



CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS Coming up after the break:
 Epigenome and Cancer: From Biology to Therapy Francis Moody Ballroom

Reaching Rural Communities Discussion
 Floral Hall A





CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Epigenome and Cancer: From Biology to Therapy

Epigenome and Cancer: From Biology to Therapy Pre-malignant Tumor Progression, Prevention and Interception

Stephen B. Baylin and colleagues

Components Of The Talk

- A little bit of history including our group's entry into the field
- Molecular mechanisms underlying origins of an epigenetic abnormality we have been studying for over 30 years – very recent insights
- An exciting era cancer evolution from normal cells of tumor origin and the role of their epigenetic "state", dependency of epigenetic changes for a) progression of these cells to point of cancer initiation and b) allowing driver mutations to induce cell transformation
- Some basic translational implications including manipulating epigenetic aspects of tumor immunology

Who Drives Cancer?



The Economist 2012

When, How? Epigenetic www.bloomberg.com/news/articles /2019-03-14/

Genetic

Abnormalities ?





Hanahan, Cancer Discovery, 2022

Epigenetics = the cell, not the DNA does the work!

Martinez Arias's apparent goal, like Ireland's, is to push aside Occam's razor and free us from the inclination to accept simple answers. Sometimes the truth is the murky old news that's been sitting right in front of us the whole time — undiluted, unsavory and complex.

"Since the discovery of the structure of DNA," Martinez Arias writes, "it's become common to refer to DNA as the 'book of life,' a text made up of a sequence of letters — A's, G's, C's and T's — that serves as an instruction manual for building organisms. But what are the instructions for, and who carries them out?"

Frankenstein Experiment

Martinez Arias builds his argument against the supremacy of DNA around Frankenstein-like experiments that involve borrowing a gene from one organism and dropping it into another. Take, for instance, the fruit fly PAX6 gene. When this gene is mutated, flies develop without eyes. Yet when a human version of PAX6 is swapped in for the fly gene, it makes a fly with fly eyes, not a fly with human eyes = <u>the cell, not the DNA does the work</u>!

NY Times Book Review – The Master Builder by Alfonso Martinez Arias, developmental biologist for over 40 years

Putative Therapeutic Target - The Epigenome

Enhancer

Insulator

What is the balance – 1) between the regions, and the types, of change? Who are the 2)



Jones, Nat Rev Genet, 2012

Genetic Alteration vs Promoter Hypermethylation



Jones and Baylin, Nat Rev Genet, 2002

Hypotheses for Molecular Progression to DNA Hypermethylation of Many PcG Target Genes in Cancer – Cancer As An Epigenetic and Genetic Disease



Easwaran, Johnstone, Collison, Ng et al, 2012

DNA methylation subtypes in colorectal cancers



What Are The Mechanisms Underlying CIMP?

- Role of DNA damage, especially ROS Exposure
- Role Of Altered Transcription Factor Expression (PcG genes dominate)

DSB's and Oxidative Damage Inducing A Systemic Signal for Repair in GC/CpG Rich Regions



O'Hagan et al Cancer Cell, 2011

Zhang et al, Mol Cell, 2017

Xia et al, Cancer Cell, 2017

A TF Drive To Sculpting Our Microcosm Of The Cancer Epigenome



Hari Easwaran



Yuba Bhandari Promoter Methylation (CIMP) versus Enhancer Enhancer Methylation (CEMP)



TF's (PcG) and their binding sites are linked for the cancer specific DNA hypermethylation of enhancers and the promoters of their designated target genes and expected gene expression relationships

Bhandari et al, PNAS, 2023

TF repertoire forms a basis for setting the DNA methylation landscape



Hypermethylated

Hypomethylated



Bhandari et al, PNAS, 2023

Importance Of "Fixing" Cell States And Oncogenesis



James DeGregori

Our lab seeks to understand how carcinogenic conditions promote cancer evolution and to discover pathway dependencies in cancers that can be exploited therapeutically.

- Evolutionary based model for cancer development, Adaptive Oncogenesis.
- In this model, mutations (including oncogenic mutations) face fitness landscapes (Cell states and memory thereof = epigenetics!)
- We propose that long-lived multicellular organisms have evolved stem cell populations with high fitness = serving to maintain the status quo, preventing somatic evolution.
- But in stem cell pools damaged by aging, irradiation or other insults, the fitness landscape will be dramatically altered = selection for mutations and <u>epigenetic events that improve</u> <u>perverse fitness and fixation of oncogenically initiated cells.</u>
- These studies could lead to discovery of adjuvants to current therapies that will more effectively treat or possibly even cure leukemias.

Importance Of "Fixing" Cell States And Oncogenesis



Parent cell of tumor origin fate!! Determined in development and parent stem cell renewal in adults

Swanton and colleagues, Cell 186, April 13, 2023

Inflammation as a Driving Agent in Tumorigenesis through Epigenetic Remodeling



Epigenetic changes further evolve in *epithelial, microenvironment,* and *immune cells* and help drive immune evasion and permit oncogenic addiction to mutated oncogenes and tumor suppressors.

Above Evolution of Events Can Be Causal for Key Cancer Risk Factors:

- Aging
- Environmental exposures
- Dietary habits (high fat/carb = metabolic imbalance)
- Obesity
- Exposure to pathogens/infections VIRUSES Mitochondria



Contributions for evolution of and causal effects for Chronic Inflammation driving cancer risk and initiation

Translational implications: targeting epigenetic reprogramming to derive

prevention, interception, early cancer therapy, and biomarker strategies

Ex vivo modeling of early steps in tumorigenesis using colon organoids



CIMP For Developmental Genes Is Functional For Aging Organoids And Susceptibility to Transformation



Old Organoids

Tao, Khang, Easwaran et al, Cancer Cell, 2019

Inducing BRAF Mutation In-Vivo In Setting Of ETBF Challenge



Preceded By Proximal Colon Cell Mucinous Cell Hyperplasia, then serrated polyps and followed by mucinous CRC

DeStefano Shields et al, Cancer Discov, 2021

Different epigenetic and transcriptional landscape in proximal and distal colon define BRAF-driven CRC initiation



Easwaran and colleagues

In revision, please do not post

Influence of cancer risk factors on carcinogenesis



Parent cell of tumor origin fate!! Determined in development and parent stem cell renewal in adults

Swanton and colleagues, Cell 186, April 13, 2023

Smoke-Induced Changes To The Epigenome Provide Fertile Ground For *KRAS* Oncogenic Mutation In NSCLC



Michelle Vaz



Hari Easwaran



Cancer Cell, 2017

SUMMARY - Airway, Normal Cell Organoids

- Chronic CSC exposure causes key shifts in populations of lung stem cells with an associated decrease in differentiation.
- These changes are accompanied by DNA methylation and gene expression changes of an increased tumorigenic potential.
- CSC treated organoids acquire growth factor independency.
- CSC treated organoids modulate the function of key immune cells associated with lung tumorigenesis from a pro- to an anti-inflammatory phenotype over the course of prolonged exposure.
- Growth capability in factor free media + induced driver mutations = NSCLC
 Unpublished, please do not post

Probing The Evolution of NSCLC With Normal Airway Cell Organoids - Michelle Vaz





Altorki, N.K., et al. Nat Rev Cancer 19, 9–31 (2019)

PHASE CONTRAST IMAGES SHOWING MORPHOLOGY OF NORMAL HUMAN LUNG ORGANOIDS (AIRWAY ORGANOIDS)



PHASE CONTRAST IMAGES SHOWING MORPHOLOGY OF MURINE LUNG ORGANOIDS



Unpublished, please do not post



Michelle Vaz



Na Wang

CSC-INDUCED MORPHOLOGICAL CHANGES IN MURINE LUNG ORGANOIDS



After CSC exposure:

- Larger size;
- > Higher density.

IMMUNOFLUORESCENT STAINING OF CELL TYPE-SPECIFIC MARKERS IN HUMAN LUNG ORGANOIDS





CSC Treatment Causes A Shift in the Basal Stem Cell Population From P63*Krt5* TO P63*Krt5*Krt14*

CSC EXPOSURE INDUCES SUBSTANTIAL SHIFTS IN BASAL STEM CELL AND DIFFERENTIATED CELL POPULATIONS



Markers of Stem Cells

Markers of Differentiated Cells



CSC-INDUCED DIFFERENTIALLY EXPRESSED GENES AT 3 MONTHS



Upregulated (Log2 FC) : 199 Downregulated (Log2 FC) : 133 Upregulated (Log2 FC : 247 Downregulated (Log2 FC) : 165

GSEA analysis of CSC-induced differentially expressed genes at 3 months





MORPHOLOGICAL CHANGES SUGGESTIVE OF GROWTH FACTOR INDEPENDENCY IN MURINE ORGANOIDS TREATED WITH CSC FOR 6 MONTHS

Control

10CSC

20CSC



CM : Complete medium BM: Base medium

Preliminary data suggest that the CSC treated organoids are susceptible to KRAS induced transformation.

Induction Of A KRAS Mutation Or A P53 Deletion At Time Of Organoid Growth In Basal Media

KRAS^{G12V}

Тр53 КО



Adenocarcinoma Highly metastatic to lung

Squamous CA
SUMMARY

- Chronic CSC exposure causes key shifts in populations of lung stem cells with an associated decrease in differentiation.
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- Growth capability in factor free media + induced driver mutation = NSCLC

Viral Mimicry Review



Increase efficacy of IO?

DeCarvalho- Jones; ours-Chiappinelli et al , Cell 2015

Dear and Phimster, NEJM, 2016

Combining DNMTi's And HDACi's To Enhance Immune Checkpoint Therapy



Vaz

Topper, Vaz et al, Cell, 2017

Pathogen Mimicry Response (PMR): DNMTi and PARPi induce STING-dependent interferon/inflammasome signaling leading to HRD in TNBC and OC



Covid And Epigenetic Rx Viral mimicry



Unpublished, please do not post

MT ARE THE GATEWAY TO IFN/INFLAMMASOME SIGNALING

Hypothesis

DNMTi and PARPi treatment in BRCA wild-type EOC triggers mt dysfunction and cytoplasmic mtDNA release that activates STING-mediated inflammatory signaling, leading to HRD





Unpublished – please do not post

The Tumor As A Target Of Epigenetic Therapy -The Triad



Clinical Trial Schema: Reversing IO Resistance – NSCLC SU2C Merck Catalyst Trial



Conclusions to date

- Kras, TP53 co-mutations are associated with response.
- Basal responders have high inflammatory signaling.
- Differential expression to therapy is modest, DEGs detected are associated with STAT3, TAM and DC recruitment
- Inflammatory pathways are augmented by therapy, MYC suppressed
- Calcium signaling associated with response in whole blood samples.

Widening A Research Effort Without Walls

Rothbart Lab





Feyruz Rassool



Hari Easwaran

Competitive renewal

Multiple PI NIEHS Grant – Role Of Inflammation And Increased ROS Induced Epigenetic Changes In The Genesis Of CRC

Peter Jones



NIF

CANCER

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Discipline based SPORE to develop Cancer Epigenetic based therapies - Issa, Jones, Baylin

DSB's and Oxidative Damage Inducing A Systemic Signal for Repair in GC/CpG Rich Regions



O'Hagan et al Cancer Cell, 2011

Zhang et al, Mol Cell, 2017

Xia et al, Cancer Cell, 2017



In preparation, You, Qinglong, Yi Cai, S Baylin, Huilin Li

Unpublished– do not post

UHRF1 MAINS ABNORMAL DNA METHYLATION IN CANCER – ELEVATED EXPRESSION CORRELATES WITH POOR OUTCOMES IN HUMAN COLORECTAL CANCER



Kong et al., 2019, Cancer Cell 35, 633–648

FUNCTION OF STELLA (DPPA1), A NATURAL INHIBITOR OF UHRF1



Du et al, J. Biol. Chem. (2019) 294(22) 8907–8917

MOUSE, BUT NOT HUMAN STELLA ACTS AS AN INHIBITOR OF UHRF1 IN HUMAN CANCER CELLS





Xiangqian Kong (Baylin Lab)

Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences



HCT116-Vector

HCT116-hStella-OE

RKO-Vector





RKO-mStella-OE

HCT116-mStella-OE





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Survival Analysis of Combination Epigenetic and Immunotherapy in αPD-1 Resistant NSCLC



Targeted Mutational Profiling (MSK-IMPACT) - Association Between Kras/TP53 Co-mutation and Tumor Regression



Mutation	w/ Unknown Samples
WT both	NS
Kras MT	NS
TP53 MT	NS
Kras MT, TP53 MT	P-value: 0.0103

Nanostring GeoMX DSP ROI Selection and Segmentation

CD45 Segmentation



Region of Interest Selection: Tumor and Immune Cells in Direct Contact (Pathologist Guided)





PanCK Segmentation



Channels:

FITC/525nm : SYTO 13 : DNA (Blue) Cy3/568nm : Alexa 532 : PanCK (Green) Texas Red/615nm : Alexa 594 : CD45 (Red)

Basal Transcriptome of Responders Display Differential Enrichment of Inflammatory and Kras Pathways Relative to Non-Responders



Basal Responder vs Non-Responder based on RECIST Response; all CR/PR patients have achieved DCB (6 Mos. No PD) DE analysis: High Class II APC, inflammatory genes and immunotherapy target MUC16 Pathways: Interferon and Allograft pathways (Up)

Responders Basally Present with Transcriptional MYC Activation and Interferon Suppression vs. Non-Responders in PanCK+ Tumor Cells

Differential Expression Analysis

p-value

O NS

× Log₂ FC

p-value and log₂ FC

HALLMARK OXIDATIVE activated suppressed PHOSPHORYLATION HALLMARK MYC TARGETS V1 HALLMARK PROTEIN SECRETION HALLMARK PROTEIN SECRETION HALLMARK MYC TARGETS V1 HALLMARK FATTY ACID METABOLISM HALLMARK OXIDATIVE PHOSPHORYLATION HALLMARK REACTIVE OXYGEN SPECIES PATHWAY HALLMARK ADIPOGENESIS HALLMARK PEROXISOME HALLMARK DNA REPAIR HALLMARK COAGULATION HALLMARK REACTIVE OXYGEN HALLMARK CHOLESTEROL SPECIES PATHWAY HOMEOSTASIS HALLMARK ANDROGEN RESPONSE Count RESPONSE HALLMARK PEROXISOME HALLMARK ADIPOGENESIS HALLMARK UNFOLDED PROTEIN HALLMARK MITOTIC SPINDLE RESPONSE HALLMARK ANDROGEN RESPONSE p.adjust HALLMARK FATTY ACID METABOLISM HALLMARK MTORC1 SIGNALING 0.025 HALLMARK COMPLEMENT 0.050 HALLMARK DNA REPAIR HALLMARK E2F TARGETS p.adiust HALLMARK COMPLEMENT HALLMARK XENOBIOTIC METABOLISM 0.075 HALLMARK UV RESPONSE UP HALLMARK UV RESPONSE UP HALLMARK PI3K AKT MTOR 0.050 SIGNALING HALLMARK MITOTIC SPINDLE 0.025 HALLMARK E2F TARGETS HALLMARK INTERFERON ALPHA HALLMARK MTORC1 SIGNALING RESPONSE HALLMARK COAGULATION -HALLMARK XENOBIOTIC METABOLISM - 6 HALLMARK INTERFERON GAMMA HALLMARK HYPOXIA RESPONSE HALLMARK ALLOGRAFT REJECTION HALLMARK INFLAMMATORY RESPONSE HALLMARK TNFA SIGNALING VIA HALLMARK APOPTOSIS NFKB HALLMARK CHOLESTEROL HALLMARK INFLAMMATORY RESPONSE HOMEOSTASIS HALLMARK TNFA SIGNALING VIA NFKB HALLMARK KRAS SIGNALING UP HALLMARK KRAS SIGNALING UP 0.10.20.30.4 0.10.20.30.4 HALLMARK HYPOXIA GeneRatio -10 10 20 300 t-score

MSigDB: Hallmark







Swanton and colleagues, Cell, 2023

Ageing-associated DNA methylation provides the permissive state for oncogenic mutations



Tao et al., Cancer Cell (2019, PMID: 30753828)

Widening A Research Effort Without Walls

Rothbart Lab





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Competitive renewal

Multiple PI NIEHS Grant – Role **Of Inflammation And Increased ROS Induced Epigenetic Changes** In The Genesis Of CRC

Peter Jones



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Discipline based SPORE to develop Cancer Epigenetic based therapies - Issa, Jones, Baylin



Cope, Danilova, Laird, Weisenberger, and the TCGA Consortium ,Nature 2014

Role of epigenetic alterations in sensitizing to key genetic driver events to drive specific pathological subtypes of NSCLC



IMMUNOFLUORESCENT STAINING OF CELL TYPE-SPECIFIC MARKERS IN MURINE LUNG ORGANOIDS



SFTPC



Human lung organoids

F-actin Cell type-specific marker DAPI

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SFTPC



Human lung organoids

F-actin Cell type-specific marker DAPI

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"Viral Mimicry" by DNMTi's – A Key Mechanistic Underpinning of our Hypothesis



Important – occurring within, and collaboratively with, a broader inflammasome and DNA repair response



Mechanisms; correlative science; trial parameters

MMSK (Chan) and Erlangen, GermanyRoulois et al, Cell, 2015Chiappinelli, et al, Cell, 2015

Clinical Trial Strategy with STING agonist CRD5500 in AML





Kong et al., 2019 Cancer Cell