PATHOLOGY AND Molecular Medicine

Laboratory Aspects of Biomarker Studies

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Disclosures

- CSO with Indoc Research
- Research partner with Life Technologies (ThermoFisher)



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Objectives

- Understand the different types of biomarkers and some of their major characteristics
- Appreciate the general approaches for measuring common biomarkers
- Understand the limitations and challenges of developing biomarkers

bi·o·mark·er

/ˈbīōˌmärkər/

noun

a measurable substance in an organism whose presence is indicative of some phenomenon such as disease, infection, or environmental exposure. "a biomarker that may predict aggressive disease recurrence in liver transplant recipients"

Molecular Biomarkers. A biomarker is a characteristic that can be objectively measured as an indicator of normal biological processes, pathogenic processes or a pharmacological response to a therapeutic intervention.

Journal of Molecular Biomarkers & Diagnosis - OMICS Group www.omicsonline.org/molecular-biomarkers-diagnosis.php



Novel Biomarker Publications by Year



http://www.biomarker-trends.com/tag/emerging-biomarkers/





Considerations

- What kind of question are you asking?
- What kind of biomarker will you measure?
- What type of sample will you have access to?
- How will your sample have been handled?
- How will your measurements be made?
- How reliable is your biomarker measurement?

What kind of question?

Uses of Biomarkers in Cancer Medicine										
Prior to Cancer		Diagnosis	After Cancer Diagnosis				Post Treatment			
	Risk Assessment	Diagnosis	Prognosis	Predicting Treatment Response	Pharmaco- kinetics	Monitoring Treatment Response	Recurrence			
	Am I at increased risk for cancer?	Do I have cancer? What type of cancer do I have?	What is the expected course of my cancer?	Will my cancer respond to this drug?	Should I receive a normal or lower dose or no dose?	How is my cancer responding to this treatment?	Will my cancer come back?			

Source: Biomarkers in Cancer- An Introductory Guide for Advocates, Research Advocacy Network, 2010.

What kind of biomarker?



Properties of common biomarkers



Richard Chahwan The Multidimensional Nature of Epigenetic Information and Its Role in Disease



What type of sample?

- Need to consider the source
- Need to consider the pre-analytic preparation
- Need to consider the timing
- Need to consider the gender
- Other factors?



Quality of macromolecules



Source: Aude Lamy, et al (2011) Mod Pathol 24: 1090-1100;



В



Effect of fixation on biomarkers

Table 1. FFPE-Related Preanalytical Factors Categorized by the Extent Each Has Been Investigated in the Literaturefor Potential Effects on DNA, RNA, Protein, and Morphology Analytes

Comprehensive (All 4 Analytes Have Been Evaluated)	Incomplete (Some but Not All Analytes Have Been Evaluated)	Unexplored (No Analytes Have Been Evaluated)
Cold ischemia	Postmortem interval	Pathology ink
Decalcification	vvarm ischemia time	Fixative age
Fixation duration	Specimen size	Commercial versus in-house fixative
Duration of paraffin block	Prefixation handling	Use of recycled formalin
storage	Fixative buffer	Movement during fixation
<u> </u>	Tissue to fixative ratio	Light exposure during fixation
	Fixation temperature	Fixation container
	Fixative delivery method	Fixation alone or with other biospecimens
	Dehydration reagent and conditions	Postfixation wash solution and conditions
	Clearing reagent and conditions	Reagents and conditions of interim alcohol storage
	Paraffin embedding reagent and conditions	Use of recycled dehydration and clearing reagents
	FFPE block size or section thickness	Automated versus manual processing
	Type of slide or adhesive	Use of recycled paraffin for impregnation and embedding
	Slide drying duration and temperature	Embedding conditions
	Storage duration of slide-mounted FFPE	Slide pretreatment
	sections	Equipment and conditions of sectioning and section transfer

Stability of dynamic markers

BMC Molecular Biology 2009, 10:31



http://www.gene-quantification.de/rna-integrity2.html Thompson KL, Pine PS, Rosenzweig BA, Turpaz Y, Retief J - (2007) http://folk.uib.no/mfapu/Pages/BV/BVSite/stability.html



Biomarker profile of selected metabolites in fresh (orange) and improperly stored (grey) serum/plasma. Arrows indicate conversions, and concentrations are given in µmol/L.

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hsa-miR-29a-3p



CLL: miRNA and protein profiling over time



timecode

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4

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Inter-tumour heterogeneity



Sample or intratumour heterogeneity



Muley T, Herth FJF, Schnabel P, Dienemann H, Meister M. From tissue to molecular phenotyping: Pre-analytical requirements Heidelberg Experience. Transl Lung Cancer Res 2012;1(2):111-121.

Liquid biopsy

- Use of blood, plasma, urine, csf
- May measure CTCs, cfDNA, protein, miRNA, mRNA, metabolites





Sample considerations

- The type of sample you have access to makes a difference in what you can measure
- The collection of the sample can influence the behaviour of a biomarker
- The processing of a sample will influence the behaviour of a biomarker
- Biomarkers don't necessarily behave the same in different sample types



Common methods to measure

- FISH- Fluorescence in situ hybridization
- Arrays
- Sequencing Sanger and NGS
- Nanostring







Sanger Sequencing



Single-stranded DNA	
to be sequenced	
^{5'} CTGACTTCGACAA ^{3'}	
	Gel
Add: <u><u> </u></u>	Larger
DNA Plymerase I	fragments
	G
	A
DITP	C
fluorescently labelled	T Solv the
ddaTP	G sequence
	A of the
	A template
ddTh	G strand
AAGCTGTT	□ →
TGAAGCTGTT	Smaller
	fragments
CTGAAGCTGTT	
	5
GACTGAAGCTGTT	

complement of bands containing labeled strands

Microarray Approach

- Global or targeted
- DNA, RNA, methylation, SNPs
- Semi quantitative
- Not great for degraded material



Next Generation Sequencing

- Global or targeted
- High throughput
- Library to sequence
- Depth controls sensitivity
- Short fragments





Next Gen Sequencing Data

Α

ID3131: MYH7 (p.Y162H)

В

ID3236: ILK (p.P70L)

CCACATCTTCTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAGGCCCTGGAA

ATCTTCTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAG ATCTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAG ATCTTCTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAG ATCTTCTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAG ATCTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAG TCTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGG TCTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGG TCTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGG TCTTCTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAC TCTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGG TCTTCTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAGG TCTTCTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAGG TCTTCTCCATCTCCGACAACGCATATCAGTACATGCTGACAGGTGAGAGG TCTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGG TCTTCTCCATCTCCGACAACGCCAATCAGTACATGCTGACAGGTGAGAGG CTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGC CTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGC CTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGC CTTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGC TTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGCC TTCTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGCC TCTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAGGCCC CTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGCCCT CTCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGCCCT CTCCATCTCCGACAACGCCTATCAGTACATGCTGACAGGTGAGAGGCCCT TCCATCTCCGACAACGCCCATCAGTACATGCTGACAGGTGAGAGGCCCTG ACGGATCAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGGCAGCCAGTCATGGA ACGGATCAATGTAATGAACCGTGGGGATGACACCC ACGGATCAATGTAATGAACCGTGGGGATGACACCC ACGGATCAATGTAATGAACCGTGGGGATGACACCC ACGGATCAATGTAATGAACCGTGGGGATGACAC ACGGATCAATGTAATGAACCGTGGGGATGACACCCC ACGGATCAATGTAATGAACCGTGGGGATGACACCCTCCT ACGGATCAATGTAATGAACCGTGGGGATGACACCCTCCTG ACGGATCAATGTAATGAACCGTGGGGATGACACCCTCCTG ACGGATCAATGTAATGAACCGTGGGGATGACACCCTCCTGC ACGGATCAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGG ACGGATCAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGG ACGGATCAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGGC CGGATCAATGTAATGAACCGTGGGGATGACACCCCCCTGCATCTGGCAGC GGATCAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGGCAGCC GATCAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGGCAGCCA CAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGGCAGCCAGTC CAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGGCAGCCAGTC CAATGTAATGAACCGTGGGGATGACACCCTCCTGCATCTGGCAGCCAGTC A TG TAATGAACCG TGGGGGATGA CACCCTCC TG CATCTGGCAGCCAGTCCC AACCGTGGGGATGACACCCTCCTGCATCTGGCAGCCAGTCATGGA GGATGACACCCTCCTGCATCTGGCAGCCAGTCATGGA CATGACACCCACCTGCATCTGGCAGCCAGTCATGGA CCCTGCATCTAGCAGCCAGTCATGGA TGCATCTGGCAGCCAGTCATGGA ACTCTGGCAGCCAGTCATGGA GGCAGCCAGTCATGGA GCAGCCAGTCATGGA CAGTCATGGA





Sensitivity of NGS vs Sanger



Nanostring

- Targeted
- RNA or DNA
- Quantitative
- Short fragments





Some further considerations

- Sensitivity and specificity
- Precision and accuracy
- Analytical validity versus clinical validity
- Data preprocessing
- Data analysis



Analytic sensitivity and specificity

	Genotype		A: True positives B: False positives	C: False negative
	Present	Absent	Di l'allo positi lo	St. 199 Nagarita
Test				
Positive	Α	В	Sensitivity:	A/(A+C)
			Specificity:	D/(D+B)
Negative	С	D	Positive predictive value:	A/(A+B)
			Negative predictive value:	D/(C+D)

If you are sequencing a tumour looking for KRAS mutations, *analytic sensitivity* refers to the proportion of time that the mutation is there and you can find it. *Analytic specificity* refers to how often the mutation is not there and you think you see it.

It has no bearing on the clinical utility of whether or not there is a KRAS mutation

Accuracy, precision



Do all biomarkers need to be accurate and precise?

Clinical versus Analytical Validity



PICO guides product development, clinical messaging and payer engagement



Data







Data Handling

- Feature extraction
- Processing, cleaning, filtering
- Alignment
- Analysis
- Pipeline for these events must be locked down prior to using biomarker

Before you get it...

Raw reads (DAT files, BCL files) QC raw and QC passed run yield, read quality, run parameters Demultiplexing QC barcoding deconvolution, sample read distribution Deconvoluted reads (FASTQ files) Alignment to reference genome QC alignment (mapping quality), library complexity Aligned reads (BAM files) QC coverage depth, coverage uniformity, allelic Coverage calculation, local alignment frequency, strand bias, GC content Parallel analysis of control samples On target alignment Variation analysis QC error rate Mutation analysis (VCF files) QC negative and positive controls Filtration Mutation filtering Mutation annotation **Clinical annotation** Clinical report **"TRUTH"**

Front. Oncol., 17 April 2014 | http://dx.doi.org/10.3389/fonc.2014.00078

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Conclusions

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