

# **Opportunities in Epigenetic**



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### To stimulate population based research on application of epigenetic markers in cancer epidemiology



# Markers in Epidemiology Research

**Currently Used:** Genetic markers Biochemical markers

Unexplored: Epigenetic markers Proteomic markers

In epidemiology, biomarkers are used to follow disease prevalence by determining their level in cohort studies with potential of identifying the high risk population



# **Characteristics of Population Studies**

In population based studies, questions of

- reliability,
- sensitivity,
- specificity,
- reproducibility, and
- scalable capacity for automation

are central in selecting assays to determine factors associated with carcinogenesis



# **Epigenetics: Background**

**Epigenetics is the study of** 

- mitotically heritable changes
- not caused by DNA sequence alterations

**Epigenetic controls** 

- essential for normal development
- misdirected in cancer cells



# Background

Misdirected epigenetic controls can cause - silencing of tumor suppressor genes - activation of oncogenes

**Epigenetic events vs. genetic events** 

- higher frequency
- can be reversed





Verma and Srivastava (2003) Lancet Oncology. 3, 755-763



Transcription Ac Ac Methylation ۰ Me MeCP2 binding ALCP2 Co-Repressor Co-repressor and deacetylase binding Deacetylase o-Represso Co-Repressor eacetylase acetyle o-Represso Histone deacetylation and chromatin compaction °-°-Co-Repressor Mailtin Acetylation Methylation Co-Represso No transcription

Jones and Laird (1999) Nat Rev Gen 21: 163

### Inhibitors of DNA Methyltransferase (5-AZA-C) and Histone Deacetylase (TSA) can Restore Gene Activation



# **Epigenetics in Epidemiology**



## **Molecular Targets**

### **Tumor suppressor Genes**

APC, p15, p16, p73, ARF/INK4A, VHL, ER, RARbeta, AR, HIC1, Rb Invasive/Metastasis suppressor Genes

E-cadherin, TIMP-3, mts-1, CD-44

### **DNA Repair Genes**

Methylguanine methyl transferase, hMLH1, BRCA1, GST

### Angiogenesis

Thrombospondin-1 (TSP-1), TIMP-3

## **Cancer Development is Lengthy**



# **Epigenetic Markers in Lung Cancer**







# Potential Epidemiological Markers in Colon Cancer



### A Model for Colorectal Tumorigenesis

Modified from Jubb et al 2001. J Path. 195: 111.



# Pancreatic Cancer: Methylation of p14ARF and p16INK4a

Division of Cancer Control & Population Sciences

Pancreatic Carcinoma (PCA) : 39 19/39 p16INK4a

**Chronic Pancreatitis (CP) : 16** 

0/16 p16INK4a

p16INK4a

0/6

Normal Pancreatogram (NAD) : 6



Sample: Pancreatic Fluid

(Klump et al. Mol Cell Path 88: 217, 2003)

		GEI		AS	SS:			
Epigenetic Patterns in	'SUE 'YPE	ASE # DKN2A SR1 YOD1	ALCA GMT MP3	<b>ຕ</b> ຸ	AF DH1 STP1 CISS2 HBS1 HBS1	TINNB1 B1 B1 B1 B1 B1 B1 B1 B1 B1 B1 B1 B1 B	C ] <b>J</b>	ASSOCIATED DYS OR T
Esophageal Adenocarcinoma	T NORMAL T STOMACH(S)	10 10 10 10 10 10 10 10 10 10		AF				NO ITO
Cancer Research 61:3410	NORMAL ESOPHAGEAL SQUAMOUS MUCOSA ( NE )	46799 44495555 1155 1155 1155 1155 1155 115						NO
Cancer Progression	BARRETT'S (IM)	467 4479 554 556 162 152 17						NO YES
	DYSPLASIA (DYS)	16L 16H 188 139 388 39						STAGE
	ADENOCARCINOMA (T)	8 113 483 97 3726 404 7 199 3399 444 517 212			N	N N N		1 2 3 4
	< 4 PM		4-20 PM	ИВ	21-50	PMR	> 50	PMR

## Esophageal Cancer: Probability of Survival



Brock et al. Clinical Cancer Research. 9: 2912 (2003)

## **Esophageal Cancer and Methylation**

	TUMOR SAMPLES					NORMAL TISSUE								
PARENT	p16	MGMT	DAP-K	TIMP-3	E-CAD	ER	APC	p16	MGMT	DAP-K	TIMP-3	E-CAD	ER	APC
1	U	Ų	M	м	м	M	М	Ų	м	U	U	U	м	U
2	M	Ų	M	U	М	M	M	Ų	М	Ų	U	U	M	U
3	M	M	U	U	М	M	М	M	М	Ų	U	U	M	M
4	U	U	U .	U	Ų	U	М	M	U	Ų	U	U	U	U
5	U	м	U	U	U	U	U	U	U	U	U	U	U	U
6	M	U	U	м	М	M	M	U	U	U	U	U	U	U
7	U	м	U	U	М	U	М	U	U	U	U	U	U	U
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10	U.	Ų	U	U	U	Ų	U	U	Ų	Ų	Ų	U	U	U
11	M	M	M	Ų	М	M	M	M	м	Ų	Ų	U	Ų	Ų
12	U.	U	M	M	м	M	U	M	U	V	U	M	M	U.
13	M	м	U	U	м	M	М	Ų	м	U	U	M	U	U
14	U	м	U	U	М	U	U	U	М	U	U	U	U	U
15	U	M	U	U	м	U	М	U	U	U	U	U	U	U
16	Ų	M	M	Ų	м	Ų	Ų	M	Ų.	M	Ų	М	U	Ų
17	U	U	U	U	м	М	M	M	U	U	U	U	U	U
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19	M	M	U	M	U	U	м	U.	U	Ų	U	U	U	U
20	М	M	U	U	м	M	м	M	U	U	U	U	Ų	U
21	U	U	U	U	U	U	м	U	U	U	U	U	U	U
22	U	м	U	M	U	U	М	U	U	U	U	U	U	M
23	U.	Ų	U	Ų	м	V	U	V	U.	U U	U	U	U	U
24	м	M	U	M	U	М	M	U	M	U	U	М	M	U
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26	U	Ų	Ų	U .	M	U	Ų	U	Ų	Ų	Ų	U	U	U
27	U	U	Ų	U	Ų	U	M	Ų	Ų	Ų	Ų	U	U	U
28	U	M	M	U	U	U	U	Ų	Ų	U	U	U	U	U
29	U	M	м	U	L L	М	M	U	Ų	U	U	U	U	U
30	м	M	U	U	L L	U	U	U	U	U	U	U	U	U
31	м	M	U	M	М	М	M	м	M	U U	U	U	U	U
32	U	U	U	M	U	М	M	U	M	U	U	U	U	U
33	U.	M	U	V	U	М	M	U U	V.	U	U.	U	U	U
34	M	M	U U	U	M	М	M	Ų	Ų	Ų	U	Ų	U	U
35	M	M	U.	Ų	Ų	м	M	Ų	Ų	Ų	Ų	Ų	U	M
36	U	M	U	U	U	U	U	U	U	U	U	U	U	U
37	U	U	U	U	M	М	M	U	U	U	U	U	U	U
38	м	M	U	U	M	U	U	U	U.	U	U	U	U	U
39	U	U	U	U	M	U	U	U	U	U	U	U	U	U
40	м	M	U	U	M	м	M	U	U	U	U	U	U	U
41	U	V	U	U	U	U	U	U	U	м	U	U	U	U

### Brock et al. Clinical Cancer Research. 9: 2912 (2003)



# Bladder Cancer: Methylation of LAMC2 in Exfoliated Cells

Division of Cancer Control & Population Sciences



Sample: Urine

(Sathyanarayana et al. Can R



## **Esophageal Cancer: Immuno-histochemistry**

### Unmethylated







Brock et al. Clinical Cancer Research. 9: 2912 (2003)

## Tumor Class Prediction by Methylation AML and ALL



В







AML: Acute Myeloid Leukemia ALL: Acute Lymphoblastic Leukemia

#### Adorjan et al (2002) Nuc Ac Res. 30: e21

### Tumor Class Prediction by Methylation AML and ALL



AML:Acute Myeloid Leukemia ALL: Acute Lymphoblastic Leukemia

Adorjan et al (2002) Nuc Ac Res. 30: e21

## **Principle of Methylation**

a Methylation	content
8888888	8888888
8 8888 8 8	8888888 8888888
8888888	8888888
8888888	8888 8 8 8
8888888	8888888
8 8888 8 8 8	888888
8888888	888 888
8888888	8888 8 8 8

b	Methy	yla	tion	level		
- 8	8888	8	88	8888	888	
-8	8888	8	88	8888	888	
-8	8888	8	8	8888	888	
- 8	****	8	88	8888	888	
-8	8888	8	88	8888	888	
-8	8888	8	88	8888	888	
-8	8888	8	8	8888	888	
- 8	8888	8	88	8888	888	

### c Methylation pattern

8 8888 8 8 8	888 888
8 8888 8 8 8	8888888
8 888 888	88888888
8 888 888	888 888
8 8888 8 8 8	888 888
8 8888 8 8 8	888 888
8 888 888	8888 888
8 888 888	8888 8 8 8

### d Level profile

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•	0	000	0	•	•	000	0	0	0	•
•	0	000	0	•	•	000	P	0	0	•
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•	9	and the	0	0	•	000	2	0	0	•

#### e Pattern profile

-8	8888	888	8888	888
	8888	888	8888	888
- 8	****	888	8888	888
	8888	888	8888	888
-				
-	2000	888	2000	000
*	8888	888	8888	888
8	8888 8888 8888 8888 8888 8888 8888 8888 8888	888	8888 8888 8888 8888	888
*	8888 8888 8888 8888 8888 8888 8888 8888 8888	888 888 888	8888 8888 8888 8888	888 888 888

### Laird (2003) Nat Rev Cancer 3:253

### Nature Reviews | Cancer

# **Circulating DNA to Detect Methylation**

Real time PCR HeavyMethyl Method (Cottrell et al NAR 32: e10, 2004)





# **Nanochip for Methylation**



Micro-array test sites connected with platinium wires



# Why Epigenetic Markers

- Multiple markers are better than single marker
- Complementary to biochemical and genetic markers
- Epigenetic events occur early in cancer development
- Easy to assay in small sample size (MS-PCR based assay)
- Source of markers: biofluids, exfoliated cells
- Automation possible (nanochips)



# **Funding Opportunities**

R03 (Small Grant): PAR-03-010

R21 and R33 (IMAT Program)

R01

R41/42 and R43/44

# **Epigenetics Interest Group**



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## **SUMMARY**



### Epigenetic markers can be used for cancer detection and risk assessment to identify populations at high risk of developing cancer

