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Identifying Novel Targets for Melanoma Treatment

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Tackett Laboratory at UAMS

• <u>Project 1</u>: We develop new tools and assays for determining how proteins interact with each other to drive cancer phenotypes

 <u>Project 2</u>: We take a translational research approach for using patient skin biopsies archived at UAMS for the identification of new targets for melanoma prevention and therapy

Melanoma

•Melanoma: a cancer that develops in melanocytes and is the most deadly of all skin cancers

- •1 person diagnosed every 8 min with melanoma
- •Melanoma claims the life of one American every 62 minutes
- •The mean age for diagnosis of melanoma is 50 •Many other cancers it is 65 to 70 years old
- •Most common form of cancer for young adults 25- to 29-years-old

•65% cases attributed to UV exposure

Risk Factors for MelanomaFair skinLight hair and eye colorMolesDysplastic neviPersonal and/or family historyNon-melanoma skin cancerWeakened immune systemSevere sunburnsExposure to UV

Age

Melanoma

Mole



Melanoma





Melanoma

- -123,590 cases in 2011
- -8,790 deaths in 2011
- -Accounts for 75% of skin cancer deaths



Stage	Description
2a	Tumor >1 but ≤2mm w/ ulcer OR >2 but ≤4mm w/no ulcer
2b	Tumor >2 but ≤4mm w/ulcer OR >4 w/o ulcer
2c	Tumor >4mm w/ ulcer



National Cancer Institute



Prognosis is bleak, little response to chemotherapy or radiation treatments



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National Cancer Institute



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Melanoma survival by stage

Stage	5-year survival (%)
IA	97
IB	92
IIA	81
IIB	70
IIC	53
IIIA	78
IIIB	59
IIIC	40
IV	10

Our Approach



 Exploit the extensive archive of patient melanoma biopsies at UAMS



Utilize the state of the art Proteomics
 Facility assembled by Dr. Tackett to find
 biomolecules in these samples to improve
 diagnosis, prognosis and treatment



Bring our findings back into Dr. Tackett's research laboratory to understand how these biomolecules activate the cancer phenotype (*study melanoma cells directly*)

Proteomics of FFPE Human Melanoma

Laser microdissection of melanoma cells



Normalized Spectral Abundance Factor







Thermo LTQ-XL



390 Proteins Differentially Regulated in Melanoma

SILV is Up-regulated in Melanoma

Benign melanocytic nevus



Malignant melanoma



What about these low molecular weight proteins?



DNA Wraps Around Histones to Form Chromosomes



THE CELL, Fourth Edition, Figure 5.17 © 2006 ASM Press and Sinauer Associates, Inc.

Unraveling a Chromosome



Natural Modifications to Histones Regulate Gene Expression



Modifications of Histones in Patient Melanoma



H3K27me3 is Up-regulated in Melanoma



Maintaining an Epigenetic Mark





H3K27me3 "WRITER" is Over-expressed and "ERASER" is Repressed in Melanoma

JMJD3 "ERASER"

Benign melanocytic nevus

Malignant melanoma



•Tissue microarrays show JMJD3 "eraser" and EZH2 "writer" are differentially expressed (*p*<0.0001)

A Cell Culture Model for Studying Melanoma in the Lab



The "WRITER" is Necessary for Melanoma Cells to Migrate



A Novel Epigenetic Program Activated in Melanoma



Summary

- Described a translational research approach for identifying novel targets for melanoma diagnosis, prognosis and treatment
 - Extensive archive of patient skin biopsies at UAMS
 - Cutting-edge Proteomic technologies
 - A laboratory model to determine mechanism
- Uncovered 390 putative melanoma biomarkers that will move to the validation stage
- Found an epigenetic program involving proteins that WRITE and ERASE the H3K27me3 mark
 - Important for the migration phenotype of melanoma cells
 - Moving forward in elucidating how this epigenetic program "sets" the cancer "clock"

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