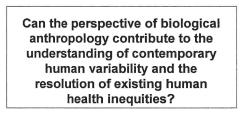
# Using Ethnogenetic Layering (EL) to Illuminate the Genetics of Health Disparities



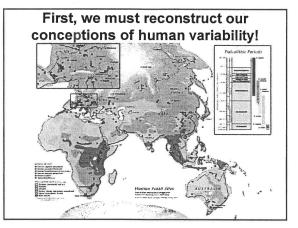
Fatimah L.C. Jackson, Ph.D. Professor Distinguished Scholar-Teacher University of Maryland College Park, MD 20742 301.405.1431 and 301.405.7643 fatimah@urrd.edu

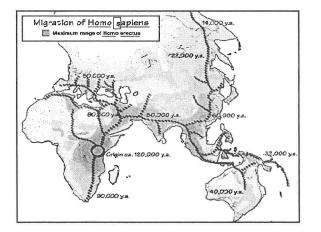
## The Problem and Its Solution

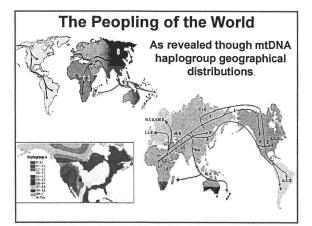
Human heterogeneity and biocultural variability presents a challenge to the classical stratification models of epidemiology and public health. New approaches are needed to capture the nuance of human biodiversity. These new models must encompass relevant cultural/behavioral diversity, genetic variation, non-genetic biological differences, and be contextualized by appropriate biological lineage histories.



Yes! If we take human evolutionary history and population biology into account.







#### Potential Genetic Diagnostic Markers for Breast Cancer

Cell Cycle: Cell Cycle Arrest and Checkpoint: MYC, RB1, TP53. Negative Regulation of the Cell Cycle: ATM, BAX, BRCA1, EGFR, ESR1, NME1, PTEN, RB1, TP53.

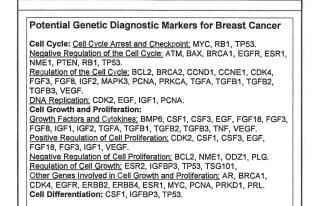
Regulation of the Cell Cycle: BCL2, BRCA2, CCND1, CCNE1, CDK4, FGF3, FGF8, IGF2, MAPK3, PCNA, PRKCA, TGFA, TGFB1, TGFB2, TGFB3, VEGF.

DNA Replication: CDK2, EGF, IGF1, PCNA.

Cell Growth and Proliferation:

Growth Factors and Cytokines: BMP6, CSF1, CSF3, EGF, FGF18, FGF3, FGF8, IGF1, IGF2, TGFA, TGFB1, TGFB2, TGFB3, TNF, VEGF. Positive Regulation of Cell Proliferation: CDK2, CSF1, CSF3, EGF, FGF18, FGF3, IGF1, VEGF.

Negative Regulation of Cell Proliferation: BCL2, NME1, ODZ1, PLG. Regulation of Cell Growth: ESR2, IGFBP3, TP53, TSG101, Other Genes Involved in Cell Growth and Proliferation: AR, BRCA1, CDK4, EGFR, ERBB2, ERBB4, ESR1, MYC, PCNA, PRKD1, PRL. Cell Differentiation: CSF1, IGFBP3, TP53.



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# Ethnogenetic Layering Approaches

Ethnogenetic layering is a new tool to better understand the role of population substructuring in identifying and assessing the biological, cultural, and biocultural risks underlying health disparities.

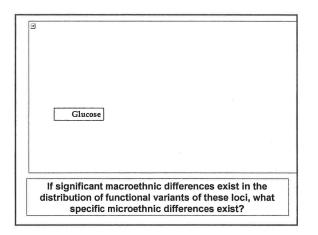


We have focused our research on groups that live in and/or have ancestral origins from one of three US regions: the Chesapeake Bay area, the Carolina Coast area, or the Mississippi Delta.

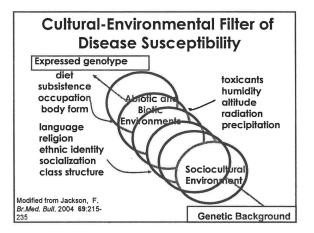
We have developed a strategy to collect and analyse geographical patterns of biological lineage data and micro-ethnic affinity within an ethnohistorical framework.

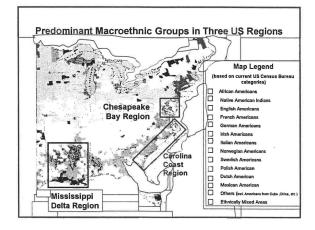
Regional frequencies of significant biocultural factors correlated with health outcomes have been identified to develop a predictive model for assessing group susceptibilities.

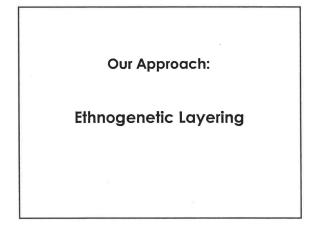
We have developed modified version of phenotype segregation network analysis to pinpoint specific genetic, cultural/behavioral, non-genetic biological contributions to existing health disparities.

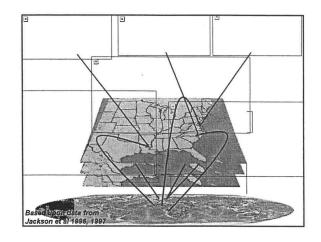


(Number of new cases each year) per 100,000 individuals (1992-1999)					
Group	Both Sexes	Males	Females		
African-American	526.6 (267.3)	703.6 (369.0)	404.8 (204.5)		
European-American	480.4 (205.1)	568.2 (258.1)	424.4 (171.2)		
Asian/Pacific Islander	348.6 (128.6)	408.9 (160.6)	306.5 (104.4)		
Hispanic/Latino	329.6 (129.2)	393.1 (163.7)	290.5 (105.7)		
Amer Ind/Alaska Nat	244.6 (128.6)	277.7 (154.5)	224.2 (104.4)		
Not accurate; ba	sed on selected	d, non-represen	tative groups.		

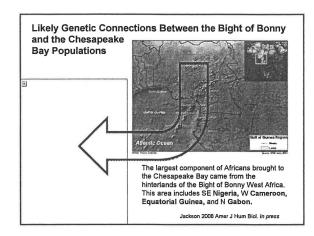


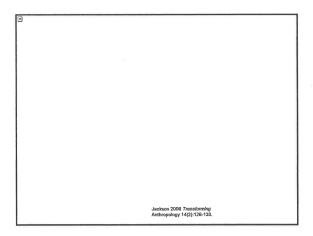


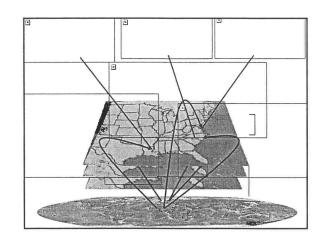




Foundation Microethnic Groups (MEGs) of the Chesapeake Bay Region						
	Major African Deportation Chesapeake Bay Regio Bight of Bonny 38% West Central Africa 16% Gold Coast 16%					
AR	Major Foundin Represente Ulster English Irish	g Europear d in the Cho Scot Scot-Irish	<b>Colonia</b> Sapeako Germa Welsh	e Bay Region		
	Major Foundin Indigenous Amonsoquath Rappahannock Assategue Chesapeake Dogues Haliwa-Saponi Meherrin		apeake -Sapon			







Recently Published Methods Paper on EL Jackson, FLC 2008 Ethnogenetic Layering (EL): An alternative to the traditional race model in human variation and health disparity studies. *Annals of Human Biology* Mar-Apr;35(2):121-144.

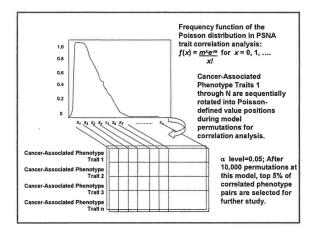


URL: http://www.informaworld.com/10.1080/0301 4460801941752

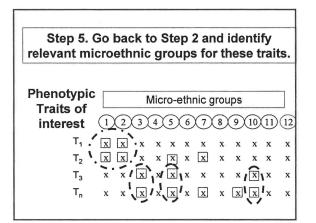
Recently Published Applications Paper based on EL

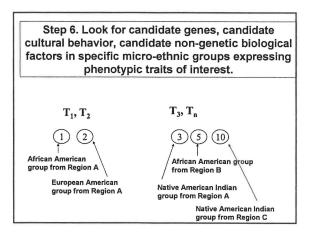
 Jackson, FLC 2008 Ancestral links of Chesapeake Bay region African Americans to specific Bight of Bonny (West Africa) microethnic groups and increased frequency of aggressive breast cancer in both regions. *American Journal of Human Biology* 20:165-173. URL:

http://www3.interscience.wiley.com/cgibin/abstract/117890563 /ABSTRACT?CRETRY=1&SRETR Latest Complement to our Ethnogenetic Layering Approach: Phenotype Segregation Network Analysis of Microethnic Groups for Candidate Gene, Cultural/Behavioral, non-genetic Biological Component Identification



Step 4. Produce a matrix of the phenotypic trait interrelationships						
Phenotypic		10K permutations; top 5% correlations				
Traits of interest	T,	T <sub>2</sub>	T <sub>3</sub>	T		
Τ <sub>1</sub>		z	z	z		
T <sub>2</sub>	z		z	z		
Τ <sub>3</sub>	z	z		z		
Tn	z	z	z			





Possible Use of Ethnogenetic Layering and Phenotype Segregation Analysis to Cancer Health Disparities Research and Intervention Strategies					
<ul> <li>Ranking of classic diagnostic procedures and techniques for specific subgroups</li> </ul>	<ul> <li>Increased resolution of roles of social and biological contributors to existing disparities</li> </ul>				
<ul> <li>Improved specificity of</li> </ul>					

Improved specificity of treatment regimes for particular individuals and groups - Integration of sophisticated genetic, sociocultural, and environmental data in cancer assessments.

## SYNOPSIS

Ethnogenetic layering (EL) is a new tool to better understand the role of population substructuring in identifying and assessing the risks underlying health disparities. By focusing on groups that live in and/or have ancestral origins from one of three US regions: the Chesapeake Bay area, the Carolina Coast area, or the Mississippi Delta, we have developed a strategy to collect and analyse geographical patterns of biological lineage data and micro-ethnic affinity within an ethnohistorical framework. Regional frequencies of significant biocultural factors correlated with health outcomes are then identified to develop a predictive model for assessing group susceptibilities.

A modified version of phenotype segregation network analysis (PSNA) is used to pinpoint specific genetic, cultural/behavioral, non-genetic biological contributions to existing disparities, allowing us to identify the role of genes and gene-environment interactions in disease diathesis and health disparities.