**Association of neighbourhood deprivation and depressive symptoms with epigenetic age acceleration: Evidence from the Canadian Longitudinal Study on Aging (CLSA)**

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**Abstract**

**Background:** Neighbourhood deprivation and depression have been linked to epigenetic age acceleration. The next generation epigenetic clocks including the DNA methalyation (DNAm) GrimAge and PhenoAge have incorporated clinical biomarkers of physiological dysregulation by selecting CpGs that are associated with risk factors for disease, and have shown improved accuracy in predicting morbidity and time-to-mortality compared to the first-generation clocks. The aim of this study is to examine the association between neighbourhood deprivation and DNAm GrimAge and PhenoAge acceleration in adults, and assess interaction with depressive symptoms.

**Methods:** The Canadian Longitudinal Study on Aging recruited 51,338 participants aged 45-85 years across provinces in Canada. This cross-sectional analysis is based on a sub-sample of 1,445 participants at baseline (2011-2015) for whom epigenetic data were available. Epigenetic age acceleration (years) was assessed using the DNAm GrimAge and PhenoAge, and measured as residuals from regression of the biological age on chronological age.

**Results:** A greater neighbourhood material and/or social deprivation compared to lower deprivation (b=0.66; 95% CI=0.21, 1.12), and depressive symptoms scores (b=0.07; 95% CI=0.01, 0.13) were associated with higher DNAm GrimAge acceleration. The regression estimates for these associations were higher but not statistically significant when epigenetic age acceleration was estimated using DNAm PhenoAge. There was no evidence of a statistical interaction between neighbourhood deprivation and depressive symptoms.

**Conclusions:** Depressive symptoms and neighbourhood deprivation are independently associated with premature biological aging. Policies that improve neighourhood environments

and address depression in older age may contribute to healthy aging among older adults living in predominantly urban areas.

**Key words:** Neighbourhood social deprivation; Neighbourhood material deprivation; GrimAge, PhenoAge; CLSA

## Introduction

The world is currently experiencing two unprecedented demographic transitions - rapid aging of the populations and urbanization.[1] The proportion of the population aged 65 years and older is expected to increase by 16% between 2020 and 2050, and during this time the proportion of population living in urban areas is also expected to increase to two-thirds of the world's entire population.[2] In parallel, there has also been an increased interest in understanding how late-life depression among older adults relates to both urbanization and aging. The hypothesis that the urban environment influences mental health dates back to Faris and Dunham, who proposed the role of "place" as a risk factor for mental health.[3] Since then, several empirical studies have examined how urban environments influence depressive symptoms.[4-7] Neighbourhood characteristics, too, have been linked to the mental health of older adults.[8-10] A large and growing body of literature suggests that people living in deprived urban neighbourhood physical, social and socioeconomic conditions experience more anxiety and depression,[5, 11-13] and faster decline in mental health.[14] There is also evidence that living in a socially deprived neighbourhood is associated with poor mental health, while higher neighbourhood social cohesion is associated with an improvement in mental health over time.[13, 14] Further, there is evidence of interaction between neighbourhood deprivation and depression on the risk of cardiovascular disease and multimorbidity.[15-17] Individuals with poor mental health may more often reside in highly deprived neighbourhoods or that living in deprived neighbourhoods may influence mental health through factors such as lack of access to health care. Thus, the simultaneous presence of both these factors may amplify the risk of poor health outcomes.

A separate body of research has also reported associations between neighbourhood deprivation and markers of biological aging, such as higher allostatic load and shorter telomere

length.[18, 19] These biological markers, too, have been linked to depression in older age: individuals with major depressive disorder are more likely to show advanced biological aging as assessed using brain imaging and telomere length.[20-22] Recently, urban environments and psychopathology have both been linked to epigenetic processes such as DNA modification through methylation.[23-26] DNA methylation-based estimators, commonly referred to as 'epigenetic clocks', assess DNA methylation (DNAm) at predetermined cytosine-phosphate-guanine (CpG) sites to estimate biological aging at the cellular level.[27, 28] An accelerated epigenetic clock where the epigenetic age is higher than the chronological age, has been associated with age-related declines in health, including faster rates of cognitive decline and higher mortality risk.[29, 30]

The aim of this study is to examine how epigenetic age acceleration assessed using the DNAm GrimAge and DNAm PhenoAge relate to both neighbourhood deprivation and depressive symptoms, and to assess interactions between these two factors among middle-aged and older adults residing in predominantly urban areas in Canada. We hypothesise that both neighbourhood depression and depressive symptoms are independently associated with epigenetic age acceleration. In addition, we expect a significant interaction so that people with more depressive symptoms experience greater epigenetic age acceleration as a result of living in deprived neighbourhoods. Our study addresses a gap in understanding how neighbourhood deprivation and depressive symptoms influence epigenetic age acceleration. In addition, most studies have used the first-generation epigenetic clocks such the original Horvath DNAm and Hannum clocks to estimate the epigenetic age. More recently, second-generation epigenetic clocks such as the DNAm GrimAge and DNAm PhenoAge incorporated clinical biomarkers of physiological dysregulation by selecting CpGs associated with risk factors for disease.[31, 32] This

offers an advantage as depression is associated with changes in inflammatory, metabolic and endocrine biomarkers.

## Methodology

### Study design and population

The complete study design and methodology for the Canadian Longitudinal Study on Aging (CLSA) has been described in detail previously.[33, 34] Briefly, the CLSA is a 20-year population-based, longitudinal cohort study involving a stratified random sample of 51,338 community-living individuals aged 45-85 years at the time of recruitment in 2011-2015. Of these 51,338 participants, 30,097 participants (Comprehensive cohort) were recruited from a 25-50 km area from one of 11 data collection sites located across provinces in Canada. The majority of the participants were from urban population centres and a small proportion were from small urban areas with rural populations and medium sized urban areas. These participants provided data through in-home interviews, physical assessments and biological samples at data collection sites. Data on epigenetic age measures were obtained from blood samples collected from a random sub-sample of 1,479 participants who were included in the analysis.

The Canadian Urban Environmental Health Research Consortium (CANUE) is an initiative created to collect and develop standard measures for environmental exposure data and link them to health databases in Canada. For each participant, the environmental data on measures including neighbourhood social and material deprivation, air quality, noise and air pollution, weather and climate, built environment and greenspaces were created by CANUE and linked to the CLSA individual participant data using the participant's six-digit postal code and interview date. For this study, the 2011 environmental exposure data on neighbourhood level material and social deprivation indices available from the CANUE were used. This study was

approved by the Hamilton Integrated Research Ethics Board (ethics approval number 09-213 and 10-423). Written consent was obtained from all participants prior to data collection.

**Study measures**

**DNA methylation age**

Genome-wide DNA methylation in peripheral blood mononuclear cells (PBMCs) were profiled using the Illumina Infinium MethylationEPIC BeadChip microarrays (Illumina, CA, USA). The EPIC array quantitatively measures DNA methylation at 862,927 CpG sites and 2,932 CHH sites across the genome. To obtain the DNA methylation data, the genomic DNA from the frozen PBMC samples were extracted using QIAsymphony DSP DNA Kits (Qiagen, Hilden, GE). Bisulfite conversion was performed using the EZ DNA Methylation kit (Zymo, CA, USA). For quality control purposes, the raw array data were preprocessed using the GenomeStudio software (Illumina, CA, USA), which transformed the raw methylation values into beta values that range from 0 to 1 and indicate the proportion of methylation at each CpG site. During a quality check of the preprocessed methylation data (RStudio v3.6.3), we identified and excluded four samples that had bisulfite-conversion scores of less than 85%. The bisulfite-conversion scores were computed by the bscon function in the wateRmelon package v1.28.0 in R. Further, inconsistenly performing non-specific probles were also excluded. The *wateRmelon* and *lumi* (v23.6.0) packages in R identified 29 additional outlier samples, which were also excluded from further processing procedures. Thus, epigenetic data were available for 1,445 participants. Complete details about procedures used to generate and process raw data are described in the CLSA Data Support Document.[35]

**Derivation of biological age estimates from epigenetic clocks**

Epigenetic aging measures were calculated from the DNA methylation beta values using the new Horvath online DNA Methylation Age calculator software (https://dnamage.genetics.ucla.edu/home). Epigenetic clocks were derived using weight and beta values that were normalized using the Noob normalization approach.[36] The DNAm GrimAge is constructed as a composite of 12 DNAm based biomarkers and smoking pack-years, and estimates mortality risk in unit of years.[32] The DNAm PhenoAge was based on a phenotypic age score developed from chronological age and nine clinically relevant blood biomarkers.[31] The unit for DNAm PhenoAge is biological years. The DNAm PhenoAge was trained to predict all-cause mortality and the DNAm GrimAge was trained to predict time-to-death. For both clocks, the residuals from regression of the biological age on chronological age are considered as "age-adjusted" and were used to measure epigenetic age acceleration.

**Depressive symptoms**

The 10-item Center for Epidemiologic Studies Short Depression Scale (CES-D10) was used to assess depressive symptoms in the past 7 days.[37] The CES-D10 includes items on depressed affect, positive affect, and somatic symptoms. Each item is scored on an ordinal scale from 0 (never or rarely, <1 day) to 3 (all of the time, 5-7 days) a week. After reverse coding the positive affect items, scores can range from 0 to 30, with higher scores indicating higher depressive symptoms. The CES-D10 has good reliability and validity, with an internal consistency of 0.86, test-retest reliability of 0.85, and convergent and divergent validity of 0.91 and 0.89, respectively, in the adult population.[38, 39]

**Neighbourhood deprivation**

Material and social deprivation refers to characteristics of individuals of the neighbourhood, and the indices were based on socioeconomic factors that were known to be associated with health.

The deprivation indices are based on the dissemination areas, which are the smallest geographical units for which Canadian census data are disseminated. These indices were developed by CANUE and were constructed from six socioeconomic factors taken from the 2011 Statistics Canada's census program.[40, 41] These indices measure deprivation among Canadians and assess inequalities in accessing material and social resources in the communities.[40, 41] Material deprivation was assessed based on the proportion of individuals without a high school diploma, the employment to population ratio, and average personal income of individuals. Material deprivation is an indicator of people's inability to access or afford goods and conveniences that are part of modern life, such as proper housing, nutritious meals, high speed internet, a car, or a neighbourhood with recreational facilities. It reflects economic hardships and is an indicator of the consequences associated with low education achievement, job insecurity, unemployment, and lack of sufficient income.[40] Social deprivation reflects presence of weak social networks in the family and the community. This index is an indication of the proportion of people who live alone, are separated, divorced, or widowed, or are a lone parent.[40] Data on the socio-economic indicators are obtained for people aged 15 years and older, and except for the proportion of people who are single parent families, have been adjusted for the age and sex distribution of the Canadian population. Data on material and social deprivation were available as quintiles with the highest quintile representing the most deprivation. As suggested in the literature, we created a combined deprivation index from the quintiles, with participants in the upper two quintiles for material and/or social deprivation considered as being highly 'materially and/or socially deprived'.[42]

**Covariates**

The analysis was adjusted for individual level covariates including sex (male or female), income (less than $20,000, $20,000-<$50,000, $50,000-<$100,000, $100,000-<$150,000, $150,000 or more, treated as a continuous variable), number of people currently living in the household not including the participant, number of poor health behaviours, and number of chronic health conditions. Smoking intensity was assessed by calculating total pack-years (number of cigarettes smoked per day divided by 20 cigarettes per pack, and multiplied by the number of years smoked), and dichotomized as 'never or less than 20 pack-years' or '20 or more pack-years'. The Physical Activity Scale for the Elderly (PASE) was used to assess physical activity levels.[43] Participants meeting the World Health Organization's age-specific cut-off of at least 75 minutes of vigorous intensity or at least 150 minutes of moderate intensity of physical activity per week were considered as 'adequate', otherwise 'inadequate'.[44] Nutritional risk was assessed using the validated 'Seniors in the Community: Risk Evaluation for Eating and Nutrition (SCREEN-II)' tool, and scores were dichotomized as "high risk" (total score < 32) or "not at-risk" (total score ≥ 32).[45] Alcohol consumption was grouped as 'did not drink alcohol in the past 12 months' or 'occasional and regular drinker'. The number of poor health behaviours tend to co-occur and therefore were summed to create a score ranging between 0 and 4. Participants were presented with a list of chronic conditions including musculoskeletal problems, respiratory diseases, cardiovascular diseases, endocrine disorders, neurological diseases, gastrointestinal disorders, genitourinary problems, ophthalmologic disorders, kidney disease, back problems, and cancer, asked to report only those chronic conditions diagnosed by a health professional that are expected to last or have already lasted at least six months. The number of conditions endorsed by each participant was summed for inclusion in the analysis. In the analysis, number of poor health behaviours and chronic conditions were modeled as continuous variables to improve statistical

power. These covariates were identified a priori and were included in the analysis as they are known to be associated with depressive symptoms, neighbourhood deprivation, and epigenetic age.

**Statistical analysis**

All analyses were adjusted for the sampling design. Descriptive analysis was performed using the inflation weights and regression analysis were performed using the analytical weights provided by the CLSA to ensure that the results are generalizable to the target population. A multilevel regression model was tested to examine the effect of neighbourhood level material and/or social deprivation after adjusting for individual level socioeconomic factors. The results produced an intraclass correlation coefficient (ICC) of less than 2% indicating lack of presence of multilevel effect by neighbourhood deprivation.[46] Therefore, multivariable linear regression models were used to examine the association of neighbourhood material deprivation and/or social deprivation and depressive symptoms with each epigenetic age acceleration measure after adjusting for the above-mentioned covariates (eFigure 1 in the Supplement). A two-way interaction between neighbourhood deprivation and depressive symptoms was tested to assess if the association between neighbourhood deprivation and epigenetic age acceleration differed by depressive symptoms. We reported unstandardized coefficients with 95 per cent confidence intervals (95% CI). Data management and analyses were performed on SAS version 9.4 software.

**Results**

Descriptive characteristics for participants in the CLSA are shown in Table 1. The mean chronological age of participants was 59.7 years (SE = 0.3 years, range 45-85 years), 49.7% were males, and 92.6% were of European ethnic background. At the individual level, 78.8% of

participants had attained a post-secondary or higher education and 40.9% had a total annual household income of CAD$100,000 or higher. The average depressive symptoms score was 5.5 (SE = 0.2) and 59.1% resided in neighbourhoods that were materially and/or socially deprived. The average DNAm GrimAge (mean = 56.3, SE = 0.3 years) was closer to the chronological age and much higher than the epigenetic age estimated using the DNAm PhenoAge estimator (Mean = 42.8, SE = 0.34 years). The correlations of each epigenetic clock with chronological age are presented in Figure 1. Both epigenetic clocks were significantly positively correlated with chronological age, with strong correlations observed for DNAm GrimAge (r = 0.90) and DNAm PhenoAge (r = 0.82).

Results from models examining the association of depressive symptoms and material and/or social deprivation with epigenetic age acceleration measures are reported in Table 2. On average, higher depressive symptoms score showed a positive association with epigenetic age acceleration estimated by DNAm GrimAge after adjusting for covariates (b = 0.07; 95% CI = 0.01, 0.13). Greater neighbourhood material and/or social deprivation compared to lower neighbourhood deprivation was associated with higher DNAm GrimAge acceleration (b = 0.66; 95% CI = 0.21, 1.12). The associations between depressive symptoms, neighbourhood material and/or social deprivation, and epigenetic age acceleration estimated using DNAm PhenoAge were positive, but not statistically significant.

Engaging in greater number of poor health behaviours including smoking, inadequate physical activity, poor nutrition, and alcohol consumption was positively associated with DNAm GrimAge acceleration only. Each additional poor health behaviour was associated with a one-year higher epigenetic age acceleration (b = 1.06; 95% CI = 0.77, 1.34). Compared to females, males had higher epigenetic age acceleration, and having greater number of chronic conditions

was positively associated with higher epigenetic age acceleration using both DNAm GrimAge and PhenoAge clocks (Table 2).

Two-way interactions between depressive symptoms and neighbourhood material and/or social deprivation were not statistically significant for both clocks (Table 2). In sensitivity analysis, we examined associations between depressive symptoms, material and/or social deprivation, and epigenetic age acceleration using the first-generation Horvath DNAm Age and Hannum DNAm Age, and found no evidence of a statistically significant interaction or main effects (eTable 1 in the Supplement). We also examined the associations after restricting the sample to individuals of European ethnicity. The results remained similar to those obtained from the overall sample for all four age acceleration measures (results not shown).

**Discussion**

This study sought to examine how living in a deprived neighbourhood and having depressive symptoms are associated with epigenetic age acceleration in a community-based sample of middle-aged and older adults residing in predominantly urban areas. The results showed that neighbourhood deprivation and depressive symptoms were positively associated with acceleration of the epigenetic age estimated using the DNAm GrimAge clock. As DNAm GrimAge estimates mortality risk in units of years, our results indicate an acceleration in the risk of mortality by one month for every point increase in depressive symptom score, and by almost one year for those exposed to greater neighbourhood deprivation (upper two quintiles for material and/or social deprivation) compared to lower neighbourhood deprivation. We did not find evidence, however, of a statistically significant interaction between neighbourhood deprivation and depressive symptoms.

Consistent with prior literature, we found that greater number of depressive symptoms were associated with acceleration of epigenetic aging estimated using DNAm GrimAge after adjusting for all covariates, suggesting that the association is above and beyond individual and neighbourhood-level factors.[25, 47-49] Emotional distress caused by depression may result in biological wear and tear and dysregulation of the physiological systems, and in turn lead to accelerated epigenetic aging.[50] Dysregulation of the hypothalamic-pituitary-adrenal (HPA) axis, and inflammatory, neurological and immune processes have been implicated in the pathophysiology of mood disorders, including major depressive disorder.[51] Changes in glucocorticoid receptor activity, cortisol levels, and presence of inflammatory biomarkers have been noted in individuals with exposure to chronic stress and/or depression, and may be linked with cellular aging.[51] Evidence also suggests that differences in the methylation levels of the aryl hydrocarbon receptor repressor (AHRR) gene and the associated immune and neuroinflammatory processes may be associated with the pathophysiology of psychiatric diseases and aging.[32, 52-55] Individuals with depressive symptoms may also have had exposure to environmental stressors such as childhood trauma, poor lifestyle and health behaviours, and weaker social networks; thus, accumulation of stressors over the life course may explain the observed epigenetic changes among these individuals.[25] However, longitudinal studies are needed to understand the causal nature of these associations.

The findings also add to the growing body of evidence that exposure to urban environment and neighbourhood deprivation is associated with accelerated epigenetic aging.[23, 24, 47, 56] Neighbourhood social environment is associated with DNA methylation of both stress and inflammation related genes.[57] Adults who lived in neighbourhoods characterized by lower aesthetic quality, safety, and social cohesion had shorter telomere length (another marker of

biological aging) than those who lived in a more socially advantaged neighbourhood.[19] Likewise, material deprivation is also associated with the epigenetic age acceleration measured using epigenetic clocks, shorter telomere length, and DNA methylation of genes involved in stress and inflammation processes.[23, 58, 59] Since the material deprivation index in the current study is based on the dissemination area level indicators, this finding highlights the potential associations of biological aging with residing in neighbourhoods characterized by lower income households, high unemployment rate, and lower education rates. The association between material and social deprivation and epigenetic age acceleration could be reflective of poor childhood environment, lifestyle and health behaviours, stress of experiencing economic hardship, weaker social networks, and fewer opportunities for social participation, which may result in premature biological aging.[58, 60, 61] Our results showed that the effect of neighbourhood deprivation on epigenetic age acceleration was similar regardless of depressive symptoms, suggesting that depression influences epigenetic age acceleration through mechanisms that are unrelated to neighbourhood deprivation.

There was no statistical association between depressive symptoms, material and/or social deprivation, and epigenetic age acceleration measured using the PhenoAge. The differences in findings between the two epigenetic clocks may be explained by the differences in the number and type of DNAm based estimators included in the algorithm. There is also little overlap of CpG sites between clocks, which may indicate that the different epigenetic clocks may be measuring different aspects of biological aging. The DNAm GrimAge may be more sensitive and may outperform other clocks, as its estimation is based on greater number of CpG sites (1030 CpGs) compared with the DNAm PhenoAge (513 CpGs), Horvath DNAm Age (353 CpGs), and Hannum DNAm Age (71 CpGs).[62]

The findings of our study should be considered in the light of some limitations. The cross-sectional study design prevents us from determining the temporal sequences between urban environment attributes, depressive symptoms, and epigenetic aging. Evidence suggests that the association between depressive symptoms and epigenetic age may be bi-directional. Therefore, longitudinal studies are needed to examine these associations further. This study also did not assess age of onset or duration of depression. Further, information regarding length of exposure or how long individuals lived in their neighbourhood was not available. It may be possible that individuals who spend more time in deprived neighbourhoods have a higher epigenetic age. Another limitation is that our sample was predominantly of European ethnic background; in addition, individuals residing in the Canadian territories, on First Nation reserves, in long-term care homes, and those with cognitive impairment were excluded from the study, which limits the generalizability of our findings to community-dwelling older adults of European ethnicity.

**Conclusions**

Taken together, these findings suggest that living in urban environments with higher levels of neighbourhood deprivation and having depressive symptoms are both associated with premature biological aging, even after accounting for individual level health and behavioural risk factors. DNAm GrimAge estimates mortality risk in units of years; therefore these results may indicate an acceleration in the risk of mortality for those with depressive symptoms as well as those exposed to neighbourhood material and social deprivation. However, longitudinal studies are needed to confirm these associations. Future studies are also needed to examine whether the associated epigenetic changes are stable or reversible over time. As next steps, future research should focus on identifying and examining the underlying biological mechanisms linking

depression, neighbourhood material and social deprivation, epigenetic age acceleration, and increased risk of morbidity and mortality.

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**Competing interests:** The authors declare no competing interests.

**Ethics approval and consent to participate:** This study was approved by the Hamilton Integrated Research Ethics Board (ethics approval number 09-213 and 10-423). The participant data were de-identified at the CLSA Data Curation Centre prior to their release to the study team. Written consent was obtained from all participants prior to data collection.

**Availability of data and materials:** Data are available from the Canadian Longitudinal Study on Aging (www.clsa-elcv.ca) for researchers who meet the criteria for access to de-identified CLSA data.

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**Table 1: Descriptive characteristics at baseline for participants in the Canadian Longitudinal Study on Aging (n=1,479)**

| | n | Mean or Frequency | SE or Percentage[a] |
|---|---|---|---|
| **Chronological age, mean (SE)** | 1479 | 59.73 | (0.32) |
| **Male sex, n (%)** | 1479 | 732 | (49.68) |
| **European ethnic background, n (%)** | 1476 | 1371 | (92.64) |
| **Post-secondary education or higher, n (%)** | 1479 | 1107 | (78.81) |
| **Annual household income, n (%)** | | | |
| **<$20,000** | 1400 | 94 | (5.75) |
| **≥$20,000-<$50,000** | 1400 | 364 | (20.08) |
| **≥$50,000-<$100,000** | 1400 | 458 | (33.28) |
| **≥$100,000-<$150,000** | 1400 | 248 | (20.20) |
| **≥$150,000** | 1400 | 236 | (20.69) |
| **Depressive symptoms, mean (SE)** | 1474 | 5.47 | (0.16) |
| **Neighbourhood material and/or social deprivation, n (%)[b]** | 1427 | 857 | (59.10) |
| **DNAm GrimAge, mean (SE)** | 1445 | 56.32 | (0.29) |
| **DNAm PhenoAge, mean (SE)** | 1445 | 42.81 | (0.34) |
| **Total number of poor health behaviours, mean (SE)** | 1479 | 1.69 | (0.03) |
| **Smoking, n (%)** | 1474 | 305 | (18.93) |
| **Inadequate physical activity, n (%)** | 1403 | 988 | (64.94) |
| **Nutritional risk, n (%)** | 1362 | 213 | (14.52) |
| **Alcohol consumption, n (%)** | 1442 | 1059 | (74.88) |

| | | | |
|---|---|---|---|
| **Number of people living in the same household, mean (SE)** | 1479 | 1.48 | (0.04) |
| **Chronic conditions** | | | |
| **Number of chronic conditions, mean (SE)** | 1479 | 2.33 | (0.07) |
| **None, n (%)** | 1479 | 244 | (21.86) |
| **One, n (%)** | 1479 | 303 | (23.20) |
| **Two, n (%)** | 1479 | 265 | (18.30) |
| **Three or nore, n (%)** | 1479 | 667 | (36.65) |

Note: DNAm = DNA methylation

[a]Estimates are weighted by the inflation weights provided by the CLSA

[b]With the exception of neighbourhood material and/or social deprivation, all variables were assessed at the individual level.

**Table 2: Association between neighbourhood material and/or social deprivation, depressive symptoms, and epigenetic age acceleration measures**

| | DNAm GrimAge Acceleration | | DNAm PhenoAge Acceleration | |
|---|---|---|---|---|
| | **b** | **95% CI** | **b** | **95% CI** |
| **Unadjusted Models** | | | | |
| Depressive symptoms (n=1,440) | 0.11* | (0.05, 0.16) | 0.06 | (-0.03, 0.15) |
| High material and/or social deprivation vs. low deprivation (n=1,393) | 1.13* | (0.65, 1.60) | 0.39 | (-0.43, 1.20) |
| **Adjusted Model[a] (n=1,315)** | | | | |
| Depressive symptoms | 0.07* | (0.01, 0.13) | 0.07 | (-0.03, 0.17) |
| High material and/or social deprivation vs. low deprivation | 0.66* | (0.21, 1.12) | 0.20 | (-0.64, 1.04) |
| Male vs. Female | 2.99* | (2.53, 3.44) | 3.90* | (3.07, 4.72) |
| Annual household income | -0.55* | (-0.79, -0.32) | -0.20 | (-0.62, 0.23) |
| Number of people living in the same household | 0.14 | (-0.06, 0.35) | -0.17 | (-0.53, 0.18) |
| Number of poor health behaviours | 1.06* | (0.77, 1.34) | 0.46 | (-0.02, 0.94) |
| Number of chronic conditions | 0.18* | (0.07, 0.28) | 0.21* | (0.03, 0.40) |
| **Interaction Model[a] (n=1,315)** | | | | |
| Depressive symptoms*High material and/or social deprivation | -0.10 | (-0.22, 0.02) | -0.07 | (-0.27, 0.13) |

Note: DNAm = DNA methylation

[a]Model is adjusted for individual level covariates including sex, annual household income, number of people living in the same household, number of chronic conditions, and number of poor health behaviours

*$p$-value<0.05

**Figure 1: Scatterplot between chronological age and epigenetic age measures**