



Paolo Vineis Imperial College London

The impact of socio-economic differentials and the environment on health: new technologies

MRC-PHE Centre for Environment & Health



Social inequalities in health



¹ Source: Analysis by London Health Observatory of ONS and GLA data for 2004-08. Diagram produced by Department of Health

Explaining social inequalities in health



Barton H, Grant M, (2006). A health map for the local human habitat. *Journal of the Royal Society for the Promotion of Health.* 126 (6), p. 252-3.

Behavioral factors and social inequalities in health



Stringhini et al. Contribution of modifiable risk factors to social inequalities in type 2 diabetes: prospective Whitehall II cohort study. BMJ 2012; 345.

Environmental factors and social inequalities in health

Concentration of PM2.5 at place of residence (estimated at neighborhood level) by 6 quantiles of neighborhood level proportion in manual class (A), with income below median (B), with primary education only (C), not owning their dwelling (D), living in flat (E), and in crowded household (F).



Næss et al. Air Pollution, Social Deprivation, and Mortality: A Multilevel Cohort Study, Epidemiology. 18(6):686-694, November 2007.

SES and biomarkers

Hypothalamic-pituitary-adrenal axis	Cortisol - Saliva, urine	
	Dehydroepiandrosterone sulfate - Blood	
Sympathetic neuro-hormonal system	Norepinephrine/Epinephrine - Urine	
	Alpha-amylase - Saliva	
Parasympathetic neuro-hormonal system	n Heart rate variability - Pulse rate recording	
Inflammatory/Immune system	C-reactive protein- Blood	
	Erythrocyte sedimentation rate- Blood	
	Interleukins- Blood	
	Lymphocyte number and function- Blood	
	Circulating serum albumin - Blood, saliva	
Cardiovascular	Diastolic/systolic blood pressure	
	Resting heart rate	
Glucose metabolism	Fasting glucose- Blood	
	Glycosylated hemoglobin- Blood	
	Fasting insulin- Blood	
Lipid metabolism	Cholesterol and lipoprotein fractions - Blood	
	BMI, waist to hip ratio	
	<i>Total body fat</i> - DXA scan	
Hematological	Serum hemoglobin- Blood	
	Clotting factors and clotting time - Blood	
Renal	Creatinine - Serum or 24h urine	
	Urine albumin leakage - Urine	
	Cystatin C - Serum or dried blood spot	
Hepatic	Circulating serum albumin - Blood, saliva	
Reproductive	Serum testosterone/estradiol- Blood	
	Follicle-stimulating hormone - Blood	
Pulmonary	Arterial oxygen saturation - Pulse oximeter	
	Peak expiratory flow - Spirometer	
Bone	Bone density - DXA scan	
	Bone turnover markers - Blood, fasting urine	
Muscle	Skeletal muscle mass - DXA scan, body impedance	
	Grip strength - Dynamometer	

Source: Wolfe B, Evans W, Seeman T. The biological consequences of health inequalities (2012). Russel Sage Foundation, New York

SES and immune system biomarkers



Fig. 1. Prevalence of very high (10+ mg/L) CRP by age group and poverty status with 95% confidence intervals (N = 7634).

Alley et al. Socioeconomic status and C-reactive protein levels in the US population: NHANES IV. Brain Behav Immun. 2006 Sep;20(5):498-504

SES and neuroendocrine biomarkers



Steptoe A et al. Socioeconomic Status and Stress-Related Biological Responses Over the Working Day. Psychosom Med 2003;65:461-470

For >50% cancer the etiology is still unknown

How can we identify new risk factors? Relationships between macro-environment and micro-environment

The exposome changes paradigms for studying lenvironmental causes of disease



S.M. Rappaport and M.T. Smith, Science, 2010: 330, 460-461

A study on omics and air pollution - Oxford Street: high exposure, Hyde Park: low exposure







Serum albumin adducts as biomarkers of exposure

["] Stephen Rappaport's group (UC Berkeley) have been profiling adducts of human serum albumin. Extended and adapted by David Phillips and George Preston at King's College



Rappaport, Williams et al., Toxicol. Lett., 2012, 213, 83-90



Sample ID

Epigenome wide association study of *in utero* exposure to air pollution in ALSPAC: design



Epigenome wide association study PM10



Number of significantly differentially hypo (-) and hyper (+) methylated loci on the genome

+	93	318	49	228
-	53	369	49	300

-> PM₁₀ exposure during trimester 2 shows many associations with methylation loci on the genome



A «socio-molecular» study from existing cohorts: LIFEPATH







We use the revised Strachan-Sheikh (2004) model of life-course functioning (Kuh D 2007; Blane et al, 2013), to describe ageing across the life-course. This model presents ageing as a phenomenon with two broad stages across life: build-up & decline.



MRC-PHE Centre for Environment & Health





Epigenetic modifications

Functionally relevant modifications to the genome that do not involve a change in the nucleotide sequence. Examples of such modifications are <u>DNA methylation</u> and <u>histone modification</u>, both of which serve to regulate gene expression without altering the underlying DNA sequence.





Difference in DNA methylation of CpG dinucleotides in siblings discordant for periconceptional exposure to Dutch famine in 1944.



"60 individuals pre-natally exposed to famine compared with matched, unexposed siblings

"Investigated several genes involved in metabolism

"Positive difference indicates higher methylation level among exposed individuals

Tobi E W et al. Hum. Mol. Genet. 2009;18:4046-4053

Dominance rank and expression level of proinflammatory genes (macaques)



Fig. 2. Rank-gene expression associations among inflammation-related immune genes. Low-ranking females tend to overexpress inflammation-related genes: (A) PTGS2 (P = 0.004); (B) IL8RB (P = 0.003); and (C) NFATC1 ($P < 10^{-3}$).

Tung et al. Social environment is associated with gene regulatory variation in the rhesus macaque immune system. Proc Natl Acad Sci U S A. 2012 Apr 24;109(17):6490-5.

SES and DNA methylation – EPIC Turin

- ["]Selection of candidate genes based on literature review: NR3C1, IL1A, CCL2, CXCL2, CCL20, GPR132, ADM, OLR1, CREBZF, TNFRSF11A, PTGS2, CXCR2, NFATC1, SAT2, MTHFR, AHRR, IGF2
- ["] A total of 599 CpG sites were examined.
- Several indicators of socioeconomic status across the lifecourse
- Adjustment for potential confounding from lifestyle factors



Indicators of socioeconomic status are associated with DNA methylation of candidate genes. The graphs represent the plot of beta coefficients and p-values from linear regression of CpG sites on socioeconomic indicators, adjusted for age, sex, season of blood collection and disease status. The red line represents the corrected overall critical p-value after a multiple-test procedure (FDR). Data points on or above the red line correspond to rejected null hypotheses (p-values that remained significant after multipletesting). For household B highest occupational position (B)26 data points are above the red line; for lifecourse socioeconomic trajectory (C), 7 data points.



Conclusions

The challenges posed by socio-economic differentials and NCDs require new tools for epidemiology and public health (P Vineis, C Wild. <u>Global cancer patterns: causes and prevention.</u>The Lancet 2014 Feb 8;383(9916):549-57) – we know the causes of less than 50% of cancers

Omic technologies allow us to investigate a range of hypotheses on disease in populations according to the paradigm of the exposome

First proof-of-principle suggests that the exposome approach can be successful in areas as diverse as the impact of SES and environmental pollution