Large US Study Finds Boosting Gut-Friendly Foods may Slow Biological Aging

Researchers assessed associations between the dietary index for gut microbiota (DI-GM) and phenotypic age acceleration (PAA).

Aging is a significant global health concern, affecting lifespan and contributing to an increased disease burden. Dietary factors have increasingly gained attention for their role in regulating aging. Healthy dietary patterns, such as the Dietary Approaches to Stop Hypertension (DASH) diet and the Mediterranean diet, can slow the aging process by decreasing oxidative stress and inflammation; however, the specific mechanisms underlying the associations between diet and aging remain unclear.

Studies indicate links between gut microbiota composition or diversity and aging-related diseases. A functionally intact and diverse gut microbiota could delay aging. In contrast, unhealthy diets rich in fats and refined grains can lead to gut dysbiosis and accelerate the aging process.

The DI-GM is a composite score balancing the intakes of foods deemed detrimental or beneficial to microbial diversity. However, its relationship with biological aging remains unclear.

Study

In the present study, researchers explored the associations between DI-GM and PAA. Data were used from the National Health and Nutrition Examination Surveys (NHANES) conducted between 1999 and 2018 in the United States. Participants were included if they were aged 20 years or older and excluded if they lacked diet or phenotypic age data.

The DI-GM score (range: 0–13) was derived from two 24-hour dietary recalls, with higher scores indicating greater benefits to the gut microbiota. The index originally included 14 components, but green tea, unavailable in NHANES, was excluded.

Scoring was based on sex-specific median food intake. One point was assigned when the intake of foods beneficial to the gut microbiota was above or at the median value, and zero points were assigned if it was below the median. Conversely, one point was assigned when the intake of foods detrimental to the gut microbiota was below the median value, and zero points were assigned if it was above or at the median.

Phenotypic age was determined using 10 physiological indicators (including chronological age), such as creatinine, albumin, glucose, lymphocyte percentage, C-reactive protein, mean cell volume, white blood cell count, alkaline phosphatase, and red cell distribution width. A linear

regression analysis was performed to calculate the age acceleration residual (ACR) by regressing phenotypic age against chronological age. PAA was defined as a positive ACR.

Potential confounding variables included gender, age, marital status, race, poverty income ratio, body mass index (BMI), alcohol intake, smoking status, education level, diabetes, cardiovascular disease (CVD), physical activity, hypertension, and hyperlipidemia. Multivariable regression models were used to evaluate the association between the DI-GM score and ACR and PAA. One was adjusted for gender and age, while the other was adjusted for all confounders.

Furthermore, restricted cubic spline analyses were used to assess the non-linear relationship between PAA and DI-GM. Notably, detrimental food components exhibited a significant non-linear association with PAA, whereas the overall DI-GM showed a linear association (P = 0.063 for non-linearity).

In addition, stratified analyses were performed to explore the consistency of associations in subgroups defined by age, gender, alcohol intake, race, smoking status, and chronic disease status (diabetes, hyperlipidemia, and cardiovascular disease).

A significant interaction emerged between DI-GM and age groups. Moreover, various sensitivity analyses, including propensity score matching and multiple imputation for missing data, were undertaken to verify the robustness of the findings.

Findings

In total, 29,435 NHANES participants aged 50.3 years, on average, were included. Of these, 50.7% were male, 48.4% were non-Hispanic White, and 61.7% were married or cohabiting. Further, 9,605 individuals exhibited PAA. Individuals with PAA were significantly older and had a higher BMI and lower average DI-GM score than those without PAA.

There were significant differences in race, gender, education level, smoking status, and chronic disease status between individuals with and without PAA. Further, higher DI-GM scores were significantly associated with lower ACR and PAA. Each one-point increment in the DI-GM score was associated with a 12% decrease in PAA risk in the age- and gender-adjusted model and a 7% reduction in the fully adjusted model. Beneficial components (OR = 0.92) contributed more strongly than avoiding detrimental foods (OR = 0.97).

Individuals with DI-GM scores of 5 (OR = 0.89) and those with scores of 6 or higher (OR = 0.74) had significantly lower PAA risks than those with scores of 0–3. A linear, negative correlation was found between DI-GM scores and PAA risk. Stratified analyses showed that higher scores were consistently associated with reduced PAA risks across subgroups. Likewise, sensitivity analyses using advanced statistical methods confirmed these results.

Conclusion

Taken together, the findings illustrate that higher DI-GM scores were significantly associated with lower ACR and PAA risks. Specifically, each unit increment in the score was associated with 7% lower PAA risk in the fully adjusted model. Increasing beneficial foods had a stronger effect than reducing detrimental ones.

This suggests that the potential benefits of dietary patterns on the gut microbiota may play a vital role in slowing biological aging. However, as a cross-sectional study based on 24-hour dietary recalls, causality cannot be inferred, and long-term dietary patterns may not be fully captured.

Additionally, the absence of direct measurements of gut microbiota limits mechanistic interpretations. Future studies should focus on long-term interventions and the integration of multi-omics to explore the interactive mechanisms between the host, microbiota, and diet.

Source:

https://www.news-medical.net/news/20250720/Boosting-gut-friendly-foods-may-slow-biological-aging-large-US-study-finds.aspx