (+)

Must reflex test with ISH (if same specimen), or order new test with IHC or dual probe ISH (if new specimen available).



HER2 testing (in situ component) by validated dual probe ISH assay

Both controls and on slide contain non-appropriate hybridization

HER2/CENT11 ratio > 2.0

- Group 1: Average HER2 copy number < 4.0 (equivocal) → ISH positive
- Group 2: Average HER2 copy number < 4.0 (equivocal) → Additional work-up required (See Fig 6)

HER2/CENT11 ratio < 2.0

- Group 3: Average HER2 copy number < 4.0 (equivocal) → Additional work-up required (See Fig 6)
- Group 4: Average HER2 copy number > 4.0 (non-equivocal) → ISH positive
- Group 5: Average HER2 copy number < 4.0 (equivocal) → Additional work-up required (See Fig 6)

NCCN Guidelines Version 2.2024 Invasive Breast Cancer. Wolff AC et al. J Clin Oncol 2018;36:2105-2122

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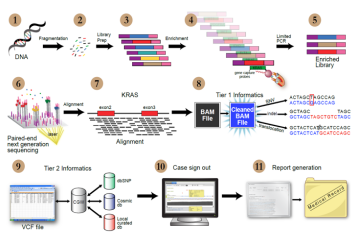
Overview of comprehensive genomic profiling

Goals

- High throughput, cost effective multiplexed sequencing assay with deep coverage
- Target clinically actionable regions important for all tumor types

Challenges

- Huge infrastructure costs
- Bioinformatic barriers
- Longer turnaround times



1. DNA → 2. Library → 3. Sequencing → 4. Enriched Library → 5. Sequencing → 6. BAM File → 7. Alignment → 8. Variant Calling → 9. Tier 1 Informatics → 10. Case sign out → 11. Report generation

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Comparison of single gene testing versus comprehensive genomic profiling

Single gene testing (SGT)	Comprehensive Genomic Profiling
<p>One or more tests ordered individually or simultaneously, but performed separately</p> <ul style="list-style-type: none"> PCR - defined regions for a limited number of mutations in <i>EGFR</i>, <i>KRAS</i> or <i>BRAF</i> FISH - known rearrangements in <i>ALK</i>, <i>RET</i>, <i>ROS1</i> or <i>MET</i> amplification IHC - known expression patterns or percentage of positive cells; loss of protein expression 	<p>One test ordered following negative SGT results or instead of SGT</p> <ul style="list-style-type: none"> DNA sequencing - simultaneously evaluate all major genomic variant types (mutations, copy number alterations, rearrangements) in oncogenes recommended for testing that have FDA-approved targeted therapies, as well those with emerging and potential clinical significance RNA sequencing - for known and novel rearrangements Microsatellite status and Tumor mutation burden - immunotherapy biomarkers

Nesline et al. Oncol Ther 2024 Mar 19.

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Cancer biomarker testing can be performed on a liquid or tissue biopsy

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Tissue acquisition: What material is available for testing?

<p>Tissue Resection</p> <ul style="list-style-type: none"> Obtained for diagnosis and symptomatic relief Tumor cell percentage may be an issue OGP and multiple assays typically not a problem for tumor-rich samples 	<p>Biopsy</p> <ul style="list-style-type: none"> Obtained for a diagnosis Testing options may be limited but depends on tumor content not necessarily tissue size 	<p>Endobronchial Ultrasound (EBUS) / Fine Needle Aspiration (FNA)</p> <ul style="list-style-type: none"> Diagnosis can be made from very few cells Considered a cytology specimen May have significant limitations for testing
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Liquid biopsy: source of circulating tumor DNA (ctDNA)

- **ctDNA:** component of cell-free DNA which is tumor related
- **Cell-Free DNA Blood Collection Tubes:** specialized tubes required allow for isolation of plasma DNA up to 14 days after sample collection

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Net Rev Clin Oncol. 2017 Sep;14(9):531-548

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ctDNA varies among tumor types

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Buttgewandt C et al. Sci Transl Med. 2014 Feb 19; 6(224): 224. Zill O et al. Clin Cancer Res. 2018 Aug 1; 24(15):3528-3536.

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Liquid biopsy and tumor tissue concordance

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Wang W et al. JAMA Netw Open. 2024 Jan 23;7(1):e235100.

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Advantages and disadvantages of tumor versus liquid biopsy

Tumor Biopsy

Histological evaluation
Tumor microenvironment analysis
Clinical gold standard

- Surgery/needle biopsy
- Risk of complications
- Difficult to repeat & expensive
- Possible sampling bias
- Highly sensitive
- Longer TAT

Liquid Biopsy

Non-invasive
Short half-life (<2 h)
Compatible with longitudinal monitoring
Representative of tumor heterogeneity

- Blood draw
- Minimal complications
- Easy & repeatable
- Quick & cost-efficient
- Less sampling bias
- Rapid TAT
- False negatives
- Detection of CHIP

Adapted from Corcoran et al Nature Medicine 2020

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ESMO Guidelines: Advanced cancer genotyping recommendations

Liquid Biopsy Best Practice

- ✓ May be used in clinical practice when results impact treatment.
- ✓ May be used in clinical scenarios first where time to result is clinically important
- ✓ Aggressive tumor type
- ✓ No available tissue or biopsy not feasible
- ✓ Collect when tumor progressing (not regressing)
- ✓ Confirm testing if pathogenic variants of cancer susceptibility genes identified
- ✓ Negative tests should prompt tissue testing

Adapted from Pascual et al. Annals of Oncology, 2022

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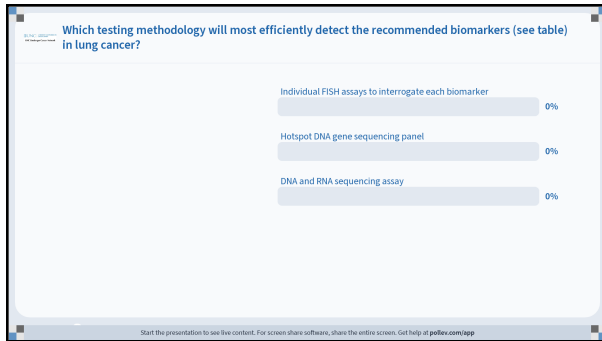
Poll everywhere question #2:

• Which testing methodology will most efficiently detect the recommended biomarkers (see table) in lung cancer?

- Individual FISH assays to interrogate each biomarker
- Hotspot DNA gene sequencing panel
- DNA and RNA sequencing assay

Recommended Testing
ALK rearrangements
BRAF mutations
EGFR mutations
ERBB2 (HER2) mutations
KRAS mutations
MET exon 14 skipping mutations
MET amplification
NTRK 1/2/3 rearrangements
RET rearrangements
ROS1 rearrangements

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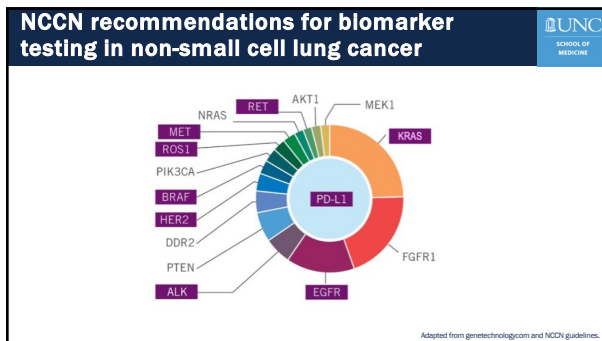
Poll everywhere question #2: Answer

Which testing methodology will most efficiently detect the recommended biomarkers (see table) in lung cancer?

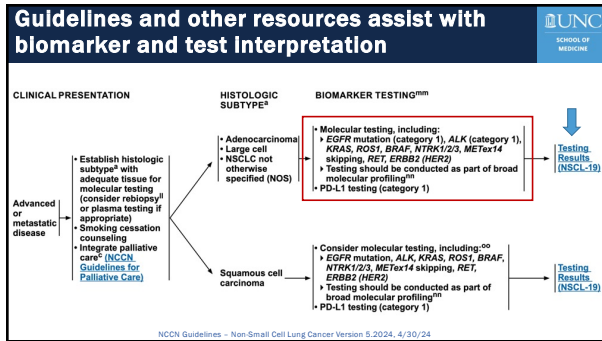
- Individual FISH assays to interrogate each biomarker
- Hotspot DNA gene sequencing panel
- DNA and RNA sequencing assay**

Recommended Testing
ALK rearrangements
BRAF mutations
EGFR mutations
ERBB2 (HER2) mutations
KRAS mutations
MET exon 14 skipping mutations
MET amplification
NTRK 1/2/3 rearrangements
RET rearrangements
ROS1 rearrangements

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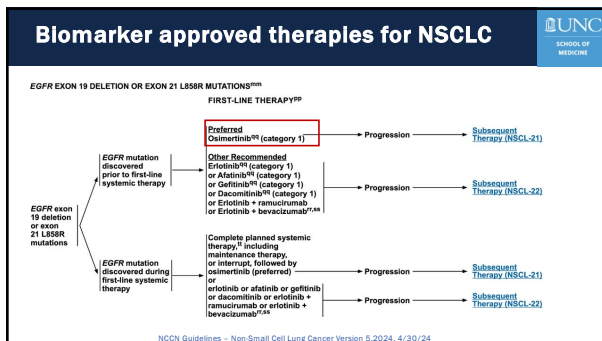
Guidelines and other resources assist with biomarker and test interpretation

TESTING RESULTS^{12,13}

EGFR exon 19 deletion or exon 21 L858R mutation positive	NSCLC-20
EGFR S768I, L861Q, and/or G719X mutation positive	NSCLC-23
EGFR exon 20 insertion mutation positive	NSCLC-24
KRAS G12C mutation positive	NSCLC-25
ALK rearrangement positive	NSCLC-26
ROS1 rearrangement positive	NSCLC-29
BRAF V600E mutation positive	NSCLC-31
NTRK1/2/3 gene fusion positive	NSCLC-32
METex14 skipping mutation positive	NSCLC-33
RET rearrangement positive	NSCLC-34
ERBB2 (HER2) mutation positive	NSCLC-35
PD-L1 ≥1% and negative for actionable molecular biomarkers above	NSCLC-36
PD-L1 <1% and negative for actionable molecular biomarkers above	NSCLC-37

NCCN Guidelines - Non-Small Cell Lung Cancer Version 5.2024, 4/30/24

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Availability of molecular biomarker testing in NSCLC impacts overall survival

- 326 consecutive treatment naïve patient with a new diagnosis of metastatic NSCLC
- Patients with molecular test results available before first line therapy (available group) had significantly longer overall survival

No. at risk:	0	6	12	18	24	30	36
Available testing group	261	208	164	111	42	14	8
Unavailable testing group	65	27	14	7	6	2	0

Aggarwal C et al. JCO Precis Oncol 2023; 7:7e2300191

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Molecular biomarkers are refining classification of tumors

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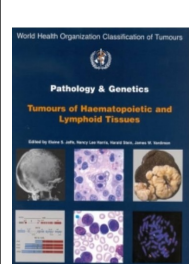
Evolution of hematologic malignancy classification

French-American-British (FAB) Classification System

60

Evolution of hematologic malignancy classification

2001



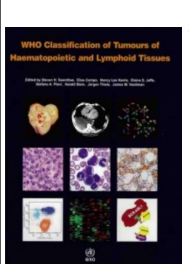
I. Acute myeloid leukaemias with recurrent cytogenetic translocations

- AML with t(8;21)(q22;q22),AML1(CBFa)/ETO
- Acute promyelocytic leukaemia (AML with t(15;17)(q22;q11-12) and variants, PML/RARA)
- AML with abnormal bone marrow eosinophils (Inv(16)(p13q22) or t(16;16)(p13;q11), CBFb/MYH11X)
- AML with 11q23 (MLL) abnormalities.

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Evolution of hematologic malignancy classification

2008



I. Acute myeloid leukemia with recurrent genetic abnormalities

- AML with t(8;21)(q22;q22); RUNX1-RUNX1T1
- AML with inv(16)(p13.1q22) or t(16;16)(p13.1q22); CBFb-MYH11
- APL with t(15;17)(q22;q12); PML-RARA
- AML with t(9;11)(p22;q23); MLLT3-MLL
- AML with t(6;9)(p23;q34); DEK-NUP214
- AML with inv(3)(q21q26.2) or t(3;3)(q21;q26.2); RPN1-EVI1
- AML (megakaryoblastic) with t(1;22)(p13;q13); RBM15-MKL1

II. Provisional entities:

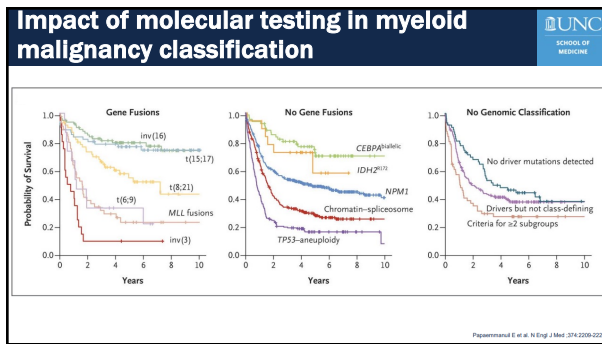
- AML with mutated NPM1
- AML with mutated CEBPA

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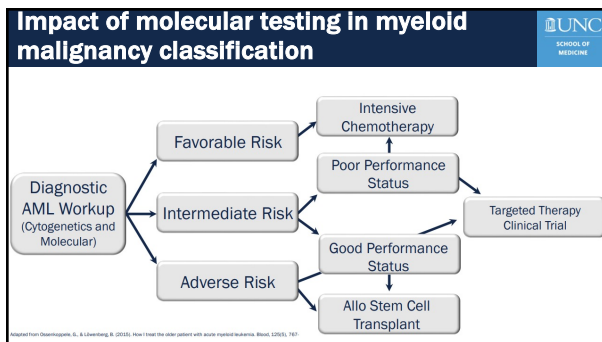
Evolution of hematologic malignancy classification

WHO 2017	WHO 2022	ICC 2022
AML with recurrent genetic abnormalities	AML with defining genetic abnormalities (no blast % cut-off, except*)	AML with recurrent genetic abnormalities (requiring equal or greater than 10% blasts, except*)
AML with t(8;21)(q22;q22.1);RUNX1-RUNX1T1	AML with RUNX1::RUNX1T1 fusion	AML with t(8;21)(q22;q22.1)/RUNX1::RUNX1T1
AML with inv(16)(p13.1q22) or t(16;16)(p13.1q22);CBFB-MYH11	AML with CBFB::MYH11 fusion	AML with inv(16)(p13.1q22) or t(16;16)(p13.1q22); CBFB::MYH11
APL with PML-RARA	Acute promyelocytic leukaemia with PML::RARA fusion	Acute promyelocytic leukaemia (APL) with t(15;17)(q24.1;q21.2)/PML::RARA; APL with other RARA rearrangements
AML with t(9;11)(p21.3;q23.3);MLLT3-KMT2A	AML with KMT2A rearrangement	AML with t(9;11)(p21.3;q23.3)/MLLT3::KMT2A; AML with other KMT2A rearrangements
AML with t(6;9)(p23;q34.1);DEK-NUP214	AML with DEK::NUP214 fusion	AML with t(6;9)(p23.3;q34.1)/DEK::NUP214
AML with inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2);GATA2-MECOM	AML with MECOM rearrangement	AML with inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2)/GATA2::MECOM(EVI1); AML with other MECOM rearrangements
AML (megakaryoblastic) with t(1;22)(p13.3;q13.3);RBM15-MKL1	AML with RBM15::MRTFA fusion	
Provisional entity: AML with BCR-ABL1	AML with BCR::ABL1 fusion*	AML with BCR::ABL1 fusion*
	AML with NUP98 rearrangement	
	AML with other (rare) defined genetic alterations*	AML with other rare recurring translocations

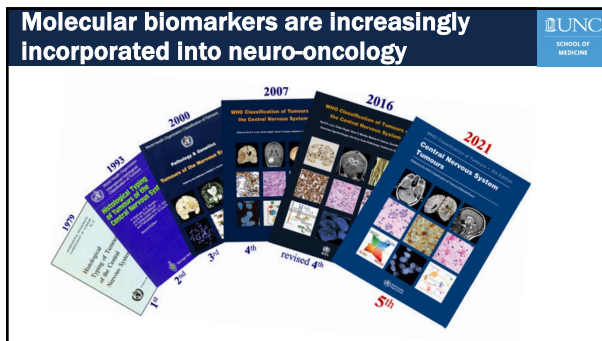
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Evolution of molecularly classified CNS tumors

WHO 2016 GLIOMAS
Diffuse Astrocytic and Oligodendroglial Tumours

Classification

- Diffuse Astrocytoma, IDH mutant
 - Gemistocytic astrocytoma, IDH mutant
- Diffuse astrocytoma, IDH wildtype
- Diffuse astrocytoma, NOS
- Anaplastic astrocytoma, IDH mutant
- Anaplastic astrocytoma, IDH wildtype
- Anaplastic astrocytoma, NOS
- Glioblastoma, IDH wildtype
 - Giant cell glioblastoma
 - Gliosarcoma
 - Ependymal glioblastoma
- Glioblastoma, IDH mutant
- Glioblastoma, NOS
- Diffuse midline glioma, H3 K27M mutant
- Oligodendroglioma, IDH mutant and 1p/19q codeleted
- Oligodendroglioma, NOS
- Anaplastic oligodendroglioma, IDH mutant and 1p/19q codeleted
- Anaplastic oligodendroglioma, NOS
- Oligosarcinoma, NOS
- Anaplastic oligosarcinoma, NOS

WHO 2021 GLIOMAS
Gliomas, Glioneural and Neuronal Tumours

Adult type diffuse gliomas

- Astrocytoma, IDH mutant
- Oligodendroglioma, IDH mutant and 1p/19q codeleted
- Glioblastoma, IDH wildtype

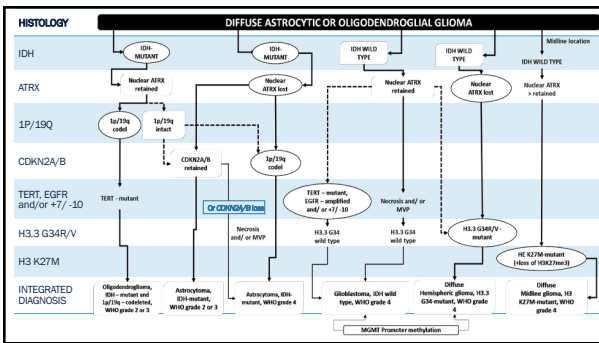
Pediatric-type diffuse low-grade gliomas

- Diffuse astrocytoma, MYB or MYBL1 altered
- Anaplastic glioma
- Polymorphous low-grade neuroepithelial tumour of the young
- Diffuse low-grade glioma, MAPK pathway altered

Pediatric-type diffuse high-grade gliomas

- Diffuse midline glioma, H3 K27 altered
- Diffuse hemispheric glioma, H3 G34 mutant
- Diffuse pediatric-type high-grade glioma, H3 wild-type and IDH wild-type
- Infant-type hemispheric glioma

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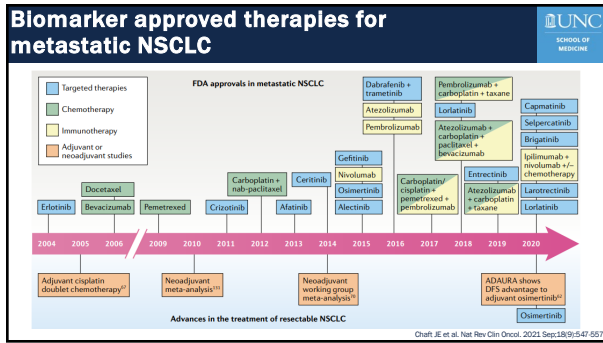


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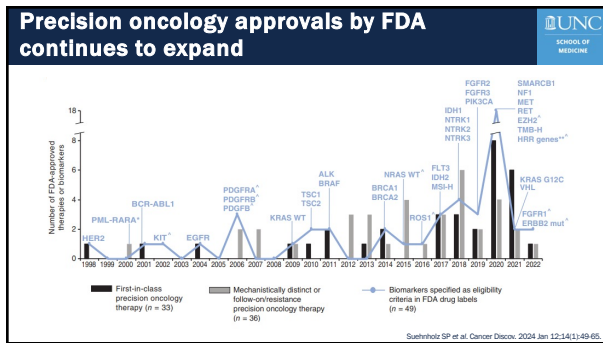
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Molecular biomarkers guide treatment decisions

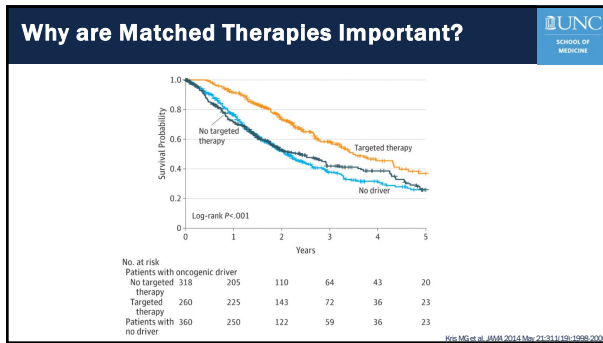
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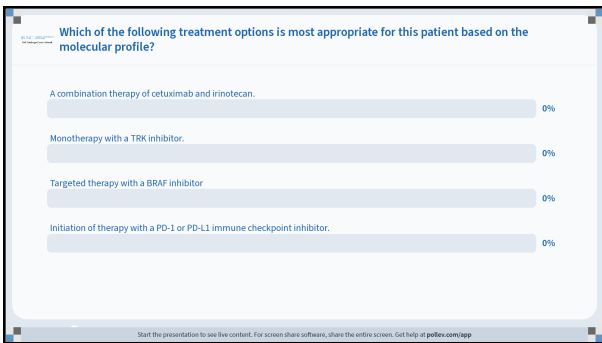
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Poll everywhere question #3:

In a patient with newly diagnosed colon cancer, testing determined that the tumor had microsatellite instability (MSI) or was MSI-high. Which of the following treatment strategies is indicated for MSI-high status?

1. A combination therapy of cetuximab and irinotecan.
2. Monotherapy with a TRK inhibitor.
3. Targeted therapy with a BRAF inhibitor
4. Initiation of therapy with a PD-1 or PD-L1 immune checkpoint inhibitor.

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3. Targeted therapy with a BRAF inhibitor
4. **Initiation of therapy with a PD-1 or PD-L1 immune checkpoint inhibitor.**

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DNA Mismatch Repair and Microsatellite Instability

- During DNA replication, errors occur in microsatellite regions
 - Short repetitive DNA sequences (1-6 base pairs) or tandem repeats
- Multi-protein complex corrects these single base pair mismatches and small insertion-deletion errors
- Failures to repair these errors during replication leads to expansion of repeats and genomic instability = **microsatellite instability**

Nature Reviews | Immunology

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Anti-PD-1/L1 therapies reactivate T cell activity

- MSI-High/dMMR tumors generate neoantigens which are recognized by the immune system
- Tumor cells also express PD-L1 to inhibit T-cell activity
- Immune checkpoint inhibitors reactivate T-cell activity

He Y et al. Int J Biol Sci 2022; 18(7):2923-2932

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Tumor agnostic Immune checkpoint inhibitor approval

FDA grants accelerated approval to pembrolizumab for first tissue/site agnostic indication

- 2017 approval for adult and pediatric patients with unresectable or metastatic solid tumors
 - microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR)
 - progressed following prior treatment

Ros J et al. Cancers (Basel). 2023 Aug 24;15(17):4245.

78

Additional FDA-approved tumor agnostic targeted therapies

- **NTRK1, NTRK2, NTRK3** transmembrane tyrosine kinases that are important for neuronal development
 - Fusions detected in 1.6% of profiled cases
 - NTRK fusions can be targeted using Larotrectinib and Entrectinib
- **Tumor mutation burden (TMB)** reflects the number of genetic alterations in the genome of cancer cells
 - Calculated using data from NGS of either tissue or plasma, mutations per megabase (mut/MB)
 - 10 mut/mb as for defining indication of pembrolizumab
- **BRAF V600E** can be targeted by using inhibitors of BRAF and MEK
 - Detected in 3% of AACR Project GENIE (version 1.3) pan-cancer cohort
 - Dabrafenib and Trametinib received FDA approval for BRAF V600E-positive solid tumors
- **RET fusion-positive** samples were identified in 1.5% of 25,972 tumors profiled for structural variants
 - Selpercatinib, ATP-dependent selective RET inhibitor, approved by FDA for solid tumors with RET fusions

Gouda MA et al. Clin Cancer Res. 2023 Aug 1;29(15):2753-2760

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Targeted therapy success story

Chronic Myeloid Leukemia

80

Visualization of first chromosome translocation

A New Consistent Chromosomal Abnormality in Chronic Myelogenous Leukaemia identified by Quinacrine Fluorescence and Giemsa Staining

JANET D. ROWLEY
 Department of Medicine,
 University of Chicago and
 Franklin McLean Memorial Research Institute,
 Chicago, Illinois 60637
 Received January 8, revised February 8, 1973.

Nature volume 243, pages290-293 (1973)

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Genomic rearrangement results in oncogenic fusion gene

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- Exchange of genetic material between chromosome 9 and chromosome 22 produces novel oncogenic fusion gene
- BCR::ABL1* creates a constitutively active tyrosine kinase

<https://www.cancer.gov/publications/dictionaries/cancer-terms/def/bcr-abl-fusion-gene>

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Understanding mechanism of *BCR::ABL1* transforms care for CML patients

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NEW ENGLAND JOURNAL OF MEDICINE

Efficacy and Safety of a Specific Inhibitor of the BCR-ABL Tyrosine Kinase in Chronic Myeloid Leukemia

Authors: Brian J. Goldstein, M.D., Mounir Tajiri, M.D., Debra J. Reiss, B.S., Bin Peng, Ph.D., Elizabeth Buchdunger, Ph.D., John M. Ford, M.D., Nicholas H. Lippman, Ph.D., Hajime Kuroki, M.D., Renaud Capdeville, M.D., Stuart Ojima Jones, B.S., and Charles L. Sawyers, M.D. Author info & #References

- 2001 Phase I clinical trial
 - 98% had complete hematologic response
 - 54% had cytogenetic response
- Imatinib is the first FDA approved drug to counteract molecular defect = targeted therapy

Mughal TI & Goldman JM. *Front Biosci*. 2006; 11:209-220.

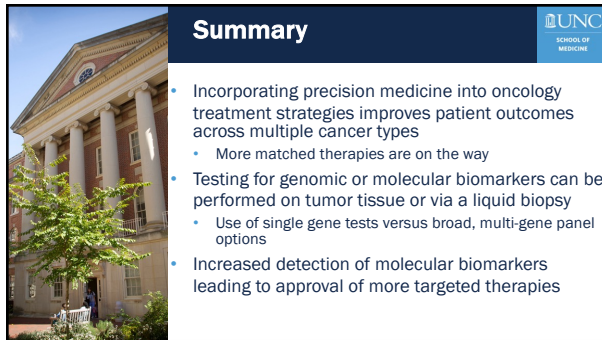
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Combining molecular methods to diagnosis and monitor CML

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Normal Abnormal

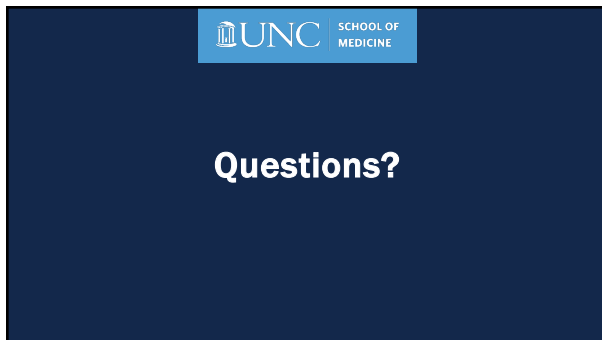
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Summary

- Incorporating precision medicine into oncology treatment strategies improves patient outcomes across multiple cancer types
 - More matched therapies are on the way
- Testing for genomic or molecular biomarkers can be performed on tumor tissue or via a liquid biopsy
 - Use of single gene tests versus broad, multi-gene panel options
- Increased detection of molecular biomarkers leading to approval of more targeted therapies

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Questions?

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Questions/Comments?

Nobody has responded yet.
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Thank You . . .

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Jon Powell, PhD - Continuing Education Specialist
Oliver Marth - Technology Support Technician

Andrew Dodgson, CRT - Continuing Education Specialist
Patrick Muscarella - Technology Support Technician
Lindsey Reich, MA - Public Communication Specialist
Barbara Walsh, DNP, APRN, MSN, RN - Nurse Planner

The song *Black Rhodes* written and performed by Tim Poe

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ADVANCED PRACTICE PROVIDER [@unccln](#) **May 15 4:00 PM**

Using Acceptance and Commitment Therapy to Help Cancer Survivors Move Forward After Treatment
Melissa Holt, DNP, PMHNP-BC **Lisa Kansner, PsyD**

RESEARCH TO PRACTICE [@unccln](#) **May 22 12:00 PM**

The Selective Use of Radiation in Solid Malignancies
Kevin Pearlstein, MD

PATIENT-CENTERED CARE [@unccln](#) **June 12 12:00 PM**

Medication-Related Osteonecrosis of the Jaw
Ricardo Padilla, DDS

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Physical Therapy Approaches to Oncology Care: Beyond Lymphedema
Sarah Richardson, PT, DPT, CLT, WCS

RESEARCH TO PRACTICE [@unccln](#)

Immune (check point) Related Adverse Events
Frances Collichio, MD

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Oncologic Emergencies
Jake Stein, MD

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