Laboratory Aspects of Biomarker Studies

Harriet Feilotter, PhD, FCCMG Department of Pathology and Molecular Medicine Queen's University

Disclosures

- ✤ Member, Indoc Research (NFP)
- Sesearch partner with ThermoFisher
- Sesearch program with Astra Zeneca
- ✤ Consultant to Labceutics, AZ

Objectives

- Understand the pre-analytic, analytic and post- analytic phases of biomarker testing
- Understand the impact of some key parameters of biomarker measurement

bi·o·mark·er

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

What kind of question?

Uses of Biomarkers in Cancer Medicine

Prior to Cancer		Diagnosis	After Cancer Diagnosis				Post Treatment
А	Risk ssessment	Diagnosis	Prognosis	Predicting Treatment Response	Pharmaco- kinetics	Monitoring Treatment Response	Recurrence
1	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?



Other

- lipids
- metabolites
- physiological
 Protein

Protein

- where
- which version
- functionality

RNA

- which type
- where
- when

DNA

- single nucleotide changes
- copy number changes
- methylation

Delineating biomarker studies

✤ pre analytical

sample quality, sample prep, sample suitability

🥩 analytical

quality issues around library prep, amplification, sequencing run

🎐 post analytical

base calling and alignment

so clinical interpretation



What type of specimen?
Is there sufficient material of interest?
Is it a tissue type that is validated for the assay?

Is it a sample type that is validated for the assay?

What type of biomarker does the assay need?
Is the quantity sufficient?
Is the quality sufficient?

Template preparation

Is the assay targeted or global?
Is there sufficient representation of molecules?

Generation of data

Analysis

Did the assay generate appropriate data?
Did the assay achieve sufficient sensitivity?
Was the quality sufficient to analyze?

Are all QC metrics met?
Are there variants of interest?
Are they clinically relevant

Analytic

Molecular Diagnostic Pre-Analytic Phase



TumorFFPEQuantification/QualSampleProcessingExtractionStorageity assessment

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
- Some the processing of a sample will influence the behaviour of a biomarker
- Biomarkers don't necessarily behave the same in different sample types

Tissue Treatment and Effects



Effect of fixation on biomarkers

 Table 1.
 FFPE-Related Preanalytical Factors Categorized by the Extent Each Has Been Investigated in the Literature for 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	Warm 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
	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



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

P08670 - Vimentin___P08670.EYQDLLNVK.2y6



Tumor Heterogeneity You can miss a biomarker, even if it is there



Even if you sample in the optimal area...



Subclonespecific Common mutation mutation error ATCGGGCTCGTGCTCGCTTATCG ATCGGGCTCGTGCTCGCTTATCG ATCGGGCTCGAGCTCGCTTATCG

ATCGGGCTCGAGCTCGCTTATCG ATCGGGCTCGAGCTCGCTTATCG ATCGGGCTCGAGCTCGCTAATCG ATCGGGCTCGAGCTCGCTTATCG **ATCGGGCTCGAGCTCGCTTATCG**

Limit of detection



For high input:

 $\frac{4 \, reads \, with \, mutation \, of \, interest}{\# \, reads} = Limit \, of \, detection$

 $\frac{4 \, reads \, with \, mutation \, of \, interest}{\# \, reads} = 0.01\% \, desired$

reads = 40,000x!

For Research Use Only

Estimating tumour %

So Roughly

- 100 tumor nuclei
- 🦻 200 normal nuclei
- So Tumor cellularity 33%



How accurate is this?

So Tumors are not always diploid

☞ If tetra-ploid: 2x 2N DNA content

✤ 50% tumor DNA and 50% normal DNA

☞ If octo-ploid: 4x 2N DNA content

✤ 66% tumor DNA and 33% normal DNA

 If hypodiploid (34 chromosomes, 0.75x 2N DNA content in tumor)

\$\mathbf{27}\% tumor DNA 63\% normal DNA

 Tumour nuclei are different sizes compared to normal

Summer nuclei at least 3x longer in one dimension than normal (and more variable in shape)

 Normal nuclei 5um diameter spheres (these are muscle nuclei so I realize they are probably tapered in the Z dimension, but for math sphere is easier)

∽ ~65 um^3 volume

Tumor nuclei 15um diameter spheres

∞ ~1767 um^3 volume (27 x larger)

Relationship of variant frequency to % tumour cells





10% tumour cells100% of the tumour cells heterozygousTherefore, the variant is present at 5%

25% tumour cells40% of the tumour cells heterozygousTherefore, the variant is present at 5%

Analytical considerations

- so have to do with the parameters of the assay itself
- so how it is run, who runs it, when, what quality metrics are available
- so are machines calibrated
- so are controls included
- so are limits of detection known
- so are pipelines locked and applied

Analytical validity

Clinical validity

Clinical utility

Sensitivity

How often is test positive when biomarker is present?

Specificity

How often is test negative when biomarker is not present?

Robustness

How repeatable and reproducible is assay within and between labs?

Stability

What is the impact of sample parameters on test result?

Sensitivity

How often is the biomarker present when disease or outcome is present?

Specificity

How often is the biomarker not present when disease or outcome is not present?

PPV

What is the probability that someone with a positive test will have the disease or outcome?

NPP

What is the probability that someone with a negative test will not have the disease or outcome? The likelihood that the test result informs clinical decision making and improves outcome

Analytical pitfalls



Most of the analytic pitfalls need to be identified and dealt with by the lab As end users of the data, you will not likely need to deal with these factors

But a well informed end user will be aware that these factors exist



Relationship Between Sequencing Quality Score and Base Call Accuracy

Quality Score	Probability of Incorrect Base Call	Inferred Base Call Accuracy
10 (Q10)	1 in 10	90%
20 (Q20)	1 in 100	99%
30 (Q30)	1 in 1000	99.9%

Post analytical considerations

- Are QC metrics established and did the assay meet these?
- So How confident can you be in the variant calling?
- What is the difference between variant calling (biomarker identification) and variant interpretation (clinical interpretation)?
- Defining when a biomarker is present or absent is part of the locked pipeline for the assay
- Interpreting what the presence or absence or behaviour of a biomarker means in the clinical context is different



Variant interpretation

- Biomarker of interest is BRCA2- looking for variants in the coding sequence
- identify a variant that is c.9976A>T which results in a stop codon being inserted at codon 3326
- ∽ c.9976A>T, p.Lys3326*
- Because protein truncation is a mechanism of loss of BRCA2 activity, one might consider this to be a pathogenic finding

Characteristics of this variant

- occurs at the end of the protein, in a region with little functional impact
- occurs in the general population at frequencies well above the frequency of hereditary breast cancer
- so all major interpretation sites list it as benign
- BUT there is limited evidence that it actually confers an increased risk of pancreatic cancer

Variant interpretation



Tools for standardization of interpretation



Before you get it...

Raw reads (DAT files, BCL files)

Demultiplexing

Deconvoluted reads (FASTQ files)

Alignment to reference genome

Aligned reads (BAM files)

Coverage calculation, local alignment

On target alignment

Variation analysis

Mutation analysis (VCF files)

Filtration

Mutation filtering Mutation annotation Clinical annotation

> Clinical report

"TRUTH"

QC raw and QC passed run yield, read quality, run parameters

QC barcoding deconvolution, sample read distribution

QC alignment (mapping quality), library complexity

QC coverage depth, coverage uniformity, allelic frequency, strand bias, GC content

QC error rate

QC negative and positive controls

Parallel analysis of control samples

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

Conclusions

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