Airway Genomics for Lung Cancer Detection and Interception



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Disclosures

Founder of Allegro Diagnostics Inc. (acquired by Veracyte Inc. Sept, 2014)

Consultant to Veracyte Inc.

Founder of Metera Pharmaceuticals Inc.

Sponsored Research Agreements with Janssen Pharmaceuticals

How airway gene-expression can personalize early detection and prevention of lung cancer

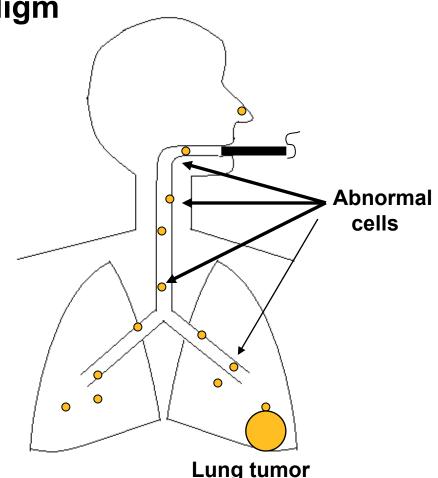
1. Airway gene expression in the "field of injury" as a diagnostic biomarker

2. Extending the "field of injury" into <u>premalignany</u> to accelerate precision <u>prevention</u>

3. Identifying the molecular determinants of premalignancy via the <u>Pre-Cancer</u> <u>Genome Atlas</u>

The airway 'field of injury' paradigm

- Smoking (and other inhaled toxins) alters epithelial cell gene expression throughout the respiratory tract
- Variability in epithelial cell genomic response to and damage from smoking linked to tobacco-associated lung cancer

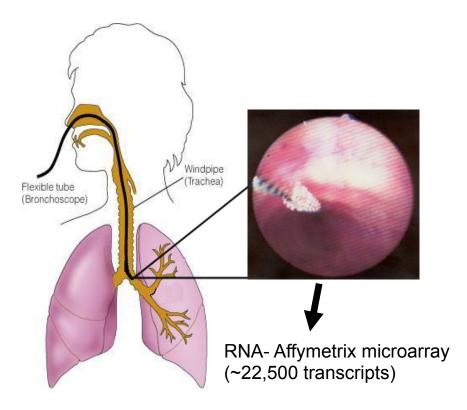


Bronchial airway gene expression as a biomarker of smoking and lung cancer

Smoking impacts airway and microRNA gene expression¹⁻³

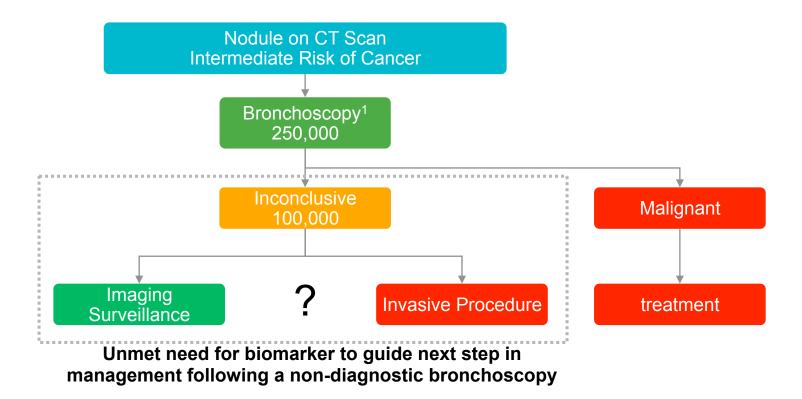
Subset of changes are irreversible upon cessation⁴

Airway gene expression can serve as an early diagnostic biomarker for lung cancer^{5,6}



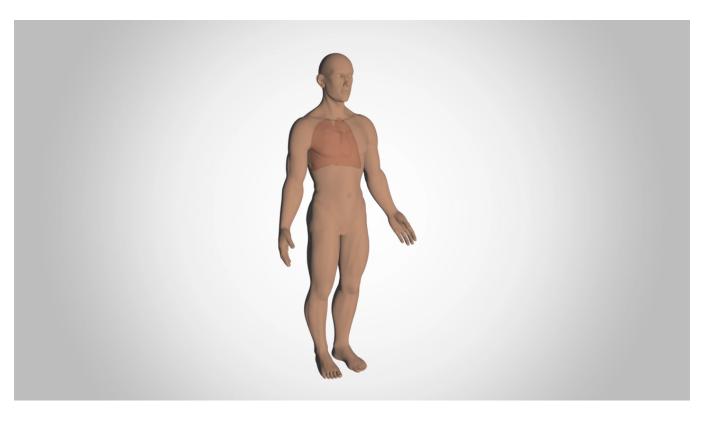
1. Spira et al. PNAS 2004;101:10143-48; 2. Shah et al. NAR 2005;33:D573-79; 3. Schembri et al. PNAS 2009:106:2319-24; 4. Beane et al. Genome Biology 2007;8:R201; 5. Spira et al. Nature Medicine 2007;13:361-366; 6. Beane et al. CAPR 2008;1:56-64

Bronchial Airway Genomic Biomarker was developed to address specific clinical unmet need

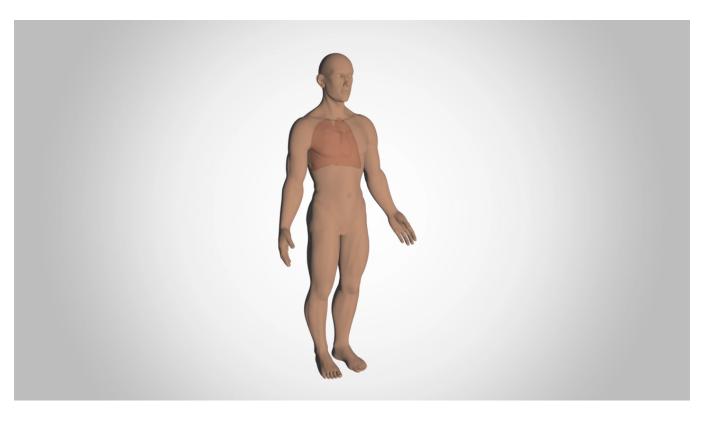


1. Centers for Medicare and Medicaid Services, Hospital Outpatient Standard Analytical Files

The elevator pitch!



The elevator pitch!



Prospective Validation of Bronchial Genomic Classifier (23 genes) in the Airway Epithelium Gene Expression In the DiagnosiS of Lung Cancer The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

A Bronchial Genomic Classifier for the Diagnostic Evaluation of Lung Cancer

Gerard A. Silvestri, M.D., Anil Vachani, M.D., Duncan Whitney, Ph.D., Michael Elashoff, Ph.D., Kate Porta Smith, M.P.H., J. Scott Ferguson, M.D., Ed Parsons, Ph.D., Nandita Mitra, Ph.D., Jerome Brody, M.D., Marc E. Lenburg, Ph.D., and Avrum Spira, M.D., for the AEGIS Study Team*

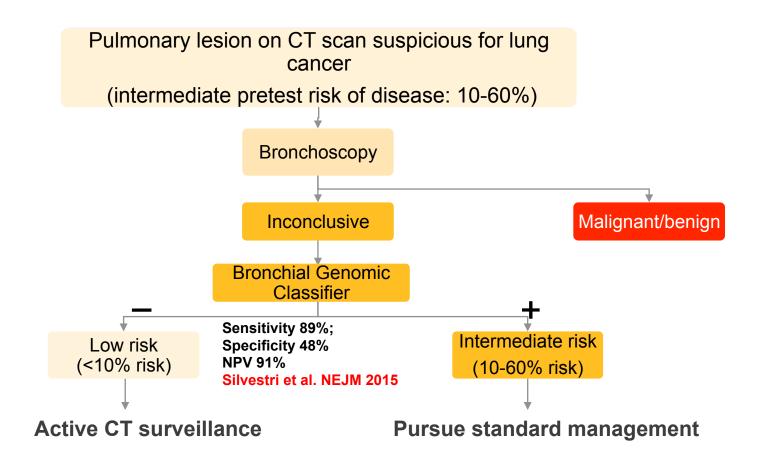


Percepta[™] launched Apr 2015 by Veracyte as CLIA test: 50+ med centers in registry trial; Recent Medicare Coverage Decision

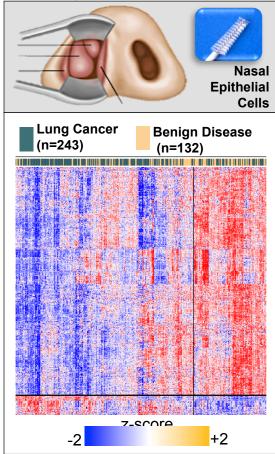
~650 current/former smokers undergoing bronchoscopy for suspect lung cancer -followed for up to 1 year until final diagnosis made



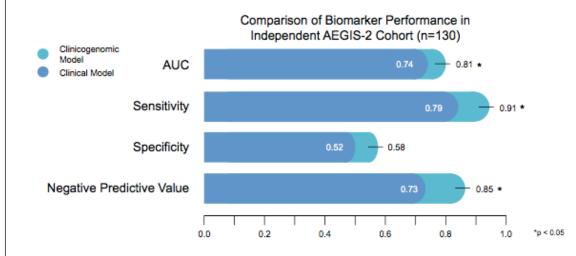
How the bronchial genomic classifier can impact the diagnostic workup



Extending the "field" to the nasal epithelium (NCI/EDRN)



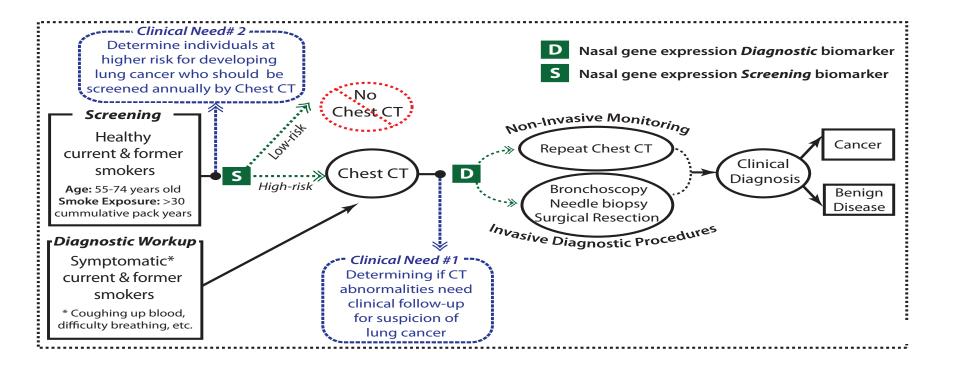
Validation of a clinical model vs. clinical model + 30 gene nasal marker (n=130)



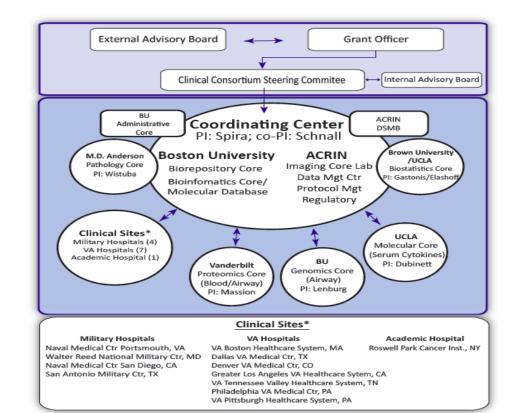
Perez-Rogers et al. JNCI In press

Concordance of bronch and nose

Potential clinical applications for a nasal biomarker



The Detection of Early Lung Cancer Among Military Personnel (DECAMP) Consortium



Funded by DOD, NCI and Janssen

How airway gene-expression can personalize early detection and prevention of lung cancer

1. Airway gene expression in the "field of injury" as an <u>diagnostic</u> biomarker (will be covered in detail tomorrow)

2. Extending the "field of injury" into <u>premalignany</u> to accelerate precision <u>prevention</u>

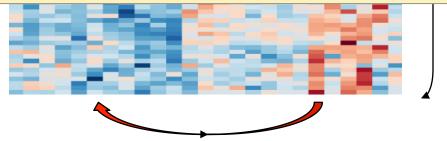
3. Identifying the molecular determinants of premalignancy via the Pre-Cancer Genome Atlas

The airway "field of injury" as a potential <u>companion diagnostic</u> and intermediate <u>marker for therapeutic efficacy</u> in chemoprevention setting

Healthy Smokers Smokers with Dysplasia

Validation in Phase-2b clinical trial: ~75 subjects with dysplasia randomized to placebo vs. myoinositol (Lam et. al CaPR 2016)

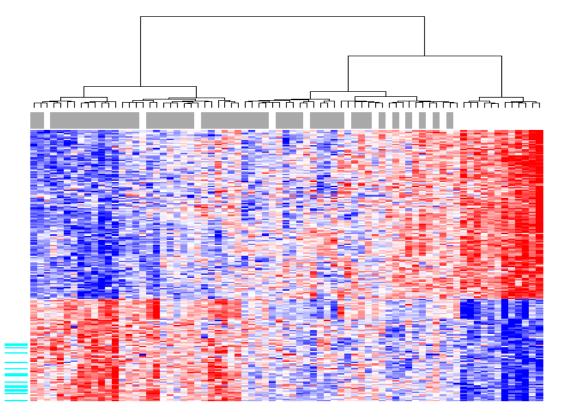
Eva Szabo, Stephen Lam, Paul Limburg



Activity of PI3K gene-expression pathway is significantly reduced post-treatment with myo-inositol in those smokers who had regression of their dysplastic lesions: potential marker for selecting patients likely to respond?

Gene expression alterations in the "field" associated with presence of premalignant lesions

RNA-seq on airway epithelium from 75 smokers with dysplasia vs. 25 without dysplasia



206 genes differentially expressed at FDR<0.001

Subjects without LesionsSubjects with Premalignant Lesions

149 pathways enriched among upregulated genes at FDR<0.05

- Oxidative Phosphorylation
- Respiratory Electron Transport
- Mitochondrial Protein Import
- Nucleotide metabolism
- DNA repair
- Cell cycle

Beane et al. under revision

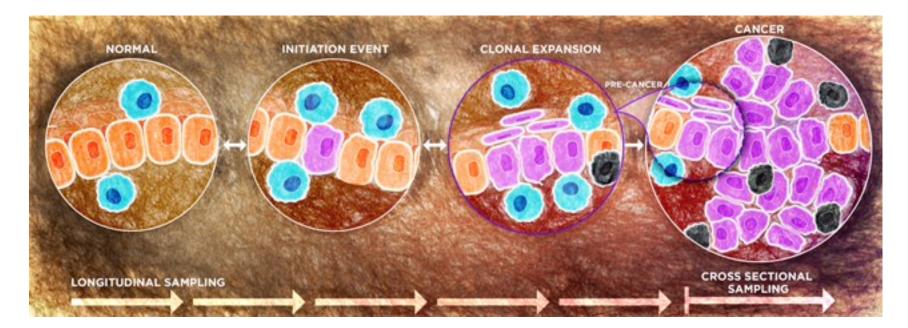
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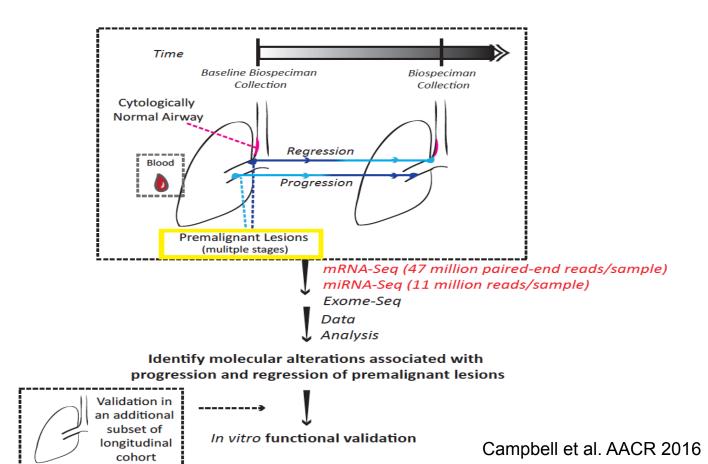
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The Case for A Pre-Cancer Genome Atlas (PCGA)



Campbell et al. CaPR 2016 Spira er al. PNAS 2016

The PCGA for Squamous cell lung carcinoma (in collaboration with Mary Reid, Roswell Park; funded by NCI/JNJ)



Summary

Airway gene expression is a biomarker of the physiological response to smoking and can serve as a <u>diagnostic biomarker</u> for lung cancer

- cancer "field of injury" extends into nasal epithelium

Alterations in airway gene-expression in the <u>premalignant setting</u> may serve as companion diagnostic and surrogate marker of efficacy in chemoprevention trials

PCGA needed to identify earliest molecular events associated with lung carcinogenesis: novel early detection biomarkers and targets for cancer interception

Acknowledgements



UCLA: Steve Dubinett, Denise Aberle, David Ellashoff

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- UPenn: Anil Vachani
- DECAMP investigators

Funded by NCI/EDRN, DOD; Janssen