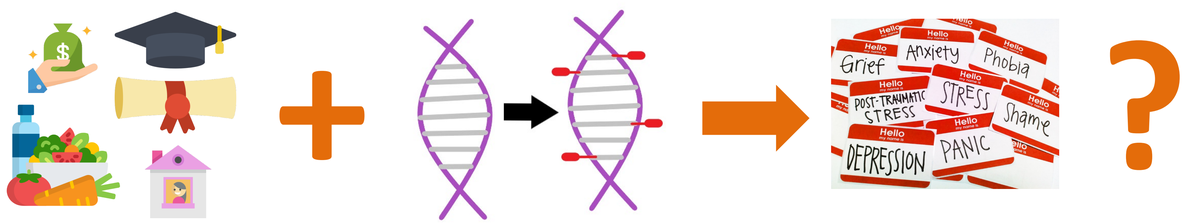
Scars of childhood stress exposures: A Systematic Review

Natasha Wood, Thomas Trebilco, & Sarah Cohen-Woods.
College of Education, Psychology, and Social Work. Flinders University
natasha.wood@flinders.edu.au

Introduction and Background

Childhood socioeconomic position (SEP) has potential to alter epigenetic pathways associated in the development of adulthood mental health outcomes.

Epigenetics refers to mechanisms that cause **changes to gene expression**, without causing changes to the genetic code of DNA (Cruceanu, Matosin, & Binder, 2017). **DNA methylation (DNAm)** is a stable chemical medication which can alter how genes are expressed (Jones & Takai, 2001).



Aim Systematically review the literature assessing the association between DNAm and childhood SEP, with insight in regards to influences on mental health outcomes.

Methods

Inclusion Criteria
- Human
- Original research
- Analysis on an association between DNAm and a measure of childhood SEP,
- Childhood SEP must have solely occurred before age 18.

Electronic Database Search
PubMed, Scopus

Key Search Terms
- DNAm
- Gene methylation, Epigenetics
- Childhood/early environment socioeconomic position and adversities

Data Extraction and Quality Check

Data Synthesis
n= 32

Full Text Screening
n= 81

Abstract Screening
n= 3941

References: Cruceanu, C., Matosin, N., & Binder, E. B. (2017). Interactions of early-life stress with the genome and epigenome: from prenatal stress to psychiatric disorders. *Current Opinion in Behavioral Sciences, 14*, 167-171. doi:https://doi.org/10.1016/j.cobeha.2017.04.001
Jones, P. A., & Takai, D. (2001). The Role of DNA Methylation in Mammalian Epigenetics. *Science, 293*(5532), 1068

Results

11 studies using only **financial** related variables.

11 studies used only **educational** related variables.

11 studies used **a single variable** to represent childhood SEP. **21** studies developed a childhood SEP measure from **2 or more variables**

5 studies investigated mental health outcomes. **Limited evidence for an association** between childhood SEP, DNAm, and mental health outcomes.

Epigenome wide
Across the entire epigenome (450,000 sites per person). **Mixed results of DNAm.**

Epigenetic Age
Measure of biological age based on DNAm. **Sign of increase with lower SEP.**

SLC6A4
Gene associated with serotonin, OCD, & depression. **Mixed results of DNAm.**

NR3C1
Gene associated with stress response. **Mixed results of DNAm.**

OXTR
Gene associated with social bonding, fear, & anxiety. **Increased DNAm with lower SEP.**

Discussion and Implications

There is evidence for **limited** associations between **childhood SEP and DNAm.**

Epigenome wide: altered patterns which **varied** between studies.
Specific genes: selection may **limit research** to existing areas of knowledge and interest.
Epigenetic age acceleration: a type of clock which revealed a **slight increase of aging** with lower childhood SEP.

Inconsistent and **varying** measures of **childhood SEP** reveals an areawide oversight. The consistent use of a **valid measure** of childhood SEP is the best way to ensure childhood SEP is consistently operationalised.

Previous research has indicated that **DNAm might link childhood SEP and general health**. This could be the case with **mental health**. A relationship needs to be established between childhood SEP and DNAm, to **identify epigenetic markers** that could link this relationship.

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