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Ultra-processed food intake, genetic polymorphisms and the risk of dyslipidaemia in the adult Korean population

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Research Paper

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Abstract

Objective: This study aimed to examine the association between ultra-processed food intake and dyslipidaemia risk and whether this association varied by the polygenic score for dyslipidaemia in the adult Korean population. *Design:* Prospective cohort study. *Setting:* Ultra-processed foods were identified under the NOVA classification. Participants were categorised into < 5, 5 to < 10, 10 to < 15, 15 to < 20 and ≥ 20 %E/d of ultra-processed food intake. The polygenic scores for dyslipidaemia were calculated from 53 950 SNPs. ORs and 95 % CIs were estimated using multivariate logistic regression models. *Participants:* 20 044 Korean adults aged ≥ 40 years in the Health Examinees (HEXA) study, the Cardiovascular Disease Association Study (CAVAS) and the Korea Association Resource (KARE) study. *Results:* During median follow-ups of 4·09, 8·67 and 15·67 years in the HEXA, CAVAS and KARE studies, respectively, there were a total of 7331, 786 and 1732 incident dyslipidaemia events. Ultra-processed food intake was not significantly associated with dyslipidaemia risk. Compared with < 5 %E/d, the pooled OR (95 % CI) of ≥ 20 %E/d of ultra-processed food intake for dyslipidaemia incidence was 1·01 (0·90, 1·13; *P* for trend = 0·83). There was no interaction by dyslipidaemia-related genetic variations; ORs (95 % CIs) were 1·04 (0·89, 1·22; *P* for trend = 0·91) and 0·98 (0·84, 1·15; *P* for trend = 0·72) for individuals with high- and low-polygenic scores, respectively (*P* for interaction = 0·90). *Conclusions:* No significant association was observed between ultra-processed food intake and the overall risk of dyslipidaemia, nor in subgroups of polygenic scores for dyslipidaemia among Korean adults with low ultra-processed food intake.

The Global Burden of Disease Study revealed a growing contribution of dyslipidaemia to the global disease burden over the past decade. In 1990, elevated LDL cholesterol levels ranked as the fifteenth leading risk factor for death, rising to eleventh in 2007 and eighth in 2017[1]. A recent meta-analysis of randomised clinical trials indicated that diets rich in unsaturated fatty acids and soluble fibre, while low in saturated and *trans* fatty acids, were associated with reduced LDL cholesterol levels[2], suggesting that modifying dietary factors could potentially prevent the risk of dyslipidaemia.

Ultra-processed foods have drawn attention for their relation to the risk of non-communicable diseases and the sustainability of food systems. The NOVA classification, introduced in 2010 to categorise foods based on the type, degree and scope of industrial processes, defines ultra-processed foods as ready-to-heat or ready-to-eat products with food additives and minimal whole foods[3]. In contrary to processed foods, which are whole foods preserved by typical methods like pickling or canning, ultra-processed foods are predominantly composed of components isolated from foods, either altered or unaltered, often consisting of five or more ingredients. Due to significant alterations in the food matrix during processing, the extensively damaged physical composition of ultra-processed foods may impact absorption processes, appetite, glucose response and the function and nature of the gut microbiota, possibly leading to health outcomes distinct from those of whole foods of comparable nutritional composition[4]. The increasing production and intake of ultra-processed foods are thus considered challenges that need to be addressed within the framework of the UN Sustainable Development Goals and the Decade of Nutrition[5]. Economic development has been linked to a steady rise in ultra-processed food intake, particularly in Korea. The Korea National Health and Nutrition Examination Survey (KNHANES) reported that the proportions of consuming sugar-sweetened beverages and Western-style fast foods, such as sandwiches, pizza, hamburgers and chicken nuggets, doubled from 1998 to 2009[6]. Despite the growing prevalence of dyslipidaemia and ultra-processed food intake in Korea, studies on the association between ultra-processed food intake and the risk of dyslipidaemia among Koreans are limited.

A recent meta-analysis of observational studies has reported positive associations between ultra-processed food intake and low HDL cholesterol levels (OR 2·02) and CVD risk (RR

1·29)[7]. Cross-sectional studies have also suggested associations between ultra-processed food intake and low levels of HDL cholesterol[8,9]. Ultra-processed foods may contribute to unfavourable lipid profiles, partly due to their high content of saturated and *trans* fatty acids and free sugars, but low content of dietary fibre and micronutrients[10]. A high intake of added sugars and refined carbohydrates and a low intake of unsaturated fatty acids and dietary fibre have been suggested as contributing factors to the elevation in LDL and non-HDL cholesterol levels[11].

Genetic factors may contribute to the development of dyslipidaemia. Genome-wide association studies (GWASs) have reported that genetic variants explain approximately 10–12 % of the total variance in lipid traits[12]. Since interactions by genetic variants may partially explain the residual susceptibility to dyslipidaemia, further research on these interactions is important[13].

The objective of this study was to examine whether ultra-processed food intake was associated with the risk of dyslipidaemia and whether this association varied by genetic susceptibility to dyslipidaemia in > 20 000 Korean adults aged 40 years or older.

Methods

Study population

The participants were drawn from three prospective cohorts within the Korean Genome and Epidemiology Study (KoGES), a nationwide initiative aimed at investigating the etiological factors of complex diseases[14]: the Health Examinees (HEXA) study, the Cardiovascular Disease Association Study (CAVAS) and the Korea Association Resource (KARE) study. These cohorts comprised community dwellers and individuals recruited from the national health examinee registry, all aged 40 years or older at baseline. Recruitment took place from 2004 to 2013 for the HEXA study, from 2005 to 2011 for the CAVAS and from 2001 to 2002 for the KARE study.

Follow-up examinations were conducted once between 2012 and 2016 for the HEXA study, with a median (interquartile range) follow-up duration of 4·09 (3·84–5·84) years. In the CAVAS, a total of four follow-ups were carried out between 2007 and 2016 at intervals of 1–3 years, resulting in a median (interquartile range) follow-up of 8·67 (7·58–8·92) years. The KARE study included a total of eight follow-ups conducted between 2003 and 2018 at 2-year intervals, with a median (interquartile range) follow-up of 15·67 (15·17–15·92) years. For the HEXA study, participants who completed the follow-up surveys were included, while for the CAVAS and KARE studies, the inclusion criteria encompassed anyone who participated in at least one of the last two follow-up periods.

In our analysis of the association between ultra-processed food intake and dyslipidaemia risk, there were a total of 211 562 participants at baseline (*n* 173 195 for the HEXA study, *n* 28 337 for the CAVAS and *n* 10 030 for the KARE study). Participants with the following characteristics were excluded: those who did not participate in a follow-up examination (*n* 131 095) (*n* 107 587 for the HEXA study, *n* 22 627 for the CAVAS and *n* 881 for the KARE study); those who did not have genetic information (*n* 13 184) (*n* 12 948 for the HEXA study, *n* 0 for the CAVAS and *n* 236 for the KARE study); those who had a history of dyslipidaemia, myocardial infarction, CHD, heart failure, stroke or cancer at baseline (*n* 45 955) (*n* 35 458 for the HEXA study, *n* 4446 for the CAVAS and *n* 6051 for the KARE study); those who did not provide FFQ at baseline (*n* 262) (*n* 170 for the HEXA study, *n* 3 for the CAVAS and *n* 89 for the KARE study); those who had implausible total energy intake at baseline (SD 3 from the mean of log-transformed total energy intake) (*n* 182) (*n* 141 for the HEXA study, *n* 11 for the CAVAS and *n* 30 for the KARE study) or those who did not have information on total cholesterol level, LDL cholesterol level, HDL cholesterol level, TAG level, self-reported diagnosis of dyslipidaemia or use of dyslipidaemia medication (*n* 840) (*n* 2 for the HEXA study, *n* 0 for the CAVAS and *n* 838 for the KARE study) (see online supplementary material, Supplemental Figure S1). A total of 20 044 participants (*n* 16 889 for the HEXA study, *n* 1250 for the CAVAS and *n* 1905 for the KARE study) were included in this study.

Ascertainment of dyslipidaemia

As part of the KoGES conducted by the Korea Centers of Disease Control and Prevention, blood samples were collected after an overnight fast, and levels of total cholesterol, HDL cholesterol and TAG were measured through biochemical assays at a central laboratory (Seoul Clinical Laboratories, Seoul, Korea). LDL cholesterol levels were calculated using the Friedewald equation for participants with TAG levels < 400 mg/dl[15]. We adopted four lipid parameters from the 2022 Korean Guidelines for the Management of Dyslipidaemia and considered levels above the normal or optimal range as cut-off values. Dyslipidaemia was defined as the presence of any one of the following criteria[16]: (1) total cholesterol ≥ 200 mg/dl, (2) LDL cholesterol ≥ 130 mg/dl, (3) TAG ≥ 150 mg/dl or (4) HDL cholesterol < 40 mg/dl. Additionally, a history of diagnosed dyslipidaemia or current use of dyslipidaemia medication was also considered as dyslipidaemia. Incident events were identified as those who did not have dyslipidaemia at baseline and met any of the aforementioned criteria during the follow-up period.

Assessment of ultra-processed food intake

Ultra-processed food intake was evaluated using a 106-item semi-quantitative FFQ in the HEXA study and the CAVAS and a 103-item semi-quantitative FFQ in the KARE study, which were developed based on the same protocols. A description of the validity and reproducibility of the FFQ can be found elsewhere[17,18]. In the KoGES, participants were required to choose from nine categories indicating the frequency of ultra-processed food intake over the preceding year, ranging from almost never to three times or more per day. For coffee, the intake frequency of coffee additives, cream and sugar, was also collected. Portion sizes were categorised as half, equal to or one and a half or twice the standard serving size.

We classified food items based on the NOVA classification[3] and previous publications[5,19,20]. In cases of aggregated food groups or mixed meals containing food items with varying processing degrees, we segmented them and applied weights using information from Korean food recipes. These weights represented the percentage of weight supplied by an ultra-processed food item within the food group or mixed meal. Consequently, the ultra-processed food items in this study included instant noodle (*ramen*), cereal/corn flakes, loaf bread/sandwich/toast, red bean bread/steamed bun/*pulppang*, other breads, bread spread (jam/butter/margarine), cake/*chocopie*, cookie/cracker/snack, candy/chocolate, pizza/hamburger, vegetable juice, tomato juice/tomato ketchup, carrot juice, orange juice, apple juice, grape juice, ham/sausage, fish cake/crab stick, processed milk, yogurt/*yoplait*, ice

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cream, processed cheese, soybean milk, carbonated drink, other drinks and coffee cream (see online supplementary material, Supplemental Table S1). We computed the percentage of total energy intake from ultra-processed foods in the total energy intake (percentage of total energy intake from ultra-processed foods = total energy of ultra-processed foods (kJ/d) × 100/total energy intake (kJ/d)). Ultra-processed food intake was categorised into five groups: < 5 %E, 5 to < 10 %E, 10 to < 15 %E, 15 to < 20 %E and ≥ 20 %E per day. As most participants had low ultra-processed food intake (see online supplementary material, Supplemental Figure S2) and to ensure a decent number of participants in each category, the top category of ultra-processed food intake was set as ≥ 20 %E/d.

Assessment of other risk factors

The following demographic and lifestyle factors were assessed by trained interviewers for each cohort study: education level, smoking status (never, past and current), the number of years spent smoking, the number of cigarettes smoked daily, alcohol drinking status (never, past and current), alcohol drinking frequency, alcohol serving size and the frequency of vigorous physical activity. In the KARE study, the frequency and duration of eight types of physical activities (aerobics, jogging, swimming, tennis, golf, bowling, walking and climbing) were also assessed. We then determined metabolic equivalent minutes per week (MET-min/week) by multiplying the minutes per week spent on each physical activity by the metabolic cost of each activity in METs[21]. We calculated pack-years of smoking by dividing the number of cigarettes smoked daily by 20 and multiplying this result by the number of years smoked. We calculated total alcohol intake as grams of ethanol per day and BMI as the weight in kilograms divided by the square of the height in metres.

Genotyping and polygenic score calculation

Genotyping of participant genomic DNA was performed by the National Research Institute of Health, Centers for Disease Control and Prevention, Ministry for Health and Welfare, Republic of Korea. Blood samples were collected at baseline and each follow-up and placed in a serum separator tube and two EDTA tubes[14]. Additional details regarding the study design have been discussed elsewhere[14]. Among the 211 562 KoGES participants, genomic DNA samples from a total of 82 459 participants were genotyped (*n* 61 562 for the HEXA study, *n* 12 057 for the CAVAS and *n* 8840 for the KARE study). In the HEXA study, genomic DNA samples from peripheral blood were genotyped by the Affymetrix Genome-Wide Human SNP Array 6·0, and genotypes were determined using the birdseed genotyping algorithm[22]. Some CAVAS participants were genotyped using the same technique, while others were genotyped by the Illumina Omni1-Quad bead microarrays[22,23]. Participants in the KARE study were genotyped by the Affymetrix Genome-Wide Human SNP Array 5·0, and genotypes were determined by the Bayesian robust linear model with the Mahalanobis distance genotyping algorithm[24]. Missing or non-typed genotypes were imputed using IMPUTE v2 with 1000 Genomes Project data[25]. Additionally, some participants in each cohort were genotyped by the Korea Biobank Array, referred to as KoreanChip, a customised Korean genome structure-based array[25]. Genotyping by Affymetrix 5·0, Affymetrix 6·0, Illumina Omni1-Quad and KoreanChip, along with the quality control methods, has been reported earlier[22–25].

We computed an individual polygenic score of dyslipidaemia using SNPs related to dyslipidaemia, obtained from the PGS Catalogue (https://www.pgscatalog.org). The SNPs, included in the polygenic score (PGS002029) of abnormal circulating lipid concentration, were selected from the publication by Privé *et al.* (2022), which included East Asian ancestry data in the GWAS or polygenic score evaluation stage[26]. As a result, a total of 764 390 genetic variants were extracted based on evidence from the PGS Catalogue, and 53 950 genetic variants with a missing call rate of < 0·2 were available from genotyping within the HEXA, CAVAS and KARE studies.

Statistical analysis

We calculated polygenic scores of dyslipidaemia using the allelic scoring command of PLINK version 1·9 (·www.cog-genomics.org/plink/1·9)[27,28]. Whether dyslipidaemia incidence occurred during the follow-up period was used as a binary outcome variable in the scoring model. Each SNP related to dyslipidaemia was assigned a value of 0, 1 or 2 based on the number of minor alleles and then weighted by its relative effect size (β coefficient obtained from the GWAS). The polygenic score was the sum of the weighted values for each candidate genetic variant, calculated using the formula: polygenic score = $i \times (\beta_1 \times SNP_1 + \beta_2 \times SNP_2 + \ldots + \beta_i \times SNP_i)/(\beta_1 + \beta_2 + \ldots + \beta_i)$ (·https://www.cog-genomics.org/plink/1·9/score)[29]. To assess whether the polygenic score of dyslipidaemia served as an interaction variable in the association between ultra-processed food intake and dyslipidaemia risk, it was categorised as either high or low based on the median value.

Multivariate logistic regression models were utilised to explore the associations between ultra-processed food intake and the risk of dyslipidaemia. ORs and 95 % CIs were estimated based on categories of ultra-processed food intake and per 5 %E/d continuous increment. All multivariable analyses included age (years, continuous) and sex (men, women). We further adjusted for BMI (< 18·5, 18·5 to < 23, 23 to < 25, ≥ 25 kg/m^2 for HEXA, < 23, 23 to < 25, ≥ 25 kg/m^2 for CAVAS and KARE), smoking status (never, < 10, 10 to < 20, 20 to < 30, ≥ 30 pack-years for men; never, < 5, 5 to < 10, ≥ 10 pack-years for women for HEXA, never, past, current for men; never, ever for women for CAVAS, never, < 10, 10 to < 20, 20 to < 30, ≥ 30 pack-years for men; non-current, current for women for KARE), alcohol drinking (never, ethanol < 10, 10 to < 20, 20 to < 30, 30 to < 40, 40 to < 50, 50 to < 60, ≥ 60 g/d for men; never, ethanol < 10, 10 to < 20, ≥ 20 g/d for women for HEXA, non-current, current for CAVAS, never, ethanol < 10, 10 to < 20, 20 to < 30, ≥ 30 g/d for men; non-current, current for women for KARE), education level (elementary school or below, middle school, high school or above), regular exercise (none, vigorous physical activity frequency 1–2, 3–4, 5–6, every day per week for HEXA, none, vigorous physical activity frequency 1–2, 3–6, every day per week for CAVAS, quartiles in MET-min/week for KARE), total energy intake (kcal/d, continuous) and total fat intake (g/d, continuous) in our final model. To analyse the interaction by polygenic scores, we included a cross-product term of ultra-processed food intake and polygenic scores in the model and assessed the interaction using a likelihood ratio test in each cohort study and a Wald test on the cross-product term for pooled analysis.

To examine linear trends across categories of ultra-processed food intake, we modelled the median intake of each category as a continuous variable. Pooled ORs were estimated using a random-effects model in the presence of heterogeneity or a fixed-effects

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Table 1. Baseline characteristics of participants according to ultra-processed food intake

	Total		Ultra-processed food intake (%E/d)									
			< 5		5 to < 10		10 to < 15		15 to < 20		≥ 20	
HEXA												
No. of participants	16 889		3284		5042		3877		2198		2488	
Age (years)	51·8	8·2	55·2	7·8	52·7	8·1	50·7	7·8	49·8	7·8	49·0	7·7
Sex												
Men	5167	30·59	1062	32·34	1642	32·57	1160	29·92	644	29·30	659	26·49
Women	11 722	69·41	2222	67·66	3400	67·43	2717	70·08	1554	70·70	1829	73·51
BMI (kg/m^2)*	23·1	2·7	23·3	2·7	23·3	2·7	23·1	2·7	22·9	2·7	23·0	2·8
Smoking status (pack-years)*	4·4	10·9	4·9	11·7	4·6	11·0	4·4	11·3	4·2	10·4	3·7	9·5
Alcohol drinking (ethanol g/d)*	6·3	26·1	7·7	49·2	5·9	15·0	6·2	18·0	6·2	15·5	5·4	15·9
Total energy intake (kcal/d)	1750·0	504·5	1543·3	380·3	1683·9	421·1	1771·7	477·1	1860·5	543·6	2025·4	640·1
Education level*												
High school or above	12 225	72·38	1934	58·89	3489	69·20	2987	77·04	1760	80·07	2055	82·60
CAVAS												
No. of participants	1250		404		392		210		121		123	
Age (years)	56·8	9·2	59·0	8·2	56·6	9·2	55·2	9·3	54·9	9·8	54·8	9·9
Sex												
Men	477	38·16	137	33·91	161	41·07	84	40·00	41	33·88	54	43·90
Women	773	61·84	267	66·09	231	58·93	126	60·00	80	66·12	69	56·10
BMI (kg/m^2)	23·5	2·9	23·4	3·0	23·4	2·9	23·8	3·0	23·4	2·9	23·5	2·9
Smoking status (pack-years)	7·3	15·5	6·3	14·3	7·9	15·7	7·6	15·5	6·2	15·0	9·7	19·1
Alcohol drinking (ethanol g/d)*	9·6	25·4	8·8	24·4	11·8	31·5	9·8	23·0	5·8	15·0	8·7	16·5
Total energy intake (kcal/d)	1672·9	479·6	1514·8	420·9	1628·4	381·5	1752·3	479·2	1833·8	516·3	2040·8	620·9
Education level*												
High school or above	339	27·12	64	15·84	106	27·04	74	35·24	51	42·15	44	35·77
KARE												
No. of participants	1905		472		492		400		279		262	
Age (years)	50·8	8·9	55·4	9·2	51·2	8·5	49·0	8·3	48·4	8·1	46·9	6·9
Sex												
Men	739	38·79	182	38·56	203	41·26	157	39·25	99	35·48	98	37·40
Women	1166	61·21	290	61·44	289	58·74	243	60·75	180	64·52	164	62·60
BMI (kg/m^2)*	23·4	3·1	23·4	3·3	23·5	3·0	23·5	3·0	23·3	2·7	23·3	3·1
Smoking status (pack-years)*	7·5	14·8	9·3	16·3	8·6	16·1	6·5	14·2	4·9	10·1	6·9	14·2
Alcohol drinking (ethanol g/d)*	8·4	19·8	9·5	19·9	9·9	23·5	6·0	14·8	6·7	18·4	9·0	20·2
Total energy intake (kcal/d)	1947·7	630·2	1784·5	610·0	1889·0	570·7	1961·9	589·8	2113·6	648·7	2153·7	711·3
Education level*												
High school or above	822	43·15	107	22·67	185	37·60	210	52·50	165	59·14	155	59·16

HEXA, the Health Examinees; CAVAS, Cardiovascular Disease Association Study; KARE, the Korea Association Resource.
Continuous variables are reported as mean (SD), and categorical variables are reported as no. (%).
*The total number of participants was not equal because of missing values.

model in its absence[30]. Heterogeneity across the studies was assessed using Q statistics[30]. The potential variation in the association between ultra-processed food intake and dyslipidaemia risk based on polygenic scores (high or low) was explored. Additionally, we performed subgroup analyses to investigate whether age (< 50 or ≥ 50 years), sex (men or women), BMI (< 25 or ≥ 25 kg/m^2) or alcohol drinking (non-current or current drinker) modified the association between ultra-processed food

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Table 2. Multivariate-adjusted ORs and 95 % CIs for the risk of dyslipidaemia according to ultra-processed food intake

	per 5 %E/d		Ultra-processed food intake (%E/d)								
			< 5	5 to < 10		10 to < 15		15 to < 20		≥ 20	
	OR	95 % CI		OR	95 % CI	OR	95 % CI	OR	95 % CI	OR	95 % CI	*P* for trend
Pooled												
Case/total no.	9849/20 044		2119/4160	2885/5926		2236/4487		1242/2598		1367/2873		
Age- and sex-adjusted model	0·99	0·97, 1·01	Reference	1·00	0·92, 1·09	1·06	0·97, 1·16	0·93	0·84, 1·03	0·96	0·87, 1·07*	0·21
Multivariate-adjusted model	1·00	0·98, 1·02	Reference	1·02	0·94, 1·11	1·09	0·99, 1·19	0·97	0·87, 1·08	1·01	0·90, 1·13*	0·83
HEXA												
Case/total no.	7331/16 889		1432/3284	2196/5042		1738/3877		916/2198		1049/2488		
Age- and sex-adjusted model	0·99	0·97, 1·01	Reference	1·01	0·92, 1·10	1·06	0·96, 1·17	0·93	0·83, 1·04	0·95	0·85, 1·05	0·14
Multivariate-adjusted model	1·00	0·98, 1·02	Reference	1·02	0·94, 1·12	1·09	0·99, 1·20	0·97	0·86, 1·09	1·00	0·89, 1·12	0·69
CAVAS												
Case/total no.	786/1250		257/404	238/392		134/210		72/121		85/123		
Age- and sex-adjusted model	1·03	0·95, 1·11	Reference	0·91	0·68, 1·21	1·03	0·72, 1·46	0·83	0·54, 1·27	1·33	0·86, 2·07	0·33
Multivariate-adjusted model	1·02	0·94, 1·11	Reference	0·91	0·68, 1·23	1·03	0·72, 1·50	0·85	0·54, 1·32	1·28	0·79, 2·06	0·44
KARE												
Case/total no.	1732/1905		430/472	451/492		364/400		254/279		233/262		
Age- and sex-adjusted model	1·00	0·91, 1·11	Reference	1·18	0·74, 1·86	1·12	0·69, 1·82	1·12	0·66, 1·92	0·92	0·54, 1·55	0·68
Multivariate-adjusted model	1·02	0·91, 1·14	Reference	1·21	0·76, 1·93	1·17	0·71, 1·95	1·21	0·69, 2·15	0·98	0·55, 1·73	0·88

HEXA, the Health Examinees; CAVAS, Cardiovascular Disease Association Study; KARE, the Korea Association Resource.
Fixed-effects model was used for pooled meta-analysis.
Multivariate-adjusted model was adjusted for age (years, continuous), sex (men, women), BMI (< 18·5, 18·5 to < 23, 23 to < 25, ≥ 25 kg/m^2 for HEXA, < 23, 23 to < 25, ≥ 25 kg/m^2 for CAVAS and KARE), smoking status (never, < 10, 10 to < 20, 20 to < 30, ≥ 30 pack-years for men; never, < 5, 5 to < 10, ≥ 10 pack-years for women for HEXA, never, past, current for men; never, ever for women for CAVAS, never, < 10, 10 to < 20, 20 to < 30, ≥ 30 pack-years for men; non-current, current for women for KARE), alcohol drinking (never, ethanol < 10, 10 to < 20, 20 to < 30, 30 to < 40, 40 to < 50, 50 to < 60, ≥ 60 g/d for men; never, ethanol < 10, 10 to < 20, ≥ 20 g/d for women for HEXA, non-current, current for CAVAS, never, ethanol < 10, 10 to < 20, 20 to < 30, ≥ 30 g/d for men; non-current, current for women for KARE), education level (elementary school or below, middle school, high school or above), regular exercise (none, vigorous physical activity frequency 1–2, 3–4, 5–6, every day per week for HEXA, none, vigorous physical activity frequency 1–2, 3–6, every day per week for CAVAS, quartiles in MET-min/week for KARE), total energy intake (kcal/d, continuous) and total fat intake (g/d, continuous).
**P* for heterogeneity across the three cohort studies > 0·10.

Table 3. Pooled multivariate-adjusted ORs and 95 % CIs for the risk of dyslipidaemia by polygenic scores according to ultra-processed food intake

			Ultra-processed food intake (%E/d)									
	per 5 %E/d			5 to < 10		10 to < 15		15 to < 20		≥ 20		
Polygenic scores*	OR	95 % CI	< 5	OR	95 % CI	OR	95 % CI	OR	95 % CI	OR	95 % CI	*P* for trend	*P* for interaction
Low-polygenic scores													0·90†
Case/total no.	4659/10 021		998/2062	1382/3004		1076/2278		565/1268		638/1409			
Age- and sex-adjusted model	0·99	0·97, 1·02	Reference	1·02	0·91, 1·15	1·07	0·94, 1·22	0·91	0·78, 1·06	0·98	0·85, 1·14	0·37	
Multivariate-adjusted model	1·01	0·98, 1·03	Reference	1·04	0·92, 1·17	1·10	0·97, 1·26	0·96	0·81, 1·12	1·04	0·89, 1·22	0·91	
High-polygenic scores													
Case/total no.	5190/10 023		1121/2098	1503/2922		1160/2209		677/1330		729/1461			
Age- and sex-adjusted model	0·99	0·97, 1·02	Reference	0·99	0·88, 1·12	1·06	0·93, 1·20	0·95	0·82, 1·10	0·94	0·81, 1·09	0·29	
Multivariate-adjusted model	1·00	0·97, 1·03	Reference	1·00	0·89, 1·13	1·09	0·95, 1·24	0·98	0·84, 1·14	0·98	0·84, 1·15	0·72	

Fixed-effects model was used for pooled meta-analysis.

Multivariate-adjusted model was adjusted for age (years, continuous), sex (men, women), BMI (< 18·5, 18·5 to < 23, 23 to < 25, ≥ 25 kg/m^2 for HEXA, < 23, 23 to < 25, ≥ 25 kg/m^2 for CAVAS and KARE), smoking status (never, < 10, 10 to < 20, 20 to < 30, ≥ 30 pack-years for men; never, < 5, 5 to < 10, ≥ 10 pack-years for women for HEXA, never, past, current for men; never, ever for women for CAVAS, never, < 10, 10 to < 20, 20 to < 30, ≥ 30 pack-years for men; non-current, current for women for KARE), alcohol drinking (never, ethanol < 10, 10 to < 20, 20 to < 30, 30 to < 40, 40 to < 50, 50 to < 60, ≥ 60 g/d for men; never, ethanol < 10, 10 to < 20, ≥ 20 g/d for women for HEXA, non-current, current for CAVAS, never, ethanol < 10, 10 to < 20, 20 to < 30, ≥ 30 g/d for men; non-current, current for women for KARE), education level (elementary school or below, middle school, high school or above), regular exercise (none, vigorous physical activity frequency 1–2, 3–4, 5–6, every day per week for HEXA, none, vigorous physical activity frequency 1–2, 3–6, every day per week for CAVAS, quartiles in MET-min/week for KARE), total energy intake (kcal/d, continuous) and total fat intake (g/d, continuous).

*Polygenic scores were calculated using 53 950 SNPs related to dyslipidaemia weighted by relative effect (β coefficient).

†*P* value was obtained using the multivariate-adjusted model.

intake and dyslipidaemia risk. All statistical tests were two-sided, and *P* values less than 0·05 were considered statistically significant. All analyses were performed using SAS software, version 9·4 (SAS Institute Inc., Cary, North Carolina).

We conducted sensitivity analyses to evaluate the robustness of our findings. First, to minimise reverse causation, we excluded participants who developed dyslipidaemia at the first follow-up in the CAVAS and KARE studies. Second, participants were categorised into tertiles based on polygenic scores instead of two categories. Third, we generated genetic risk scores specific to our study participants, using fourteen dyslipidaemia-related SNPs that were genome-wide significant ($P < 5 \times 10^{-8}$) in the study population. To calculate the genetic risk scores, we examined whether the selected genetic variants were associated with dyslipidaemia in our study population. Among the genetic variants associated with dyslipidaemia with suggestive significance ($P < 1 \times 10^{-6}$) extracted from the GWAS Catalogue (https://www.ebi.ac.uk/gwas), we selected those reported from GWAS that included ≥ 100 000 individuals of East Asian descent only. We performed a GWAS in our study population, adjusting for age (years, continuous) and sex (men, women). As a result, fourteen dyslipidaemia-related SNPs were identified as genome-wide significant ($P < 5 \times 10^{-8}$) through GWAS, and these SNPs were incorporated into the genetic risk scores. The genetic risk score was calculated as the sum of the weighted number of each candidate genetic variant using the equation: genetic risk score $= 14 \times (\beta_1 \times \mathrm{SNP}_1 + \beta_2 \times \mathrm{SNP}_2 + \ldots + \beta_{14} \times \mathrm{SNP}_{14})/(\beta_1 + \beta_2 + \ldots + \beta_{14})$. Online supplementary material, Supplemental Table S2 provides details of the SNPs included in the genetic risk score calculation. In a sensitivity analysis, participants were categorised into high- or low-genetic risk score groups based on the median. Additionally, we aggregated the three cohort studies to examine the association between ultra-processed food intake and dyslipidaemia risk with a higher cut-off for the top category of ultra-processed food intake (≥ 30 %E/d).

Results

During the follow-up period across the three studies, a total of 9849 (49·14 %) incident dyslipidaemia events were identified among 20 044 participants. The median follow-up durations for the HEXA study, the CAVAS and the KARE study were 4·09, 8·67 and 15·67 years, respectively.

The general characteristics of participants from the three cohort studies according to ultra-processed food intake are presented in Table 1. Generally, participants with higher ultra-processed food intake were younger, exhibited higher total energy intake and had higher education levels than those with lower intake.

Table 2 presents the ORs and 95 % CIs for dyslipidaemia incidence according to ultra-processed food intake. There was no significant association between ultra-processed food intake and the risk of dyslipidaemia. Compared with < 5 %E/d of ultra-processed food intake, the pooled ORs (95 % CIs) were 1·02 (0·94, 1·11) for 5 to < 10 %E/d, 1·09 (0·99, 1·19) for 10 to < 15 %E/d, 0·97 (0·87, 1·08) for 15 to < 20 %E/d and 1·01 (0·90, 1·13) for ≥ 20 %E/d of ultra-processed food intake (*P* for trend = 0·83; *P* for heterogeneity across the three cohort studies = 0·60) (Table 2). An increment of 5 %E/d in ultra-processed food intake did not show a significant association with the risk of dyslipidaemia (pooled OR 1·00; 95 % CI 0·98, 1·02). No significant associations were found in each cohort study. When compared with < 5 %E/d of ultra-processed food intake, the ORs (95 % CIs) for ≥ 20 %E/d of ultra-processed food intake were 1·00 (0·89, 1·12; *P* for trend = 0·69) in the HEXA study, 1·28 (0·79, 2·06; *P* for trend = 0·44) in the CAVAS and 0·98 (0·55, 1·73; *P* for trend = 0·88) in the KARE study.

We investigated whether the association between ultra-processed food intake and dyslipidaemia risk was modified by genetic susceptibility to dyslipidaemia (Table 3). The non-significant associations were consistent across dichotomous polygenic score categories of dyslipidaemia (pooled *P* for interaction = 0·90). No statistically significant interactions were observed in each cohort study (*P* for interaction = 0·61, 0·13 and 0·99 in the HEXA study, the CAVAS and the KARE study, respectively) (see online supplementary material, Supplemental Table S3).

Subgroup analyses according to age, sex, BMI and alcohol drinking revealed no significant association between ultra-processed food intake and dyslipidaemia risk (see online supplementary material, Supplemental Table S4). Compared with < 5 %E/d of ultra-processed food intake, the pooled ORs (95 % CIs) for ≥ 20 %E/d of ultra-processed food intake were 0·89 (0·74, 1·06; *P* for trend = 0·16) for age < 50 years, 1·09 (0·94, 1·27; *P* for trend = 0·21) for age ≥ 50 years, 0·93 (0·76, 1·15; *P* for trend = 0·63) for men, 1·06 (0·93, 1·21; *P* for trend = 0·86) for women, 1·07 (0·94, 1·21; *P* for trend = 0·43) for BMI < 25 kg/m^2, 0·83 (0·66, 1·05; *P* for trend = 0·05) for BMI ≥ 25 kg/m^2, 1·10 (0·94, 1·28; *P* for trend = 0·46) for non-current drinkers and 0·90 (0·76, 1·06; *P* for trend = 0·20) for current drinkers. The lack of a significant association did not vary by sex, BMI or alcohol drinking (*P* for interaction = 0·17, 0·12 and 0·46, respectively). Although the pooled ORs were slightly higher in those aged ≥ 50 years compared to those aged < 50 years overall (*P* for interaction = 0·01), the associations within each age group were not statistically significant.

In sensitivity analyses, the association between ultra-processed food intake and dyslipidaemia risk remained non-significant, even after excluding participants who had dyslipidaemia at the first follow-up in the CAVAS and KARE studies (see online supplementary material, Supplemental Table S5). When polygenic scores were categorised into tertiles (high-, medium- and low-polygenic scores), no significant interaction was observed (*P* for interaction = 0·74) (see online supplementary material, Supplemental Table S6). Similar results were found in sensitivity analyses using genetic risk scores instead of polygenic scores (*P* for interaction = 0·70) (see online supplementary material, Supplemental Table S7). Additionally, when we aggregated the three cohort studies, no significant association between ultra-processed food intake and dyslipidaemia risk was observed in the higher top category (≥ 30 %E/d) (see online supplementary material, Supplemental Table S8).

Discussion

In this pooled analysis of 20 044 participants from three Korean prospective studies, we found no significant association between ultra-processed food intake and the risk of dyslipidaemia. The association between ultra-processed food intake and the risk of dyslipidaemia did not vary by genetic variants related to dyslipidaemia. Since our study participants were Korean adults aged 40 years or older, who had low ultra-processed food intake, future studies involving younger populations with higher ultra-processed food intake demand ongoing attention and careful consideration.

In contrast to our findings, a number of explanations have been proposed to elucidate the potential unfavourable effects of ultra-processed foods on dyslipidaemia risk. Ultra-processed foods are

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characterised by a high content of saturated and *trans* fatty acids, which are assumed to elevate dyslipidaemia risk and negatively influence lipid profiles, and a low content of PUFA[31,32]. Ultra-processed foods may result in low dietary intakes of fibre, micronutrients and other naturally occurring bioactive substances present in whole foods but high intakes of sugars and Na[33]. The combination of elevated blood glucose and pressure, resulting from such dietary patterns, has been suggested to synergistically accelerate atherosclerosis through mechanisms like insulin resistance, endothelial dysfunction and oxidative stress[34].

A prospective cohort study on Spanish adults aged 60 years or older revealed an association between high ultra-processed food intake and incident dyslipidaemia[35]. In that study, a high intake of ultra-processed foods was associated with a higher risk of hypertriglyceridaemia (OR 2·66; 95 % CI 1·20, 5·90; *P* for trend = 0·01) and low HDL cholesterol levels (OR 2·23; 95 % CI 1·22, 4·05; *P* for trend = 0·01). However, there was no association between ultra-processed food intake and high LDL cholesterol levels (OR 1·03; 95 % CI 0·43, 2·47) or changes in HDL and LDL cholesterol levels. A cross-sectional study of young adults in Canada showed an association of ultra-processed food intake with a higher prevalence of reduced HDL cholesterol levels (OR 2·05; 1·25, 3·38 (Q5 *v.* Q1); *P* for trend = 0·02) but not with hypertriglyceridaemia (OR 0·93; 95 % CI 0·57, 1·52 (Q5 *v.* Q1); *P* for trend = 0·71)[8]. Among Brazilian adolescents aged 11·3 (SD 1·3) years, ultra-processed food intake was not correlated with baseline levels of total cholesterol ($\rho = -0{\cdot}16$, $P = 0{\cdot}07$), LDL cholesterol ($\rho = -0{\cdot}16$, $P = 0{\cdot}07$), HDL cholesterol ($\rho = -0{\cdot}04$, $P = 0{\cdot}67$) or TAG ($\rho = -0{\cdot}07$, $P = 0{\cdot}44$), nor with levels of total cholesterol ($\rho = 0{\cdot}05$, $P = 0{\cdot}43$), LDL cholesterol ($\rho = 0{\cdot}06$, $P = 0{\cdot}38$), HDL cholesterol ($\rho = 0{\cdot}06$, $P = 0{\cdot}37$) or TAG ($\rho = 0{\cdot}001$, $P = 0{\cdot}99$) after a 4-year follow-up[36]. These mixed outcomes from previous studies may not provide strong evidence for a clear association between ultra-processed food intake and the risk of dyslipidaemia. The heterogeneity in the populations studied, differences in dietary assessment methods, various intake levels of ultra-processed foods and the diverse composition of ultra-processed foods could explain the discrepancies.

Moreover, Asian studies remained limited and exhibited inconsistent results. Among Iranian adults aged 20–50 years, high ultra-processed food intake was associated with a higher risk of TAG and HDL cholesterol abnormalities (OR 3·69; 95 % CI 1·67, 8·16; *P* for trend < 0·01 (Q3 *v.* Q1) and OR 3·38; 95 % CI 1·42, 8·07; *P* for trend = 0·01 (Q3 *v.* Q1), respectively)[37]. However, no associations were observed between ultra-processed food intake and total or LDL cholesterol levels in that study. In another cross-sectional study from Lebanon, medium or high adherence to a dietary pattern rich in ultra-processed foods, compared with low adherence, was not associated with high TAG levels (OR 1·08; 95 % CI 0·28, 4·11) or low HDL cholesterol levels (OR 1·82, 95 % CI 0·52, 6·42)[38].

It is noteworthy that ultra-processed food intake is higher in Western populations than in our study population. The contribution of ultra-processed foods to total energy intake in Korea is 25·1 %[39], considerably lower than in the United States (57·9 %)[9], the United Kingdom (56·8 %)[33], Canada (45 %)[40] and France (29 %)[41]. Korean dietary patterns, although gradually, are becoming closer to Western dietary patterns. Predictions indicate that ultra-processed food sales in Asian countries will approach those in high-income countries by 2035[5]. Our study included participants aged 40 years or older, who likely had a lower intake of ultra-processed foods than young adults. Therefore, further prospective studies focusing on young Asian adults are warranted.

We did not observe significant interactions of polygenic scores in the association between ultra-processed food intake and dyslipidaemia risk. Nonetheless, recent studies have presented evidence supporting interactions by genetic variants for components in ultra-processed foods and lipid profiles. Several epidemiological studies in Western countries have reported potential interactions between saturated and unsaturated fats and *CETP* gene polymorphisms[42], dietary sucrose and *APOE* gene polymorphisms[43] and Na and *AGT* gene polymorphisms[44]. While investigations involving diverse ethnic groups are necessary to explore population-specific associations, develop effective nutrition strategies and generalise study results, the current evidence is mostly from Caucasian populations. The KARE study found that a dietary pattern rich in whole grains and soybean products was inversely associated with hypercholesterolaemia risk (HR 0·74; 95 % CI 0·59, 0·93 (Q4 *v.* Q1); *P* for trend = 0·01; *P* for interaction = 0·08) among Korean adults with higher genetic risk scores related to dyslipidaemia[45]. In young Chinese Han adults, changes in levels of LDL and HDL cholesterol after a high-carbohydrate low-fat diet were different according to the genotypes of *LEPR* gene polymorphisms[46]. However, Asian studies on gene–diet interactions for ultra-processed food intake and lipid profiles or cardiovascular diseases are limited.

The present pooled analysis has several limitations. First, the potential for residual confounding could persist; however, we adjusted for possible confounding factors, and the associations remained largely unchanged after adjustment. Second, dietary information was collected only at baseline and lacked repeatedly measured exposures. Additionally, FFQ may introduce measurement errors and challenges in accurate portion quantification compared with prospective approaches relying on weighing and recording foods consumed. Third, our questionnaire was not specifically designed to assess ultra-processed food intake as defined by the NOVA classification. Fourth, even though the NOVA classification is widely acknowledged, it may not be universally applicable because of diverse dietary and cultural habits, as well as variations in food processing. Finally, our study population had a low intake of ultra-processed foods, and there was a small proportion with ≥ 30 %E/d of ultra-processed food intake. Given the increasing intake of ultra-processed foods, notably among younger populations, further studies in younger populations are required. Nonetheless, this study possesses some strengths. First, we included prospective cohort studies with data collected in a temporal sequence, enabling the distinction of a temporal relationship[47]. Second, the study involved an Asian population with a relatively large sample size, addressing Asian gene–diet interaction studies on ultra-processed food intake and the risk of dyslipidaemia.

In conclusion, we found no significant association between ultra-processed food intake and the risk of dyslipidaemia in an adult Korean population aged 40 years or older. This lack of association did not differ by polygenic scores and genetic risk scores. Further epidemiological and intervention studies including younger Asian populations with a higher intake of ultra-processed foods are needed to clarify the effects of dyslipidaemia-related genetic variation and high ultra-processed food intake on cardiometabolic disease risk.

Supplementary material. For supplementary material accompanying this paper visit https://doi.org/10.1017/S1368980024002337

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Ethics of human subject participation. Data in this study were from the Korean Genome and Epidemiology Study (KoGES, 4851-302), National Research Institute of Health, Centers of Disease Control and Prevention, Ministry for Health and Welfare, Republic of Korea. The KoGES was conducted according to the guidelines laid down in the Declaration of Helsinki, and all procedures involving the KoGES participants were approved the Institutional Review Board of all the participating hospitals or institutes. The written informed consent in the KoGES was signed by participants prior to their participation.

References

1. GBD 2017 Risk Factor Collaborators (2018) Global, regional, and national comparative risk assessment of 84 behavioural, environmental and occupational, and metabolic risks or clusters of risks for 195 countries and territories, 1990–2017: a systematic analysis for the Global Burden of Disease Study 2017. *Lancet* **392**, 1923–1994.
2. Schoeneck M & Iggman D (2021) The effects of foods on LDL cholesterol levels: a systematic review of the accumulated evidence from systematic reviews and meta-analyses of randomized controlled trials. *Nutr Metab Cardiovasc Dis* **31**, 1325–1338.
3. Monteiro CA, Cannon G, Levy RB, *et al.* (2019) Ultra-processed foods: what they are and how to identify them. *Public Health Nutr* **22**, 936–941.
4. Juul F, Vaidean G & Parekh N (2021) Ultra-processed foods and cardiovascular diseases: potential mechanisms of action. *Adv Nutr* **12**, 1673–1680.
5. Monteiro CA, Cannon G, Moubarac JC, *et al.* (2018) The UN Decade of Nutrition, the NOVA food classification and the trouble with ultra-processing. *Public Health Nutr* **21**, 5–17.
6. Lim H, Lee HJ, Choue R, *et al.* (2018) Trends in fast-food and sugar-sweetened beverage consumption and their association with social environmental status in South Korea. J Acad Nutr Diet 118, 1228–1236.e1221.
7. Pagliai G, Dinu M, Madarena MP, *et al.* (2021) Consumption of ultra-processed foods and health status: a systematic review and meta-analysis. *Br J Nutr* **125**, 308–318.
8. Lavigne-Robichaud M, Moubarac JC, Lantagne-Lopez S, *et al.* (2018) Diet quality indices in relation to metabolic syndrome in an Indigenous Cree (Eeyouch) population in northern Québec, Canada. *Public Health Nutr* **21**, 172–180.
9. Martínez Steele E, Baraldi LG, Louzada ML, *et al.* (2016) Ultra-processed foods and added sugars in the US diet: evidence from a nationally representative cross-sectional study. *BMJ Open* **6**, e009892.
10. Louzada M, Ricardo CZ, Steele EM, *et al.* (2018) The share of ultra-processed foods determines the overall nutritional quality of diets in Brazil. *Public Health Nutr* **21**, 94–102.
11. Kirkpatrick CF, Sikand G, Petersen KS, *et al.* (2023) Nutrition interventions for adults with dyslipidemia: a clinical perspective from the National Lipid Association. *J Clin Lipidol* **17**, 428–451.
12. Teslovich TM, Musunuru K, Smith AV, *et al.* (2010) Biological, clinical and population relevance of 95 loci for blood lipids. *Nature* **466**, 707–713.
13. Corella D & Ordovas JM (2005) Single nucleotide polymorphisms that influence lipid metabolism: interaction with dietary factors. *Annu Rev Nutr* **25**, 341–390.
14. Kim Y & Han BG (2017) Cohort profile: the Korean Genome and Epidemiology Study (KoGES) consortium. *Int J Epidemiol* **46**, e20.
15. Friedewald WT, Levy RI & Fredrickson DS (1972) Estimation of the concentration of low-density lipoprotein cholesterol in plasma, without use of the preparative ultracentrifuge. *Clin Chem* **18**, 499–502.
16. The Korean Society of Lipid and Atherosclerosis (2022) Korean Guidelines for the Management of Dyslipidemia, 5th ed. Seoul, South Korea: The Korean Society of Lipid and Atherosclerosis.
17. Ahn Y, Kwon E, Shim JE, *et al.* (2007) Validation and reproducibility of food frequency questionnaire for Korean genome epidemiologic study. *Eur J Clin Nutr* **61**, 1435–1441.
18. Kim J, Kim Y, Ahn YO, *et al.* (2003) Development of a food frequency questionnaire in Koreans. *Asia Pac J Clin Nutr* **12**, 243–250.
19. Shim JS, Shim SY, Cha HJ, *et al.* (2021) Socioeconomic characteristics and trends in the consumption of ultra-processed foods in Korea from 2010 to 2018. *Nutrients* **13**, 1120.
20. Kityo A & Lee SA (2023) The intake of ultra-processed foods, all-cause, cancer and cardiovascular mortality in the Korean Genome and Epidemiology Study-Health Examinees (KoGES-HEXA) cohort. *PLoS One* **18**, e0285314.
21. Korea Disease Control and Prevention Agency (2017) Korean Genome and Epidemiology Study User Guideline. (Ministry for Health and Welfare, editor). Cheongju, South Korea: Korea Disease Control and Prevention Agency.
22. Kim YJ, Go MJ, Hu C, *et al.* (2011) Large-scale genome-wide association studies in East Asians identify new genetic loci influencing metabolic traits. *Nat Genet* **43**, 990–995.
23. Kim YK, Moon S, Hwang MY, *et al.* (2013) Gene-based copy number variation study reveals a microdeletion at 12q24 that influences height in the Korean population. *Genomics* **101**, 134–138.
24. Cho YS, Go MJ, Kim YJ, *et al.* (2009) A large-scale genome-wide association study of Asian populations uncovers genetic factors influencing eight quantitative traits. *Nat Genet* **41**, 527–534.
25. Moon S, Kim YJ, Han S, *et al.* (2019) The Korea Biobank Array: design and identification of coding variants associated with blood biochemical traits. *Sci Rep* **9**, 1382.
26. Privé F, Aschard H, Carmi S, *et al.* (2022) Portability of 245 polygenic scores when derived from the UK Biobank and applied to 9 ancestry groups from the same cohort. *Am J Hum Genet* **109**, 12–23.
27. Purcell S, Neale B, Todd-Brown K, *et al.* (2007) PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* **81**, 559–575.
28. Chang CC, Chow CC, Tellier LC, *et al.* (2015) Second-generation PLINK: rising to the challenge of larger and richer datasets. *GigaScience* **4**, 7.
29. Igo RP Jr, Kinzy TG & Cooke Bailey JN (2019) Genetic risk scores. *Curr Protoc Hum Genet* **104**, e95.
30. Cochran WG (1954) The combination of estimates from different experiments. *Biom* **10**, 101–129.
31. Mensink RP, Zock PL, Kester AD, *et al.* (2003) Effects of dietary fatty acids and carbohydrates on the ratio of serum total to HDL cholesterol and on serum lipids and apolipoproteins: a meta-analysis of 60 controlled trials. *Am J Clin Nutr* **77**, 1146–1155.
32. Wijendran V & Hayes KC (2004) Dietary *n*-6 and *n*-3 fatty acid balance and cardiovascular health. *Annu Rev Nutr* **24**, 597–615.
33. Rauber F, da Costa Louzada ML, Steele EM, *et al.* (2018) Ultra-processed food consumption and chronic non-communicable diseases-related dietary nutrient profile in the UK (2008–2014). *Nutrients* **10**, 587.
34. Neves JS, Newman C, Bostrom JA, *et al.* (2022) Management of dyslipidemia and atherosclerotic cardiovascular risk in prediabetes. *Diabetes Res Clin Pract* **190**, 109980.
35. Donat-Vargas C, Sandoval-Insausti H, Rey-García J, *et al.* (2021) High consumption of ultra-processed food is associated with incident dyslipidemia: a prospective study of older adults. *J Nutr* **151**, 2390–2398.
36. Gadelha P, de Arruda IKG, Coelho PBP, *et al.* (2019) Consumption of ultraprocessed foods, nutritional status, and dyslipidemia in school-children: a cohort study. *Eur J Clin Nutr* **73**, 1194–1199.
37. Nouri M, Eskandarzadeh S, Makhtoomi M, *et al.* (2023) Association between ultra-processed foods intake with lipid profile: a cross-sectional study. *Sci Rep* **13**, 7258.

https://doi.org/10.1017/S1368980024002337 Published online by Cambridge University Press

38. Nasreddine L, Tamim H, Itani L, *et al.* (2018) A minimally processed dietary pattern is associated with lower odds of metabolic syndrome among Lebanese adults. *Public Health Nutr* **21**, 160–171.
39. Shim JS, Shim SY, Cha HJ, *et al.* (2022) Association between ultra-processed food consumption and dietary intake and diet quality in Korean adults. *J Acad Nutr Diet* **122**, 583–594.
40. Nardocci M, Leclerc BS, Louzada ML, *et al.* (2019) Consumption of ultra-processed foods and obesity in Canada. *Can J Public Health* **110**, 4–14.
41. Schnabel L, Kesse-Guyot E, Allès B, *et al.* (2019) Association between ultraprocessed food consumption and risk of mortality among middle-aged adults in France. *JAMA Intern Med* **179**, 490–498.
42. Wuni R, Kuhnle GGC, Wynn-Jones AA, *et al.* (2022) A nutrigenetic update on CETP gene-diet interactions on lipid-related outcomes. *Curr Atheroscler Rep* **24**, 119–132.
43. Erkkilä AT, Sarkkinen ES, Lindi V, *et al.* (2001) APOE polymorphism and the hypertriglyceridemic effect of dietary sucrose. *Am J Clin Nutr* **73**, 746–752.
44. Norat T, Bowman R, Luben R, *et al.* (2008) Blood pressure and interactions between the angiotensin polymorphism AGT M235T and sodium intake: a cross-sectional population study. *Am J Clin Nutr* **88**, 392–397.
45. Park SJ, Kim MS, Choi SW, *et al.* (2020) The relationship of dietary pattern and genetic risk score with the incidence dyslipidemia: 14-year follow-up cohort study. *Nutrients* **12**, 3840.
46. Tang H, Zhang Z, Li Z, *et al.* (2017) High-carbohydrate/low-fat diet-induced gender-specific serum lipid profile changes are associated with LEPR polymorphisms in Chinese youth. *Ann Nutr Metab* **70**, 1–8.
47. Mann CJ (2003) Observational research methods. Research design II: cohort, cross sectional, and case-control studies. *Emerg Med J* **20**, 54–60.

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