Master of Public Health

Master de Santé Publique

<Associations of plant-based dietary patterns with gut microbiota profiles and metabolic health in Korean adults: a cross-sectional study>

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List of Acronyms

PDIs: Plant-based Diet Indices

PDI: Overall Plant-based Diet Index

hPDI: Healthy Plant-based Diet Index

uPDI: Unhealthy Plant-based Diet Index

HPFG: Healthy Plant Food Group

UPFG: Unhealthy Plant Food Group

AFP: Animal Food Group

CHO: Carbohydrates

FFQ: Food Frequency Questionnaire

GM: Gut Microbiota

B-type: *Bacteroides*-dominant enterotype

P-type: *Prevotella*-dominant enterotype

MetS: Metabolic Syndrome

TG: Triglyceride

HDL-C: HDL-cholesterol

WC: Waist Circumference

BMI: Body Mass Index

PA: Physical Activity

Abstract

Background: Plant-based diets are increasingly adopted worldwide, yet not all plant-based foods confer equal metabolic advantages. Plant-based diet indices (PDIs), including healthy PDI (hPDI) and unhealthy PDI (uPDI), differentiate plant-based food quality, but their relationships with gut microbiota and metabolic health remain unclear.

Objective: This study investigated associations between PDIs, gut microbial diversity, and metabolic markers in Korean adults, examining enterotype- and age-specific differences.

Methods: We analyzed data from 336 Korean adults aged 18-60 years across two cross-sectional studies (2018, 2021). Dietary intake was assessed using a 106-item semi-quantitative food frequency questionnaire. Gut microbiota data were obtained through 16S rRNA gene sequencing. Associations were analyzed using general linear regression models adjusted for confounding variables, with further stratified by enterotype and age.

Results: Higher PDI and hPDI scores were positively associated with gut microbial α-diversity (Chao1 and Shannon indices), while uPDI showed inverse associations. Higher α-diversity correlated with favorable metabolic markers, including lower glucose and triglyceride levels and higher HDL-cholesterol (HDL-C). Notably, uPDI was negatively associated with HDL-C levels (effect size = -0.35 ± 0.11 per unit increase, $p = 0.001$), mediated through alterations in bacterial genera including *Lactobacillus, Catenibacterium*. The uPDI-HDL-C relationship was particularly pronounced in participants under 40 years or *Bacteroides*-dominant enterotype, but not in older or *Prevotella*-dominant enterotype groups.

Conclusions: Plant-based food quality determines metabolic benefits through alterations in gut microbiota. Age-dependent and enterotype-specific responses highlight the potential for personalized nutrition approaches considering gut microbial profiles and demographic factors. These findings support refining current dietary guidelines to incorporate plant-based food quality and individual microbial, thereby enhancing their effectiveness in promoting health benefits.

Key words: Plant-based diets; Human gut microbiota; Metabolic health markers; Korean population; Plant food quality

Introduction

Plant-based diets, characterized by low or no consumption of animal foods such as meat, fish, eggs, and dairy products, are gaining increasing global popularity due to their potential health and environmental benefits. (1) Such diets provide a wide range of health benefits, particularly helping in the prevention and management of chronic diseases. (2) Numerous epidemiological studies and meta-analyses have shown that individuals adhering to plant-based diets such as vegetarians or vegans tend to have a lower risk of chronic diseases including coronary heart disease, cardiovascular disease, cancer, diabetes, and overall mortality. (3–5)

However, not all plant-based diets confer health benefits. A recent meta-analysis has highlighted that the food choices and the quality of plant-based food groups are as important as their quantities in the context of a healthy dietary pattern. (6) Therefore, to better capture variations in the quality of plant-based foods, plant-based dietary indices (PDIs), including overall plant-based dietary index (PDI), healthy PDI (hPDI), and unhealthy PDI (uPDI), have been developed. (7) These indices differentiate between healthy plant foods (e.g., whole grains, vegetables, legumes) and less healthy ones (e.g., refined grains, sugary beverages), allowing for a more accurate evaluation of diet quality in relation to health outcomes. (8)

A recent study found that adherence to a healthy plant-based diet was significantly associated with a lower risk of metabolic syndrome (MetS), while an “unhealthy” plant-based diet was significantly associated with higher risks of obesity, hypertriglyceridemia, low high-density lipoprotein (HDL) cholesterol, and elevated fasting blood glucose. (9) In addition, higher adherence to unhealthy plant-based diets was associated with greater odds of dyslipidaemia, highlighting that simply increasing overall plant-based foods is not enough without considering their nutritional components. (10) Moreover, a study among UK adults found that the hPDI was associated with lower risks of myocardial infarction and ischemic stroke, while uPDI scores were associated with higher risks of mortality, cardiovascular disease, and cancer. (1)

Beyond dietary intake alone, emerging evidence shows that the gut microbiota plays an important role in linking diet and health. Diet is a key factor modulating gut microbial diversity and composition, which in turn may exert either beneficial or harmful effects on metabolic health. (11) For example, a previous study among UK, US, and Italian populations found that red meat intake strongly influenced omnivore-associated microbiomes, with signature microbes such as *Bilophila wadsworthia*, and *Alistipes putredinis* being negatively correlated with cardiometabolic markers, such as BMI, blood pressure, and lipoproteins. In contrast, vegan-associated microbes such as *Streptococcus thermophilus, Lachnospiraceae,*

Butyricicoccus, were linked to more favorable cardiometabolic markers and were enriched even in omnivores who consumed more plant-based foods. (12) However, most research exploring diet–microbiota relationships has focused on Western or Mediterranean dietary patterns in European or North American populations. (13) Furthermore, despite growing interest in PDIs, studies examining their associations with gut microbiota diversity and composition remain limited, leaving an important gap in our understanding of how plant-based dietary patterns may influence the gut microbial ecosystem.

Moreover, limited data exist on these associations in Asian populations, including Koreans. Compared to the European or Western diets, Korean diets include a diverse array of plant-based foods, such as vegetables, legumes, and various grains, which may shape a distinct gut microbiome profile. Understanding these unique dietary patterns is crucial for evaluating diet–microbiota–health relationships in this context.

Therefore, this study aimed to investigate associations between plant-based dietary patterns using PDIs and gut microbial diversity and taxonomic composition, and to examine how these are related to metabolic health markers in a Korean adult population (as described in **Figure 1**).

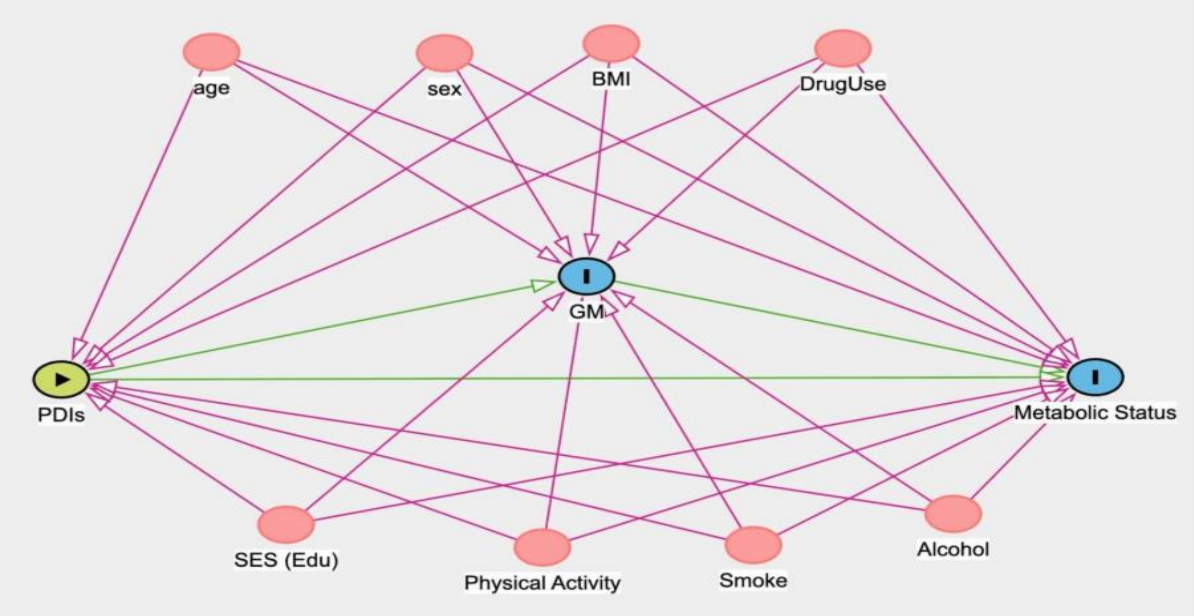


Figure 1. Directed Acyclic Graph (DAG) illustrating the study hypotheses and potential confounders in associations between plant-based dietary indices and metabolic health through alterations in gut microbiota. PDIs, Plant-based Dietary Indices; BMI, Body Mass Index; GM, Gut Microbiota; SES, Socio-Economic Status; Edu, Education level, representing SES.

Materials and Methods

Study population

This study integrated data from two cross-sectional studies carried out in 2018 (Study 1) and 2021 (Study 2) within an international collaborative study between the National Institute of Agricultural Sciences (NAS) and the International Agency for Research on Cancer (IARC-WHO). Details of the study have been previously described. (11,14) Participants aged 18 to 60 years were recruited from communities in Jeollabuk-do, Korea. Initially, Study 1 enrolled 222 individuals between March and October 2018 for a different project. Among them, 179 participants provided additional written informed consent for the extended use of their biospecimens for the diet-gut microbiota-metabolic health project, so only their data were included in the present analysis. Study 2 recruited 172 participants between January and October 2021 for the same project.

Study 1 recruited relatively healthy participants, excluding those who were underweight or obese (BMI <18.5 or ≥30 kg/m²), had taken antibiotics or hormone-related medications (e.g., oral contraceptives or hormone replacement therapy) within the previous two weeks, were pregnant or breastfeeding within the past six months, or had a history of metabolic disorders, inflammatory bowel disease, or cancer. Study 2, to broaden the metabolic profile of the study population, intentionally included a higher proportion of overweight or obese individuals with metabolic abnormalities. It applied the same exclusion criteria as Study 1, except that it included participants with obesity (BMI ≥30 kg/m²) or with metabolic abnormalities such as hyperglycemia and dyslipidemia, including those taking related medications.

All participants provided written informed consent. The study protocol was approved by the Public Institutional Review Boards of the Ministry of Health and Welfare, Korea (approval no. P01-202011-11-003) and by the IARC Ethics Committee (approval no. IEC 19-03-A1 and A2). The study was registered at the Clinical Research Information Service (CRIS) of the Centers for Disease Control and Prevention of Korea (registration no. KCT0005676).

Of the 351 eligible participants, we further excluded those with low-quality measures of metabolic markers (n=4), excessive energy intake (n=4) and missing gut taxonomic composition data (n=7), resulting in a final study population of 336 Korean adults (aged 18–60 years; 52% male; BMI 18.5–44.4 kg/m²) (**Figure 2**).

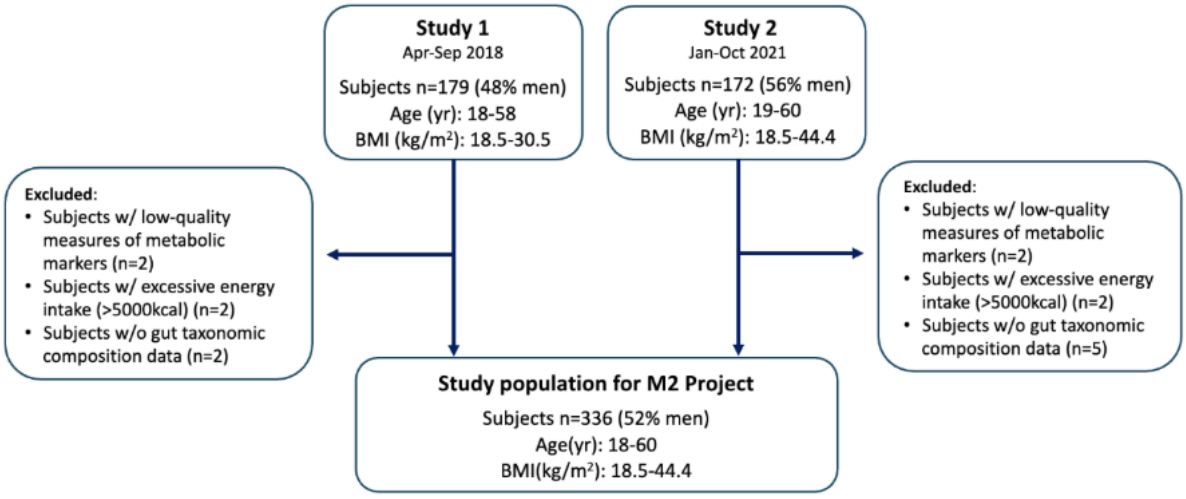


Figure 2. Flow chart of included study population

Dietary data collection

Dietary intake was assessed using a semi-quantitative, self-administered food frequency questionnaire (FFQ), specifically developed and validated for the Korean population by the Korea National Institute of Health. (15) Participants reported their average consumption of 106 food items and beverages over the past year, reporting both frequency and portion size.

Plant-based diet scores

To identify patterns of plant-based diets, the 106 food items were categorized into 19 food groups based on similarities in their nutrient composition. These 19 food groups were further classified into three broader categories: healthy plant foods (whole grains, fruits, vegetables, nuts, legumes, coffee and tea, and vegetable oils), unhealthy plant foods (refined grains, potatoes, fruit juices, sugar-sweetened beverages, sweets and desserts, and salty foods), and animal foods (animal fat, dairy, eggs, fish, meat, and miscellaneous animal-based foods) (**Annex Table 1**). (16) Intakes of food groups and macronutrients were calculated as grams per day (g/day) based on the consumption frequency and average portion size according to a food composition database established for the FFQ.

In constructing the PDIs, energy-adjusted daily intake of each food group was estimated using the residual method and ranked by sex-specific quintiles. For the PDI, all plant food groups—regardless of their healthfulness—were positively scored, with the highest quintile assigned a score of 5 and the lowest quintile a score of 1. For the hPDI, only healthy plant foods were positively scored, while unhealthy plant foods were reverse scored. In contrast, the uPDI assigned positive scores only to unhealthy plant foods, while healthy plant foods were reverse

scored. Animal food groups were reverse scored across all indices, with the highest quintile assigned a score of 1 and the lowest quintile a score of 5.

Gut microbial diversity and taxonomic composition

Stool samples from each participant were collected using stool nucleic acid collection tubes (Norgen Biotek Co., Thorold, Canada). All gut microbiome measurement and bioinformatics analysis, from bacterial DNA extraction to microbial data generation, were conducted by Macrogen Inc. (Seoul, Korea). Details of the methods have been previously described. (11,14) Briefly, DNA was extracted using the Powersoil DNA Isolation Kit (Cat. No. 12,888, MO BIO). The 16S rRNA gene, covering the V3-V4 regions, was sequenced on the MiSeq platform (Illumina, San Diego, CA, USA). Sequenced data were processed using QIIME2, with quality control and denoising performed using the DADA2 pipeline to generate the amplicon sequence variant (ASV) table. α-diversity was assessed to capture species richness and/or evenness within each individual sample, using two commonly used indices: Chao1 (species richness) (17,18) and Shannon (species richness and evenness) (19). β-diversity was assessed to evaluate differences in microbial composition between individuals, using weighted UniFrac, a widely used distance matrix (20). Based on weighted UniFrac, enterotypes, clusters of similar gut microbial profiles, were previously defined following established methods (14,21), using principal coordinate analysis (PCoA) and k-means clustering. In the study population, two dominant enterotypes were identified in our previous study (11) - *Bacteroides* (B-type, 62.8%) and *Prevotella* (P-type, 37.3%), which were used in the present study. Relative abundances of bacterial taxa at different taxonomic levels from phylum to genus were calculated as the percentage of ASVs. Taxonomic classification was conducted using the NCBI BLAST database.

Metabolic health marker measurements

Metabolic health markers were measured in plasma from at least 8-hour fasting blood samples at NAS in Korea, as described previously. (11) This study primarily focuses on markers related to MetS, including glucose, triglyceride (TG), high-density lipoprotein cholesterol (HDL-C), and waist circumference. Glucose and TG levels were measured using a colorimetric assay kit (Sigma-Aldrich, MI, USA). HDL-C was quantified from the HDL fraction after precipitating low-density lipoprotein (LDL) using an HDL and LDL/VLDL cholesterol assay kit (Cell Biolabs Inc., CA, USA). Waist circumference was measured by trained staff following a standardized protocol. Additional metabolic health and inflammatory markers, including insulin, homeostatic model assessment of insulin resistance (HOMA-IR), total cholesterol, and C-reactive protein (CRP), were considered in further analyses. Insulin and CRP levels were measured using an immunoassay kit (R&D Systems, MN, USA) and an immunometric assay kit (Cayman

Chemicals, MI, USA), respectively. Total cholesterol was estimated from the HDL-C and LDL-C fractions. HOMA-IR was estimated from glucose and insulin levels [glucose (mmol/L) X insulin (μU/mL) / 22.5]. All plasma marker levels were measured using a microplate reader (Molecular Devices Inc., CA, USA).

Statistical analysis

Data were expressed as frequencies and percentages for categorical variables and means ± standard deviations (SD) for continuous variables. Linear associations between PDI scores and food group intakes (healthy plant-based food groups, HPFG; unhealthy plant-based food groups, UPFG; animal food groups, AFG), gut microbial diversity and taxonomic composition, and metabolic markers were used using generalized linear regression models - unadjusted (Model 1) and adjusted (Model 2) for age (years), sex (male/female), BMI (kg/m^2), drug use (yes/no), regular physical activity (yes/no), alcohol drink (never/former/current), smoke status (never/former/current), education level (low/middle/high/missing), and study (1&2) variables. Effect sizes were estimated per 1-unit increase in PDI scores or per 1-SD increase in gut microbial and metabolic marker variables. Differences in α-diversity distribution across PDI tertiles were assessed using the Kruskal-Wallis test. Prior to the test, α-diversity indices (Chao1 and Shannon) were log-transformed to reduce skewness and improve interpretability in boxplots. Stratified analyses by age groups (age < 40 vs. ≥ 40 years) and enterotypes (B-type vs. P-type) were conducted due to distinct distributions of α-diversity by age (**Annex figure 1**). Interactions between PDIs and age were examined using ANOVA tests comparing models with and without interaction terms to assess age as a potential effect modifier.

Prior to analyses of gut microbial taxonomic composition, relative abundances at the phylum and genus levels were transformed using centered log-ratio (clr) after handling zero/missing values – removing taxa with > 80% zeros/unobserved values and imputing using a Bayesian-multiplicative replacement approach. Multiple comparisons were corrected using the false discovery rate (FDR, q-value <0.05).

All statistical analyses were conducted using R statistical software (version 4.3.1).

Results

Population characteristics

The basic characteristics of study participants across tertiles of PDI, hPDI, and uPDI (tertile 1 vs. 3) are presented in **Table 1**. Individuals in tertile 3 of PDI and hPDI were more likely to be older and more physically active, compared to those in tertile 1. They were also more likely to be never-smokers, have lower education levels, and be never or former alcohol consumers. In contrast, participants in tertile 3 of uPDI tended to be younger, less physically active, and former/current alcohol drinkers. Smoking status did not differ significantly across uPDI tertiles. No significant differences in BMI were observed across any of the diet indices.

When examining dietary intake across PDI tertiles, total energy intake was higher among participants in tertile 3 of hPDI and uPDI, but lower in tertile 3 of PDI. Regarding macronutrient intake, participants in tertile 3 of PDI and hPDI had higher intakes of carbohydrates and dietary fiber, and lower intakes of protein and fat (as a percentage of total energy). uPDI showed a similar trend, except for dietary fiber, which was lower in tertile 3.

Table 1. Basic characteristics of the study population by tertiles (tertile 1 vs. 3) of plant-based diet indices

	PDI				hPDI				uPDI			
	Tertile 1		Tertile 3		Tertile 1		Tertile 3		Tertile 1		Tertile 3	
Subjects (n)	n=115		n=101		n=113		n=98		n=124		n=107	
Score range	36-54		61-77		43-54		60-75		33-54		61-76	
Age (yr)	30.7	10.5	39.2	12.9	29.7	10.1	37.5	13.1	35	12.1	32.2	11.3
Male (n, %)	63	54.8	57	56.4	61	54.0	55	56.1	62	50.0	58	54.2
BMI (kg/m^2)	24.5	4.6	24.7	3.2	23.9	3.9	25	4.2	24.4	4.1	24.2	3.8
Drug use (n, %)												
Yes	5	4.3	11	10.9	2	1.8	10	10.2	8	6.5	7	6.5
No	110	95.7	90	89.1	111	98.2	88	89.8	116	93.5	100	93.5
Regular PA (n, %)												
Yes	56	47.0	61	60.4	53	45.3	65	66.3	73	57.9	50	45.0
No	64	53.0	40	39.6	64	54.7	33	33.7	53	42.1	61	55.0
Smoking (n, %)												
Never	85	70.8	74	73.3	84	71.8	73	74.5	87	69.0	77	69.4
Former	18	15.0	15	14.9	8	6.8	17	17.3	24	19.0	10	9.0
Current	17	14.2	12	11.9	25	21.4	8	8.2	15	11.9	24	21.6
Education (n, %)												
Low	9	7.5	18	17.8	7	6.0	17	17.3	17	13.5	8	7.2
Middle	46	38.3	25	24.8	48	41.0	27	27.3	35	27.8	44	39.6
High	57	47.5	52	51.5	54	46.2	45	45.9	67	53.2	51	45.9
Missing	8	6.7	6	5.9	8	6.8	9	9.2	7	5.6	8	7.2
Alcohol drink (n, %)												
Never	14	11.7	19	18.8	14	12.0	14	14.3	23	18.3	16	14.4
Former	6	5.0	11	10.9	8	6.8	13	13.3	12	9.5	13	11.7
Current	100	83.3	71	70.3	95	81.2	71	72.4	91	72.2	82	73.9

Energy (kcal/day)	1988	778	1662	689	1748	737	1984	754	1706	771	1932	654
CHO (%)	60.4	8.3	67.2	6.9	61.9	6.7	65.3	8.6	59.8	8.4	67.7	6.6
Protein (%)	15.8	3.1	14.4	2.2	15.4	2.1	14.6	3.1	16.5	2.8	13.3	2.0
Fat (%)	23.8	5.9	18.4	5.2	22.7	5.2	20.1	6.2	23.6	6.3	19.0	5.3
Dietary fiber (g/1000kcal)	8.4	2.3	11.1	3.0	8.8	2.4	10.5	3.1	10.6	2.9	8.3	2.3

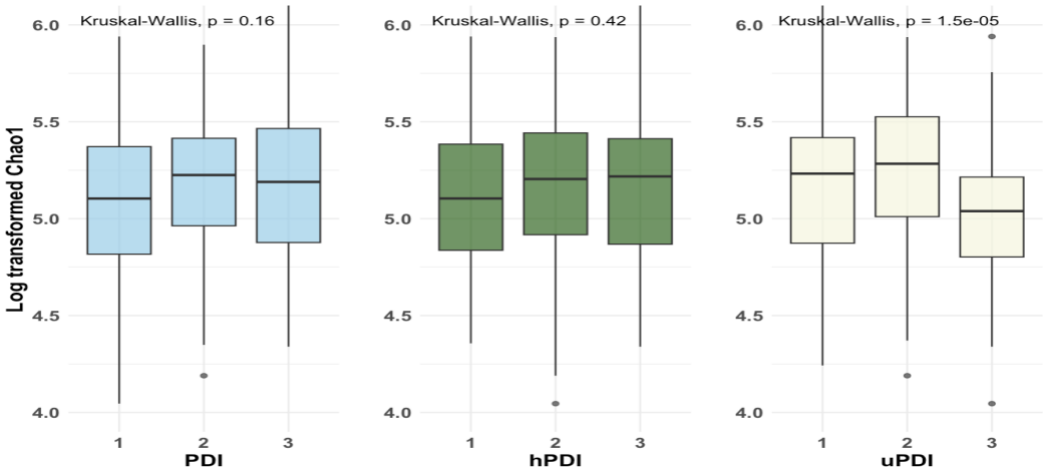
PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index; BMI, Body Mass Index; PA, Physical Activity; CHO, Carbohydrates

Data are presented as mean and standard deviation (SD) for continuous variables and as frequency (n) and percentage (%) for categorical variables.

Associations between plant-based dietary indices, gut microbial diversity and metabolic markers

Distributions of gut microbial α-diversity using two indices, Chao 1 and Shannon, across the PDIs tertiles are presented in **Figure 3**. PDI scores were significantly associated with greater α-diversity according to the Shannon index, but not the Chao1 index. In contrast, uPDI was significantly associated with lower α-diversity in both indices. No significant associations were observed between hPDI and gut microbial α-diversity.

a. Chao1



b. Shannon

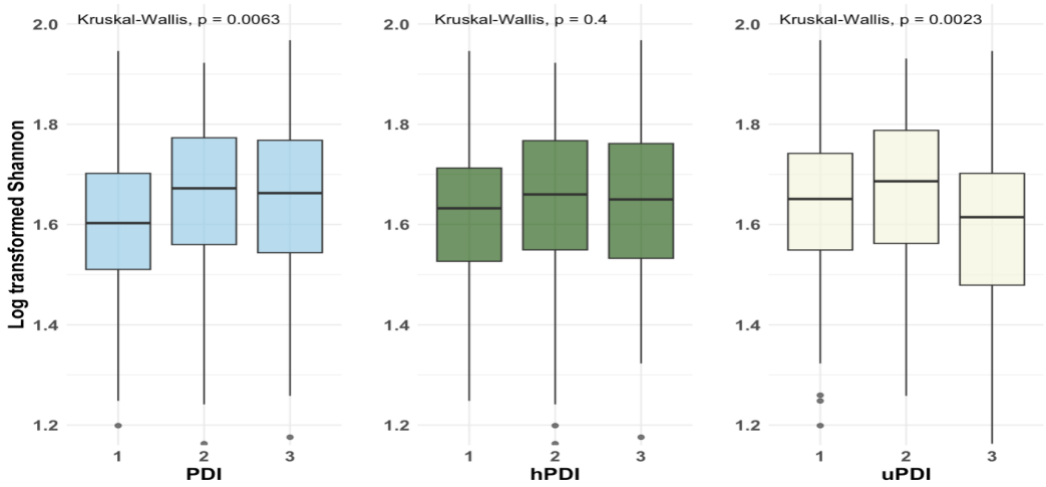


Figure 3. Distribution of gut microbial α-diversity (a. Chao1 and b. Shannon indices) across tertiles of plant-based dietary indices. PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index; Box plots represent the distribution of α-diversity with boxes for Interquartile ranges and center lines for medians, stratified by tertiles of each PDI, hPDI, and uPDI. Kruskal-Wallis tests were used to examine differences in distributions across tertiles. Both Chao1 and Shannon indices were log-transformed prior to the test.

We further investigated the associations between gut microbial α-diversity and metabolic markers (**Table 2**). Higher Chao1 and Shannon indices were inversely associated with glucose levels in the crude models (Chao1 effect size= – 3.20±1.39 for 1SD increase, p=0.021; Shannon effect size = – 5.46±1.37 for 1SD increase, p<0.001). The association remained significant only with the Chao1 index after adjusting for potential confounders (Chao1 effect size=– 3.05±1.25 for 1SD increase, p=0.015). In addition, we found that the Shannon index was inversely associated with TG levels in the adjusted model (Shannon effect size= – 11.71±5.37 for 1SD increase; p=0.030), and positively associated with HDL cholesterol levels in the crude model (Shannon effect size = 4.16±0.95 for 1SD increase, p<0001), but the significance didn't remain after adjustment. However, no significant associations were observed between gut microbial α-diversity indices and waist circumferences.

Table 2. Associations between gut microbial α-diversity (Chao1 and Shannon indices) and metabolic markers

	β_{raw}	SE_{raw}	*P*-value	β_{adj}	SE_{adj}	*P*-value
Chao 1						
Glucose (mg/dL)	-3.20	1.39	0.021	-3.05	1.25	0.015
Triglycerides (mg/dL)	-4.41	5.36	0.412	-7.56	5.16	0.143
HDL cholesterol (mg/dL)	1.08	0.97	0.268	0.40	0.82	0.629
Waist circumference (cm)	-0.49	0.59	0.407	-0.182	0.26	0.482
Shannon						
Glucose (mg/dL)	-5.46	1.37	<0.001	-1.50	1.32	0.255

Triglycerides (mg/dL)	-2.44	5.36	0.649	-11.71	5.37	0.030
HDL cholesterol (mg/dL)	4.16	0.95	<0.001	1.51	0.85	0.078
Waist circumference (cm)	0.26	0.59	0.657	-0.13	0.27	0.626

General linear regressions (GLM) models were used without adjustment (-raw) and with adjustment (-adj) for age (years), sex (male/female), BMI (kg/m2), drug use (yes/no), regular physical activity (yes/no), alcohol drink (never/former/current), smoke status (never/former/current), education level (low/middle/high/missing), and study (1 & 2) variables. B-coefficients were estimated per 1 SD increase in each index.

Additionally, we examined associations between PDIs and metabolic markers (**Table 3**). For uPDI, higher adherence was significantly associated with lower HDL cholesterol levels after adjustment for potential confounders such as age, sex, BMI, drug use, physical activity, alcohol drink, smoke status, education level, study (uPDI effect size= – 0.35±0.11 for 1 unit increase, p=0.001), suggesting a potential adverse metabolic impact of uPDI. PDI and hPDI showed significant associations with some metabolic markers, such as TG or waist circumference, in crude model, but they did not remain significant after adjustment for potential confounders.

Table 3. Associations between plant-based dietary indices and metabolic markers

	β_{raw}	SE_{raw}	*P*-value	β_{adj}	SE_{adj}	*P*-value
PDI						
Glucose (mg/dL)	-0.32	0.21	0.130	-0.30	0.19	0.109
Triglycerides(mg/dL)	1.65	0.80	0.038	0.73	0.78	0.346
HDL cholesterol (mg/dL)	-0.04	0.15	0.783	-0.05	0.12	0.691
Waist circumference (cm)	0.16	0.09	0.060	0.07	0.04	0.066
hPDI						
Glucose (mg/dL)	0.01	0.24	0.974	-0.15	0.22	0.493
Triglycerides(mg/dL)	1.01	0.92	0.270	0.18	0.89	0.841
HDL cholesterol (mg/dL)	-0.17	0.17	0.311	-0.03	0.14	0.830
Waist circumference (cm)	0.21	0.10	0.036	0.05	0.04	0.303
uPDI						
Glucose (mg/dL)	0.13	0.19	0.513	0.08	0.17	0.656
Triglycerides(mg/dL)	0.43	0.75	0.565	0.70	0.69	0.311
HDL cholesterol (mg/dL)	-0.31	0.14	0.022	-0.35	0.11	0.001
Waist circumference (cm)	-0.07	0.08	0.362	0.04	0.03	0.210

PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index; General linear regressions (GLM) models were used without adjustment (-raw) and with adjustment (-adj) for age (years), sex (male/female), BMI (kg/m^2), drug use (yes/no), regular physical activity (yes/no), alcohol drink (never/former/current), smoke status (never/former/current), education level (low/middle/high/missing), and study (1 & 2) variables. B-coefficients were estimated per 1-unit increase in each index.

We further examined the associations by age groups (**Table 4**). The association between uPDI and HDL cholesterol was more pronounced in the younger age group (< 40 years) (uPDI effect size = – 0.42±0.12 for 1-unit increase; p=0.001), but not significant in the older age group (≥

40 years). However, all *P*-values for interaction exceeded 0.05, indicating no statistically significant effect modification by age.

Table 4. Associations between plant-based dietary indices and HDL cholesterol levels, stratified by age

	β_{raw}	SE_{raw}	*P*-value	β_{adj}	SE_{adj}	*P*-value	*P*-interaction
PDI							
Age (yr)							0.614
< 40	-0.04	0.19	0.821	-0.10	0.14	0.471	
≥ 40	0.17	0.27	0.533	0.09	0.24	0.714	
hPDI							
Age (yr)							0.471
< 40	-0.16	0.21	0.464	-0.01	0.17	0.964	
≥ 40	-0.29	0.28	0.304	-0.09	0.26	0.717	
uPDI							
Age (yr)							0.612
< 40	-0.46	0.16	0.004	-0.42	0.12	0.001	
≥ 40	0.02	0.25	0.926	-0.16	0.22	0.455	

PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index. General linear regressions (GLM) models were used without adjustment (-raw) and with adjustment (-adj) for age (years), sex (male/female), BMI (kg/m^2), drug use (yes/no), regular physical activity (yes/no), alcohol drink (never/former/current), smoke status (never/former/current), education level (low/middle/high/missing), study (1 & 2) variables. B-coefficients were estimated per 1-unit increase in each index. Significances of interactions between PDIs and age were examined using ANOVA tests comparing models with and without interaction terms for a potential effect modifier.

We subsequently explored associations between PDI, hPDI, uPDI and metabolic markers, stratified by enterotypes (**Table 5**). For hPDI, higher scores were inversely associated with glucose levels after adjustment for potential confounders in B-type group (hPDI effect size=− 0.70±0.33 for 1 unit increase, p=0.035). Additionally, positive associations were found between hPDI and TG in adjusted models in the B-type group (hPDI effect size= 3.13±1.47 for 1 unit increase, p=0.034). These associations were not observed in the P-type group. For uPDI, higher scores were significantly associated with lower levels of HDL cholesterol in the B-type group after adjusting for potential confounders (uPDI effect size= − 0.37±0.14 for 1 unit increase, p=0.009). Although a similar trend was observed in the P-type group, the association did not reach statistical significance.

Associations between plant-based diet indices, gut microbial taxa composition and metabolic markers

We examined associations of PDIs (PDI, hPDI, uPDI) and food intake groups (HPFG, UPFG, AFG) with gut microbial composition (phylum to genus levels), then with metabolic markers (**Figures 4 & 5**). At the phylum level, after pre-processing including zero-value handling and

imputation as described in the Method section, seven out of 19 bacterial phyla, including *Actinobacteria*, *Bacteroidetes*, *Firmicutes, Fusobacteria, Lentisphaerae, Proteobacteria,* and *Verrucomicrobia,* were included in the analysis. In the total subjects (**Fig. 4a**), PDI, hPDI, and HPFG were positively associated with the relative abundance of *Firmicutes* (effect sizes = 0.05±0.02, 0.06±0.02, 0.06±0.02 for 1SD increase, respectively, all $p<0.05$). However, no significant associations were observed between the *Firmicutes* phylum and metabolic markers. Additionally, PDI was negatively associated with the relative abundances of *Fusobacteria* and *Proteobacteria* (effect sizes = − 0.22±0.10 and − 0.10±0.05 for 1SD increase, both $p<0.05$), while only *Fusobacteria* was positively associated with fasting glucose (effect size=0.07±0.03 for 1SD increase, $p=0.035$). No significant association of PDIs and food group intakes with *Bacteroidetes* was observed, but the relative abundance of this phylum was inversely associated with fasting glucose (effect size=− 0.22±0.11 for 1SD increase, $p=0.034$).

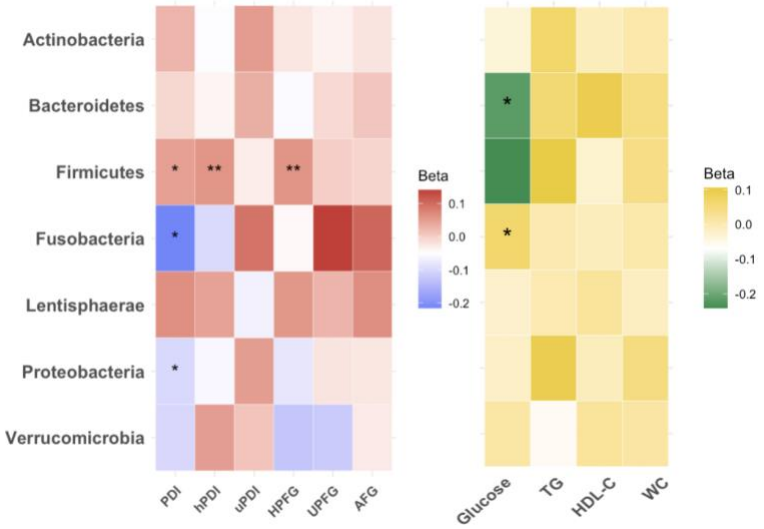
Table 5. Associations between plant-based diet indices and metabolic markers, stratified by gut microbial enterotypes

	Total (n=336)											
	B-type (n= 211)						P-type (n=125)					
	β_{raw}	SE_{raw}	*P*-value	β_{adj}	SE_{adj}	*P*-value	β_{raw}	SE_{raw}	*P*-value	β_{adj}	SE_{adj}	*P*-value
PDI												
Glucose (mg/dL)	-0.40	0.28	0.161	-0.29	0.25	0.243	-0.23	0.31	0.459	-0.33	0.30	0.268
Triglycerides(mg/dL)	2.00	1.09	0.068	1.30	1.11	0.245	1.16	1.18	0.329	0.28	1.13	0.806
HDL cholesterol (mg/dL)	0.02	0.20	0.899	0.06	0.16	0.696	-0.10	0.22	0.650	-0.21	0.19	0.286
Waist circumference (cm)	0.13	0.12	0.284	0.05	0.05	0.357	0.21	0.13	0.108	0.11	0.06	0.070
hPDI												
Glucose (mg/dL)	-0.54	0.37	0.151	-0.70	0.33	0.035	0.39	0.31	0.214	0.25	0.30	0.403
Triglycerides(mg/dL)	3.65	1.42	0.011	3.13	1.47	0.034	-0.92	1.19	0.441	-1.39	1.13	0.221
HDL cholesterol (mg/dL)	-0.39	0.26	0.129	-0.12	0.22	0.582	0.00	0.22	0.988	-0.03	0.19	0.895
Waist circumference (cm)	0.28	0.16	0.080	0.02	0.07	0.733	0.16	0.13	0.212	0.07	0.06	0.267
uPDI												
Glucose (mg/dL)	0.30	0.27	0.260	0.00	0.22	0.999	-0.07	0.29	0.799	0.10	0.26	0.690
Triglycerides(mg/dL)	-0.28	1.03	0.790	0.23	1.00	0.815	1.29	1.09	0.237	1.03	0.99	0.301
HDL cholesterol (mg/dL)	-0.39	0.18	0.036	-0.37	0.14	0.009	-0.23	0.20	0.259	-0.29	0.17	0.085
Waist circumference (cm)	-0.15	0.11	0.193	0.1	0.05	0.894	0.01	0.12	0.914	0.08	0.05	0.125

PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index
Enterotype B-type refers to the Bacteroides-dominant group and Enterotype P-type refers to Prevotella-dominant group.
General linear regressions (GLM) models were used without adjustment (-raw) and with adjustment (-adj) for age (years), sex (male/female), BMI (kg/m^2), drug use (yes/no), regular physical activity (yes/no), alcohol drink (never/former/current), smoke status (never/former/current), education level (low/middle/high/missing), and study (1 & 2) variables.
B-coefficients were estimated per 1-unit increase in each index.

Interestingly, these associations among the total subjects differed by enterotypes (**Fig. 4b**). The positive associations of PDI, hPDI, and HPFG with *Firmicutes* and the inverse association of PDI with *Fusobacteria*, observed in the total subjects, were retained only in the B-type group. Conversely, among those in the P-type group, only HPFG was inversely associated with *Actinobacteria* (effect size= − 0.33±0.14 for 1 SD increase, p=0.017) and *Verrucomicrobia* (effect size= − 0.36±0.18 for 1 SD increase, p=0.042). Regarding metabolic markers, the inverse association between *Bacteroidetes* and glucose remained significant only in the B-type group (effect size= − 0.29±0.12 for 1 SD increase, p=0.015), while the positive association between *Fusobacteria* and glucose persisted only in the P-type group (effect size=0.13±0.07 for 1 SD increase, p=0.049).

a. Total subjects



b. Subjects stratified by gut microbial enterotypes

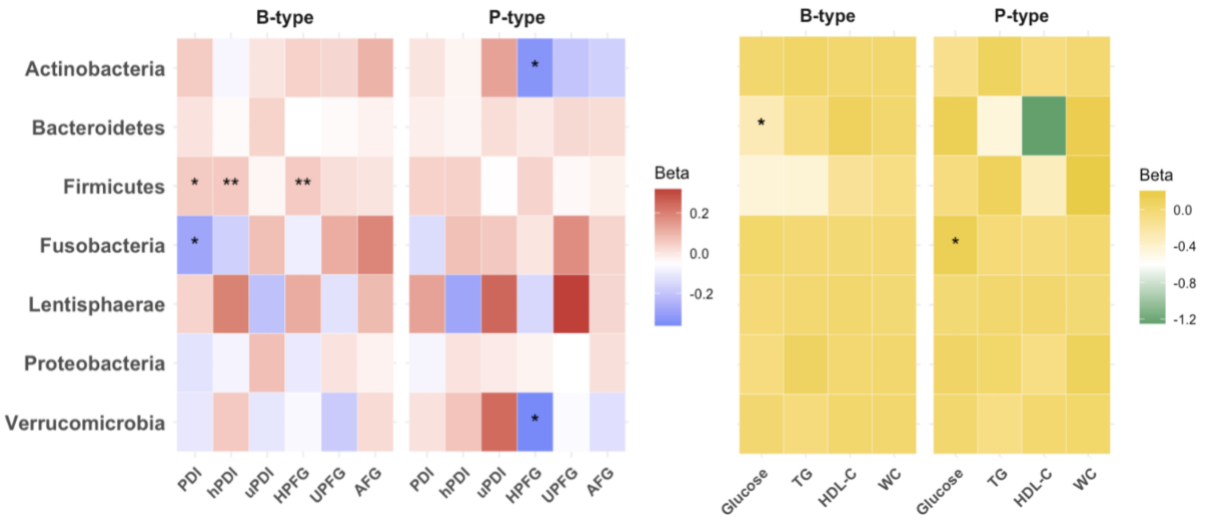


Figure 4. Associations between gut microbial phyla and plant-based diet indices, food groups and metabolic markers in total subjects (a) and subjects stratified by enterotypes (b) PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index; HPFG, Healthy Plant Food Group; UPFG, unhealthy Plant Food Group; AFG, Animal Food Group; TG, Triglycerides; HDL-C, HDL cholesterol; WC, Waist circumference; Enterotype B-type refers to the Bacteroides-dominant group and Enterotype P-type refers to Prevotella-dominant group; Heatmaps are based on β-coefficients per 1SD increase in each variable derived from linear regression models adjusted for age, sex, BMI, study, drug use, physical activity, smoke status, alcohol drink and education level. Results are shown for seven dominant phyla. Statistical significance is indicated as follows: p<0.05(*), < 0.01(**).

Among the seven phyla analyzed (Figure 4), only genera belonging to the six phyla, except for *Lentisphaerae*, showed significant associations with PDIs, food groups (HPFG, UPFG, AFG), or metabolic markers were included in further analysis. After pre-processing the genus-level data, including zero-value handling and imputation as described in the Method section, only 102 out of 504 genera were retained: *Actinobacteria* (n = 3), *Bacteroidetes* (n = 11), *Firmicutes* (n = 79), *Fusobacteria* (n = 1), *Verrucomicrobia* (n = 1), and *Proteobacteria* (n = 7) (**Figure 5**).

When examining genera linked to the uPDI-HDL-C association observed in the total subjects (**Fig. 5a**), within *Firmicutes*, uPDI was inversely associated with *Lactobacillus* and *Catenibacterium*. *Lactobacillus* was positively, while *Catenibacterium* was negatively, associated with HDL-C. In addition, UPFG was inversely associated with *Flintibacter,* which in turn was positively associated with HDL-C, further supporting the observed uPDI-HDL-C association.

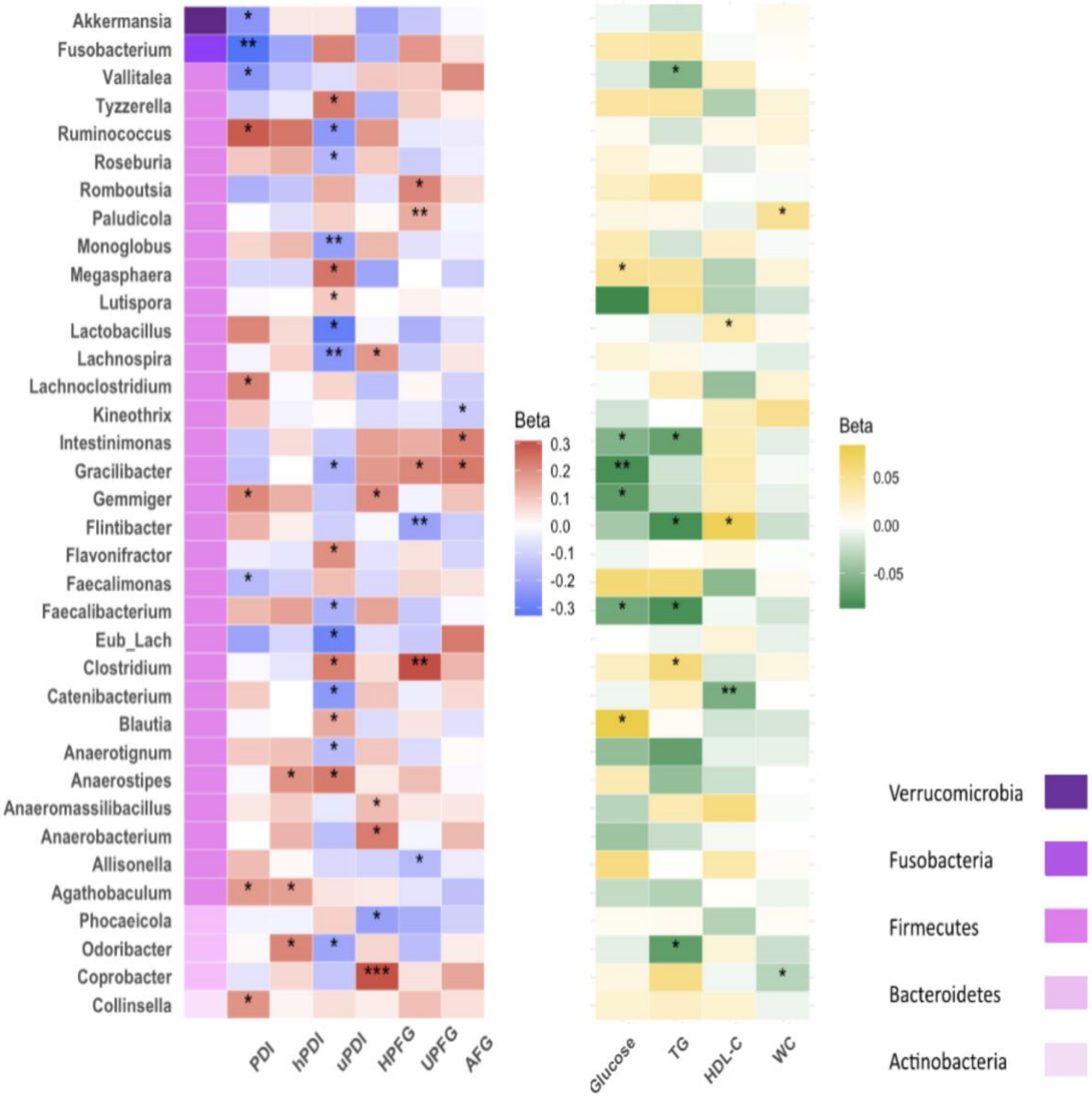
When stratified by enterotypes, significant differences were observed in the associations (**Fig. 5b**). Among the genera linked to the uPDI-HDL-C association in total subjects, *Catenibacterium* remained significant only in the P-type, where it was positively associated with TG as well as negatively associated with HDL-C. In contrast, the UPFG-*Flintibacter*

association was significant only in the B-type group. However, it was linked to TG negatively rather than HDL-C.

Notably, HPFG displayed a strong positive association with *Coprobacter*, even after FDR, which, in turn, was inversely associated with waist circumference. These associations differed by enterotypes, persisting remained only in the B-type group but was no longer significant after FDR correction. Within metabolic markers, *Coprobacter* was inversely associated with waist circumferences in the P-type group, despite its significant associations with food groups, HPFG and AFG were observed in the B-type group.

In the B-type group, the PDI and *Fusobacterium* association observed in the total subjects remained significant, with hPDI and uPDI also showing inverse association with *Fusobacterium,* which were positively associated with TG. In the P-type groups, *Pseudescherichia* was inversely associated with uPDI in the B-type, which showed strong associations with TG while significant retained after FDR correction. Among Firmicutes genera, *Paludicola* showed similar trends to those in the total subjects, which showed positive association with waist circumference. The inverse association between UPFG and *Allisonella* in total subjects was retained in the B-type group, showing positive association with glucose.

a. Total subjects



b. Subjects by gut microbial enterotypes

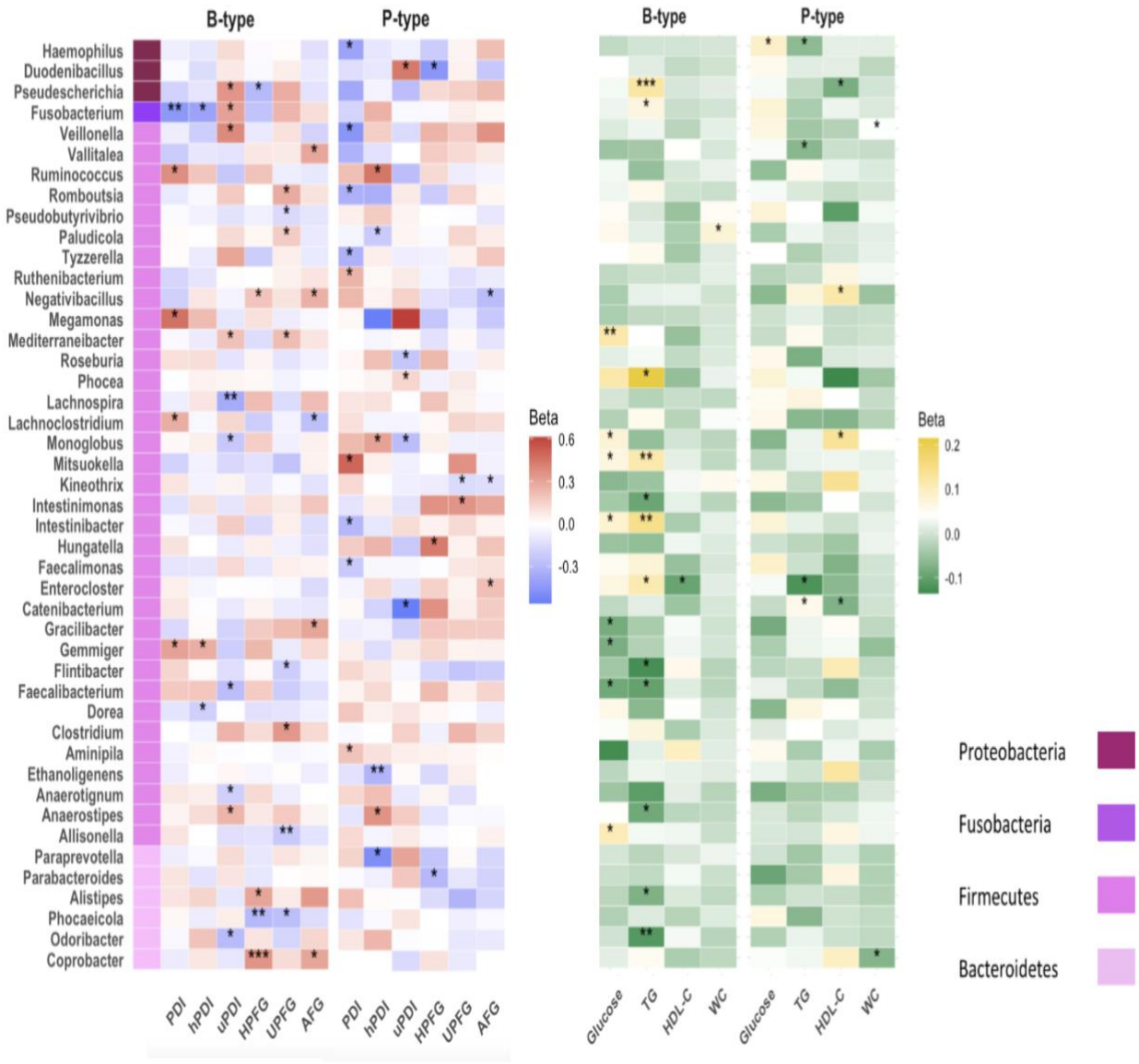


Figure 5. Associations between gut microbial genera and plant-based diet indices, food groups and metabolic markers in total subjects (a) and subjects stratified by enterotypes (b) PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index; HPFG, Healthy Plant Food Group; UPFG, Unhealthy Plant Food Group; AFG, Animal Food Group; TG, Triglycerides; HDL-C, HDL cholesterol; WC, Waist circumference; Enterotype B-type refers to the Bacteroides-dominant group and Enterotype P-type refers to Prevotella-dominant group; Heatmaps are based on β-coefficients per 1SD increase in each variable derived from linear regression models adjusted for age, sex, BMI, study, drug use, physical activity, smoke status, alcohol drink and education level. Results are shown for genera within the five phyla with significant associations in Figure 4. Statistical significance is indicated as follows: p<0.05(*), < 0.01(**). After multiple comparison correction using the false discovery rate (FDR), HPFG-Coprobacter (in total subjects) and Pseudescherichia-TG (in B-type) associations remained significant (q-value <0.05)

Discussion

In this study, we found that plant-based dietary patterns showed differential associations with gut microbial α-diversity and metabolic markers. While higher PDI scores were associated with greater α-diversity, uPDI showed the opposite pattern, with higher scores associated with significantly lower microbial diversity. Higher α-diversity was associated with more favorable metabolic markers, including lower glucose and TG levels and higher HDL-C. Notably, uPDI was inversely associated with HDL-C, with differences emerging across age groups and enterotypes. At the bacterial taxa level, uPDI showed negative associations with the *Lactobacillus* and *Catenibacterium* genera, which were also related to HDL-C, exhibiting differing patterns by enterotype.

Previous studies have examined the associations between plant-based dietary patterns and metabolic health. One study with a Korean population aged ≥ 19 years (n=14 450) (16) found that greater adherence to uPDI was associated with greater odds of MetS, particularly hypertriglyceridemia in men and abdominal obesity, high fasting glucose, and hypertriglyceridemia in women, highlighting the importance of quality of plant foods in Korean adults. Similarly, recent findings with 500,000 UK participants aged 40 and 69 years highlighted that while greater hPDI was associated with lower levels of insulin, TG, and higher levels of HDL-C, uPDI, characterized by processed foods, sugary beverages, and refined grains, was associated with higher levels of insulin, HOMA-IR, CRP and lower levels of HDL-C. (22) In line with previous evidence, the current study found that uPDI was significantly associated with decreased levels of HDL-C, reinforcing the critical distinction between different plant-based dietary patterns in their metabolic effects.

Our findings provide mechanistic insights into how uPDI affects HDL-C through alterations in gut microbiota. The inverse association between uPDI and microbial diversity observed in our study aligns with the "diversity hypothesis" of gut health, which posits that a more diverse microbiome enhances metabolic flexibility and beneficial health effects. (23) Plant-based diets rich in fruits, vegetables, whole grains, and legumes supply diverse prebiotic substrates that promote the growth of different bacterial species, including short-chain fatty acid (SCFA)-producing bacteria, such as *Bifidobacterium adolescentis*, *Ruminococcus bromii*, *Eubacterium rectale*, and *Parabacteroides distasoniseach*. (24,25) SCFAs, such as butyrate, propionate, and acetate, play crucial roles in lipid metabolism and HDL-C regulation. Our findings align with this. PDI was positively associated with *Ruminococcus,* whereas uPDI showed negative associations with both *Ruminococcus* and *Latobacillus*. This suggests that the quality of plant-based foods may differentially shape SCFA-producing bacterial populations. Moreover, a diverse microbiota can produce a broader spectrum of metabolites that collectively contribute

to improved metabolic health, whereas reduced diversity may limit these beneficial metabolic outcomes. (26)

Previous studies have shown that processed plant foods - characterized by reduced fiber complexity and high added sugar content - may decrease microbial diversity and the abundance of beneficial bacteria such as *Ruminococcus, Lactobacillus,* and *Faecalibacterium*. (27,28) Our findings are consistent with these observations. The genus-level analysis revealed that uPDI was negatively associated with *Lactobacillus*, which in turn was positively associated with HDL-C. The positive link between *Lactobacillus* and HDL-C supports previous evidence suggesting its role in bile acid metabolism. For instance, a randomized controlled trial of *Lactobacillus acidophilus* together with *Bifidobacterium bifidum* in hypercholesterolemic patients (29) demonstrated significant improvements in HDL-C levels after a six-week intervention, proposing an underlying mechanism that *Lactobacillus* and other probiotics produce bile salt hydrolase (BSH), which deconjugates bile salts, leading to increased cholesterol excretion via BSH activity and improved cholesterol homeostasis. (30) These results suggest that poor-quality plant-based diets may affect HDL-C levels not only through reduced microbial diversity but also by altering specific beneficial bacterial taxa that directly influence lipid metabolism.

Additionally, we newly identified a potential link of the *Catenibacterium* and *Flintibacter* genera to the uPDI/UPFG and HDL-C association. Yet, to date, relationships of these genera with diet and the host metabolic health have not yet been elucidated in human studies. However, a study among 53 obese women (31) exploring gut microbiota features related metabolic markers suggested that *Catenibacterium mitsuokai* may be involved in lipid metabolism, showing significant positive correlations with total cholesterol and LDL-C, rather than HDL-C. This suggests it might play a role in the lipid profile regulation, though the exact mechanisms is not yet understood. An in vitro study also reported a significant change in the relative abundance of *Flintibacter* in dietary fat-fed mouse models (32), although its role in host metabolism remains largely unknown. Further research is needed to determine its exact functions and how it may influence metabolic health.

One of the most striking findings of our study was the age- and enterotype-dependent effect of uPDI on HDL-C levels. Higher uPDI were significantly associated with lower HDL-C levels in the overall population, with this association remaining significant among participants under 40 years of age and in B-type enterotype, but not among those aged ≥40 years or in the P-type group. This age-stratified pattern suggests that younger adults may be more vulnerable to the adverse metabolic effects of poor-quality plant foods. First, younger adults may have

more malleable metabolic programming that is sensitive to dietary influences during their metabolic prime years. The establishment of gut microbiota-host metabolic relationships during early adulthood may create lasting patterns that influence long-term health outcomes. (33,34) Second, older adults may have developed compensatory mechanisms or different baseline risk profiles that buffer against the immediate metabolic effects of dietary quality. (35) However, this apparent resilience in older adults should not be interpreted as protection against long-term consequences of poor dietary patterns.

In addition, our enterotype-stratified analysis revealed distinct microbial and metabolic responses to plant-based diet intakes between B-type and P-type enterotypes, highlighting the potential for personalized nutrition approaches. In the B-type enterotype, we observed stronger associations between healthy plant foods and metabolic results, including positive associations between *Firmicutes* abundance and PDI/hPDI and HPFG, and more pronounced relationships between *Bacteroidetes* and glucose level. These associations support previous evidence that gut *Firmicutes* are key mediators of dietary fiber degradation and that dietary fiber–induced *Firmicutes* and their metabolites exert beneficial effects on health. (32) Moreover, previous studies have shown that individuals with a B-type enterotype respond more favorably to dietary interventions and exhibit beneficial shifts in gut microbiome composition. This may be explained by the distinct functional traits of B-type communities, including enriched bacterial secretion systems and protein export pathways, as well as a higher abundance of carbohydrate-active enzymes (CAZymes) involved in the degradation of both plant- and animal-derived carbohydrates. These features likely enable more efficient processing of plant nutrients and their conversion into health-promoting metabolites. (36)

Our findings have important implications for dietary guidelines and clinical practice. The demonstration that unhealthy plant foods can have adverse metabolic associations challenges current recommendations that broadly promote plant-based diets without adequate consideration of food quality. The enterotype-specific and age-dependent responses observed in our study suggest that personalized nutrition approaches based on gut microbiome profiling and demographic factors may enhance the effectiveness of dietary interventions targeting gut microbiota and metabolic health.

Several limitations should be considered when interpreting our findings. The cross-sectional design precludes causal interferences about the relationships between diet, gut microbiota, and metabolic health. Longitudinal and interventional studies are needed to establish temporal relationships and determine whether dietary changes can predictably alter microbiome composition and metabolic outcomes. Additionally, our analysis was conducted in a specific

population in South Korea, and the generalizability of our findings to other ethnic and geographic regions requires validation. Although we adjusted for multiple established confounders, including age, sex, BMI and lifestyle and socioeconomic factors, residual confounding cannot be fully excluded. In particular, information on mode of birth delivery and other early-life factors was not available in our study. The relatively stable enterotype classifications in our study may not capture the dynamic nature of gut microbiome composition, which can vary with seasonal diet changes, medications, and other environmental factors. Future research should investigate the stability of enterotype-specific dietary responses over time and under different conditions.

Despite these limitations, our study provides valuable insights into the nuanced relationships between plant-based dietary patterns and metabolic health through alterations in gut microbiota. The integration of dietary quality assessment, microbiome analysis, and metabolic profiling offers a comprehensive framework for understanding how plant-based food choices influence human health through microbial intermediates.

Conclusion

Our findings demonstrate that the quality of plant foods is a critical determinant of their metabolic effects, through alteration of gut microbiome composition and diversity. The adverse effects of unhealthy plant-based diets, particularly among younger adults in the B-type group, highlight the inadequacy of dietary recommendations based solely on food origin rather than processing and nutritional quality. The enterotype-specific responses observed in our study support the potential for personalized nutrition approaches that consider individual microbiome characteristics. Future research should focus on developing and validating personalized dietary interventions based on microbiome profiling, while longitudinal studies are needed to establish causal relationships and optimize intervention strategies for different population group. Ultimately, this work contributes to the growing evidence base supporting precision nutrition approaches that can maximize the health benefits of dietary interventions while minimizing potential adverse effects.

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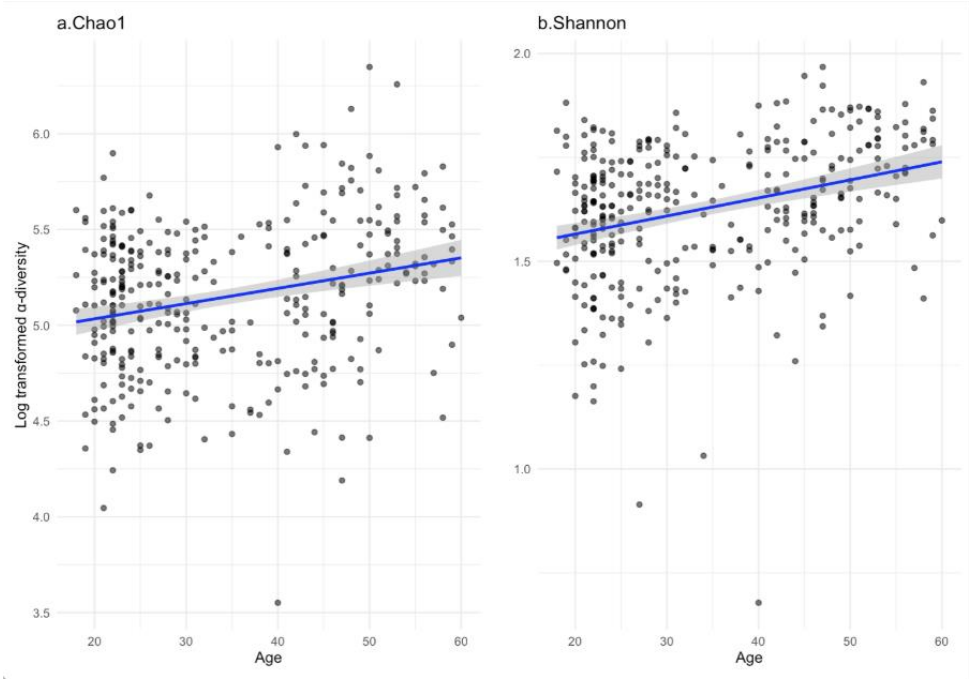
Annex

Annex Table1. Food group classification

	Food Groups	Food Items
Healthy Plant Foods	Whole grains	Various whole grains including black/brown rice
	Fruits	Apple, Banana, Grape, Muskmelon / Melon, Orange, Peach, Plum, Pear, Strawberry, Tangerine, Watermelon, Persimmon, hard / Dried persimmon
	Vegetables	Bean sprouts, Bracken, Sweet potato stalk/ Stem of taro/ Carrot/ Carrot juice, Crown daisy / Leek / Water dropwort, Cucumber, Deoduck / Doraji (kind of white root), Green pepper, Immature pumpkin, Kelp / Sea mustard, Lettuce, Mature pumpkin / Pumpkin juice, Onion, Other green vegetables, Other Mushrooms, Oyster Mushroom, Pepper leaves / Chamnamul / Asterscaber, Perilla leaf, Radish / Salted radish, Spinach, Tomato / Cherry tomato / Tomato juice/ Ketchup, Vegetable juices, Garlic, Sweet potatoes, Wasabi leaf
	Nuts	Peanut, Almond, Pine nut, Starch jelly, Sesame, Perilla seeds
	Legumes	Soybean and other Beans, Tofu, Soybean milk
	Coffee and Tea	Coffee, Coffee with cream, Green tea
	Veg Oils	Soybean oil, Sesame oil
Unhealthy Plant Foods	Refined grains	Buckwheat vermicelli/ Buckwheat noodle, Breakfast cereals, corn flakes, Chajangmyon / Jambbong, Loaf bread / Sandwich / Toast, Other bread, Parched cereal powder, Ramen, Rice cake, Bread with red bean paste, Flour

	Potatoes	fried potatoes, steamed boiled potatoes, Starch vermicelli
	Fruit juices	Fruit juices
	Sugar sweetened beverages	Carbonated drinks, other drinks
	Sweets and desserts	Cakes, Chocopie, Candy / Chocolate, Cookie / Cracker / Snack, Jam, Honey, Sugar, Starch syrup, Sherbet, Castella
	Salty food group	Cabbage Kimchi*, Radish Kimchi, other type of Kimchi (Green onion, mustard leaves etc.), Pickled vegetables, Salt, Soy sauce, Soy bean paste, Chilli pepper paste, Jjajang
Animal Foods	Animal fat	Butter, Beef tallow
	Dairy	Milk, Yogurt, Cheese, Ice cream
	Eggs	Eggs / Quail eggs
	Fish	Sushi, Yellow croaker / Sea bream/ Flat fish, Alaska pollack, Canned tuna, Clam / Whelk, Crab, Cuttlefish / Octopus, Dried anchovy, Dried laver, Eel, Fish paste / Crab flavored, Hair tail, Oyster, Salted-fermented fish, Shrimp, Yellow croaker / Sea bream / Flat fish, Squid
	Meat	Beef, Prok, Chicken & Processed meat
	Miscellaneous animal foods	Pizza, Hamburger



Annex figure 1. Distribution of gut microbial α-diversity (a. Chao1 and b. Shannon indices) across age. Linear regression models were used to examine differences in distributions across PDIs. Both Chao1 and Shannon indices were log-transformed prior to the test.

Annex table 2. Associations between gut microbial α-diversity (Chao1 and Shannon indices) and metabolic markers

	β_{raw}	SE_{raw}	*P*-value	β_{adj}	SE_{adj}	*P*-value
Chao 1						
Insulin (pmole/L)	-2.91	1.83	0.112	-0.87	1.82	0.634
HOMA-IR	-0.15	0.10	0.132	-0.06	0.10	0.538
Total Cholesterol (mg/dL)	4.67	1.98	0.019	1.323	1.95	0.497
C-reactive protein (ug/ml)	-0.09	0.07	0.179	-0.098	0.07	0.166
Shannon						
Insulin (pmole/L)	-1.02	1.83	0.580	0.52	1.90	0.786
HOMA-IR	-0.11	0.10	0.268	0.01	0.11	0.898
Total Cholesterol (mg/dL)	6.35	1.96	0.001	0.18	2.04	0.931
C-reactive protein (ug/ml)	-0.21	0.07	0.003	-0.23	0.07	0.002

General linear regressions (GLM) models were used without adjustment (-raw) and with adjustment (-adj) for age (years), sex (male/female), BMI (kg/m^2), drug use (yes/no), regular physical activity (yes/no), alcohol drink (never/former/current), smoke status (never/former/current), education level (low/middle/high/missing), and study (1 & 2) variables. B-coefficients were estimated per 1 SD increase in each index.

Annex table 3. Associations between plant-based dietary indices and metabolic markers

	β_{raw}	SE_{raw}	*P*-value	β_{adj}	SE_{adj}	*P*-value
PDI						

Insulin (pmole/L)	-0.03	0.27	0.911	0.20	0.27	0.459
HOMA-IR	0.00	0.01	0.840	0.01	0.02	0.672
Total Cholesterol (mg/dL)	0.73	0.30	0.014	0.25	0.29	0.394
C-reactive protein (ug/ml)	0.00	0.01	0.749	-0.01	0.01	0.469
hPDI						
Insulin (pmole/L)	0.25	0.31	0.432	0.34	0.31	0.286
HOMA-IR	0.02	0.02	0.341	0.02	0.02	0.352
Total Cholesterol (mg/dL)	0.40	0.34	0.238	-0.02	0.34	0.957
C-reactive protein (ug/ml)	0.03	0.01	0.023	0.02	0.01	0.048
uPDI						
Insulin (pmole/L)	-0.23	0.26	0.375	-0.09	0.24	0.709
HOMA-IR	-0.01	0.01	0.392	-0.01	0.01	0.659
Total Cholesterol (mg/dL)	-0.64	0.28	0.021	-0.48	0.26	0.066
C-reactive protein (ug/ml)	-0.02	0.01	0.041	-0.02	0.01	0.049

PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index; General linear regressions (GLM) models were used without adjustment (-raw) and with adjustment (-adj) for age (years), sex (male/female), BMI (kg/m^2), drug use (yes/no), regular physical activity (yes/no), alcohol drink (never/former/current), smoke status (never/former/current), education level (low/middle/high/missing), and study (1 & 2) variables. B-coefficients were estimated per 1-unit increase in each index

Annex table 4. Associations between plant-based diet indices and metabolic markers, stratified by gut microbial enterotypes

	Total (n=336)											
	B-type (n= 211)						P-type (n=125)					
	βraw	SEraw	P-value	βadj	SEadj	P-value	βraw	SEraw	P-value	βadj	SEadj	P-value
PDI												
Insulin (pmole/L)	-0.19	0.19	0.325	-0.09	0.19	0.633	0.10	0.54	0.860	0.64	0.53	0.229
HOMA-IR	-0.01	0.01	0.310	-0.01	0.01	0.598	0.00	0.03	0.951	0.02	0.03	0.428
Total Cholesterol (mg/dL)	0.98	0.41	0.018	0.58	0.41	0.161	0.44	0.43	0.306	-0.07	0.43	0.866
C-reactive protein (ug/ml)	-0.01	0.01	0.334	-0.02	0.01	0.203	0.01	0.02	0.641	0.00	0.02	0.841
hPDI												
Insulin (pmole/L)	-0.29	0.25	0.254	-0.32	0.25	0.209	0.58	0.54	0.282	0.98	0.53	0.069
HOMA-IR	-0.02	0.01	0.120	-0.03	0.01	0.050	0.04	0.03	0.178	0.05	0.03	0.068
Total Cholesterol (mg/dL)	0.58	0.55	0.291	0.26	0.55	0.640	0.29	0.43	0.502	-0.23	0.43	0.590
C-reactive protein (ug/ml)	0.04	0.02	0.023	0.03	0.02	0.053	0.02	0.02	0.249	0.02	0.02	0.233
uPDI												
Insulin (pmole/L)	0.07	0.18	0.684	0.18	0.17	0.277	-0.56	0.49	0.259	-0.28	0.47	0.559
HOMA-IR	0.00	0.01	0.622	0.01	0.01	0.542	-0.03	0.03	0.265	-0.01	0.03	0.618
Total Cholesterol (mg/dL)	-0.85	0.39	0.031	-0.65	0.36	0.075	-0.40	0.39	0.310	-0.25	0.38	0.517
C-reactive protein (ug/ml)	-0.04	0.01	0.002	-0.04	0.01	0.000	0.00	0.02	0.970	0.00	0.02	0.844

PDI, Plant-based Diet Index; hPDI, healthy Plant-based Diet Index; uPDI, unhealthy Plant-based Diet Index Enterotype B-type refers to the Bacteroides-dominant group and Enterotype P-type refers to Prevotella-dominant group. General linear regressions (GLM) models were used without adjustment (-raw) and with adjustment (-adj) for age (years), sex (male/female), BMI (kg/m2), drug use (yes/no), regular physical activity (yes/no), alcohol drink (never/former/current), smoke status (never/former/current), education level (low/middle/high/missing), and study (1 & 2) variables. B-coefficients were estimated per 1-unit increase in each index.

Abstract in French

Contexte : Les régimes alimentaires à base de plantes gagnent en popularité, mais tous les aliments végétaux n'offrent pas les mêmes bénéfices métaboliques. Les indices d'alimentation à base de plantes (PDI), incluant l'indice sain (hPDI) et l'indice malsain (uPDI), permettent d'évaluer la qualité des aliments végétaux, mais leurs liens avec le microbiote intestinal et la santé métabolique restent peu étudiés.

Objectif : Évaluer les associations entre les PDI, la diversité microbienne intestinale et les marqueurs métaboliques chez des adultes coréens, en tenant compte des différences selon l'entérotype et l'âge.

Méthodes : Nous avons analysés les données de 336 adultes coréens âgés de (18 à 60 ans) dans le cadre de deux études transversales (2018, 2021). L'apport alimentairea été évalué par un questionnaire de fréquence alimentaire comprenant 106 items. Le microbiote intestinal a été caractérisé par séquençage du gène 16S rRNA. Les relations ont été analysées par régressions linéaires ajustées, avec stratificationselon l'entérotype et l'âge.

Résultats : Des scores élevés de PDI et hPDI étaient associés à une diversité α plus importante (indices Chao1, Shannon), tandis que l'uPDI montrait des corrélations inverses. Une diversité α plus élevée était liée à des marqueurs métaboliques favorables (glycémie et triglycérides plus bas, HDL-cholestérol plus élevé). L'uPDI était inversement associé au HDL-C (effet = -0,35 ± 0,11, p = 0,001), via des modifications de genres bactériens bénéfiques (Lactobacillus, Flintibacter). Cette relation était marquée chez les sujets de moins de 40 ans ou d'entérotype *Bactéroïdes*, mais absente chez les sujets plus âgés ou d'entérotype *Prevotella.*

Conclusions : La qualité des aliments végétaux influence les bénéfices métaboliques via le microbiote intestinal. Les variations selon l'âge et l'entérotype soulignent l'intérêt d'approches nutritionnelles personnalisées intégrant la composition microbienne et les facteurs démographiques.

Mots-clés : Régimes à base de plantes ; Microbiote intestinal ; Marqueurs métaboliques ; Population coréenne ; Qualité des aliments végétaux