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Contribution ID: **3** Type: **TALK**

Couples who live together longer develop more similar DNA methylation patterns

Pairs of individuals who live together for long periods of time, e.g., spouses, tend to share similar lifestyles, behaviours, and risk events. As environmental exposures can affect the epigenome, it is hypothesised that pairs of long-term cohabiting couples may exhibit greater similarity in their DNA methylation marker patterns.
Using the ESTHER study, a population-representative cohort from Saarland, one hundred and seventy pairs of individuals and their spouses were profiled for genomics, epigenomics, behaviour, and health history cross-sectionally (median age 71.3 years; median cohabitation time 44.7 years). To assess epigenomic similarity, the correlation of functionally normalised DNA methylation values across the entire methylome was calculated per pair.
Linear regression models showed that epigenomic similarity decreased with average age of couples (p=1.48×10⁻⁴), but increased with longer durations of cohabitation (p=1.89×10⁻⁴). Behavioural and health history similarity were also assessed, including smoking, alcohol intake, heart disease, cholesterol, and diabetes, plus the SF-12 Health Survey. Cohabiting couples were found to share smoking and heart disease history at greater than chance, and were correlated in alcohol intake and SF-12 scores. Pairs who shared smoking behaviours were significantly more similar epigenetically (p=0.026), adjusting for age and cohabitation duration. Smoking-related methylation scores suggested a dose-dependent effect of smoke exposure on epigenomic similarity (p=1.96×10⁻³).
Our results support the hypothesis that shared environment can lead to harmonisation of the epigenome through more similar methylation of DNA. Studying cohabiting pairs of individuals could extend research focus beyond genetically-related family members, provide greater control for environmental effects, and increase power for studies of the epigenome, particularly for rare diseases.

Research type

Other

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Session Classification: Short talks #3