SUPPLEMENTAL MATERIAL

Supplemental Methods

Parameterization of Main Model

The parameterization of the main model, which is a random intercept model or multi-level model, is outlined below. Covariates are not listed for clarity. *BP* represents the predictor of interest.

The Level 1 equation represents the repeated measures level, which allows us to estimate the expected mean log-transformed white matter hyperintensity volume for the *i*th region for the *j*th participant. β_{0i} represents the expected mean log-transformed white matter hyperintensity for the $\it j^{\rm th}$ participant. $\beta_{1 \it j}$ represents the effect of brain region on mean log-transformed white matter hyperintensity volume. e_{ij} represents the within-subject effect (deviation of an individual's logtransformed white matter hyperintensity volume from their individual-specific mean of overall log-transformed white matter hyperintensity volume).

The Level 2 equations allow us to estimate the expected mean log-transformed white matter hyperintensity for the j^{th} participant, where γ_{00} is the expected overall mean log-transformed white matter hyperintensity, γ_{01} is the expected effect of *BP* measure of interest, and r_{0i} is the random subject effect (deviation of an individual's expected mean log-transformed white matter hyperintensity from the population mean). We also specify an equation for β_{1i} , which allows us to specify a two-way interaction term between *BP* and region of interest in the combined equation.

The combined equation represents the parameterization of the simplest model (i.e. no covariates). The two-way interaction term between *BP* and region of interest allows us to examine whether the effect of *BP* measure on log-transformed white matter hyperintensity volume is different across regions of interest.

Level 1 equation (repeated measures): $Y_{ij} = \beta_{0j} + \beta_{1j}(region_{ij}) + e_{ij}$ Level 2 equations (person): $\beta_{0j} = \gamma_{00} + \gamma_{01}(BP_{ij}) + r_{0j}$ $\beta_{1i} = \gamma_{10} + \gamma_{11}(BP_{ii})$

Combined equation: $Y_{ij} = \gamma_{00} + \gamma_{01}(BP_{ij}) + \gamma_{10}(region_{ij}) + \gamma_{11}(BP_{ij})(region_{ij}) + r_{0i} + e_{ij}$

Model Selection Procedure

Covariate Measurement

We chose known confounders of the association of interest *a priori* as covariates, which were measured at study entry. Standardized questionnaires based on the CDC Behavioral Risk Factor Surveillance System were used to collect self-reported demographic, medical, and risk factor data. Participants self-reported their age, sex, and race/ethnicity in response to questions based on the US Census. Smoking status was self-reported as never (reference), current, or former. Physical activity was measured using a questionnaire adapted from the National Health Interview Survey of the National Center for Health Statistics¹. Moderate alcohol consumption was measured using a modified Block National Cancer Institute Food Frequency questionnaire²,

and defined as current drinking of >1 drink per month up to 2 drinks per day as previously described³. All medication use was self-reported. Anthropomorphic measurements, including height and weight, were obtained using standardized protocols as previously described⁴. Body mass index (BMI) was calculated as weight in kilograms divided by height in meters squared kg/m^2). Diabetes was defined as fasting serum glucose level >126 mg/dL or self-reported history of diabetes⁵. Hypercholesterolemia was defined as total cholesterol of >200 mg/dL or self-reported lipid-lowering medication use. Years between the original NOMAS baseline and MRI visit were computed for each participant.

Rationale for and Calculation of Stabilized Inverse Probability of Selection Weights and Weighted Analysis

By selecting participants who had regional white matter lesion load data available, we are effectively conditioning on survival to the MRI sub-study and thus introducing selection bias into our estimates $6,7$. This selection process is illustrated by the directed acyclic graph above. By using inverse probability of selection weights 8 , we can estimate the associations of interest in the pseudo-population of original NOMAS cohort participants, i.e. the entire original NOMAS cohort survived to the MRI sub-study.

Predicted probabilities of selection were computed using binary logistic regression models adjusted for the following covariates: age, sex, race/ethnicity, anti-hypertensive medication use, BMI, any physical activity, history of cardiac disease, education, marital status, diabetes mellitus, hypertension, hypercholesterolemia, diabetes medication use, and cholesterol medication use. Stabilized inverse probability of selection weights were calculated as the predicted probability of selection divided by the predicted probability of selection conditional on $covariates⁸$ and truncated at 1% to further stabilize the weights. Weighted analyses were conducted using generalized estimating equations with an independent correlation structure that use robust variance estimators, accounting for the induced within-subject correlation due to the weights⁹.

Supplemental Tables

Supplemental Table I. Comparison of Original NOMAS Cohort Members and Household Members

P-values obtained from chi-squared tests for categorical variables, one-way ANOVAs for normally distributed variables, and Wilcoxon rank-sum test for non-normally distributed variables.

Supplemental Table II. Re-Analysis of the Association between Systolic and Diastolic Blood Pressure Levels with Regional White Matter Lesion Load, Weighted by Stabilized Inverse Probability of Selection Weights, In Subsample of Participants Recruited from the Original NOMAS Cohort (N=1022*)

*3 missing weights due to missing covariates. Generalized estimating equations used to generate estimates and robust standard errors. Beta coefficients and 95% confidence are transformed such that they represent the expected percent change in WMHV for each category, compared to SBP 140+ mmHg or DBP 90+ mmHg. Model adjusted for age at study entry, sex, race/ethnicity, total intracranial volume (TIV), region (ref=occipital), anti-hypertensive medication use, baseline BMI, baseline smoking status, baseline physical activity, baseline moderate alcohol consumption, years between baseline and MRI, region*age, region*sex, region*race/ethnicity, region*TIV, region* anti-hypertensive medication use, region*smoking status, and region*years between baseline and MRI.

Supplemental Table III. Re-Analysis of the Association between Systolic and Diastolic Blood Pressure Levels with Regional White Matter Lesion Load, Among Original NOMAS Members (N=1025)

Beta coefficients and 95% confidence are transformed such that they represent the expected percent change in WMHV for each category, compared to SBP 140+ mmHg or DBP 90+ mmHg. Model adjusted for age at study entry, sex, race/ethnicity, total intracranial volume (TIV), region (ref=occipital), anti-hypertensive medication use, baseline BMI, baseline smoking status, baseline physical activity, baseline moderate alcohol consumption, years between baseline and MRI, region*age, region*sex, region*race/ethnicity, region*TIV, region* anti-hypertensive medication use, region*smoking status, and region*years between baseline and MRI.

Supplemental Figure I. Segmentation of Regional Lobar WMHV by FSL. Credit: Noam Alperin, PhD.

References

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