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Sleep duration as a mediator in the association between dietary intake of live microbes and insulin resistance: a cross-sectional study

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Abstract

Background Insulin resistance and associated metabolic health symptoms remain a primary global health concern. In addition to healthy dietary and nutritional programs, sleep duration is closely related to and has been linked to healthy metabolism. This study aimed to determine the link between insulin resistance and sleep duration and the dietary intake of live microbes.

Methods Data were collected from 15,927 participants in the National Health and Nutrition Examination Survey database from 2005 to 2018; this sample is equivalent to 209,316,590 individuals in the United States. The participants were categorized according to their consumption of foods containing live microbes: low, medium, high, and medium-high. The relationship between diets containing live microbes and the triglyceride-glucose index was analysed using a weighted multivariate linear regression model with a multistage sampling approach. The individuals were deemed to have insulin resistance if their homeostatic model assessment score for insulin resistance was ≥ 2. The relationship between diets containing live microbes and insulin resistance status was assessed using weighted multivariate logistic regression analyses. The mediating role of sleep duration on the relationship between diets containing live microbes and the triglyceride-glucose index was also examined.

Results After accounting for potential confounders, diets containing live microbes at medium and medium-high levels were significantly associated with a reduced triglyceride-glucose index. The medium and medium-high levels of live microbial intake were also associated with a lower risk of insulin resistance. Within the 6–9 hours' sleep duration range, the indirect effect of medium and medium-high levels of live microbes on the triglyceride-glucose index was observed, accounting for 2.95% and 6.08% of the overall change, respectively.

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Conclusions This study suggests an association between a diet rich in medium and medium-high viable microbes, lower triglyceride-glucose index values, and a reduced risk of developing insulin resistance. Additionally, a sleep duration of 6–9 h may mediate this association.

Keywords Cross-sectional study, Insulin resistance, Live microbes, Mediation analysis, Sleep duration

Background

Disturbances in sleep and dietary behaviours have been linked to insulin resistance (IR) [1]. The ramifications of these disruptions, such as the fact that the total prevalence of diabetes and pre-diabetes exceeds 50% in the United States (US), pose a significant strain on socioeconomic frameworks and healthcare infrastructure [2].

The triglyceride-glucose (TyG) index and homeostasis model assessment of IR (HOMA-IR) are essential metrics for evaluating IR and play a crucial role in the early identification and management of metabolic disorders [3]. The TyG index offers a straightforward assessment method, achieving accuracy comparable to the estimated hyperinsulinaemic-euglycemic clamp technique [4] and even surpasses HOMA-IR in diagnostic efficacy [5].

IR is influenced by several lifestyle factors, including obesity and sleep deprivation [6]. Substantial evidence suggests that the modulation of the gut microbiota through dietary interventions can significantly influence protein, energy, lipid, and glucose metabolism [7]. Incorporating live microflora into the diet, especially foods abundant in live microorganisms, such as fermented products, has significant health benefits, including anti-infective, antioxidant, and antidiabetic properties [8]. Nonetheless, the complex connections between the live microbe-containing (LMC) diet and indices, such as TyG index and HOMA-IR, remain relatively unexplored.

The American Academy of Sleep Medicine emphasises the importance of sleep for health, equates sleep with diet, and advocates sleep care as a public health strategy [9]. Sleep duration varies and is inversely associated with age [10]. Insufficient sleep is a risk factor for glucose intolerance and IR [11, 12], potentially leading to metabolic syndrome [13], obesity [14], and cardiovascular disease [15]. Elevated TyG index values are associated with an increased prevalence of sleep disorders [16]. Further studies into the interplay between sleep duration, TyG index, and insulin sensitivity assessment remain warranted.

This study hypothesised that consuming foods with high levels of viable microbes is associated with lower IR and TyG index and is mediated by sleep duration. The present cross-sectional analysis elucidated the association between diets containing live microbes and the TyG index and IR using the dataset from the National Health and Nutrition Examination Survey (NHANES). The mediating function of sleep duration within the relationship between diets containing live microbes and the TyG index was also assessed. To date, this cross-sectional study is among the first to explore the mediating role of sleep duration in the relationship between dietary live microbe intake and the TyG index.

Methods

Research design and participants

This study utilised data from the NHANES, a program operating under the auspices of the National Centre for Health Statistics (NCHS), which serves as a cross-sectional study that provides a nationally representative snapshot of the nutritional profile and health in the US. This study focused on the NHANES' unrestricted public data from seven cycles (2005–2018). Public data are also freely accessible to researchers without a licence, according to the NHANES policy on data dissemination. The study was ethically reviewed, and all participants provided informed consent. Given the absence of personal identifiers in this study, which constituted a secondary analysis of the existing data, further ethical approval was not necessary.

In this study, the following groups were excluded: participants < 20 years of age; individuals lacking LMC foods due to their close relevance to the core relationship under investigation in this study; participants without data on triglycerides, glucose, and fasting insulin as these data are crucial for calculating the TyG index and HOMA-IR; individuals who responded with "refused" or "did not know" in the questionnaires regarding marital status, educational attainment, poverty income ratio (PIR), alcohol consumption, and smoking status.

The final analytical cohort comprised 15,927 individuals. The dataset is accessible to the public via the NHANES official webpage: http://www.cdc.gov/nchs/nhanes/, which was logged on 1 May 2024.

Measurement of live microbial levels in the diet

Information on dietary intake was sourced from the 'Dietary Data' subset, comprising two 24-h dietary recall assessments. These data were used to determine the diversity and volume of dietary intake, encompassing food and beverages, over 24 h (from midnight to midnight). Furthermore, the data quantified macronutrients, micronutrients, and other dietary constituents of the reported food items. Sanders et al. allocated the estimated live microbial counts per gram of food based on over 9,000 food items classified into subgroups within the NHANES database [17]. The authors conducted a

systematic categorisation of foods harbouring live microorganisms, delineating three distinct groups: foods with low microbial content (Lo, $<10^4$ CFU/g), such as pasteurised or thermally processed products, including milk, processed meats, poultry, sauces, and gravies; foods with medium microbial content (Med, 10^4–10^7CFU/g), mainly composed of unpeeled fruits and vegetables, unpasteurised seasonings, and partially fermented foods; foods with high microbial content (Hi, $>10^7$CFU/g), primarily comprising fermented dairy products. For fermented dairy products, such as yoghurt, during the fermentation process, specific strains, such as *Lactobacillus bulgaricus* and *Streptococcus thermophilus* are added. Utilising this classification system in conjunction with the initial 24-h dietary recall data, the four groups were formed by dividing the participants based on the LMC levels of the live microbes: low, medium (Med), high (Hi), and medium-high (Med-Hi, participants consumed foods in both medium and high microbial content categories). The Med-Hi group is distinct from Med and Hi groups due to its unique dietary intake combination, determined by the presence of both medium and high-level food codes in 24-h dietary recall data.

Measurement of sleep duration

Information on sleep status was recorded from 2005 to 2018 by qualified interviewers using the computer-assisted personal interviewing methodology, which has built-in consistency-checking features that reduce the possibility of data entry errors and presented in seven datasets. Sleep duration was measured by self-report and determined by a specific question in the questionnaire: "How much sleep do you get (hours)?" This refers to the sleep duration per night on weekdays or workdays.

Measurement of TyG index and HOMA-IR

Triglycerides and fasting blood glucose levels were measured using standardised enzymatic and hexokinase assays, respectively. Insulin levels were quantified with a two-site immunoenzymatic method, as described in the NHANES Laboratory/Medical Technician Procedures Manual [18]. The TyG index is a measure of metabolic imbalance that assesses the levels of triglycerides and glucose in fasting blood samples. The TyG index, HOMA-IR, and TyG-body mass index (BMI) were ascertained using the following formulas: TyG index = ln ([triglycerides (mg/dL) × fasting blood glucose (mg/dL)]/2) [19], HOMA-IR = (fasting blood glucose [mmol/L] × fasting insulin [μU/mL])/22.5 [20], and TyG-BMI = TyG index × BMI. IR was defined as the threshold of HOMA-IR ≥ 2.0, consistent with earlier studies [21–23]. The participants were categorized into two groups predicated on the participants' IR profiles.

Measurement of covariates

The covariates assessed were collected using standardised survey instruments and physical examinations. The foundational elements were demographic variables, such as sex, age, and race. Additionally, the interplays between economic and social status in relation to health results were examined by integrating variables, such as marital status, educational attainment, and PIR (categorised into tertiles: "<1", "1–3", and ">3"). Smoking status was classified as non-smoker, former smoker, or current smoker. Alcohol consumption patterns were stratified into three categories: non-drinkers, moderate alcohol consumers, and excessive alcohol consumers. Using smoking and alcohol consumption as covariates, the relationship between lifestyle choices and health was elucidated. To account for the potential confounding effects of chronic conditions, this study included patients with BMI data, diabetes mellitus, and hypertension, thereby enabling an evaluation of their prospective influence on outcomes. Participants who responded with "refused" or "did not know" to the question "Has a doctor or health professional ever told you that you have hypertension or diabetes?" in the questionnaire was excluded. Further examinations were conducted for those who self-reported a doctor's diagnosis of such diseases. Fasting blood glucose ≥ 7.0 mmol/L, 2-h postprandial glucose ≥ 11.1 mmol/L in the oral glucose tolerance test, or the glycated haemoglobin (HbA1c) ≥ 6.5% indicated confirmed diabetes. For hypertension, systolic ≥ 140 mmHg and/or diastolic ≥ 90 mmHg in at least two measurements suggested that the participant was hypertensive. Multiple imputation methods were used to interpolate missing values for marital status, educational attainment, PIR, and alcohol consumption. The Multiple Imputation method was based on repeated sampling and imputation [24, 25].

Statistical analyses

Data analysis was performed following the complex analysis guidelines provided by the Centres for Disease Control and Prevention. The sample data from 2005 to 2018 were weighted as per the NCHS specifications, utilising the 'WTSAF2YR' weight variable. The formula for calculating the weights, i.e., the sample weights, was Weight = 1/7 × WTSAF2YR. The Kolmogorov–Smirnov test was used to assess variable distribution normality, while the variance inflation factor (VIF) was used to evaluate multicollinearity in multiple linear regression models, with a VIF of > 10 indicating high multicollinearity. Data are expressed as weighted means ± standard deviations (SD) for continuous variables with a Gaussian distribution. In contrast, skewed distributions of continuous variables are represented using medians and interquartile ranges, whereas categorical variables are expressed as

weighted percentages. The relationships between dietary intake, sleep duration, TyG index, and IR status were explored using a survey design-weighted nested regression model structured across three analytical models: Model 1 was a raw model that illustrates the fundamental relationships being studied; Model 2 was modified for key demographic factors—age, sex, and ethnicity—that were considered primary determinants within the study context; Model 3 was a comprehensive model that expanded the adjustments to include a broader spectrum of covariates and confounders, such as educational attainment, relationship status, PIR, smoking status, alcohol consumption, BMI, diabetes mellitus, and hypertension, to account for potential influences. Subgroup analysis and regression were employed to test interactions after adjusting for confounders. For the continuous TyG index, a multiple linear regression model was used; for the binary IR status, a logistic regression model was applied. Coefficients, confidence intervals, and *P*-values (including interaction *P*-values) were calculated to assess the interactions between live microbe intake and the TyG index or IR status across different strata. Regression-based mediation analyses were conducted to determine the direct effects of LMC products on the TyG index and the indirect effects mediated by sleep duration [26–28]. In this approach, the TyG index was regressed on the levels of diets with live microbes to assess the direct effect, sleep duration was regressed on the levels of diets with live microbes, and the TyG index was regressed on the levels of diets with live microbes and sleep duration to determine the indirect effect mediated by sleep duration. Using this approach, three distinct effects were identified: (1) a total effect, encapsulating the overall association between the dietary levels of live microbes and the TyG index, including direct associations and sleep duration-mediated effects; (2) a direct effect, illustrating the immediate impact of live dietary microbial levels on the TyG index; (3) an indirect effect, highlighting the mediated relationship between live dietary microbial intake and the TyG index via sleep duration.

All analyses were performed using the DecisionLinnc (DecisionLinnc Core Team 2023) analytical platform, a comprehensive platform that combines various programming environments and enables data processing and analysis. HangZhou, CHN. Retrieved from https://www.statsape.com/. All the statistical tests were two-tailed, with a significance threshold of $P < 0.05$.

Results

Participant characteristics

The study cohort was used to project an approximate demographic-weighting encompassing 209,316,590 individuals across the US. Among the weighted data of this projected demographic, 48.54% were males and 51.46% were females, creating a balanced sex distribution. Table 1 lists the participants' attributes covering a range of demographic and socioeconomic characteristics. Notably, a significant proportion (67.77%) self-identified as non-Hispanic white, suggesting that the cohort predominantly comprised this ethnicity. Additionally, a significant proportion of the 60.50% age group had a university or higher education. Consumption patterns indicated that the intake of low-level LMC foods represented 33.28% and medium-to-high level LMC foods 20.89% of the total population. The TyG index, a key parameter in the study, was 8.62 ± 0.66 (mean ± SD) in the weighted population, which significantly differed among the dietary microbial intake groups. Sleep duration and two additional IR indicators, TyG-BMI index and HOMA-IR, significantly differed between the dietary microbial intake groups ($P < 0.001$).

Relationship of dietary levels of live microbes with the TyG index and IR status

Weighted multivariate regression models were employed to examine the association between live dietary microbial levels, the TyG index, and IR in the four groups. As presented in Supplementary Table 1, the medium dietary levels of live microbes were negatively associated with the TyG index in both models (Model 1, β [95% CI]: -0.034 [-0.064, -0.003], $P = 0.030$; Model 2, β [95% CI]: -0.080 [-0.109, -0.051], $P < 0.001$; Model 3, β [95% CI]: -0.040 [-0.063, -0.016], $P = 0.001$). Med-Hi dietary live microbe intake was negatively associated with TyG index (Model 1, β [95% CI]: -0.114 [-0.152, -0.075], $P < 0.001$; Model 2, β [95%CI]: -0.140 [-0.180, -0.101], $P < 0.001$; Model 3, β [95% CI]: -0.054 [-0.088, -0.019], $P = 0.003$). Logistic regression analysis, as presented in Supplementary Table 2, revealed that compared with the low dietary LMC group, the remaining dietary LMC intake groups were associated with a reduced risk of IR across all three models (except for the high LMC group in Model 3 [odds ratio (OR): 0.826 [0.679, 1.005], $P = 0.056$]). There was a significant dose-response association between live dietary microbial intake and TyG index in all models (*P* for trend < 0.05).

Subgroup analyses were performed in accordance with sex, age, diabetes, and hypertension status. For each stratified analysis, adjustments were made for age, sex, race, PIR, educational status, alcohol use, smoking status, BMI, diabetes, and hypertension, except for the stratifying variable. The results (Figs. 1, 2 and 3) revealed no significant interactive effects between the consumption of live microbes and the TyG index and IR stratification variables. No significant interaction was observed for sex differences; male and female Med and Med-Hi groups were significantly negatively associated with TyG index, whereas lower risk of IR was associated with the male

Table 1 Demographic and clinical characteristics stratified based on live microbial dietary intake

Characteristic	Total (*n* = 15,927)	Low (*n* = 5,805)	Med (*n* = 6,558)	Hi (*n* = 960)	Med-Hi (*n* = 2,604)	*P* value
Age						< 0.001
20–39	5,291 (36.76)	2,033 (40.80)	1,999 (32.92)	335 (40.07)	924 (36.53)	
40–59	5,270 (37.33)	1,910 (36.87)	2,170 (38.03)	315 (35.33)	875 (37.35)	
≥ 60	5,366 (25.91)	1,862 (22.33)	2,389 (29.05)	310 (24.60)	805 (26.12)	
Sex (%)						< 0.001
Female	8,162 (51.46)	2,776 (47.05)	3,386 (52.16)	505 (52.13)	1,495 (53.01)	
Male	7,765 (48.54)	3,029 (52.95)	3,172 (47.84)	455 (47.87)	1,109 (46.99)	
Race (%)						< 0.001
Mexican	2,540 (8.48)	781 (7.80)	1,295 (10.79)	97 (5.22)	367 (6.19)	
Other Hispanic	1,574 (5.54)	557 (5.80)	6,49 (5.63)	126 (6.78)	242 (4.54)	
Non-Hispanic White	6,944 (67.77)	2,244 (61.92)	2,785 (66.38)	474 (72.21)	1,441 (78.34)	
Non-Hispanic Black	3,215 (10.97)	1612 (16.43)	1,155 (9.79)	157 (8.87)	291 (5.13)	
Other race	1,654 (7.25)	611 (8.05)	674 (7.41)	106 (6.91)	263 (5.79)	
Education level (%)						< 0.001
Less than high school	3,957 (16.11)	1,684 (20.80)	1,686 (16.35)	200 (13.33)	387 (9.04)	
High school or GED	3,648 (23.38)	1,472 (27.00)	1,460 (22.63)	220 (24.35)	496 (18.74)	
Above high school	8,322 (60.50)	2,649 (52.20)	3,412 (61.01)	540 (62.32)	1,721 (72.22)	
PIR (%)						< 0.001
< 1	3,020 (12.89)	1,346 (17.62)	1,153 (11.38)	179 (12.70)	342 (8.26)	
1–3	7,544 (40.62)	2,948 (45.91)	3,095 (39.88)	426 (39.35)	1,075 (33.98)	
> 3	5,363 (46.49)	1,511 (36.47)	2,310 (48.74)	355 (47.95)	1,187 (57.76)	
Marital status (%)						< 0.001
Never married	2,764 (17.61)	1,162 (20.84)	998 (15.41)	169 (18.26)	435 (16.42)	
Married/living with partner	9,676 (64.50)	3,223 (58.86)	4,165 (66.97)	602 (65.72)	1,686 (68.47)	
Widowed/divorced	3,487 (17.89)	1,420 (20.30)	1,395 (17.62)	189 (16.02)	483 (15.12)	
Smoking status (%)						< 0.001
Never smoker	8,728 (54.94)	2,955 (49.81)	3,678 (56.22)	528 (55.23)	1,567 (60.60)	
Former smoker	3,959 (25.33)	1,325 (23.37)	1,728 (26.84)	244 (24.17)	662 (25.94)	
Current smoker	3,240 (19.74)	1,525 (26.81)	1,152 (16.94)	188 (20.60)	375 (13.47)	
Alcohol status (%)						< 0.001
Non-drinker	4,436 (22.87)	1,705 (24.93)	1,840 (23.12)	269 (23.09)	622 (19.04)	
Moderate alcohol consumption	8,005 (50.38)	2,928 (50.98)	3,295 (26.61)	500 (54.57)	1,282 (48.33)	
Excessive alcohol consumption	3,486 (26.75)	1,172 (24.09)	1,423 (26.66)	191 (22.34)	700 (32.63)	
Diabetes (%)						< 0.001
No	13,843 (90.61)	5,025 (90.15)	5,631 (89.49)	824 (89.41)	2,363 (93.80)	
Yes	2,084 (9.39)	780 (9.85)	927 (10.51)	136 (10.59)	241 (6.20)	
Hypertension (%)						0.2
No	10,098 (67.39)	3,623 (66.89)	4,116 (66.55)	600 (67.46)	1759 (69.73)	
Yes	5,829 (32.61)	2,182 (33.11)	2,442 (33.45)	360 (32.54)	845 (30.27)	
IR (%)						< 0.001
No	6,091 (42.38)	2,067 (38.25)	2,488 (42.27)	376 (43.46)	1,160 (49.68)	
Yes	9,836 (57.62)	3,719 (61.75)	4,071 (57.73)	588 (56.54)	1,458 (50.32)	
BMI	29.17 ± 6.95	29.55 ± 7.14	29.04 ± 6.77	29.31 ± 7.05	28.59 ± 6.87	< 0.001
TyG Index	8.62 ± 0.66	8.66 ± 0.67	8.62 ± 0.67	8.65 ± 0.64	8.54 ± 0.64	< 0.001
TyG-BMI, median (IQR)	241 (202-–289)	247 (205–296)	242 (203–289)	243 (205–289)	233 (196–276)	< 0.001
HOMA-IR, median (IQR)	2.34 (1.40–4.07)	2.56 (1.50–4.42)	2.35 (1.43–4.14)	2.36 (1.34–3.98)	1.99 (1.25–3.51)	< 0.001
Sleep duration	7.15 ± 2.55	7.07 ± 2.57	7.14 ± 2.63	7.12 ± 1.41	7.29 ± 2.64	< 0.001

The percentage is based on the weighted sample

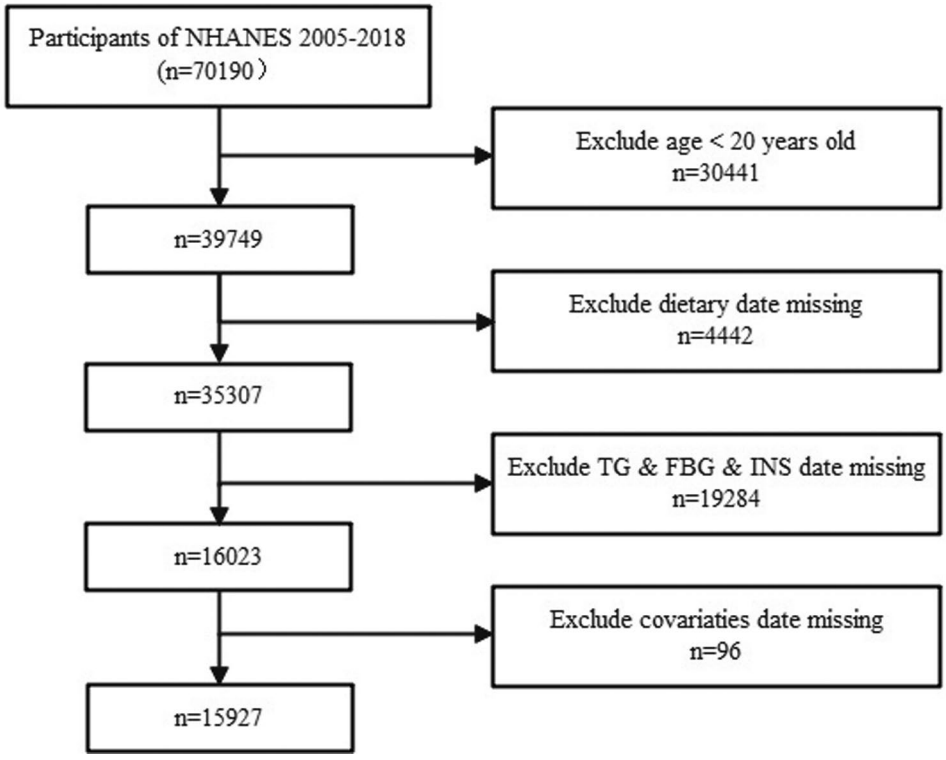

Fig. 1 Flow of study participants and enrolment

Med and Med-Hi groups and female Med-Hi group. In age stratification, in the age group 40–60 years, dietary LMC intake was associated with lower TyG index and risk of IR in the Med and Med-Hi groups (TyG: Med, β [95% CI]: -0.064 [-0.107, -0.020], $P < 0.05$; Med-Hi, β [95% CI]: -0.089 [-0.145, -0.034], $P < 0.001$. IR: Med, OR [95% CI]: 0.761 [0.603, 0.961], $P < 0.05$; Med-Hi, OR [95% CI]: 0.756 [0.578, 0.989], $P < 0.05$). These associations held true even after accounting for the effects of the aforementioned confounding factors. In the presence of diabetes and hypertension, there were significant differences in the interactions between live microbe intake, TyG index, and IR. Specifically, dietary live microbe intake was not significantly associated with the TyG index in the diabetic population but was with the non-diabetic population (P for interaction = 0.011); however, the results of hypertension stratification showed that medium and Med-Hi dietary LMC intake was significantly and negatively associated with lower TyG index in both subgroups of the hypertensive population (P for interaction = 0.084). No interaction was observed between dietary live microbial levels and IR in the diabetes stratum (P for interaction = 0.091); only Med-Hi LMC was associated with a lower risk of IR in the diabetic population (OR 0.482 [0.267, 0.871], $P < 0.05$). Whereas a significant interaction was observed between dietary live microbe intake and IR in the hypertension stratum (P for interaction = 0.009), all groups of dietary LMC intake were not significantly associated with IR in the hypertensive population.

Differences in baseline characteristics such as sex, race, and marital status between diabetic and non-diabetic patients could have influenced the TyG index through diverse metabolic pathways, distorting the relationship between dietary live microbes and the TyG index. Propensity score matching was employed to address these issues. This involved meticulously adjusting for several variables, including age, sex, race, marital status, education degree, PIR, alcohol consumption, smoking status, and BMI index.

After matching and eliminating confounding effects, the P-value for the interaction, which was previously 0.011, increased to 0.598 (Supplementary Table 3), suggesting that the relationship was not as pronounced as initially thought. This shift is consistent with the current understanding of diabetes pathophysiology, where complex metabolic derangements may limit the direct impact of dietary live microbes on the TyG index, and unmatched results could have been distorted due to uncontrolled confounding factors.

A sensitivity analysis was conducted using two models: Model 1, adjusting for age, sex, and race, yielded a P-value of 0.240 for the interaction in the diabetic subgroup (Supplementary Table 4); Model 2, incorporating additional factors such as marital status, education degree, PIR, smoking and alcohol consumption, BMI

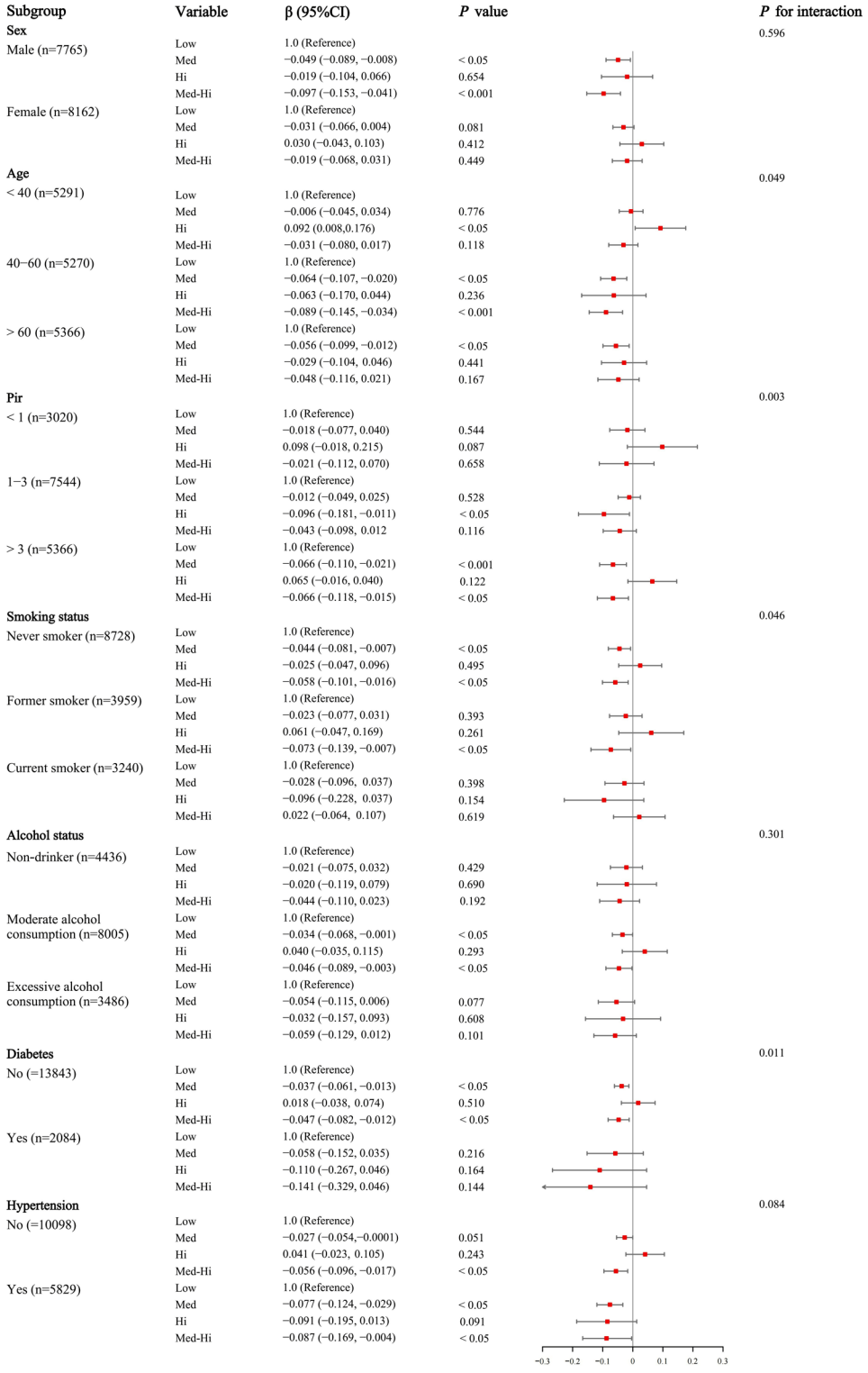

Fig. 2 Subgroup analysis of the association between dietary levels of live microbe and TyG index

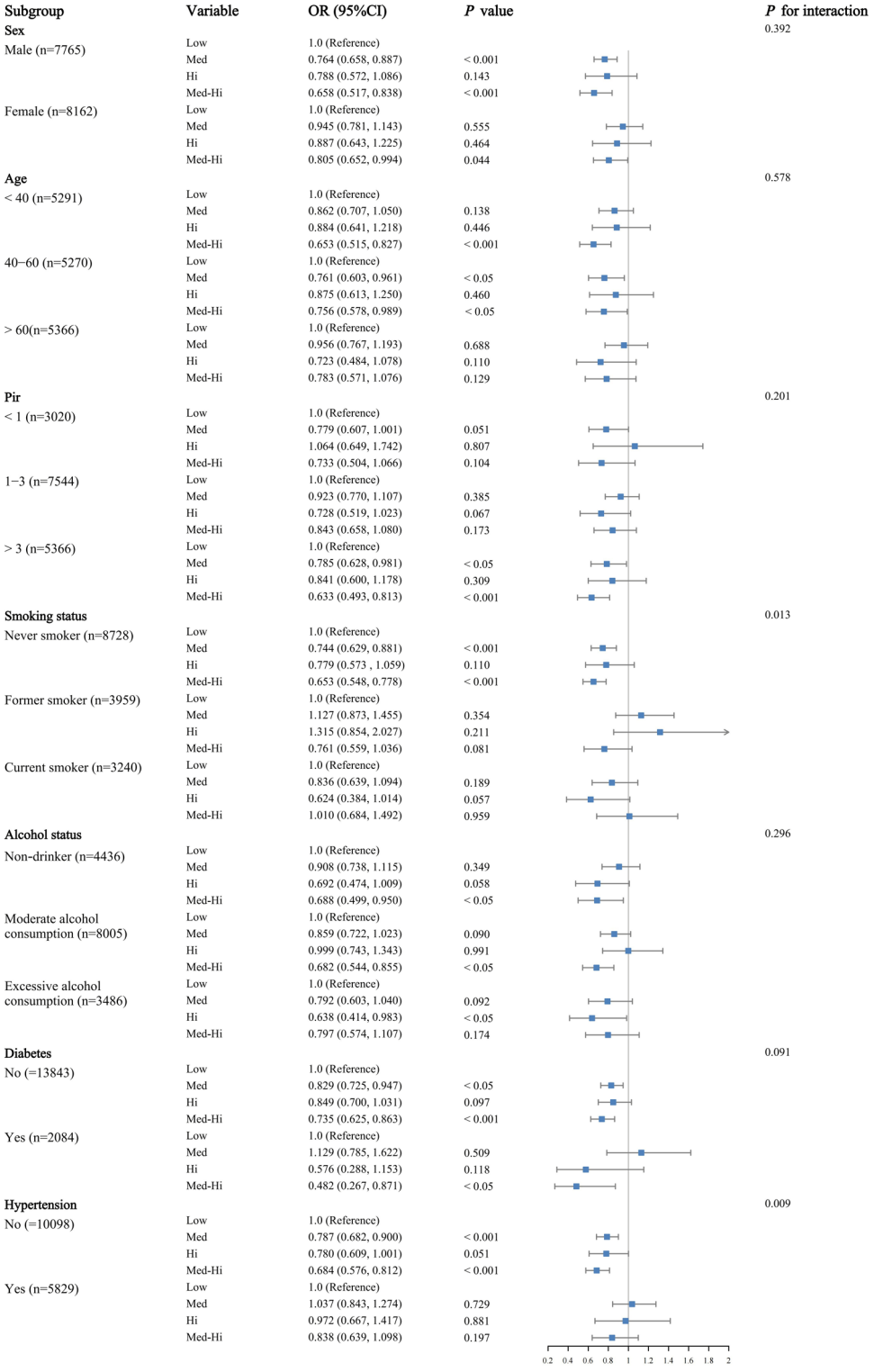

Fig. 3 Subgroup analysis of the association between dietary levels of live microbes and insulin resistance

Table 2 Associations between sleep duration and dietary live microbe intake

Model	variable	β (95%CI)	*P*-value
	< 9 h		
Model 1	Low	1.0 (Reference)	
	Med	0.181(0.118, 0.244)	< 0.001
	Med-Hi	0.347(0.276, 0.417)	< 0.001
	< 9 h		
Model 2	Low	1.0 (Reference)	
	Med	0.141(0.075, 0.206)	< 0.001
	Med-Hi	0.278(0.204, 0.351)	< 0.001
	< 9 h		
Model 3	Low	1.0 (Reference)	
	Med	0.077(0.014, 0.139)	0.018
	Med-Hi	0.168(0.097, 0.239)	< 0.001

index, and hypertension, increased the *P*-value to 0.598. The progressive increase in *P*-values with more confounding factor control confirms that the unmatched significant results were attributed to confounding and that the matched analysis provides reliable insights with good stability across different model settings.

Relationship between dietary levels of live microbes and sleep duration

Sleep duration was associated with dietary LMC intake (Table 2). After adjusting for all covariates, dietary LMC intake was positively associated with sleep duration of < 9 h in the Med and Med-Hi groups: (Med: β [95% CI]: 0.077 (0.014, 0.139), $P = 0.018$) and (Med-Hi: β [95% CI]: 0.168, (0.097, 0.239), $P < 0.001$). As the sleep duration extended to < 9.5 h, < 10 h, < 10.5 h, < 11 h, < 11.5 h, < 12 h, and < 15 h, the significance and strength of the associations for the Med and Hi groups gradually diminished. Particularly, the β and *P*-values of the Med group exhibited a decreasing trend in statistical significance (Supplementary Table 5).

Nonlinear relationship between sleep duration and the TyG index and IR status

Restricted cubic splines (RCS) were employed to investigate the influence of sleep duration on the relationship between the TyG index and IR (Fig. 4). RCS works by dividing the range of a predictor variable (in this case, sleep duration) into several segments and fitting a cubic polynomial function within each segment. This enables the model to capture more complex curvature and nonlinear patterns in the data.

The *P* for overall was < 0.001, which indicated that the entire model was highly significant in explaining the relationship between sleep duration and the TyG index and IR status. Among all models, a significant nonlinear relationship was observed between sleep duration and the TyG index and IR status (*P* for nonlinear < 0.05). Sleep

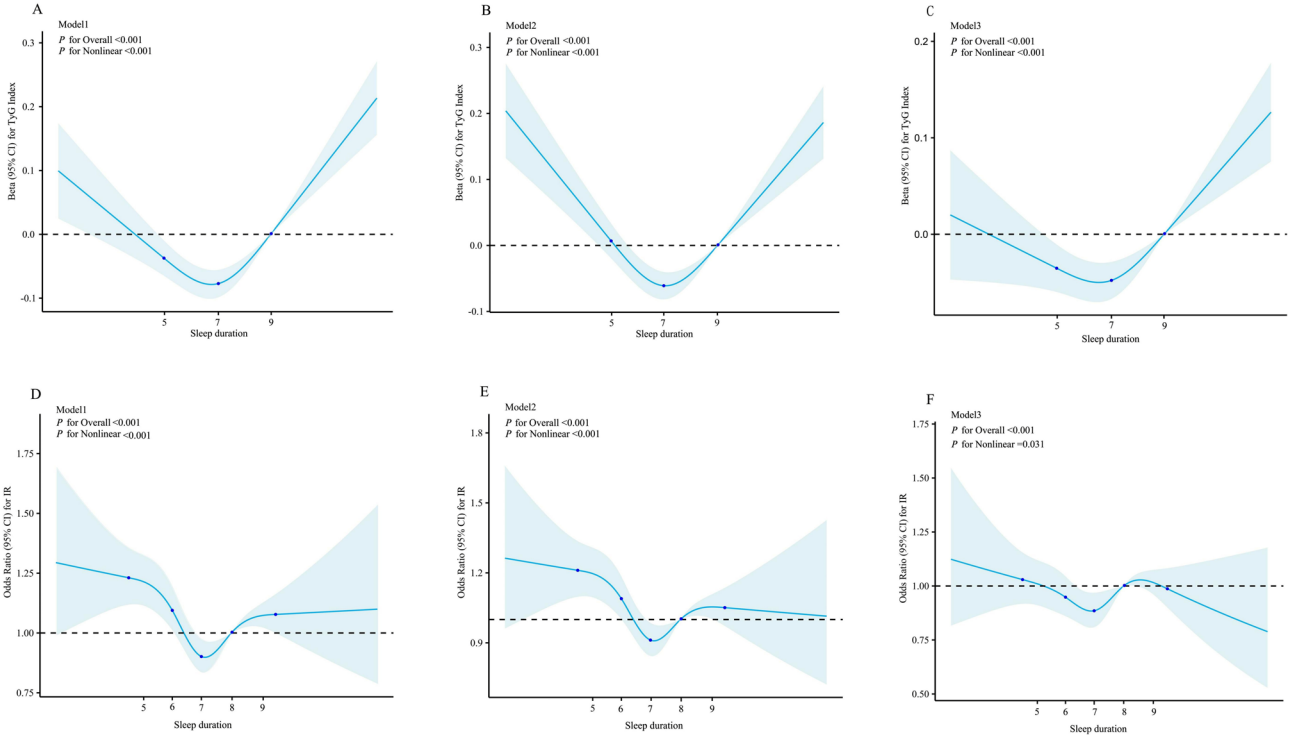

Fig. 4 Associations of sleep duration with triglyceride-glucose index and insulin resistance (IR). The RCS revealed a non-linear (U-shaped) relationship between sleep duration and the TyG (**A**–**C**) index and IR (**D**–**F**). The fitted regression curve is depicted by a continuous blue line; the black dashed line indicates where β equals 0 and OR equals 1

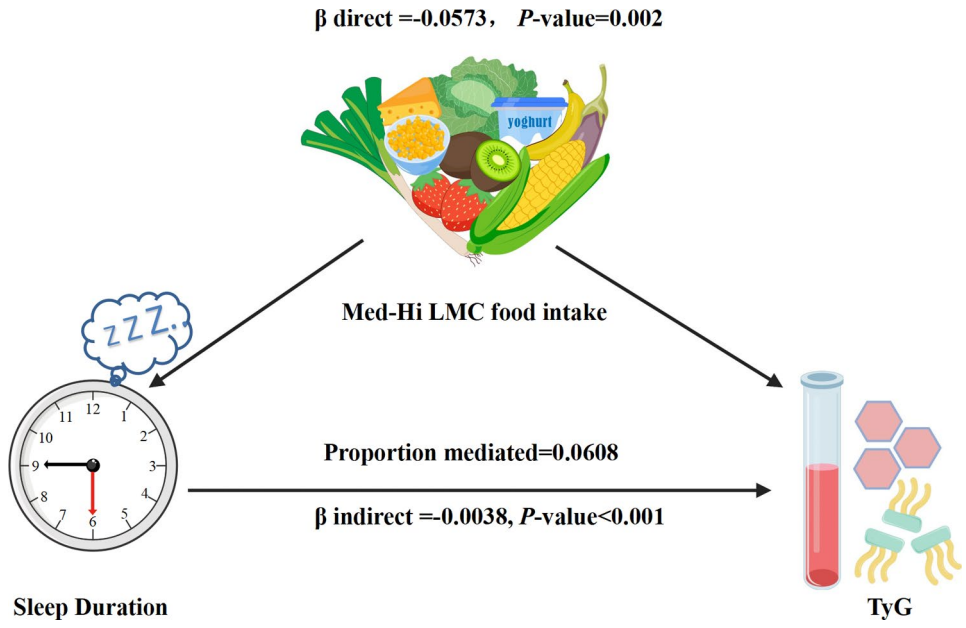

Fig. 5 Path diagram of the mediation analysis of the relationship between sleep duration, dietary Med-Hi LMC intake, and TyG index showing statistical significance ($P < 0.05$). This Figure was produced by leveraging the CNSknowall platform (https://cnsknowall.com), a specialised web service dedicated to comprehensive data analysis and visualisation

duration exhibited a pronounced "U-shaped" relationship with the TyG index, necessitating further analysis of threshold effects, which identified an inflection point. The RCS curves show that when sleep duration falls below a specific threshold, it significantly negatively correlates with the TyG index. That is, as sleep duration decreases, the TyG index tends to increase. After adjusting for confounding factors in Model 3, the inflection point was 6 h. Observations reveal a significant negative association between sleep duration and the TyG index when sleep duration falls below a certain threshold. Conversely, the TyG index increases as sleep duration surpasses this point. Similar results were found in the RCS model for sleep duration and IR, with 6.5 h of sleep demonstrating a positive effect on the risk of IR in Model 3. This indicates that sleep duration and IR have a nonlinear relationship, with an inflection point at 6.5 h of sleep.

Mediating effect of sleep duration on dietary live microbe intake and TyG indices

Mediation analyses examined whether sleep duration (6–9 h) mediates the association between dietary LMC intake and TyG index in the Med and Med-Hi groups (Fig. 5 and Supplementary Table 6). In the adjusted model, the Med-Hi group had a total effect of 6.11% on the TyG index (β [95% CI]: -0.0611 [-0.0969, -0.0250], $P < 0.001$), with a direct effect of 5.73% (β [95% CI]: -0.0573 [-0.0939, -0.0216], $P = 0.002$) and an indirect effect of sleep of 0.38% (β [95% CI]: -0.0038 [-0.0038, -0.0015], $P < 0.001$).

Discussion

This study analysed 15,927 participants from NHANES 2005–2018 to explore the links between dietary live microbes, sleep duration, TyG index, and IR status. The Med and Med-Hi groups' LMC foods showed negative associations with TyG and a reduced IR risk. The Med-Hi group, which consumed more fermented dairy products, exhibited a stronger link to TyG reduction and improvements in IR, as the quantity and diversity of live microbes increased. However, the Hi-group LMC foods showed no significant differences, possibly due to insufficient sample size, inadequate live microbe intake, and gut microbiota variability.

Ingestible live microbes and "probiotics" are beneficial for lowering cholesterol and glycaemic index [29]. For example, in patients with chronic kidney disease, probiotic, prebiotic, and symbiotic supplementation decreased HOMA-IR [30]. Sanders et al. found that a diet containing live microbes improved health by regulating BMI, lipids, glucose, and insulin [31]. The Mediterranean diet, characterized by a high intake of fruits, vegetables, and fermented foods, has been linked to reduced IR [32]. Ross et al. found that long-term intake of high-fibre-rich plant foods increased the abundance of intestinal *Bifidobacteria* and *Lactobacillus*, which was synchronously associated with decreased total cholesterol [33]. These findings reinforce metabolic health benefits of dietary live microbes, particularly in improving insulin sensitivity and reducing cardiovascular risk factors.

Dietary LMC intake can modify the composition and function of the gut microbiota. In this study, dietary

LMC intake in the Med and Med-Hi groups may have stimulated the growth of beneficial gut bacteria, including *Bifidobacteria* and *Lactobacillus*, which produce key metabolites such as short-chain fatty acids (SCFAs). SCFAs function as signalling molecules by binding to G protein-coupled receptors (such as FFAR2/3) on enteroendocrine L cells, triggering the release of key intestinal hormones, such as glucagon-like peptide-1 (GLP-1) and peptide YY (PYY). GLP-1 promotes insulin secretion, slows gastric emptying and intestinal transit, and enhances glucose-dependent insulin release, thereby regulating blood glucose levels. PYY can regulate appetite and food intake and indirectly affect insulin sensitivity [34, 35]. In addition, the gut microbiota participates in regulating insulin secretion and blood glucose homeostasis through its interaction with the enteric and central nervous systems. For example, SCFAs can stimulate enteroendocrine cells to secrete hormones, activate vagal afferent fibres, and transmit signals to the brain, regulating insulin secretion [36].

The human body undergoes metabolic and endocrine changes during sleep [37]. A shortened sleep duration (<6 h/day) is linked to a 38% increased absolute risk of obesity, while an extended sleep duration (>9 h/day) shows an 8% absolute increase in the prevalence of obesity in comparison to normal sleep duration [38, 39]. Sleep deprivation can lead to a reduction in the intake of vegetables, fruits, and whole grains, which is associated with a higher risk of cardiovascular and metabolic disorders [40]. Shan et al. found a U-shaped relationship between sleep duration and the likelihood of developing type 2 diabetes mellitus, determining that an ideal sleep length duration of 7–8 h per day is associated with the lowest risk [41]. In this study, a similar U-shaped relationship was also observed between sleep duration and the TyG index, as well as IR. In this study, sleep durations for 6–9 h is associated with a downregulated TyG index, with 6.5 h identified as the optimal duration for reducing IR risk.

In addition, mediation analyses revealed that the relationship between dietary Med and Med-Hi LMC foods and TyG index was partially mediated by sleep duration in a fully adjusted model (2.95% and 6.08%, respectively). Whether directly or through dietary means, such as increasing the intake of live microbes, longer sleep durations were associated with potentially significant beneficial changes in the TyG index and IR. From a mechanistic perspective, the composition and function of the gut microbiota change following the intake of foods rich in live microbes. Notably, sleep duration and gut microbiota exhibit a bidirectional regulatory relationship. Information is transmitted, and interactions occur through the microbiota-gut-brain axis that modulate glycolipid metabolic responses and explain the underlying mechanisms. Sleep acts as a key modulator of the brain-gut axis through neuroactive compounds that influence metabolic homeostasis. The gut microbiota can produce various metabolites, such as SCFAs, that can reach the brain through the bloodstream, affect the synthesis and metabolism of neurotransmitters [42], and increase the expression of brain-derived neurotrophic factors, which are involved in regulating sleep-related neural circuits. At the same time, SCFAs can regulate the synthesis and release of serotonin [43]. Serotonin, as a key neurotransmitter, is directly involved in regulating the sleep-wake cycle, and changes in its levels are closely related to sleep duration and quality.

Strengths and limitations

This study has several strengths. First, this study leveraged data from the US NHANES, a nationally representative dataset with a robust sample size, ensuring high validity and generalizability of the findings. These, findings holds substantial public health significance, emphasizing the potential role of dietary live microbes in mitigating TyG-associated illnesses. Accordingly, individuals can be targeted to control live microbial intake and adjust sleep duration to prevent TyG-related diseases.

This study has some limitations. Considering the cross-sectional design, potential recall bias in the dietary data derived from the questionnaires could not be ruled out, limiting causal judgements and evaluations of initial discrepancies. Recall bias may have influenced the precision of the dietary intake estimates affecting the observed strength of associations. The results should be interpreted with caution since the actual associations could be stronger or weaker than those observed in this study. Future studies, should explore alternative data collection methods to minimize recall bias and enhance dietary assessment reliability. In clinical studies, food diaries or mobile applications should be considered for more real-time recording of dietary intake. Moreover, advanced sleep trackers, such as the Oura Ring 4 and Whoop 4.0, provide continuous and accurate sleep monitoring, offering an objective complement to self-reported sleep data [44].

Conclusion

This study demonstrated that higher dietary intake of live microbes and adequate sleep duration are associated with lower TyG index, offering potential strategies for preventing and managing chronic metabolic conditions related to elevated TyG index. The study explored a rational LMC dietary pattern and the optimum sleep duration and suggested interventions in individuals with unreasonable sleep duration and poor dietary patterns to control and reduce TyG index and IR. Utilising dietary and sleep interventions to regulate metabolic and IR response

is of profound significance. Lifestyle modification, including improved sleep and dietary patterns, are crucial in reducing the incidence of public health-related diseases, such as diabetes and coronary heart disease, linked to high TyG index. Future studies should investigate the impact factors such as sleep timing, exercise, stress, and emotional states on TyG index and IR. Furthermore, the abundance and diversity of microorganisms in the diets of the Med and Med-Hi groups necessitate further research to identify specific microbial targets that may contribute to reduction in TyG index and IR. Variations in microbial population composition, genetics, and broader dietary environments may influence the outcomes of these interactions and should be considered in future investigations.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12944-025-02507-8.

Supplementary Table 1

Supplementary Table 2

Supplementary Table 3

Supplementary Table 4

Supplementary Table 5

Supplementary Table 6

Acknowledgements

Figure 5 was produced by leveraging the CNSknowall platform (https://cnsknowall.com), a specialised web service dedicated to comprehensive data analysis and visualisation.

Author contributions

LP, JDL and WGY designed the research. LP prepared the manuscript. LP, YML analyzed and interpreted the data. YJD collected data. JNJ, GHC, YL, MFW reviewed and revised the manuscript. All contributors approved the completed 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 was approved by the Research Ethics Review Board of the National Centre for Health Statistics (NCHS). Informed consent was obtained from all participants involved in the NHANES.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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