



TISSULAR AND CIRCULATING BIOMARKERS IN ONCOLOGY: PROGRESS, LIMITATIONS AND PERSPECTIVES.

Yassine LALAMI, MD Oncology Medicine Department Institut Jules Bordet

> Annual Symposium LHUB-ULB 15th October 2022



Pathological Diagnosis of Cancer

- Histology
- Immunohistochemistry
- Molecular biology
- Tumor sequencing
- Genomic profiling
- Liquid biopsy

Subdivided tumors into multiple cancers based on genomics











	IHC	FISH	PCR	NGS
Target	Protein expression	1 Gene rearrangement, amplification, deletion	1Gene DNA: mutation RNA : rearrangement	Genes DNA: mutation, indels, amplification RNA : rearrangement
Example	MSI	HER2 amplification	BRAF V600	Gene panels
Precision	+	++	+	+++
Hands on time	-	+++	+	++
Cost	+-++	++	+-++	+++-++++
TAT	48h	10 days	10 days	10 days





Hallmarks of Cancer and Molecular Therapeutic Targeting





Hallmarks of Cancer and Molecular Therapeutic Targeting



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Progress in Systemic Cancer Care





From Empirical Cancer Chemotherapy to Oncogenic Addiction Approach.

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Importance of Biomarker Testing



OS Among NSCLC Patients with Driver Alteration

*Agents selected per NCCN recommendations for specific driver mutations

Singal et al. JAMA 2019

Active treatment A

Placebo •

Biomarker positive - solid lines; Biomarker negative - dotted lines



Kerr DJ et al. EBioMedicine 2021





Types of Biomarkers and Clinical Utility

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Molecular Analysis Techniques for the Practicing Oncologist



Genetic Biomarkers

Next-generation DNA sequencing technologies

Ex: circulating tumor DNA (i.e. liquid biopsies), BRAF^{V600VE} mutation in melanoma predicts sensitivity to BRAF inhibitors (vemurafenib, dabrafenib), ALK gene rearrangement in lung cancer predicts response to crizotinib.

Epigenetic Biomarkers

Changes in the status of DNA methylation and chromatin modifications.

Ex: SHOX2 promoter methylation in bronchial aspirates for early lung cancer diagnosis and CDKN2A promoter methylation as a prognostic indicator. VIM promoter methylation in feces and SEPT9 promoter methylation ("SEPT9) in plasma for detection of CRC.

Transcriptomic Biomarkers

Global measurement of mRNA expression, microarray and RNAseg technologies.

Ex: KAT2B, PCNA, CD86, miR-192-5p, and miR-215-5p, identified as potential prognostic biomarkers from an analysis of cervical cancers.

Proteomic Biomarkers

Analysis of proteins' functionality, post-translational modifications, interaction with other biological molecules, and response to environmental factors. Use of mass spectrometry (MS). Ex: CTCs which are detected according to several proteins (i.e. EpCAM, CD45, and cytokeratins 8, 18, and 19), and are useful to monitor patients with metastatic disease. Estrogen receptors used to evaluate prognosis and response to therapy.

Metabolomic Biomarkers

Mass spectrophotometry used to identify specific metabolites.

Ex:. Decreased choline and linoleic acid in serum of lung cancer patients. Elevated 3-hydroxypropionic acid reduced pyruvic acid (specific) in serum of gastric cancer patients.

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Heitzeret al., Nat Rev Genetics 2019 The Cancer Genome Atlas et al. Nature Genetics 2013

The Partners of Personalized Oncology







Circulating Tumor Markers

	Utilité clinique	Diagnostic	Pronostic	Suivi thérapeutique
PSA	Cancer prostatique	V	1	1
CA-125	Cancer ovarien, des trompes et des séreuses	x	x	V
CA-15.3	Cancer mammaire	x	x	1
CA-19.9	Cancer pancréatique	x	x	V
CEA	Cancer colique	x	x	4
α -FP	Tumeurs germinales testiculaires non seminomateuses et hépatocarcinome	1	V	V
β-HCG	Choriocarcinomes et tumeurs germinales testiculaires	V	V	V
Thyroglobuline	cancer bien différencié de la thyroïde	V	x	V
Calcitonine	Cancers médullaires de la thyroïde	V	x	V

Alpha-fetoprotein (AFP)	Blood	Liver cancerGerm cell tumors	Diagnosis, staging, prognosis, and treatment response
B-cell immunoglobulin gene rearrangements	Blood, bone marrow, tumor tissue	B-cell lymphoma	Diagnosis and recurrence
Beta-2-microglobulin (B2M)	Blood, urine cerebrospinal fluid	 Multiple myeloma Chronic lymphocytic leukemia lymphomas 	Prognosis and treatment response
Beta-human chorionic gonadotropin (Beta-hCG)	Blood, urine	ChoriocarcinomaGerm cell tumors	Disease staging, prognosis and treatment response
Bladder tumor antigen (BTA)	Urine	 Bladder cancer Kidney cancer Ureter cancer 	Screening in patients already having bladder cancer
CA 15-3/CA 27.29	Blood	Breast cancer	Treatment response and recurrence
CA 19-9	Blood	 Gastrointestinal tract cancers 	Treatment response
CA- 125	Blood	Ovarian cancer	Diagnosis, recurrence, and treatment response
Chromogranin A (CgA)	Blood	 Neuroendocrine tumor 	Diagnosis, recurrence



Biomarkers and Types of Breast Cancer





Perou C et al. Nature 2000 Sotiriou C et al. NEJM 2009



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Multiple Gene Assays as Prognostic Clinical Marker





Perou C et al. Nature 2000 Sotiriou C et al. NEJM 2009



Oncotype DX



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Major Importance of Genomics-Driven Cancer Therapy



But there are many challenges and limitations which need to be overcome !!!





Solid Tumors = Mixture of Rare Molecular Entities



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Major Milestones for Precision Oncology Across Indications





Evolution of support for genomic testing within guidelines. CRC, colorectal cancer; ESCAT, ESMO Scale for Clinical Actionability of molecular Targets; ESMO, European Society for Medical Oncology; FDA, Food and Drug Administration; NGS, next-generation sequencing; NSCLC, nonsmall cell lung cancer; PCR, polymerase chain reaction; TMB, tumor mutational burden.



Selected Clinical Studies Evaluating Personalized Oncology (NGS)

Table 1. Clinical Studies That	Have Evaluated Personalized C	ancer Medicine.*				
Clinical Study	Design	Screened Sample	Patients with Genetic Profile	Patients with Mutation That Might Be Targeted by Drugs	Patients Receiving Matched Drug	Main Outcome Result
SHIVA trial ^a	Randomized, controlled trial of matched molecular targeted agent or physi- cian's choice	741 patients with metastatic solid tumors who were amenable to biopsy	496(67%)	293 (40%), of whom 195 underwent randomization	96 (100% of experi- mental-therapy group)	No significant difference in progression-free survival (primary end point); haz- ard ratio for death or dis- ease progression, 0.88 (95% CI, 0.65–1.19)
Lung Cancer Mutation Consortium	Testing for driver mutations in metastatic lung adeno- carcinomas at multiple centers			0	Many treated as per guidelines for an approved biomarker	Longer overall survival in the subgroups with a muta- tion treated with directed therapy than in those without the mutation or those that do not receive directed therapy
Study I ^s		1007 patients	733 (73%) tested for ≥10 genes	466(46%)	260(26%)	
Study II ^e		1315 patients	919 (70%) tested for ≥8 genes	529 (40%) had mutations, with 187 (14%) of them that could be targeted by drugs and had follow-up	127(10%)	
SAFIR-01 ⁹	Treatment chosen after genetic profiling by comparative genomic hybridization and gene sequencing	423 women with met- astatic breast cancer	299 (71%)	195 (46%)	55 (13%)	4 patients had a partial re- sponse and 9 had stable disease for >16 wk (3% of screened sample)
M.D. Anderson Study ¹⁰	Treatment chosen after gene sequencing of patients with advanced cancer	2601 patients	2000 (77%)	789(30%)	83 (3%) in geno- type-matched trials; 116 (4%) with common mutations not in trial	Not stated
Princess Margaret IMPACT- COMPACT study ²¹	Treatment chosen after gene sequencing of archival tissue	1893 patients with advanced solid tumors	1640 (87%)	938 (50%) had mutations, approximately 20% of which could be targeted by drugs	84 (4%) treated in genotype- matched trials	Response rate of 20% in gen- otype-matched trial vs. 11% in unmatched trials
Cleveland Clinic Study ³²	Treatment chosen after gene sequencing	250 patients	223 (89%)	109 (44%)	24 (10%)	Not stated



* CI denotes confidence interval, COMPACT Community Oncology Molecular Profiling in Advanced Cancers Trial, and IMPACT Integrated Molecular Profiling in Advanced Cancers Trial.

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Tannock IF, Hickman JA. N Engl J Med 2016

Selected Molecular Pathology Biomarker Testing and Expressions

Entity	Biomarker	Routine molecular diagnostics	Expressions
Entity-specific			
Non-small cell lung	ALK	Immunohistochemistry, ISH, RNA sequencing	ALK translocation (e.g. EML4-ALK)
cancer (NSCLC)	BRAF	DNA sequencing	BRAF-V600E
	EGFR	DNA sequencing	EGFR exon 21 mutation (e.g. p.L858R), EGFR exon 19 deletion, EGFR exon 20 insertion, EGFR exon 18 mutation
	ROS1	Immunohistochemistry, ISH, RNA sequencing	ROS1 translocation (e.g. CD74-ROS1)
Colorectal cancer	BRAF	DNA sequencing	BRAF-V600E
	KRAS	DNA sequencing	Mutations in Exon 2, 3 and 4 (mainly codon 12 and 13, e.g. p.G12C)
	NRAS	DNA sequencing	Mutations in Exon 2, 3 and 4 (mainly codon 61, e.g. p.Q61K)
Malignant melanoma	BRAF	DNA sequencing	BRAF-V600E
Breast cancer	BRCA1/2	DNA sequencing	Mainly mutations in BRCA2 (e.g. p.D752fs)
	HER2	Immunohistochemistry, ISH	Overexpression, amplification
	PIK3CA	DNA sequencing	Mutations in exon 8, 10 and 21 (e.g. p.E545K)
Stomach cancer	HER2	Immunohistochemistry, ISH	Overexpression, amplification
Pancreatic cancer	BRCA1/2	DNA sequencing	Mutations in the entire genes (e.g. p.R1856fs)
Ovarian cancer	BRCA1/2	DNA sequencing	Mainly mutations in BRCA1 (e.g. p.S1403fs)
Cross-entity			
	NTRK1-3	Immunohistochemistry, ISH, RNA sequencing	NTRK translocations (e.g. ETV6-NTRK3)
_	PD-L1	Immunohistochemistry	TPS (%), CPS, IC score (%)
	dMMR	Immunohistochemistry, fragment length analysis,	MSI, MSS

DNA sequencing





Selected Molecular Pathology Biomarker Testing and Expressions

Entity	Biomarker	Frequency	Examples of clinical trials
Entity-specific			
Non-small cell lung	ALK	5%	PROFILE-1014
cancer (NSCLC)	BRAF	2–4%	Planchard et al., 2017
	EGFR	15–20%	FLAURA
	ROS1	3–5%	Shaw et al., 2014
Colorectal cancer	BRAF	10%	BEACON
	KRAS	50%	PRIME
	NRAS	4%	-
Malignant melanoma	BRAF	50%	Robert et al., 2015
Breast cancer	BRCA1/2	5%	OlympiAD
	HER2	15–20%	EMILIA
	PIK3CA	10%	SOLAR-1
Stomach cancer	HER2	5%	ToGA
Pancreatic cancer	BRCA1/2	5%	POLO
Ovarian cancer	BRCA1/2	5%	SOLO-2



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Oncogenic Addiction

Target	Tumor	Inhibitor	Predictive markers of sensitivity/resistance	Disease setting
ER	Breast	Tamoxifen, Aromatase Inhibitors, Fulvestrant	ER expression ER mutation (Resistance)	Adjuvant & Metastatic
EGFR	Head&Neck	Cetuximab	NA	Locally/advanced & Metastatic
EGFR	NSCLC	Gefitinib/Erlotinib/ Dacomitinib/Afatinib/ Osimertinib	Mutation of EGFR (T790M)	Metastatic NSCLC Adjuvant NSCLC (Osimertinib)
EGFR	Colorectal	Cetuximab Panitumumab	RAS status (mutation predicts resistance to anti EGFR MAb)	Metastatic
HER-2/ Neu	Breast, Gastric, NSCLC, CRC	Trastuzumab, Pertuzumab Lapatinib, Tucatinib Neratinib T-DM1, Trastuzumab- Deruxtecan	HER-2/Neu amplification	Adjuvant (Breast) & Metastatic (Breast, Gastric)

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Oncogenic Addiction

Target	Tumor	Inhibitor	Predictive markers of sensitivity/resistance	Disease setting
C-Kit	GIST	Imatinib (Sunitinib, Regorafenib)	C-Kit mutation PDGFR mutation	High risk or metastatic GIST
ALK ROS1	NSCLC	Crizotinib, Ceritinib, Alectinib	EML4-ALK translocation R0S1	Metastatic
Hedgehog	Basal cell carcinoma	Vismodegib	NA	Metastatic
BRAF, MEK	Melanoma (NSCLC, CRC)	Vemurafenib, Dabrafenib Trametinib, Cobimetinib,	BRAF mutation	Adjuvant Melanoma & Metastatic
PARP	Breast, Ovary, Prostate (BRCA tumors)	Olaparib, Niraparib, Talazoparib	BRCA mutation HRD	Metastatic Maintenance (Ovary)
Androgen receptor	Prostate	Aberaterone, Enzalutamide, Sipuleucel-T	NA/ Androgen receptor variant 7 (Resistance)??	Metastatic
NTRK	Solid tumors	Larotrectinib Entrectinib	TRK Fusion	Metastatic
NTRK	Solid tumors	Larotrectinib Entrectinib	TRK Fusion	Metastatic



Targets* importantly involved in <u>carcinogenesis</u> process and their inhibitors (* Outside PD-L1) NA: not available

Oncogenic Addiction

Target	Tumor	Inhibitor	Predictive markers of sensitivity	Disease setting
VEGF	NSCLC, colorectal, renal, breast, ovary, cervix, HCC, gastric	Bevacizumab, Aflibercet (colon), Ramucirumab	NA	Metastatic
VEGFR	Hepatocarcinoma Colorectal Gastric	Sorafenib, Lenvatinib, Cabozantinib Regorafenib Ramucirumab	NA	Metastatic
VEGF(R); M- TOR	Renal	MTKs, Bevacizumab Everolimus, Temsirolimus	NA	Metastatic
VEGFR; M-TOR PDGFR	Neuroendocrine, Soft tissue sarcomas	Sunitinib, Everolimus Pazopanib, Olaratumab	NA	Metastatic
VEGFR, RET,	Thyroid	Vandetinib, Sorafenib Lenvatinib, Selpercatinib	NA	Metastatic
M-TOR PI3K	Breast	Everolimus Alpelisib	NA Mutateted PI3K	Metastatic
CDK 4/6	Breast	Palbociclib, Ribociclib, Abemaciclib	NA	Metastatic Adjuvant (Abemaciclik

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Breast Cancers



Her2+ / PIK3CA mut
Her2+ / p95
Her2+
TNBC / FGFR2+
TNBC / BRCA1 mut
TNBC / PTEN loss
TNBC
Her2- / ER+ / FGFR1+
Her2- / ER+ / PIK3CA mit
Her2- / ER+ / AKT mut
Her2- / ER+ / BRCA2 mit
Her2- / ER+

Standard, Investigational Biomarkers and Molecular Breast Cancer subtypes and therapies

- HR+ (expression) \leftarrow Endocrine therapy \pm biologicals
- HR+ plus PIK3CA mutations ← PIK3CA inhibitor + fulvestrant
- ESR1 mutations ← SERDs ?
- HER2+ (amplification, mutations) \leftarrow anti-HER2 \pm systemic therapies
- Low HER2 expressions ← ADCs (e.g., T-deruxtecan)
- BRCA 1 and 2 mutations ← PARP inhibitors / Platinums
- PD-L1 positivity in advanced TNBC ← Chemo + CPIs



Towards molecular segmentation!



Many Other Targetable Genomic Alterations in Breast Cancer Ongoing Investigation

Table 1	Table 1 Targetable genomic alterations in breast cancer				
Gene	Alteration	Frequency (%)	Candidate drug	Level of evidence for the target	
Growth fa	ctor receptors				
ERBB2	Amplifications Mutations	>10	HER2 inhibitor	1 3	
FGF3	Amplifications	5–10	FGFR inhibitor	4	
FGFR1	Amplifications	5–10	FGFR inhibitor	2	
FGFR2	Amplifications	1–5	FGFR inhibitor	2	
IGF1R	Amplifications	1-5	IGFR inhibitor	4	
EGFR	Amplifications	1–5	EGFR inhibitor	2	
PI3K/AKT	/mTOR				
PIK3CA	Amplifications Mutations	>10	PI3K inhibitor	1–2	
PIK3R1	Mutations	1-5	Not known	4	
PTEN	Mutations Deletions	5–10	AKT inhibitor	3	
AKT1	Amplifications Mutations	1-5	AKT inhibitor	2	
AKT2	Amplifications	1–5	AKT inhibitor	2	
AKT3	Amplifications	1-5	AKT inhibitor	4	
INPP4B	Deletions	1-5	AKT inhibitor	NA	

Gene	Alteration	Frequency (%)	Candidate drug	Level of evidence for the target
MEK path	way			
NF1	Mutations	1-5	MEK inhibitor	2c
KRAS	Amplifications	1-5	MEK inhibitor	2c
BRAF	Amplifications	1-5	MEK inhibitor	2c
JNK pathy	vay			
MAP2K4	Mutations Deletions	5–10	Not known	NA
МАРЗК1	Mutations Deletions	5-10	Not known	NA
GPS2	Mutations	1-5	Not known	NA
Cell cycle				
CCND1	Amplifications	>10	CDK4 inhibitor	4
CDKN2A	Deletions	5	Not known	NA
CDKN1B	Alterations	1-5	Not known	NA
CDK4	Amplifications	1-5	CDK4 inhibitor	4
Rb	Mutations Deletions	5–10	Resistance to CDK4 inhibitor	3
DNA repa	ir			
BRCA1	Mutations	1–5	PARP inhibitor	1



Biomarker Testing in CRC Precision medicine

RAS mut +/-

For all colon cancers:

MMR

Microsatellite stability Metastatic disease:

- KRAS, NRAS, BRAF
- HER2 amplification
- Panels: ± fusion, broad NGS



Advanced Non-Squamous Lung Cancer (NSCLC) Targetable Driver Mutations







Advanced Non-Squamous Lung Cancer (NSCLC)





Pao W et al. Nat Rev Cancer 2010







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Only Few Successful Combinations of Genomic Alterations and Approved Drug in Clinical Practice

EXaCT-1 overview: detected genomic alterations

- 85.8% 4.2% 0.4%
- Somatic alterations in currently not targetable cancer genes
- Somatic alterations in targetable cancer genes (potential off-label drug use)
- Somatic alterations in cancer genes with FDAapproved drugs
- Somatic alterations with unknown clinical and biological significance





Kandoth C et al. Nature 2013. Pauli C et al. Cancer Discovery 2017 HÓPITAL UNIVERSITAIR

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Average Mutational Burden in Various Cancers





Alexandrov LB et al. Nature 2013 Lawrence M et al. Nature 2013



Predictive Biomarkers for Immune Checkpoint Inhibitors Efficacy

(i) Tumor cells

- PD-L1 expression;
- TMB;
- DDR pathways: dMMR/MSI;
- Specific mutated gene pathways: IFN-γ pathway, KRAS, STK11;
- Neoantigen load;

(ii) Tumor microenvironment

- · PD-L1 expression;
- Tumor-infiltrating immune cells: *Immune status of TME:* immunologic classification, immunoscore; *Immune cells with specific phenotypes:* CD39⁺CD8⁺T, CD4⁺T cells, FOXP3⁺T cells, TAMs, myeloid cells, NKp46⁺ cells; *Diversity of immune repertoires:* TIL richness and clonality, TCR clonality;

(iii) Circulating factors

- Peripheral blood cells: myelogenous cells, eosinophils, nacrophages, CD4*ICOS*T cells, CTCs;
- ctDNA;
- Other circulating molecular: exosomal PD-L1, soluble proteins, cytokines and inflammatory factors;

(iv) Host-related markers

- General characteristics: gender, age, body fat distribution;
- Intestinal commensal microbiota;
- Host germline genetics: HLA diversity and other specific mutations;

(v) Immune-related adverse events

- Endocrine irAEs: thyroid dysfunction;
- Skin irAEs: vitiligo, pruritus, lichenoid toxicity;



Combination of biomarkers ? (e.g., immunogram,...)



TMB as a Predictive Biomarker for Immune Checkpoint Inhibitors efficacy KEYNOTE 158 (Pembrolizumab)

C Α TMB-high 110 -Non-tTMB-high 100-1 year 2 years 2/2 0/1 tTMB-high group 100tTMB-high group: tTMB-high group: Non-tTMB-high group 1/3 26% (95% CI 18-35) 22% (95% CI 14-30) 90-90-Non-tTMB-high group: Non-tTMB-high group: 2/5 13% (95% CI 11-16) 80-7% (95% CI 5-9) 80rate (%) 7/15 survival (%) 70-70-Objective response 5/16 60-60-2/12 free 50-10/34 50-40-30/102 40-1/14 5 Pro 30-30-7/59 4/42 8/75 1 1 1 1 100 1 11 1 11 9/84 20-20-4/67 2/59 2/63 3/79 3/78 43/688 10-1/82 10-Cervical Endo-SCLC Thyroid Biliary Salivary Vulvar Total Anal Meso-Neuro-12 18 21 24 30 33 36 39 0 15 27 42 metrial thelioma endocrine



ORR related to TMB

PFS related to TMB



Genomics-Driven Cancer Management Limitations

- Medical education and recommandations.
- Tumor biology, prioritization of targets and MDTs.
- Inter and intra-tumor heterogeneity.
- Serial tumor biopsies (± invasive) → liquid biopsies.
- Emerging of CNS metastases.

- Evolving and validation of sequencing technologies and data.
- "Druggable" targets.
- Challenges in drugs access, clinical methodology and healthcare organization.
- New designs (innovative) clinical trials.
- Ethical and legal challenges (e.g germinal mutations and ethical considerations).





Evolving Clinical Trials Framework for Drug Approval



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Unselected patients exclusively based on the type of tumor.

Biomarker-defined patients within a tumor type.

Biomarker-defined patients across different cancers sharing abnormality.

Tumor Agnostic Therapeutic Approaches

- B-RAF mutation (e.g., melanoma, NSCLC, Thyroid)
- MMR deficiency (e.g., colon, endometrium, ...)
- Tropomyosin receptor tyrosine kinase inhibitors (e.g., several solid tumors)
- PARP inhibitors (breast, ovary, pancreas, prostate, ...)

More to come



Patient survival and clinical response to pembrolizumab across 12 different tumor types with MMR deficiency



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Larotrectinib (TRK inhibitor): Efficacy



	Patients with confirmatory response data available (n=50)
Objective response rate (95% CI)	76% (62–87%)
Partial response	64%
Complete response	12%
Stable disease	12%
Progressive disease	12%



Drilon A et al. N Engl J Med 2018

Inter and Intra-Tumor Heterogeneity

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Single biopsy specimens of primary tumors, may not fully represent the genetic diversity of multiple metastatic sites.

Important molecular changes will be missed if repeated biopsies are not performed during the evolution of the disease.

Future clinical trials and biomarkers might consider longitudinal analyses of tumour evolution through the disease course.

Swanton C et al. NEJM 2012 Fisher R et al. British Journal of Cancer 2013



Liquid Biopsy



Two techniques to analyze ctDNA



- Mutation(s) are known or first identified in the primary tumor and then followed in plasma
- ✓ Higher sensitivity, feasible even when low disease burden
- ✓ Only few mutations can be tracked

Digital PCR, targeted sequencing

- ✓ Direct plasma ctDNA detection without prior analysis of tumor
- Lower sensitivity, high disease burden required
- ✓ Genome-wide analysis





Liquid Biopsy







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Potential Clinical Applications of Circulating Tumor DNA (ctDNA)

- Early detection of cancer (e.g., NPC, ...)
- Prognostic indicator
- Tumor mutation burden
- Predictor of response to therapy
- Treatment response monitoring
- Residual disease monitoring
- Resistance mechanisms



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ctDNA for Early Cancer Diagnosis





Cohen J et al. Science 2018.

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ctDNA and detection of molecular residual disease (MRD)



ctEBV DNA as a Prognostic Marker in Nasopharyngeal Carcinoma





Lin et al. NEJM 2004



Prognostic and Predictive Role of HPV16 ctDNA in OPSCC

Chera BS et al. J Clin Oncol. 2020



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Longitudinal changes HPV16 ctDNA correlate with treatment response. ctDNA responses could be observed earlier than conventional imaging(average 70 days, range: 35–166).



Haring CT et al. Oncotarget 2021 H.U.



Take-Home Messages

- Ongoing and marked developments in the field of cancer biomarkers.
- Treatment of unselected populations should be abandoned.
- The identification of a driver genetic abnormality as well as the discovery of a selective agent are key for efficacy (and need for prospective validation).
- Molecularly segmented or "rare" tumors are "good" niches for molecular-targeted therapies.
- Discovery of the resistance mechanisms is a high priority as well as the development of selective agents.





Take-Home Messages

- One gene may predict resistance, but no single gene, protein, pathway can predict full efficacy.
- Chemotherapy remains important for the synergy with targeted agents in selective settings, but combinations complicate choices of appropriate biomarker.
- Better clinical outcomes observed in the metastatic setting, but much less evidence and breakthroughs in the adjuvant setting.
- Rise of expected and unexpected side effects.

Pharmacogenomics: potential tool for individualized therapy.



Thank You for Your Attention.





