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Original article

Higher adherence to the 'vegetable-rich' dietary pattern is related to longer telomere length in women

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SUMMARY

Background & aims: Increasing evidence suggests a role of nutrition in aging process measured by telomere length (TL). However, data from Chinese are scarce. Moreover, the potential mechanism underlying diet and aging is not clear. Although inflammation has been hypothesized as one of the main factors, direct evidence is lacking. We examined whether dietary patterns were associated with TL in Chinese adults, with particular attention paid to body fat (excessive accumulation of body fat is a state of high-systematic oxidative stress and inflammation) and C-reactive protein (CRP, a marker of inflammation).

Methods: Principal components analysis was used to identify dietary patterns from a 66-item food frequency questionnaire. TL was measured by Southern blots-based assay (Telomere restriction fragments, TRF). Data on sociodemographic characteristics, lifestyle behaviors, anthropometry and metabolism were collected. Multivariate linear regressions were performed in 553 Chinese adults (50.8% men) aged 25–65 years.

Results: Four main dietary patterns were identified. After adjustment for potential confounders, only the 'vegetable-rich' pattern characterized by higher intake of fruits, whole grains, various vegetable groups, dairy products, nuts, eggs and tea, was positively related to TL in women ($\beta = 160.81$, P for trend <0.05). The strength of this relation was almost identical with further adjustment for body fat ($\beta = 160.50$, P for trend <0.05), but was attenuated slightly with additional adjustment for CRP ($\beta = 152.02$, P for trend <0.05). No significant relations were observed in men between dietary patterns and TL.

Conclusions: Chinese women with higher adherence to 'vegetable-rich' dietary pattern have a longer TL. This relation was partially explained by CRP but not by body fat.

1. Introduction

The rapid pace of population aging coupled with the raising prevalence of several age-related diseases has prompted the search for modifiable risk factors that can influence biological aging process, as indicated by telomere length (TL) [1]. To date, increasing evidence suggests a role of nutrition in aging [2]. Dietary factors (nutrients, food groups, or both) that influence oxidative and inflammatory responses, which have been recognized as the main underlying mechanisms responsible for TL shortening, may therefore affect TL [3,4].

Compared with separate dietary factors, an overall dietary pattern seems to have a stronger impact on TL [5,6]. To date, six studies conducted in Western [7] and Korean [8] adults have investigated the relations between dietary patterns and TL. However, most [7] of these studies have focused on the predefined

Abbreviations: TL, Telomere length; CRP, C-reactive protein; TRF, Telomere restriction fragments; PCA, Principal components analysis; FFQ, Food frequency questionnaire; KMO, Kaiser-Meyer-Olkin; MVPA, Moderate-to-vigorous physical activities; WC, Waist circumference; % BF, Percent body fat; BMI, Body mass index; bp, base pairs; SE, Standard error.

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patterns (e.g. Mediterranean pattern), which may neglect important dietary factors not reflected in these diets, especially considering TL research is a particularly new field and there is insufficient knowledge on what dietary factors actually influence TL. It is thus desirable to use an exploratory approach such as principal components analysis (PCA) that may be much more informative in detecting diet-TL relations. Additionally, the potential mechanism underlying diet-TL is not clear. Although inflammation has been hypothesized as one of the main incentives causing telomere shortening, direct evidence is lacking.

Obesity, characterized by excessive accumulation of body fat, is a state of high-systematic oxidative stress and inflammation [9]. Prior studies have reported relations between different indicators of body fat (body mass index and total body fat etc.) and TL [10,11]. Given the possible impact of diet on body fat, it should be noted that different levels of body fat might be in at least one of the causal pathways between diet and TL. However, most [7] previous studies have eliminated this possible influence, which would attenuate direct diet-TL relations.

Therefore, in the current study, we investigated associations between dietary patterns derived by PCA and TL in Chinese adults, with particular attention paid to body fat and inflammation measured by C-reactive protein (CRP).

2. Materials and methods

2.1. Study sample

We used data from an ongoing, population-based, prospective study conducted (9 urban and 12 rural areas) of Chengdu, Guizhou and Xiamen in South China since 2013, which aimed to investigate the nutritional and lifestyle determinants of several chronic diseases, as described elsewhere [12]. The participants were invited to the study centre for interviews. Generally, each visit included anthropometric measurements, medical examinations, questionnaires and face-to-face interviews by trained investigators about nutrition-related behaviors (dietary habits, food and beverage intake), lifestyles and social status. All participants are followed biennially to obtain updated information. Participants who were cooperative, who volunteered and who signed an informed consent form were included in this cohort study. The following participants were excluded: (1) if they had cancer, mental diseases; (2) if they were taking hormone-based drugs and other medicines that affect blood glucose and lipids; (3) if they were pregnant or lactating women. The Ethics Committee of Sichuan University approved the study and all participants gave their written informed consent for all examinations.

Eligible data in the present analysis were identified from the baseline survey of this ongoing prospective study between 2013 and 2016. Participants in the present analysis have been shown to be comparable to age-matched adults in our cohort study and the general population of urban and rural areas in Southwest China for social-demographic and lifestyle characteristics. Initially, 637 adults aged 20–70 years were identified. Of these participants, 84 were excluded because diagnosed with disease (n = 27), e.g. cardiovascular disease and cancer; with incomplete information on diet (n = 3), anthropometry (n = 40) and other covariates (n = 5); with inappropriate energy intake [13] (n = 9) (i.e. >4200 or <800 kcal/d for men and >3500 or <500 kcal/d for women). Finally, data of 553 participants (281 men and 272 women) aged 25–65 y were used for the present analysis.

2.2. Dietary intake assessment

At baseline, usual dietary intake during the previous year was assessed using a 66-item semi-quantitative food frequency questionnaire (FFQ). This FFQ was based on the validated questionnaire [14,15] that was used in the 2002 China National Nutrition and Health Survey, and additionally modified to 1) include a few individual food groups that were rich in unique antioxidants with suspected biological effects, e.g. coffee [16] and tea [17]; 2) disaggregate some food groups into more clearly defined categories, e.g. wheat flour products were disaggregated into noodles, steamed bread, steamed twisted rolls, steamed dumplings and wontons. Participants were asked to recall their frequency (daily, weekly, monthly, annually, never) of consumption of each food item and the estimated portion size, using a common unit of weight in China, i.e. 1 liang = 50 g or natural units, e.g. bottles. To increase the accuracy of the portion-size estimates, standard tableware including bowls, plates and glasses was provided. Food intake was then converted into grams per day and total energy intake was calculated from all these items according to the China Food Composition Table [18].

2.3. Dietary patterns derivation

Because no participants reported the consumption of coffee, white wine and cheese, these foods were excluded in subsequent analyses. The remaining food items from FFQ were then categorized into main food groups based on similar nutrient profiles [18] or hypothesized biological effects. Consideration was also given to individual food items because of the high reported intake, e.g. rice and noodles. As a result, 25 foods or food groups were entered into the analysis in absolute weights [19].

Dietary patterns were identified using PCA through the PROC FACTOR procedure in SAS (version 9.3, SAS Institute Inc., Cary, NC, USA.) software. Factors were rotated orthogonally to obtain a simpler structure with better interpretability. On the basis of the eigenvalues (>1), the scree plot and the interpretation of the factors [20], a 4-factor solution was selected. A factor score for each participant was then calculated by summing intake of all foods or food groups weighted by their rotated factor loadings which illustrated their correlations with that factor. A higher factor score indicated a higher adherence to that dietary pattern. Labeling of the factors was primarily descriptive and based on our interpretation of the pattern structures.

Since factor solutions may differ by sex [21], it is recommended that dietary pattern analyses should be conducted separately for men and women. However, because the current sample size was relatively small, when we derived dietary patterns by sex, the Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy declined from 0.65 in all participants to 0.58 in women, which did not meet the minimum required value (i.e. 0.6) for factor analysis [22]. So we had to perform analyses on the whole population.

2.4. Telomere length measurement

Venous blood samples that were used for measurement of TL and other biochemical markers were collected after an overnight fast at baseline. The analysis of TL has been described elsewhere [23]. In brief, genomic DNA was extracted from isolated leukocytes with standard procedures using AxyPrep Blood Genomic DNA Miniprep kit (Axygen Biosciences, Union City, CA, USA). The mean length of the terminal restriction fragment, an absolute leukocyte TL, was measured using the Southern blot based in-gel hybridization technique, in which ^{32}P-labeled telomeric probe was used for hybridization, and the weighted mean TL was calculated [24]. The laboratory staffs conducting the TL measurement were blinded to all characteristics of the leukocyte donors. Quality control samples were interspersed on each gel to assess variability. With random sampling, the coefficient of variation for three independent measurement of same sample display very small coefficient of variation

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