HIMSS 2016
Precision Medicine--The Future of Healthcare is Here

The Clinical Implementation of Precision Cancer Medicine

Lincoln Nadauld MD, PhD
Executive Director, Precision Genomics
Intermountain Healthcare

DISCLAIMER: The views and opinions expressed in this presentation are those of the author and do not necessarily represent official policy or position of HIMSS.

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Conflict of Interest

Lincoln Nadauld, MD

Has no real or apparent conflicts of interest to report.
Learning Objectives

• Identify what components are necessary to implement a precision medicine strategy

• Discuss the challenges and opportunities associated with using genomics in daily practice

• Evaluate the concerns around patient access including data security and patient privacy/consent requirements
Overview

• Challenges in Precision Cancer Medicine

• Intermountain Clinical Cancer Genomics Program

• IT Platform and Architecture
Identify and Target Genomic Alterations

Cancer cell

Genomic analysis

Variants
1. FGFR1
2. P53
3. MEK1
4. EGFR
5. HER2

*drug 1*
*drug 2*
*drug 3*
*drug 4*
Is it really that simple?
Tumor Heterogeneity

Gerlinger, NEJM, 2012
Tumor Evolution

Mutations driving relapse present at low frequency

Anticipation-based chemotherapy
Number of Mutations in Human Cancers

B. Vogelstein, Science. 2013
Precision Cancer Medicine

1. Molecular Profiling

2. Prognostic Markers
   - Markers predictive of drug sensitivity/resistance
   - Markers predictive of adverse events
Intermountain Healthcare

- Integrated Healthcare system
- 22 hospitals and 182 clinics
- “Open system” (facilities open to MDs and patients)
Clinical Cancer Genomics Program

• Personalized Medicine Clinic

• Genomic Testing

• Molecular Tumor Board

• Drug Procurement
# Cancer Genomics Workflow

<table>
<thead>
<tr>
<th>PM Clinic</th>
<th>Biopsy or FFPE</th>
<th>Pathology Review</th>
<th>Sample Prep</th>
<th>Molecular analysis (NGS)</th>
<th>Analytics</th>
<th>Molecular Tumor Board</th>
<th>Results and Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Day 1</td>
<td>Day 2-4</td>
<td>Day 5</td>
<td>Day 6</td>
<td>Day 7-8</td>
<td>Day 9-11</td>
<td>Day 12-13</td>
<td>Day 14-15</td>
</tr>
</tbody>
</table>

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Molecular Tumor Board

• Multi-institutional participants

• Experts in Cancer Genomics

• Interpretation of Genomics
Intermountain Cancer Genomics

• www.precisioncancer.org
Precision Genomics Workflow

IT Platform (Syapse)

Receive Test Order  Accession Specimen  Generate Runsheet  Pick up FASTQ File  Initiate Analytical Pipeline  Receive VCF File  Initiate Annotation Pipeline  Receive Annotation File  Report Generation & Delivery

API

Illumina MiSeq  DNAnexus  N-of-One
Integrations / Workflow

1. Upload FASTQ
2. Send status to Syapse
3. Notify DNAnexus
4. Download FASTQ
5. Send VCF and qc metrics
6. Send XML with variants and patient disease
7. Send XML with interpretation

Intermountain Firewall

Intermountain sFTP server

Syapse

DNAnexus

N-of-One
Precision medicine at the point of care.

- Review patients’ molecular & clinical history
- Order molecular testing
- Receive clinical decision support
- Implement and document decisions within optimized workflow
- Revise individual care strategy
Ordering, lab mgmt., results delivery

Select Enter Test Request

Create a new patient

Order test for an existing patient
Molecular tumor board reviews case

Click to edit the recommendation

<table>
<thead>
<tr>
<th>DENE</th>
<th>RANKED LIST OF AGENTS</th>
</tr>
</thead>
<tbody>
<tr>
<td>EGFR</td>
<td>Afatinib</td>
</tr>
<tr>
<td></td>
<td>Erlotinib</td>
</tr>
</tbody>
</table>
Final sign out and report delivery
Intermountain Precision Medicine Cohort Study

- Patients received standard trx within Intermountain
  - 36 standard trx
  - match: dx, age, gen, #prev. trx
  - Assess:
    - PFS
    - Cost of care

- 61 with actionable mutation, and received targeted trx
  - 36 genomics+trg trx
  - match: dx, age, gen, #prev. trx
  - Assess:
    - PFS
    - Cost of care

- 25 without match: dx, age, gen, prev. trx
Patient Case: Lung Cancer

• 56 year old man with metastatic lung cancer

• Progressed through standard chemotherapy regimen

• Genomic analysis: BRAF mutation (not V600E)
Patient Case: Lung Cancer (cont’d)

• Targeted treatment x 9 months
Intermountain BioRepository

- 4 million archival samples
- Accumulated from 1975-present
- Longitudinal healthcare outcome data (30yrs)
High Throughput Sequencing

• Accommodated by HiSeq X10

• 20,000 genomes per year

• Enables sequencing of our biorepository
Genomics Data Sharing Consortium

- Multi-institutional genomics data consortium
- Data shared = data viewed
- Solves n=1 problem
Summary and Conclusions

• Precision cancer medicine is clinically available now.

• Genomic testing generates enormous data sets.

• IT infrastructure for managing genomic data is absent at most institutions.

• Emerging IT applications require EMR integration.
Acknowledgements

- Intermountain Precision Genomics:
  - Derrick Haslem
  - Gary Stone
  - Pravin Mishra
  - David Loughmiller
  - Genomics Core Lab
  - Cancer Clinical Program
  - Sharanya Raghunath
  - Jason Gillman
  - Robin Romero
  - Raj Srivastava
  - Brent James

- Stanford University
- Jim Ford
- Hanlee Ji

- NCI
- ASCO
HIMSS 2016
Precision Medicine--The Future of Healthcare is Here
Clinical decision support in the era of genome informed cancer medicine

Mia Levy, MD, PhD
Ingram Assistant Professor of Cancer Research, Director Cancer Health Informatics and Strategy, Assistant Professor of Biomedical Informatics, Assistant Professor of Medicine, Division of Hematology and Oncology, Vanderbilt University

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Conflict of Interest

Mia Levy, MD, PhD

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Cancer Care Continuum

- Risk Assessment, Reduction & Screening
- Diagnosis
- Treatment Selection
- Treatment Plan Management
- Host & Disease Response Assessment
Biomarkers in the Cancer Care Continuum

Risk Assessment, Reduction & Screening
- Risk Biomarker: BRCA1/2

Diagnosis
- Diagnostic Biomarker: Estrogen Receptor

Treatment Selection
- Prognostic Biomarkers: OncotypeDx, Predictive Biomarkers
  - Estrogen Receptor
  - CYP2D6

Treatment Plan Management
- Predictive Biomarkers
- Supportive Care Pharmacogenomics

Host & Disease Response Assessment
- Response Biomarker:
  - Tumor Burden
  - Tumor Resistance
  - Host Toxicity
Decision Support
Cancer Care Continuum

Types of Decision Support:
Which tests to order?
How to interpret and report results?
How to apply results to patient care?

Mode of Decision Support:
When
How
To Whom

Risk Assessment, Reduction & Screening → Diagnosis → Treatment Selection → Treatment Plan Management → Host & Disease Response Assessment

Predictive Biomarkers
Unselected Population
Treat Unselected

Response

No Response
2002
Comparison of 4 Chemotherapy Regimens in Advanced Lung Cancer

Response rate – 19%
Median TTP – 3.7 mos
Median OS – 8 mos

1207 pts

Schiller et al, NEJM ‘02
2009
EGFR mutated lung cancer

Initial phase III first line EGFR TKI trial: “IPASS”
EGFR TKI vs. Carboplatin - Paclitaxel in Never- or Light Ex-Smokers

Ref: Mok et al NEJM 2009; updated data Fukuouka et al JCO 2011
Unselected Population
Selected Population

Predictive Biomarker

Predict Treatment Efficacy

Informs Drug Selection
Treat Selected

Targeted Therapy

Primary Sensitivity

Disease Progress

Acquired Resistance

Primary Resistance
Riding the Tsunami of Genomic Data

Evolution of testing strategies
Single mutation -> Hot spot panels -> NGS
Levels of Evidence

Pre-clinical
- Animal Models
- Cell Lines
- Case Reports

Clinical Validity
- Retrospective Cohort Studies
- Non-randomized Prospective Studies

Clinical Utility
- Randomized Prospective Studies
- Guidelines

Separates one population into two or more groups with distinctly different outcomes

Incorporated into standard of care clinical decision making
### 2015

**Non-small cell lung cancer**

<table>
<thead>
<tr>
<th>Molecular alteration</th>
<th>Drugs</th>
<th>Level of evidence</th>
</tr>
</thead>
<tbody>
<tr>
<td>EGFR mutation</td>
<td>erlotinib, gefitinib, afatinib</td>
<td>FDA approved</td>
</tr>
<tr>
<td>ALK rearrangements</td>
<td>crizotinib, ceritinib</td>
<td>FDA approved</td>
</tr>
<tr>
<td>EGFR T790M mutation</td>
<td>osimertrinib</td>
<td>FDA approved</td>
</tr>
<tr>
<td>PD-L1 expression</td>
<td>pembrolizumab</td>
<td>FDA approved</td>
</tr>
<tr>
<td>BRAF mutation</td>
<td>Trametinib, dabrafenib</td>
<td>FDA approved</td>
</tr>
<tr>
<td>ROS1 rearrangements</td>
<td>crizotinib</td>
<td>NCCN</td>
</tr>
<tr>
<td>MET amplifications</td>
<td>crizotinib</td>
<td>NCCN</td>
</tr>
<tr>
<td>HER2 mutations</td>
<td>trastuzumab, afatinib</td>
<td>NCCN</td>
</tr>
<tr>
<td>KRAS mutations</td>
<td>Resistance to TKI’s</td>
<td>NCCN</td>
</tr>
</tbody>
</table>
To curate and disseminate knowledge regarding the clinical significance of genomic alterations in cancer
Manually Curated Content

21 Cancers

ALL
ALCL
AML
CML
MDS
GIST
IMT
Breast
Glioma
Gastric
Lung
Colorectal
Basal Cell Carcinoma
Bladder
Medulloblastoma
Melanoma
Neuroblastoma
Ovarian
Rhabdomyosarcoma
Thymic
Thyroid

20 Pathways
823 Genes
21 Cancers
429 Variants
552 Drugs
# EGFR c.2369C>T (T790M) Mutation in Non-Small Cell Lung Cancer

<table>
<thead>
<tr>
<th>Properties</th>
<th>Kinase domain (exon 20)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Location of mutation</td>
<td>Kinase domain (exon 20)</td>
</tr>
<tr>
<td>Frequency of EGFR mutations in N301G</td>
<td>10% in the USA</td>
</tr>
<tr>
<td>Published clinical trial results</td>
<td>Published clinical trial results</td>
</tr>
<tr>
<td>Retrospective cohort analysis</td>
<td>Retrospective cohort analysis</td>
</tr>
<tr>
<td>Case Reports</td>
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</tr>
<tr>
<td>Clinical trial eligibility criteria</td>
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</tr>
<tr>
<td>Pre-clinical studies</td>
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</tr>
</tbody>
</table>

## Levels of Evidence
- FDA Approvals
- Guidelines
- Published clinical trial results
- Retrospective cohort analysis
- Case Reports
- Clinical trial eligibility criteria
- Pre-clinical studies

## Frequency of Alteration in Disease
- EGFR mutant tumors ([Inukai et al. 2006](#))
- T790M EGFR mutant tumors with acquired resistance to gefitinib ([Ishibashi et al. 2005; Pao et al. 2005](#))

## Response to Drug Sensitivity/Resistance
- Currently no role for EGFR inhibitors.

## Location of Alteration in Gene
- Kinase domain (exon 20)
Worldwide Collaboration

68 Contributors
26 Institutions
10 Countries
4 Continents
Dissemination

Publically Available Resources
- Website
  - >2.5M page views, 201 countries
- Mobile App
  - >3634 Downloads, 22K sessions

Clinically Integrated Solutions
- Vanderbilt EHR
  - >5800 patients
- Laboratory Reporting Tool
  - >3200 specimens
Decision Support for Variant Interpretation & Reporting

NGS RESULTS

Detected Alterations With Therapeutic Implications

<table>
<thead>
<tr>
<th>Gene</th>
<th>Alteration</th>
<th>Type of Mutation</th>
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<tbody>
<tr>
<td>EGFR</td>
<td>T790M</td>
<td>Substitution - Missense</td>
</tr>
<tr>
<td>EGFR</td>
<td>L858R</td>
<td>Substitution - Missense</td>
</tr>
</tbody>
</table>

Genes With Potentially Relevant Targeted Clinical Trials: EGFR

Genes With Other Non-Synonymous Alterations: None

Alterations that Failed Testing: EGFR (L861Q)

Therapeutic Implications of Genomic Analysis, For Patient's Tumor Type - Level 1

<table>
<thead>
<tr>
<th>Approved Drugs</th>
<th>Variants Detected</th>
<th>Response to Therapy</th>
<th>Condition</th>
<th>Line of Therapy</th>
<th>Level of Evidence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aflatinib</td>
<td>EGFR L858R, EGFR T790M</td>
<td>Acquired resistance</td>
<td>Non-Small Cell Lung Cancer, When resistance mutation occurs secondary to primary sensitizing mutation in EGFR</td>
<td>Metastatic</td>
<td>NCCN</td>
</tr>
<tr>
<td>Erlotinib</td>
<td>EGFR L858R, EGFR T790M</td>
<td>Acquired resistance</td>
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Potentially Relevant Targeted Clinical Trials - Level 3 (see note)

<table>
<thead>
<tr>
<th>Trial Title</th>
<th>Conditions</th>
<th>Relevant Genes</th>
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<tr>
<td>Trial of Erlotinib and BKM120 in Patients With Advanced Non Small Cell Lung Cancer Previously Sensitive to Erlotinib (NCT01487205)</td>
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<td>EGFR</td>
</tr>
<tr>
<td>Phase II AZD9291 Open Label Study in NSCLC After Previous EGFR TKI Therapy in EGFR and T790M Mutation Positive Tumours (NCT02094261)</td>
<td>Non Small Cell Lung Cancer</td>
<td>EGFR</td>
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<td>Lung Cancer</td>
<td>EGFR</td>
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<tr>
<td>AZD9291 in Combination With Ascending Doses of Novel Therapeutics (NCT02143466)</td>
<td>Advanced Non Small Cell Lung Cancer</td>
<td>EGFR</td>
</tr>
</tbody>
</table>
**Decision Support for Variant Interpretation & Reporting**

**Patient Information**
- **Name:** Charles P. Bingley
- **DOB:** 4/12/75  Gender: Male  MRN: 10101
- **Pathologic Diagnosis:**

**Specimen Information**
- **Specimen Type:** primary
- **Collection Date:** 11/1/14
- **Date Received:** 11/2/14

## NGS RESULTS

### Detected Alterations With Therapeutic Implications

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**Variants with Potential Clinical Utility**

---

**Drug Sensitivity**
- **In Disease (Level 1)**
- **In Other Disease (Level 2)**

### Therapeutic Implications of Genomic Analysis

#### For Patient's Tumor Type - Level 1

<table>
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<tbody>
<tr>
<td>Afatinib</td>
<td>EGFR L858R, EGFR T790M</td>
<td>Acquired resistance</td>
<td>Non-Small Cell Lung Cancer; When resistance mutation occurs secondary to primary sensitizing mutation in EGFR</td>
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AZD9291 in Combination With Ascending Doses of Novel Therapeutics (NCT02143466)

---

**Advanced Non Small Cell Lung Cancer**

**EGFR**
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<tbody>
<tr>
<td></td>
<td>EGFR L858R</td>
<td>Acquired</td>
<td>Non-Small Cell Lung Cancer, When resistance mutation occurs</td>
<td>Maintenance</td>
<td>NCCN</td>
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**Potentially Relevant Targeted Clinical Trials - Level 3 (see note)**

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</table>
Detected Alterations With Therapeutic Implications in Patient's Tumor Type - Level 1

Gene: EGFR
Nucleotide: c.2369C>T
Condition: Non-Small Cell Lung Cancer
Alteration Detected: T790M
Variation Type: Substitution - Missense

About this Gene
EGFR (epidermal growth factor receptor, also known as ERBB1 and HER1) is a gene that encodes for the epidermal growth factor receptor protein. Missense mutations, deletions, and insertions are observed in cancers such as lung cancer and glioblastoma. Activating EGFR mutations increase the kinase activity of EGFR, leading to hyperactivation of downstream pro-survival signaling pathways (Sordella et al. 2004).

Pathways
Receptor tyrosine kinase

Mutation Location in Gene and/or Protein
Kinase domain (exon 20)

Mutation Prevalence
Frequency of EGFR mutations in NSCLC: 10% in the USA and 35% in Asia (Lynch et al. 2004)
Frequency of T790M mutations in EGFR-mutated NSCLC: < 5% of untreated EGFR mutant tumors (Inukai et al. 2006); 50% of EGFR mutant tumors with acquired resistance to erlotinib/gefitinib (Kobayashi et al. 2005; Pao et al. 2005)

Response to Drugs
Response to anti-EGFR antibodies: Currently no role for EGFR mutation in predicting response in NSCLC
Response to EGFR TKIs: Confers decreased sensitivity

Reference
http://www.mycancergenome.org/content/disease/lung-cancer/egfr/4

Content from My Cancer Genome

Link to MyCancerGenome.org
Only 5% of cancer patients participate in clinical trials
Learning Cancer System
Learning Cancer System

Outcomes

Treatment Selection

Population Analysis
83% of US physicians have EHR System

Adoption of EHRs by US Physicians

Office of the National Coordinator:
EHR Data Created Each Year at Vanderbilt

- 7M Clinical Notes
- 9M Scanned Image Pages
- 5M Lab Orders
- 8M Medications Dispensed
- 15M Clinical Communications
- 1.6M Vital Signs
- 1.7M Outpatient Prescriptions

- 55K hospital discharges
- 1.9M ambulatory visits
190M Nursing Data Elements
WHAT LIES BENEATH?
A COMPARISON OF CLAIMS DATA AND EHR DATA AVAILABLE FOR 500 PATIENTS

CLAIMS DATA
The foundation for most healthcare analytics, Claims Data is easy to come by, but delayed, and short on details.

EHR DATA
Real-time, rich in clinical content, and right under your fingertips. EHR data enhances risk algorithms and informs outcomes-based measures.

© 2015 Arcadia Solutions
Health Information Exchange
2.5 Quintrillion bytes of data are created everyday

90% of the data in the world today has been created in the last two years alone

-Big Data Beyond the Hype

Susan Genulius: Data Never Sleeps
Vanderbilt’s De-identified Synthetic Derivative of EHR Linked to Germ line DNA biobank (BioVU) and pathology tissue library

- **Patient Records**: 2.5 M Number of patient records accessible in Synthetic Derivative – the largest database of its kind

- **Genetic Data**: 211,000 Number of clinical records that have matching genetic data (75k already genotyped)

- **Amount Invested**: $12 M
  Investment to create BioVU over the last 10 years

- **Advantages of BioVU**
  - 27K Breast Cancer ICD code
  - 6.6K Tumor Registry Data
  - 4K germ line DNA samples
  - 5.7K tumor specimens

- **Novel Methods**: 180 Peer-reviewed publications in the last 7 years from VUMC researchers creating / validating methodologies
Many Are Looking at Different Parts of the Same Problem
President Obama’s State of the Union Address pushes for precision medicine

- 2015 – 1 Million person precision medicine cohort
- 2016 – Moonshot to “cure” cancer (Biden named “Cancer Czar”)
THERE ARE TWO KINDS OF PEOPLE:

1) THOSE THAT CAN EXTRAPOLATE FROM INCOMPLETE DATA.
Evolution of Clinical Decision Support

Evidence Driven
Protocol Driven
Pathway Driven
Data Driven?
If You Can't Measure It, You Can't Improve It

(William Thomson, Lord Kelvin)
AND WARREN HERE IS IN CHARGE OF OUR GUT FEELINGS
Data fluency: the ability to use the language of data to fluidly exchange and explore ideas within an organization.

Gemignani, Gemignani, “Data Fluency: Empowering Your Organization with Effective Data Communication” 2014
Summary

• Rise of genomic profiling in cancer
• My Cancer Genome knowledge base provides decision support for clinical utility of alterations in cancer
• Strategies for content generation and dissemination
• Strategies for clinical decision support
# Acknowledgements

<table>
<thead>
<tr>
<th>Mia Levy</th>
<th>Lucy Wang</th>
<th>Tracy Shields</th>
</tr>
</thead>
<tbody>
<tr>
<td>Christine Lovly</td>
<td>Danny Wenner</td>
<td>Hassan Naqvi</td>
</tr>
<tr>
<td>Christine Micheel</td>
<td>Mikhail Zemmel</td>
<td></td>
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<tr>
<td>Ingrid Anderson</td>
<td>Nunzia Giuse</td>
<td>MCG Contributors</td>
</tr>
<tr>
<td>Kate Mittendorf</td>
<td>Taneya Koonce</td>
<td>MCG Alumni</td>
</tr>
<tr>
<td>Scott Sobecki</td>
<td>Sheila Kusnoor</td>
<td>And many more…</td>
</tr>
<tr>
<td>Joey Schneider</td>
<td>John Clark</td>
<td></td>
</tr>
<tr>
<td>Mik Cantrell</td>
<td>Katy Justiss</td>
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<td>Daniel Carbone</td>
<td>Batia Karabel</td>
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<tr>
<td>Ross Oreto</td>
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<td>Melissa Stamm</td>
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![Images of authors]
Thank You

mia.levy@vanderbilt.edu