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Associations of healthy eating patterns with biological aging: national health and nutrition examination survey (NHANES) 1999–2018

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Abstract

Background Healthy dietary patterns have been negatively associated with methylation-based measures of biological age, yet previous investigations have been unable to establish the relationship between them and biological aging assessed through blood chemistry-based clinical biomarkers. We sought to assess the associations of 4 dietary metrics with 4 measures of biological age.

Methods Among 16,666 participants in NHANES 1999–2018, 4 dietary metrics [Dietary inflammatory index (DII), Dietary approaches to stop hypertension index (DASH), Alternate mediterranean diet score (aMED), and Healthy eating index-2015 (HEI-2015)] were calculated through the 'dietaryindex' R package. Twelve blood chemistry parameters were utilized to compute 4 indicators of biological age [homeostatic dysregulation (HD), allostatic load (AL), Klemera–Doubal method (KDM), and phenotypic age (PA)]. Binomial logistic regression models and restricted cubic spline (RCS) regression were employed to evaluate the associations.

Results All 4 dietary metrics were significantly associated with biological age acceleration or deceleration. In comparison to the lowest DII, the odds ratios (ORs) for accelerated HD, AL, KDM, and PA were 1.25 (1.08,1.45), 1.29 (1.11,1.50), 1.34 (1.08,1.65), and 1.61 (1.39,1.87) for the highest. The multivariable-adjusted ORs of the highest quartile of DASH, aMED, and HEI-2015 were 0.85 (0.73,0.97), 0.88 (0.74,1.04), and 0.84 (0.74,0.96) for HD, 0.64 (0.54,0.75), 0.61 (0.52,0.72), and 0.70 (0.59,0.82) for AL, 0.68 (0.54,0.85), 0.62 (0.50,0.76), and 0.71 (0.58,0.87) for KDM, and 0.50 (0.42,0.59), 0.64 (0.54,0.76), and 0.51 (0.44,0.58) for PA when compared with the lowest level. The findings were validated by the best-fitting dose-response curves for the associations. Among participants consuming dietary supplements ($P_{interaction} < 0.05$), the positive effects of a healthy dietary pattern on biological aging were more pronounced. Systemic immune inflammation index (SII) and atherogenic index of plasma (AIP) were identified as being involved in and mediating the associations.

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Conclusions Biological aging assessed through blood chemistry-based clinical biomarkers is negatively associated with diet quality. The anti-aging benefits of improving the diet may be due to its ability to reduce inflammation and lower blood lipids.

Keywords Healthy eating patterns, Dietary metrics, Biological aging, Biological age, National Health and Nutrition Examination Survey (NHANES)

Background

Nutrition is a significant ecological stimulus associated with every aspect of health and lifespan [1]. Healthier food choices are associated with lowered risks of cancer [2], cardiovascular disease (CVD) [3], and death [4]. The intricate mechanisms that connect diet and disease are multifaceted and may be related to the process of aging, such as epigenetic modifications [5–7]. Additional investigation on the relationship between dietary intake and aging is imperative, which could potentially present novel outlooks on the association of nutrition with disease.

Various molecular and physiological markers of aging have been devised and explored in numerous species [8, 9]. The utilization of biological age as an indicator of disease risk and mortality is acknowledged to be more informative than chronological age [10, 11]. Biological age metrics developed based on age-related clinical indicators have proven to be reliable predictors of longevity, mortality, age-related diseases, comorbidities, and physical function impairment [12, 13], such as HD [14], AL [15], KDM [16], and PA [17]. Individuals with a higher biological age would be more susceptible to disease and experience accelerated aging [18].

One issue with past studies that predominantly investigated the associations of age acceleration metrics with specific nutrients or food items is that focusing exclusively on individual food components may disregard the broader beneficial effects of improving the overall diet [19, 20], since these constituents are consumed in combination and have interconnected associations [21, 22]. Although there are studies on dietary patterns and methylation-based measures of biological age [6], research centered on the biological age measures derived from age-related clinical parameters outcomes is scarce, potentially constraining the ability to compare and comprehensively analyze the findings regarding diet and aging, undermining the scientific validity of studies, and impeding a thorough comprehension of the impact of diet on aging.

We proposed that improved dietary quality, as determined by various recommended guidelines, would be associated with decreased age acceleration, which is intended as a prognosticator of mortality. Here, we evaluated how different dietary indices (DII, DASH, aMED, and HEI-2015) were related to biological aging indicators (HD, KDM, PA, and AL) using data from the 1999–2018 NHANES.

Methods

Study population

NHANES is an extensive, nationwide survey performed by the National Center for Health Statistics (NCHS) to capture an exact analysis of the health and nutritional state of Americans [23]. We utilized cross-sectional data from NHANES 1999–2018 that encompassed 16,666 individuals who satisfied the following criteria: non-pregnant adults (n=57,540), standard daily energy intake (800–4200 kcal/d for male and 500–3500 kcal/d for female) (n=48,741) [24], possess all the components of biological ages (n=35,367), and dietary score components are complete (n=16,666) (Fig. 1).

Assessment of dietary metrics

Dietary information was obtained through a 24-hour dietary recall for two days that were not consecutive and computed following the guidelines provided by the U.S. Department of Agriculture's Food and Nutrient Database for Dietary Studies [25]. Using the standardized algorithms for dietary index calculations, 4 dietary metrics (DII, DASH, aMED, and HEI-2015) were computed based on the dietary intake data. Access to the corresponding algorithms and R code for the package 'dietaryindex' was made available at https://github.com/jamesjiadazhan/dietaryindex. Dietaryindex is a flexible and validated tool that enables standardized calculations of dietary indices in epidemiological and clinical studies [26]. The calculation process consists of two steps: initially determining the serving size for each food and nutrient category, and then computing individual dietary indexes. In developing the DII, forty-five components identified as having inflammatory properties were included (Supplementary Table 1) [27, 28]. After adding up the scores for each component, the DII produces a single score, where a higher value suggests that the diet has a greater potential for inflammation. Comprising numerous foods and nutrients known to be connected to hypertension [29], the DASH eating plan recommends the consumption of fruits, vegetables, nuts/legumes/vegan protein, whole grains, low-fat dairy, and limiting the intake of sodium, red or processed meats, and sugar-sweetened drinks (Supplementary Table 2). The aMED encompasses 9 components associated with lower risks of chronic diseases [30, 31], including fruits, vegetables, nuts, legumes, whole grains, fish, red and processed meat, the ratio of monounsaturated fat to saturated fat, and alcohol intake (Supplementary Table

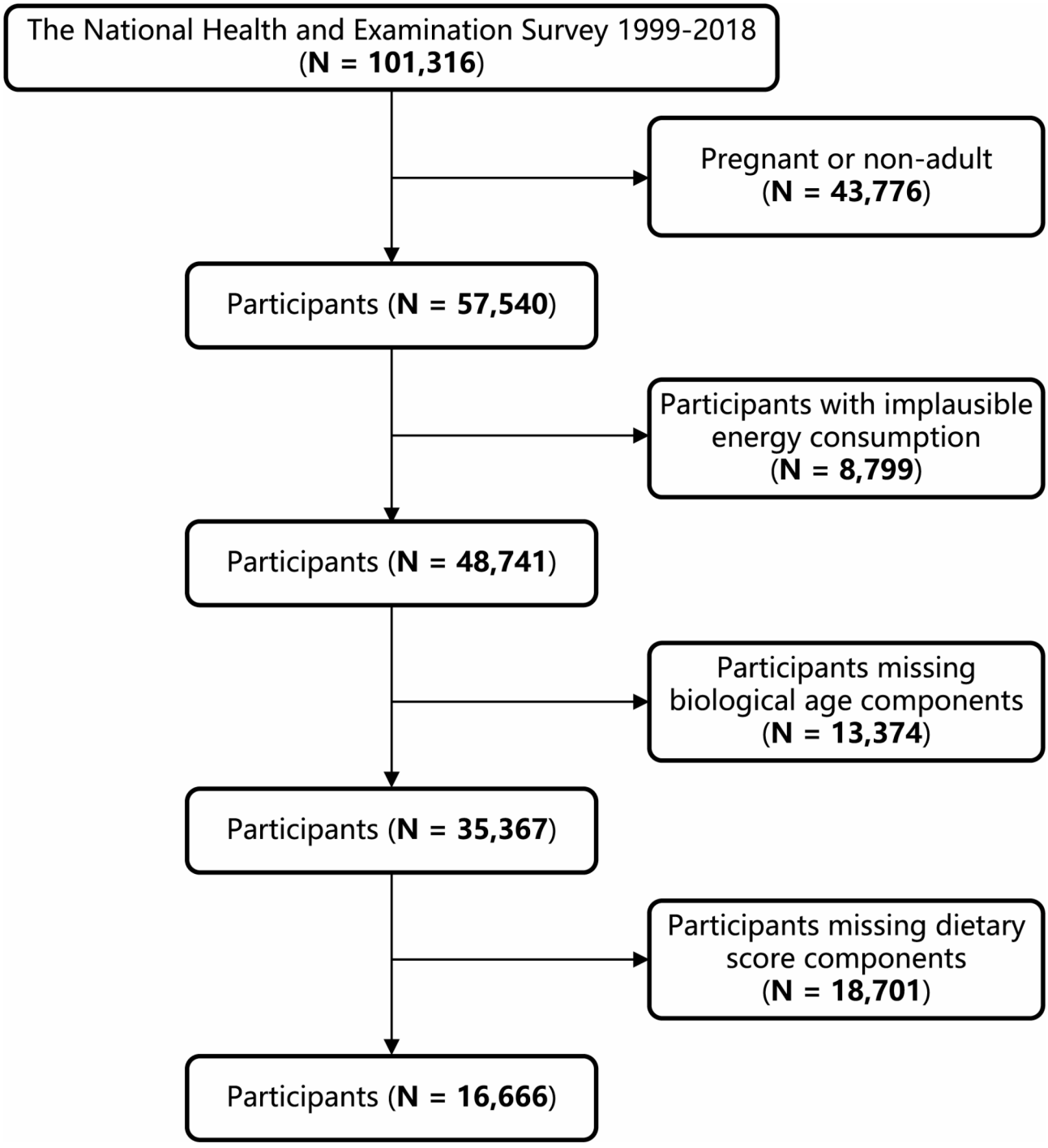

Fig. 1 Step-by-step diagram depicting the methodology for participant selection

3). The HEI-2015 serves as a summary measure of compliance with the USDA 2015–2020 Dietary Guidelines for Americans [32], assessing the consumption of total fruits, whole fruits, total vegetables, greens and beans, total protein food, seafood and plant protein, whole grain, dairy, fatty acids, refined grain, sodium, added sugar, and saturated fat (Supplementary Table 4).

Assessment of biological ages

Using twelve clinical markers (Supplementary Tables 5–8), HD, KDM, and PA were calculated. The algorithms were first calibrated utilizing NHANES 1988–1994 (NHANES III) and originally described by Nakazato et al. [33], Klemera et al. [12], and Levine et al. [13], respectively. The corresponding code was available through the R package "BioAge" at https://github.com/dayoonkwon/

BioAge. The Mahalanobis distance metric was used by HD to quantify the difference between an individual's clinical measurements and the reference established from a young and healthy population [34]. Conducting regression analyses between particular biomarkers and chronological age in the reference population enabled the measurement of KDM [35]. Through the application of elastic-net Gompertz regression, PA was computed by analyzing a range of factors related to mortality risks [36]. AL captured the cumulative effects of chronic stress and life events, and its measurement involved examining the proportion of biomarker levels indicating an increased risk for disease [37]. In our research, we assigned the risk level by identifying individuals in the top quartile of the distribution for eleven of the twelve biomarkers. For albumin, those who fall into the lowest quartile were deemed at risk, as supported by prior research findings [15]. The AL, with values between 0 and 1, denoted the ratio of biomarkers identified as "at risk".

Assessment of biological aging

To gauge disparities in biological aging, those whose KDM or PA exceeded their chronological age were regarded as experiencing accelerated aging [38]. Participants with higher HD or AL, categorized into groups based on their medians, were deemed to undergo accelerated aging [18].

Assessment of mediation variables

Combining the levels of triglyceride (TG) and high-density lipoprotein cholesterol (HDL-C) [39], AIP was calculated by mathematically deriving it from lg[TG(mmol/L)/HDL-C(mmol/L)] [40]. The SII, a novel inflammation index, was determined by dividing the multiplication of the platelet count and neutrophil count by the lymphocyte count [41].

Assessment of covariates

Information on age, sex, and race was obtained through a standardized questionnaire. Weight in kilograms divided by the square of height in meters yielded the calculation of body mass index (BMI). Data on smoking, drinking, physical activity, education, annual household income, and dietary supplement usage were acquired through questionnaires specifically designed for each. Physical activity was assessed by determining the metabolic equivalent scores for weekly recreational activities, and regular exercise was defined as engaging in a minimum of 150 min of moderate to high-intensity physical activity per week [42]. Information on cancer, CVD, hypertension, and diabetes was collected through individual interviews using a standardized medical condition questionnaire. The definition of chronic kidney disease involves estimated glomerular filtration rate (eGFR) < 60 mL/min/1.73m^2 and albumin to creatinine ratio (ACR) ≥ 30 mg/g [43]. A missing indicator category has been used to code covariates with missing data in categorical variables (missing values: smoking n = 387, drinking n = 993, exercise n = 23, income n = 820, nutrient supplement use n = 6, self-reported cardiovascular diseases n = 904, self-reported cancer n = 747, self-reported hypertension n = 21, self-reported diabetes n = 381, and chronic kidney disease n = 2,358).

Statistical analyses

Consultation of the NHANES analytic guidelines ensured proper consideration of sample weights, stratification, and clustering. For continuous variables, baseline characteristics were displayed as means (95% CI), while for categorical variables, they were listed as percentages (n). Multivariate linear regression models were utilized to analyze the associations of different dietary indexes with SII or AIP and the relationships between SII or AIP and biological age indicators. Associations of DII, DASH, aMED, and HEI-2015 with biological age indicators were examined through binomial logistic regression models. The associations between different dietary indexes and biological age indicators were then modeled using RCS regression. The effects of mediation were evaluated using mediation analysis. Several analyses were conducted according to the stratified variable: age (>60/≤ 60), sex (male/female), race (non-hispanic white/others), BMI (<30/≥ 30), smoking (yes/no), drinking (yes/no), regular exercise (yes/no), education (above college/others)), income (< $55,000/≥ $55,000), dietary supplements use (yes/no), and self-reported hypertension (yes/no). R 4.1.1 was utilized to perform all the analyses. A significance level of less than 0.05 was used to determine the statistical significance, employing a two-tailed P-value threshold.

Results

Baseline characteristics

The detailed characteristics of participants according to different dietary indexes were presented in Table 1 and Supplementary Tables 9–11. Participants with lower DII or higher DASH, aMED, and HEI-2015 were more likely to be older, non–drinkers, and regular exercisers; have higher education, annual household income, dietary supplement usage, KDM, and PA; as well as lower BMI, SII, AIP, HD, and AL.

Associations of different dietary indexes with SII and AIP

Positive correlations were observed between DII and SII (β 48.28, 95% CI 30.09–66.47) and AIP (β 0.04, 95% CI 0.02–0.06), whereas negative associations were found between DASH, aMED, HEI-2015 and SII and AIP (Supplementary Table 12). In comparison to the lowest

Table 1 Participants' characteristics according to DII quintiles[a]

	Dietary inflammatory index (DII)				*P*	P_{test}
	Q1 (≤ -0.35)	Q2 (-0.34–2.99)	Q3 (3.00–5.58)	Q4 (> 5.59)		
	N = 4167	*N* = 4166	*N* = 4167	*N* = 4166		
Age, years	49.82(49.29,50.35)	49.76(49.21,50.31)	49.77(49.20,50.33)	49.30(48.72,49.89)	0.542	0.150
Male, *n* (%)	2599(62.4)	2183(52.4)	1754(42.1)	1442(34.6)	0.000	0.000
Non-Hispanic white, *n* (%)	2028(48.7)	1833(44.0)	1712(41.1)	1727(41.5)	0.000	1.000
BMI, kg/m2	28.51(28.32,28.71)	29.14(28.94,29.35)	29.78(29.57,30.00)	30.10(29.88,30.32)	0.000	0.000
Current smoking, *n* (%)	1757(42.2)	1770(42.5)	1681(40.3)	1941(46.6)	0.000	0.319
Current drinking, *n* (%)	3264(78.3)	3016(72.4)	2831(67.9)	2659(63.8)	0.000	0.000
Regular exercise, *n* (%)	2031(48.7)	1636(39.3)	1458(35.0)	1226(29.4)	0.000	0.000
College graduate or above, *n* (%)	2669(64.1)	2324(55.8)	1972(47.3)	1661(39.9)	0.000	0.000
> 55,000 annual household income, *n* (%)	1814(43.5)	1523(36.6)	1266(30.4)	1011(24.3)	0.000	0.000
Dietary supplements use, *n* (%)	2504(60.1)	2263(54.3)	2063(49.5)	1712(41.1)	0.000	0.000
Dietary inflammatory index	-4.50(-4.62,-4.37)	1.43(1.40,1.46)	4.30(4.28,4.32)	7.27(7.24,7.31)	0.000	0.000
Dietary approaches to stop hypertension index	28.66(28.57,28.75)	27.20(27.12,27.28)	26.24(26.16,26.32)	24.85(24.78,24.92)	0.000	0.000
Alternate mediterranean diet score	6.26(6.23,6.29)	5.87(5.84,5.90)	5.58(5.55,5.61)	5.11(5.08,5.13)	0.000	0.000
Healthy eating index 2015	59.33(58.98,59.67)	53.06(52.73,53.38)	49.37(49.06,49.68)	43.17(42.88,43.46)	0.000	0.000
Chronic kidney disease, *n* (%)	70(1.9)	81(2.3)	125(3.5)	154(4.4)	0.000	0.000
Self-reported cancer, *n* (%)	428(10.3)	436(10.5)	413(9.9)	404(9.7)	0.000	0.000
Self-reported cardiovascular diseases, *n* (%)	342(8.2)	423(10.2)	469(11.3)	552(13.3)	0.000	0.000
Self-reported hypertension, *n* (%)	1388(33.3)	1458(35.0)	1542(37.0)	1590(38.2)	0.000	0.000
Self-reported diabetes, *n* (%)	434(10.4)	548(13.2)	604(14.6)	630(15.1)	0.000	1.000
Systemic immune inflammation index	501.81(492.03,511.59)	521.48(511.95,531.01)	538.25(528.06,548.44)	547.95(537.79,558.11)	0.000	0.000
Atherogenic index of plasma	0.03(0.02,0.04)	0.04(0.03,0.05)	0.03(0.02,0.04)	0.03(0.02,0.04)	0.591	0.063
Homeostatic dysregulation	1.61(1.58,1.63)	1.64(1.62,1.67)	1.73(1.70,1.75)	1.79(1.76,1.82)	0.000	0.000
Phenotypic age	48.38(47.81,48.95)	48.53(47.94,49.13)	48.92(48.31,49.54)	49(48.36,49.64)	0.415	0.681
Klemera - Doubal method	41.29(40.79,41.79)	41.87(41.36,42.39)	42.76(42.22,43.30)	43.28(42.72,43.84)	0.000	0.004
Allostatic load	0.27(0.27,0.27)	0.28(0.27,0.28)	0.29(0.28,0.29)	0.30(0.29,0.30)	0.000	0.000

[a]Continuous variables were listed as mean (95% CI). Categorical variables were listed as *n* (%). And general linear models and chi-square tests were conducted to compare continuous and categorical baseline characteristics, respectively. And P_{test} was the result of Bonfreni correction

quartiles, the beta estimates for SII concerning DASH, aMED, and HEI-2015 were −52.84 (-69.95, -35.73), -48.86 (-68.15, -29.57), and −46.49 (-62.97,1–30.00), respectively. There was a positive correlation between AIP and DASH −0.04 (-0.06, -0.02), aMED −0.05 (-0.07, -0.02), and HEI-2015 -0.05 (-0.08, -0.03) (Supplementary Tables 13–15).

Associations of SII and AIP with biological age indicators

In terms of SII, participants within the top quartile exhibited a higher HD (β 0.09, 95% CI 0.05–0.13), AL (β 0.01, 95% CI 0.00–0.02), KDM (β 2.36, 95% CI 1.92–2.81), and PA (β 3.95, 95% CI 3.69–4.21) (Supplementary Table 16). AIP also showed positive associations with HD (β 0.17, 95% CI 0.12–0.21), AL (β 0.06, 95% CI 0.05–0.07), KDM (β 2.40, 95% CI 1.93–2.87), and PA (β 1.56, 95% CI 1.25–1.86) (Supplementary Table 17).

Associations of different dietary indexes with biological age indicators

Consistent with expectations, different dietary indexes were meaningfully correlated with measures of biological age (Fig. 2, Supplementary Tables 18–21). In the case of DII, individuals in the top 25% displayed a greater propensity to possess higher HD (OR 1.25, 95% CI 1.08–1.45), AL (OR 1.29, 95% CI 1.11–1.50), KDM (OR 1.34, 95% CI 1.08–1.65), and PA (OR 1.61, 95% CI 1.39–1.87) (Supplementary Table 18). DASH demonstrated significant associations with HD (OR 0.85, 95% CI 0.73–0.97), AL (OR 0.64, 95% CI 0.54–0.75), KDM (OR 0.68, 95% CI 0.54–0.85), and PA (OR 0.50, 95% CI 0.42–0.59) (Supplementary Table 19). HEI-2015 also indicated connections to HD (OR 0.84, 95% CI 0.74–0.96), AL (OR 0.70, 95% CI 0.59–0.82), KDM (OR 0.71, 95% CI 0.58–0.87), and PA (OR 0.51, 95% CI 0.44–0.58) (Supplementary Table 20), whereas aMED displayed statistically significant patterns solely with AL (OR 0.61, 95% CI 0.52–0.72), KDM (OR 0.62, 95% CI 0.50–0.76), and PA (OR 0.64, 95% CI 0.54–0.76) (Supplementary Table 21).

Best-fitting dose-response curves of the associations between different dietary indexes and biological age indicators

As depicted in Fig. 3, DII exhibited both roughly linear and non-linear relationships with accelerated HD, AL, KDM, and PA (all $P_{overall} < 0.001$). With the exclusion of PA ($P_{overall} < 0.001$, $P_{nonlinearity} < 0.031$), DASH revealed linear connections with HD, AL, and KDM (all $P_{overall} < 0.001$, all $P_{nonlinearity} > 0.050$). Similarly, aMED and HEI-2015 showed monotonic linear associations with lower risks of higher HD, AL, KDM, and PA (all $P_{overall} < 0.001$, $P_{nonlinearity} > 0.050$).

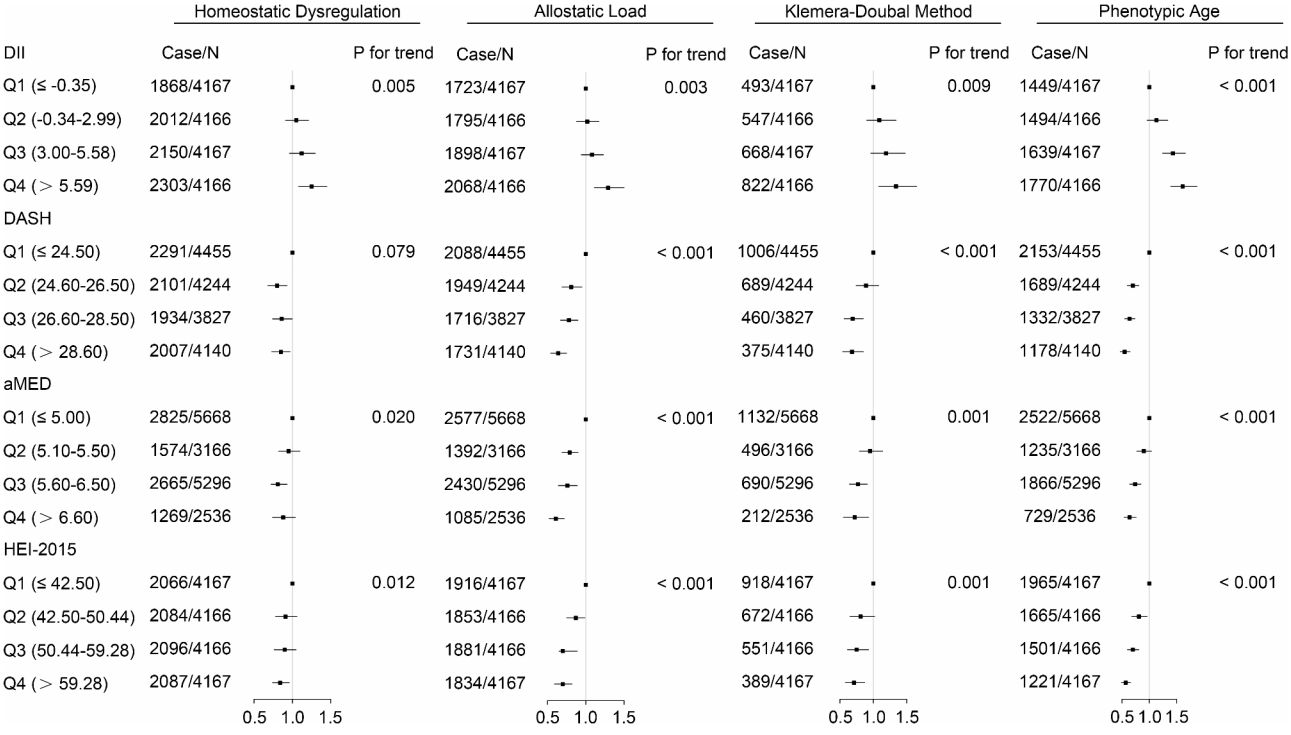

Fig. 2 Associations of dietary metrics with accelerated HD, AL, KDM, and PA. The adjustments involved age, sex, ethnicity, year, BMI, smoking, exercise, education, income, nutrient supplement use, self-reported cancer, cardiovascular diseases, hypertension, diabetes, and chronic kidney disease. Models for DASH and HEI-2015 were additionally adjusted for drinking. Case/N, the number of case subjects/total. Q, quintile

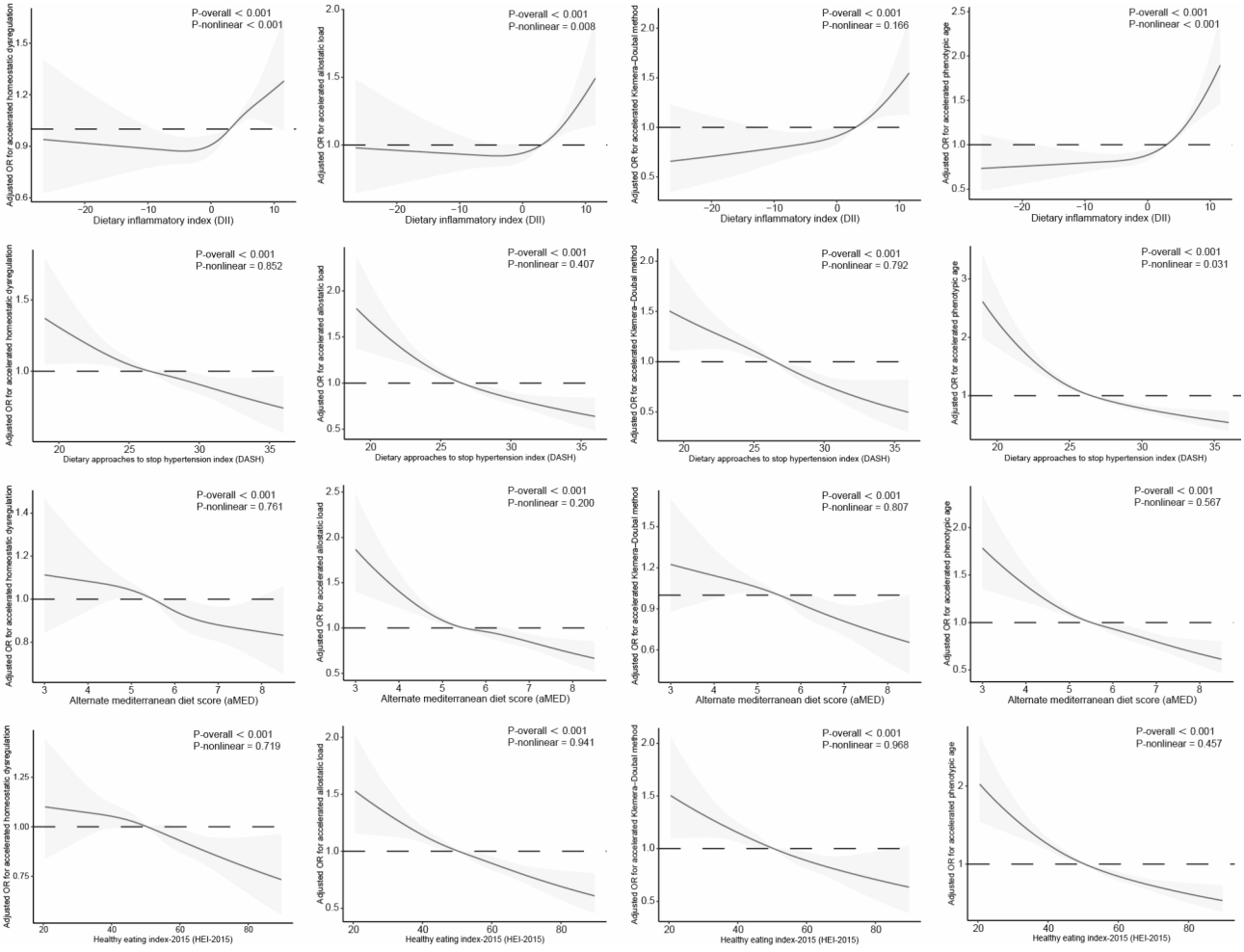

Fig. 3 Smoothing curves between dietary metrics and accelerated HD, AL, KDM, and PA. Binomial logistic regression models and RCS were performed with adjusting for age, sex, ethnicity, year, BMI, smoking, exercise, education, income, nutrient supplement use, self-reported cancer, cardiovascular diseases, hypertension, diabetes, and chronic kidney disease. Models for DASH and HEI-2015 were additionally adjusted for drinking. The solid black lines correspond to the central estimates, and the gray-shaded regions indicate the 95% confidence intervals

Mediation effects of SII and AIP on the associations between different dietary indexes and biological age indicators

Our results revealed significant associations between diverse dietary indexes and SII and AIP, as well as between SII and AIP with biological age indicators, prompting us to explore the mediation effects in-depth to uncover the underlying relationship (Fig. 4). The total effects of DII on HD (β_{Tot}=0.08, P<0.001), AL (β_{Tot}=0.06, P<0.001), KDM (β_{Tot}=0.07, P<0.001), and PA (β_{Tot}=0.06, P<0.001) were demonstrated. Quantitative measures based on standardized regression coefficients revealed the total effects of DASH on HD (β_{Tot} = -0.02, P<0.01), AL (β_{Tot} = -0.05, P<0.001), KDM (β_{Tot} = -0.13, P<0.001), and PA (β_{Tot} = -0.16, P<0.001). The total effects of aMED and HEI-2015 on HD (β_{Tot} = -0.03, P<0.001 and β_{Tot} = < -0.01, P>0.05), AL (β_{Tot} = -0.04, P<0.001 and β_{Tot} = -0.03, P<0.01), KDM (β_{Tot} = -0.08, P<0.001 and β_{Tot} = -0.12, P<0.001), and AL (β_{Tot} = -0.10, P<0.001 and β_{Tot} = -0.14, P<0.001) were assessed after controlling for the covariates in the comprehensive RCS regression model. The percentage contributions of the indirect effects of DII on HD, KDM, PA, and AL mediated by SII and AIP were evaluated to be 5.28, 4.45, 4.59, 6.33, 6.11, 3.58, 16.57, and 7.62%, respectively. The proportions of the total effects of DASH and aMED on HD (29.02, 23.49, 17.17, 35.37%), AL (9.87, 13.12, 8.9, 29.20%), KDM (5.16, 2.85, 6.44, 9.04%), and PA (9.31, 4.07, 10.33, 11.62%) were attributed to the indirect effects mediated by SII and AIP. SII and AIP-mediated indirect effects also accounted for the specific proportions of the total effects of HEI-2015 on AL (19.00, 36.31%), KDM (6.24, 4.98%), and PA (11.51, 7.34%).

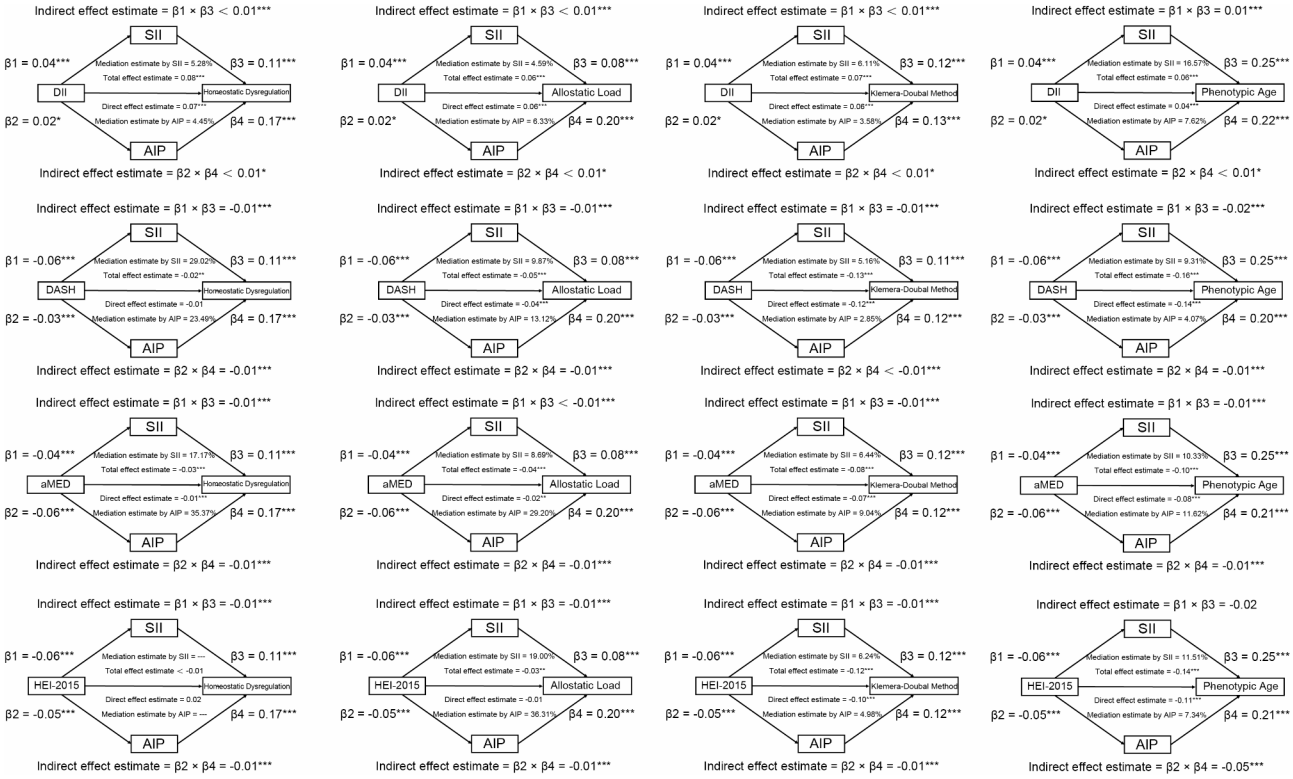

Fig. 4 Effects mediated by SII and AIP on the relationships. The results were presented as standardized regression coefficients after adjusting for the covariates in the full model of binomial logistic regression. *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$

Associations of different dietary indexes with biological age indicators stratified by the factors under consideration

When performing comprehensive stratified analyses based on the factors under consideration (Supplementary Tables 22–37), comparable significant associations were observed among participants consuming dietary supplements ($P_{interaction} < 0.05$). The relationships were also found to be strengthened among drinkers, highly educated individuals, and participants with hypertension, although the lack of statistical significance ($P_{interaction} > 0.05$).

Discussion

During our relatively large, national cross-sectional research of the general Americans, we observed that dietary patterns showed significant associations with 4 biological age metrics utilized as predictors of chronological age, and displayed specific dose-response patterns. Exhibiting a higher dietary inflammatory potential was related to a minimum of a 25% elevated risk of larger HD, AL, KDM, and PA. Meanwhile, individuals exhibiting higher DASH, aMED, and HEI-2015 experienced at least a 12% reduced risk of accelerated HD, AL, and KDM, PA. The associations of diet quality with biological aging were partly mediated by SII and AIP, underscoring the vital importance of a moderate diet in anti-inflammatory and lipid-lowering. Stratified analyses indicated that the relationships differed according to dietary supplement use, primarily due to the lack of robustness in those who do not consume.

This research was centered around the associations of well-established dietary indices with biological age metrics developed based on age-related clinical indicators, which may deliver more comprehensive assessments and insights into how food intake and nutrient consumption are associated with biological aging [44]. After all, focusing exclusively on individual food components may disregard the broader beneficial effects of improving the overall diet since these constituents are consumed in combination and have interconnected associations [21, 22]. Epigenetic clocks, relying on DNA methylation at specific locations, are developed to predict disease risk and death, and are utilized to determine the impact of various factors on biological aging [45, 46]. The extent of attrition on telomeres, DNA sequences situated at the termini of chromosomes that aid in preserving genome stability [47], can be employed to investigate the processes that detrimentally affect health and lifespan, such as inflammation, oxidative stress, and dietary intake [48–50]. Biological age metrics developed based on age-related clinical indicators, which are reliable predictors of longevity, mortality, and age-related diseases, have also

been used to assess potential factors associated with biological aging [12, 13].

Previous research examining the association between diet and biological aging has primarily centered on specific diets and nutrients, biological age indices derived from methylation, or telomere length [6, 51–57]. The consistent results of our study coincided with prior investigations employing one or multiple of the biological age markers examined in this research, which indicated that the intake of α-tocopherol, vitamin K, and caloric restriction were related to decreased instances of accelerated aging [51–53]. The strongest relationships have been observed between higher quality diets (measured using DASH, HEI-2015, and aMED) and methylation-derived assessments of biological age (including Hannum AgeAccel, Horvath AgeAccel, PhenoAgeAccel, and GrimAgeAccel), which reinforces the significant associations between diet quality and longevity [6, 54, 55]. In addition, multiple nutritional patterns and habits, like the Mediterranean diet, exhibit a significant correlation with extended leukocyte telomere length (LTL) [56, 57]. The consistent observations of our research were in line with prior investigations carried out among NHANES 2003–2014, which indicated anti-inflammatory and antioxidant dietary intake was inversely associated with accelerated HD, PA, KDM, and AL [58].

Furthermore, another revelation from our study was the advantageous effects of healthier dietary patterns on SII and AIP, both of which were interconnected with the intricate aging mechanism. As a significant risk factor with the potential to accelerate and exacerbate aging besides chronological age, inflammation could induce cellular impairment and organ injury [59, 60]. Lipids in the bloodstream are indispensable for cellular metabolism [61], and dyslipidemia is a recognized hazard for age-related diseases [61]. There are reports of research suggesting an association between dyslipidemia and its lipid markers, particularly HDL-C, and alterations in telomere length [61]. As an uncomplicated and workable approach, dietary adjustment could help to regulate inflammation and dyslipidemia [62, 63]. The relationship of a rational diet with the body's reactivity to both internal and external changes implied possible health perks [62]. Based on our findings, it can be inferred that there exist mediation effects of SII and AIP on the associations of healthier dietary patterns with biological aging, highlighting the potential of a balanced diet as a preventive strategy against aging via the modulation of inflammation and blood lipids. Nevertheless, more research is needed to assess alternative mechanisms connecting a balanced diet to the deceleration of aging.

The stratified analyses that explored the potential modifying impacts of the factors generally considered to be crucial in examining health-related issues especially emphasized the decelerated PA, KDM and decreased HD, AL among participants using dietary supplements. In addition to dietary intervention, an expanding body of research has demonstrated the potential for nutritional supplements to be a viable intervention in a comprehensive health-promoting strategy [64], which may be composed of diverse components with immunomodulatory, antioxidant, and specific nutritional properties [65]. Dietary supplement utilization tends to be elevated in pregnant or lactating women, athletes, individuals with dietary limitations, individuals leading busy or highly stressed lifestyles, and individuals with specific medical conditions [66–68]. Our study findings suggest that individuals consuming dietary supplements were more prone to being older, having chronic kidney disease (CKD), cancer, CVD, diabetes, and exhibiting higher levels of HD, AL, KDM, PA, as well as certain age-related clinical markers (Supplementary Tables 38–39). Therefore, it is plausible to assume that those with suboptimal health conditions can attain enhanced anti-aging benefits by incorporating dietary supplements into their regimen and complementing them with a higher-quality dietary intervention.

Moreover, besides inflammation and lipid regulation, there is still a great deal unelucidated about the biological pathways through which various dietary patterns might be associated with the aging process. Even though aging may be affected by diabetes and CVD [69, 70], the fundamental connection between quality meals and decelerated aging remained unchanged even when considering these chronic conditions. Given that it is a common epigenetic modification, the pattern and degree of DNA methylation have been validated to be associated with cellular aging as well as age-related diseases [55]. The consumption of certain foods and specific nutrients can bring about changes in DNA methylation through modulation of enzyme activity or modification of substrates and coenzymes [71], such as omega-3 polyunsaturated fatty acids (PUFAs) [46], and vegetables [19]. The microbiome functions as a modulator of healthy aging by transducing environmental signals, conditioning host immunity and metabolism, and modifying the vulnerability to age-related diseases [72]. Gut microbial communities exhibit specificity to their hosts, co-evolve alongside their hosts, and are shaped by dietary habits [73]. To be specific, a diverse range of dietary choices is associated with the stability of the microbiome [74], and meals that are low in fat and high in fiber can have a positive impact on the health of the gut microbiome by increasing the number of probiotic bacteria [75].

The primary features of our study were the substantial sample size that accurately represented the population across the United States, the application of multiple accelerated aging measures, and comprehensive data on

various covariates and clinical outcomes. Nevertheless, several notable constraints should be taken into account when interpreting our findings. Initially, this research was conducted in a cross-sectional manner, meaning that both diet and age acceleration were evaluated at the beginning of the study. Consequently, some misclassification was inevitable, and any modifications or persistent dietary routines may not have been fully captured. Although the health benefits of higher-quality diets were widely recognized, there was evidence indicating that unhealthy conditions were associated with reduced compliance with healthy eating [76]. Constrained by the nature of cross-sectional studies, we could not ascertain causation from the observed findings. Considering the lack of comprehensive and detailed food component data from dietary supplements, we excluded this portion of the data from our calculations of various dietary indexes, potentially resulting in a certain difference between our estimates and the actual exposure of individuals. Moreover, when it comes to HD and AL, we stratified individuals with an increased vulnerability to homeostatic disorder or health strain using the median as a cutoff, potentially influencing the precision of age-related risk assessment through the absence of information. Lastly, despite our exploration of various eating patterns, we encountered consistent associations of different dietary indexes with biological age indicators, complicating the determination of the superiority of particular dietary patterns.

Conclusions

Findings derived from our relatively sizable, countrywide, cross-sectional study demonstrated the associations of healthier eating patterns with the deceleration of biological aging, with SII and AIP serving as mediating factors. Notably, this relationship appeared to be more pronounced among individuals who incorporated dietary supplements into their routines. Future research is imperative to confirm our findings, including research with larger cohorts, research encompassing individuals from diverse racial and ethnic backgrounds, investigations into the biological mechanisms involved, and examinations of the causal relationship between dietary factors and biological aging.

Abbreviations

NHANES	National Health and Nutrition Examination Survey
DII	Dietary inflammatory index
DASH	Dietary approaches to stop hypertension index
aMED	Alternate mediterranean diet score
HEI-2015	Healthy eating index-2015
HD	Homeostatic dysregulation
AL	Allostatic load
KDM	Klemera–Doubal method
PA	Phenotypic age
RCS	Restricted cubic spline
ORs	Odds ratios
SII	Systemic immune inflammation index
AIP	Atherogenic index of plasma
CVD	Cardiovascular disease
NCHS	National Center for Health Statistics
TG	Triglyceride
HDL-C	High-density lipoprotein cholesterol
BMI	Body mass index
eGFR	Estimated glomerular filtration rate
ACR	Albumin to creatinine ratio
LTL	Leukocyte telomere length
CKD	Chronic kidney disease
PUFAs	Polyunsaturated fatty acids

Supplementary Information

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Supplementary Material 1

Supplementary Material 2

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Author contributions

X.W., X.Y., and Y.L. were led the design and the main contributors to the final content. X.W., X.Y., J.Z., and K.D. offered statistical assistance and conducted the data analysis. X.W., L.C., X.Q., P.S., and X.X. drafted the paper. All authors contributed to revising the manuscript and examined and endorsed the final manuscript.

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Data availability

No datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate

The study received ethical clearance from the Institutional Review Board of NCHS, and all subjects agreed to participate after signing the required documentation.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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