# Psychosocial adversity, socioeconomic position during childhood and epigenetic age: analysis of two prospective cohort studies

RB Lawn, EL Anderson, M Suderman, AJ Simpkin, C Relton, IS Penton-Voak, LD Howe.

MRC Integrative Epidemiology Unit and School of Experimental Psychology rebecca.lawn@bristol.ac.uk

# Background

Life history Theory (Chisholm, 1999) addresses variation in the allocation of finite resources to growth and reproduction. 'Fast' life history strategies involve increased effort directed towards reproduction such as earlier puberty and sexual activity, in response to harsh environmental conditions.

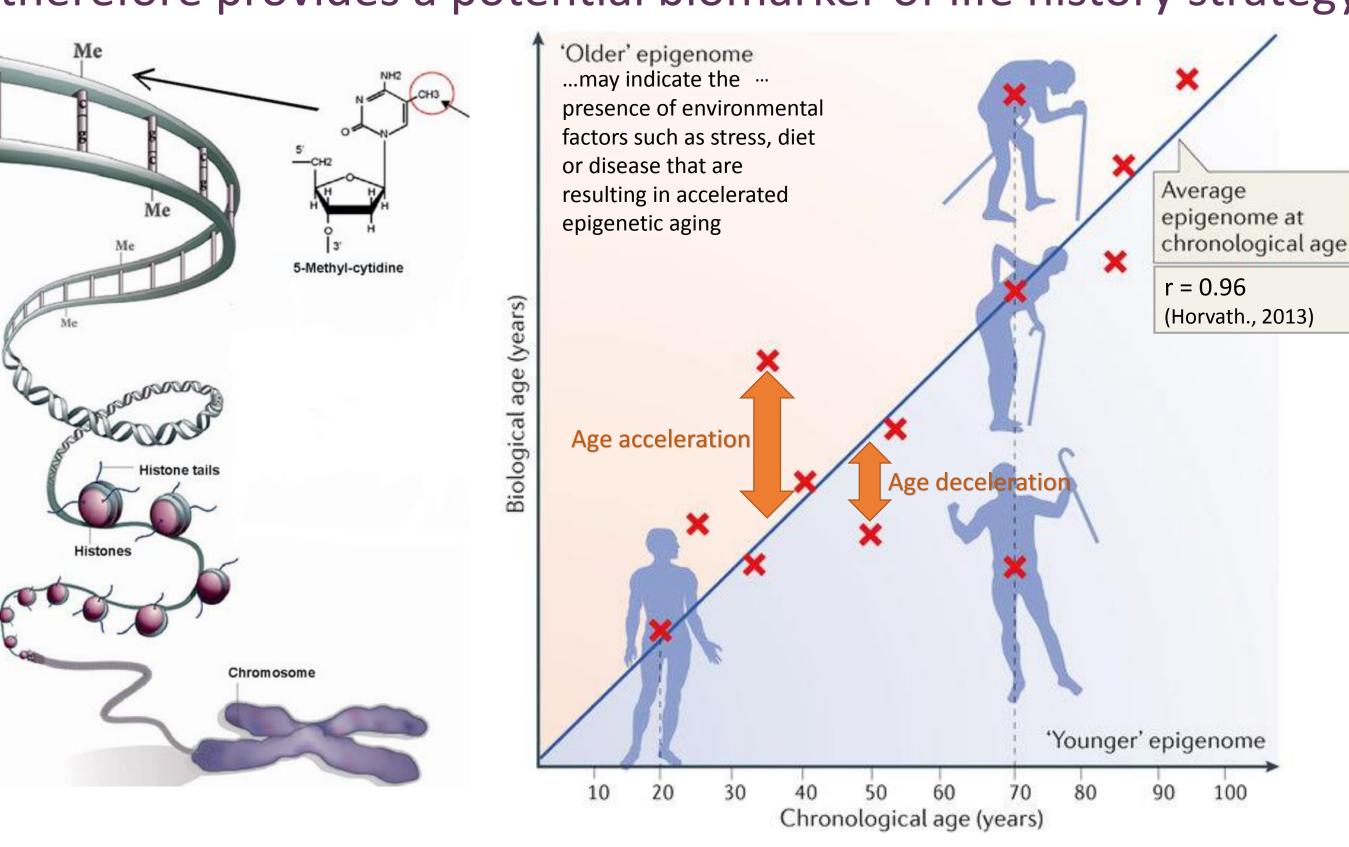
Childhood psychosocial adversity is associated with fast life history traits:

- 1. Accelerated reproductive histories (e.g. early menarche Ellis & Bjorklund, 2012)
- 2. Earlier onset of morbidity and premature death (Norman et al., 2012)

The pathways & mechanisms for the effects of such adversity are unclear, but one implication of these findings is that a Fast Life History Strategy is associated with accelerated aging.

# **Epigenetic age**

The 'epigenetic clock' predicts the rate of aging derived from DNA methylation (the addition of methyl groups to nucleotide bases) and therefore provides a potential biomarker of life history strategy.



Figures from: Maleszewska & Kaminska, 2013, doi:10.3390/cancers5031120; Benayoun et al., 2015, doi:10.1038/nrm4048.

#### Aim

# To investigate whether childhood psychosocial adversity associates with accelerated epigenetic age

#### Methods

#### Data

- Avon Longitudinal Study of Parents and Children (ALSPAC), mothers, N=989 parental mental illness associated with age deceleration for the ALSPAC 29yr
- MRC National Survey of Health and Development (NSHD), females, N=773

#### Psychosocial adversity

- Parental physical or mental illness or death, parental separation, parental absence, sub-optimal maternal bonding, maltreatment, childhood illness
- Cumulative score of psychosocial adversity in childhood

#### **Epigenetic age**

- Based on DNA methylation in adulthood (measured in peripheral blood at 29 and 47 years in ALSPAC and in buccal cells at age 53 years in NSHD)
- Epigenetic age derived using the Horvath method and adjusted for cell heterogeneity by estimated cell-type proportions (ALSPAC)

#### Statistical analysis

- Restricted analysis to participants with data on at least one type of psychosocial adversity and one measure of epigenetic age in adulthood
- Conducted a multiple imputation to estimate missing data for participants
- Used multivariable linear regression models for the cumulative score and individual items of psychosocial adversity
- Meta-analysed findings from the 47-year ALSPAC results and NSHD

# Results

No evidence for associations of cumulative psychosocial adversity and only parental mental illness associated with age deceleration for the ALSPAC 29vi

(n = 989)	results
Mean difference in methylation age acceleration (years) (95% CI)	
0.23 (-0.71, 1.16)	0.68 (-0.00, 1.35)
-0.48 (-1.55, 0.59)	-0.07 (-0.88, 0.74)
-0.29 (-1.26, 0.69)	-0.12 (-1.04, 0.80)
	0.23 (-0.71, 1.16) -0.48 (-1.55, 0.59)

#### **Discussion**

It is possible that adversity during certain developmental periods (such as below 5 years old – Simpson et al., 2012) could have a greater effect on methylation age as accumulation of adversity up to 17 years was measured. Additionally, resilient individuals that experience adversity but remain active cohort participants may possess protective characteristics for the consequences of adversity. Furthermore, associations may only exist short-term as this study included a large time lag between exposure and outcome.

#### **Future research**

Should validate findings and investigate other life history measures with epigenetic age or other epigenetic processes

# Limitations

- Used a cumulative score which assumes individual adversity measures have the same magnitude and direction
- Observed 10 year mean difference between chronological and methylation age in NSHD which has been previously found (Simpkin et al., 2015)
- Due to low variability in chronological ages (clustered around 29, 47 and 53 years) there were low correlations between chronological and epigenetic age





