Differences in DNA Methylatiun Associated with Area Based Deprivention





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Introduction

- Multiple deprivation is linked to adverse mental- and physical health.
- This link is only partly due to known environmental exposures (smoking, alcohol and BMI).
- DNA methylation (**DNAm**) changes with environmental exposures and differences in DNAm have as been linked to smoking, alcohol and BMI.
- To date there is no epigenome wide study on DNAm differences and socioeconomic status
- We used the single largest DNAm dataset to identify epigenome wide differences in DNAm associated with Scottish Index of Multiple Deprivation (SIMD)

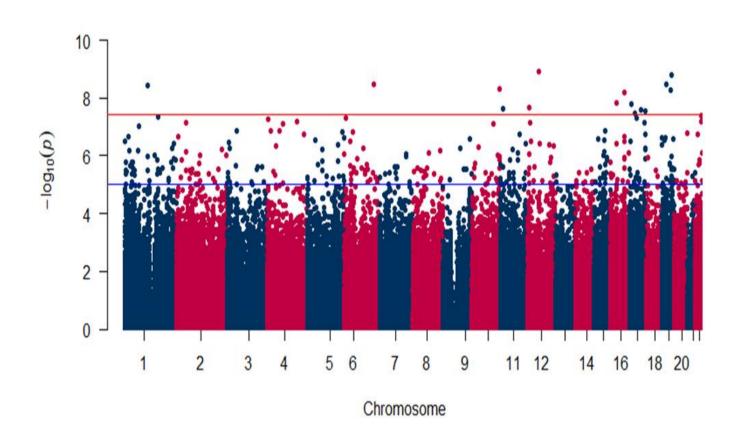
Methods

- Data from generation SCOTLAND N = 7,373
- DNA obtained from whole blood DNAm profiled using Illumina EPIC array
- Differentially methylated point (DMP) and Differentially methylated region (DMR) analysis
- EWAS regression model:

 $DNAm \sim SIMD + smoking status + pack years$

- + BMI + alcohol consumption + age + sex
- + white blood cell estimates
- + 20 Principal Components

Results



15 CpGs reach epigenome wide significance.

Manhattan plot of SIMD rank. Alternating blue and red panels to indicate different chromosomes, blue line = suggestive significance threshold (p < 1e-5), red line = epigenome wide significance threshold (p < 3.6e-8).



DMP (N = 15) Phenotypes:



Bone health

(cg03536474, cg20210689, cg16800968, cg12828075)



Height

(cg07626482, cg16800968, cg19504123)



Cardiovascular disease

(cg03536474, cg20210689)



Blood protein levels (cg13407975, cg10575067

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Respiratory disease (cg21327712, cg11047325)



Multiple sclerosis (cg05210412)

Discussion

- DNAm near genes previously linked to bone health, cardiovascular diseases, inflammatory diseases, and major depression
- ↑ 4/15 DMPs previously associated with age. SIMD has previously been associated with accelerated epigenetic ageing.
- Pervasive biological consequences of deprivation at the molecular level.
- © Current findings congruent with the known mental and physical health burden of low socioeconomic status



DMR (N = 399) Phenotypes:



Cardiovascular disease (28 contributing genes)



Blood protein levels (37 contributing genes)



Obesity-related traits (30 contributing genes)



Type 2 diabetes (16 contributing genes)



Depression
(9 contributing genes)



Mild cognitive impairment (7 contributing genes)