Diabetes, Metabolic Syndrome and Obesity

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REVIEW

The Interaction Between Body Mass Index Genetic Risk Score and Dietary Intake on Weight Status: A Systematic Review

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Background: The escalating global obesity epidemic and the emergence of personalized medicine strategies point to the pressing need to investigate the interplay between genetic risk scores (GRSs), dietary intake, and their combined impact on weight status. This systematic review synthesizes evidence from diverse studies to elucidate how dietary patterns and individual foods interact with genetic predisposition to obesity.

Methods: Literature searches were conducted in the PubMed, Embase, Science Direct, and Scopus databases until August 2023, following PRISMA guidelines. Out of 575 articles, 15 articles examining the interaction between genetic risk score for body mass index and dietary intake on weight outcomes met the inclusion criteria. All included studies were cross-sectional in design and were assessed for quality using the Newcastle–Ottawa Scale.

Results: Unhealthy dietary intake exacerbated the genetic predisposition to obesity, evident in studies assessing Western diet, sulfur microbial diet, and individual macronutrients, including saturated fatty acids, sugar-sweetened beverages and fried foods. Conversely, adhering to healthier dietary intake mitigated the genetic predisposition to obesity, as observed in studies involving Alternative Healthy Eating Index, Alternative Mediterranean Diet, Dietary Approach to Stop Hypertension scores, healthy plant-based diets, and specific foods such as fruits, vegetables, and n-3 polyunsaturated fatty acids.

Conclusion: This is the first systematic review to explore the interaction between genetics and dietary intake in shaping obesity outcomes. The findings have implications for tailored interventions; however, more controlled clinical trials with robust designs are needed to be able to recommend personalized nutrition based on nutrition for obesity prevention and management.

Keywords: Body Mass Index, Genetic Risk Score, Dietary Intake, Weight Status, Systematic Review

Introduction

Obesity is a complex multifactorial health condition with a profound impact on global public health.[1] The etiology of this morbid disease involves an interplay between genetic predisposition and environmental factors, of which dietary intake is an important modifiable risk factor.[2] In recent years, advanced studies of genetics have given rise to genetic risk scores (GRSs), which represent a summary of an individual's genetic susceptibility to various phenotypes, such as obesity.[3] The GRS represents a predictive genetic model that can be calculated by including all identified risk alleles associated with the investigated phenotype and creating a score.[4] The GRS can be calculated through two methods: a weighted method, which considers the reported magnitudes of effect for the chosen alleles and may be adjusted for the total quantity of risk alleles and their respective effect sizes assessed, or an unweighted approach, which simply involves the summation of the number of risks the person carries in their genetic makeup.[4] Concurrently, research has increasingly recognized that the relationship between dietary intake and obesity is not straightforward, suggesting that genetic factors may modulate the effects of dietary intake on weight status. Genome-wide association studies (GWAS) have identified numerous genetic

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loci linked to body mass index (BMI). Nevertheless, these associations can account for only approximately 3–5% of the BMI variation observed in the general population.[2,5–8]

Dietary intake is a central determinant of energy balance and, consequently, weight status. The distinction between the impact of a comprehensive dietary pattern and the effects of individual foods or nutrients is a noteworthy topic among researchers. Whole diets include the holistic consumption of various foods and nutrients, which reflects the complex interplay of multiple dietary components.[9] This, in turn, can demonstrate the synergistic effects that influence health outcomes in ways that single foods or nutrients may not fully elucidate.[9] In contrast, investigating the effects of individual foods or nutrients refers to a more targeted examination into their specific effects on health. Nonetheless, this approach is valuable for understanding the effect of isolated single dietary components, which enables researchers to mechanisms of action and assess dietary sufficiency.[9] Understanding whether specific dietary patterns and/or foods mitigate genetic predisposition to obesity is crucial for tailoring effective strategies for obesity prevention and management. This systematic review aims to explore the complex relationship between GRSs, dietary intake, and weight status, with a primary focus on understanding how different dietary interventions and/or intakes impact the weight status of individuals with varying GRSs.

Methods

Registration of Protocol and Reporting

The registration of the review protocol on PROSPERO (Record ID: CRD42023452734; https://www.crd.york.ac.uk/prospero/) was completed before finalizing data extraction. Essential details such as the review title, timeline, team composition, methodologies, and general particulars were uploaded onto the PROSPERO register.

Literature Searches

The Preferred Reporting of Systematic Reviews and Meta-Analyses (PRISMA) statement served as the basic guideline followed in this systematic review. Relevant articles were obtained by conducting an extensive search in online databases, including PubMed, Embase, Science Direct, and Scopus, from their respective index dates until August 2023. An additional free-hand search was conducted to ensure the collection of all relevant articles. All possible combinations of the following MeSH terms and test keywords were used to conduct the search: ”BMI” OR “body mass index” AND “GRS” OR “genetic risk score” AND “dietary intake” OR “dietary pattern” AND “obesity” OR ”weight change” OR “overweight” OR “body weight”. Retrieved articles were then imported into Endnote, where duplicates and articles written in non-English languages were excluded. An initial screening was then performed, and articles were evaluated based on the inclusion criteria to then be either included or excluded from this systematic review.

Eligibility Criteria

Scholarly articles were included in the systematic review if they met the following inclusion criteria: adult individuals of any gender; available BMI GRS; studies investigating the impact of different dietary interventions on weight status; studies that compare the effects of various dietary interventions on weight status in individuals with varying GRSs; studies that report quantitative data on weight status outcomes; randomized controlled trials, prospective cohort studies, cross-sectional studies, and case–control studies. On the other hand, articles were excluded if they included individuals with health conditions that may influence weight status independently of GRSs and dietary interventions; exclusively included pediatric or geriatric populations; solely focused on pharmacological or surgical interventions without a significant dietary component; did not assess dietary interventions or did not provide sufficient information on the dietary intervention; did not report weight-related outcomes or have inadequate reporting of these outcomes; did not test the interaction between GRS, dietary intervention and obesity outcomes, animal studies, reviews, editorials, commentaries, and opinion pieces; and studies not published in English.

Study Selection

Screening of the retrieved articles from the comprehensive search was conducted using Rayyan (https://rayyan.ai/). The filtration and screening process was completed by two independent researchers (SS and HA), and any disagreements were resolved by consensus. Following the removal of duplicates, titles and abstracts of studies were screened and classified as

included, excluded or possibly through Rayyan. Studies classified as possible were accessed in full text to decide their inclusion or exclusion. Any study not following our inclusion criteria was excluded. At the end of the screening, the full text of the included articles was obtained to retrieve pertinent information. The PRISMA flow chart demonstrating the details of the screening and selection process is shown in Figure 1.

Data Extraction

The data extraction of the included articles was conducted independently by two authors (SS and HA), and a discussion took place to finalize the extracted data, including information on the study characteristics, which were author details, year of publication, study design, country, study population, cohort name, sample size, age range or mean, percentage of females, and main outcomes (Table 1). We also extracted information regarding the number of SNPs selected in the study; GRS computation method; GRS construction criteria; dietary intervention; dietary assessment method and duration; association analysis model used; nongenetic covariates the model was adjusted for; and main study findings with their respective p values (Table 2).

Quality Assessment

Two authors conducted the quality assessment of the included articles (SS and HA). Since all included studies were cross-sectional in design, the Newcastle–Ottawa Scale (NOS) tool[25] was used for quality assessment. The NOS tool includes three criteria for evaluation, which are selection, comparability, and outcome, each of which can be given a maximum of two points except selection, which can be given a maximum of three points. The quality of the study is indicated by the given number of stars

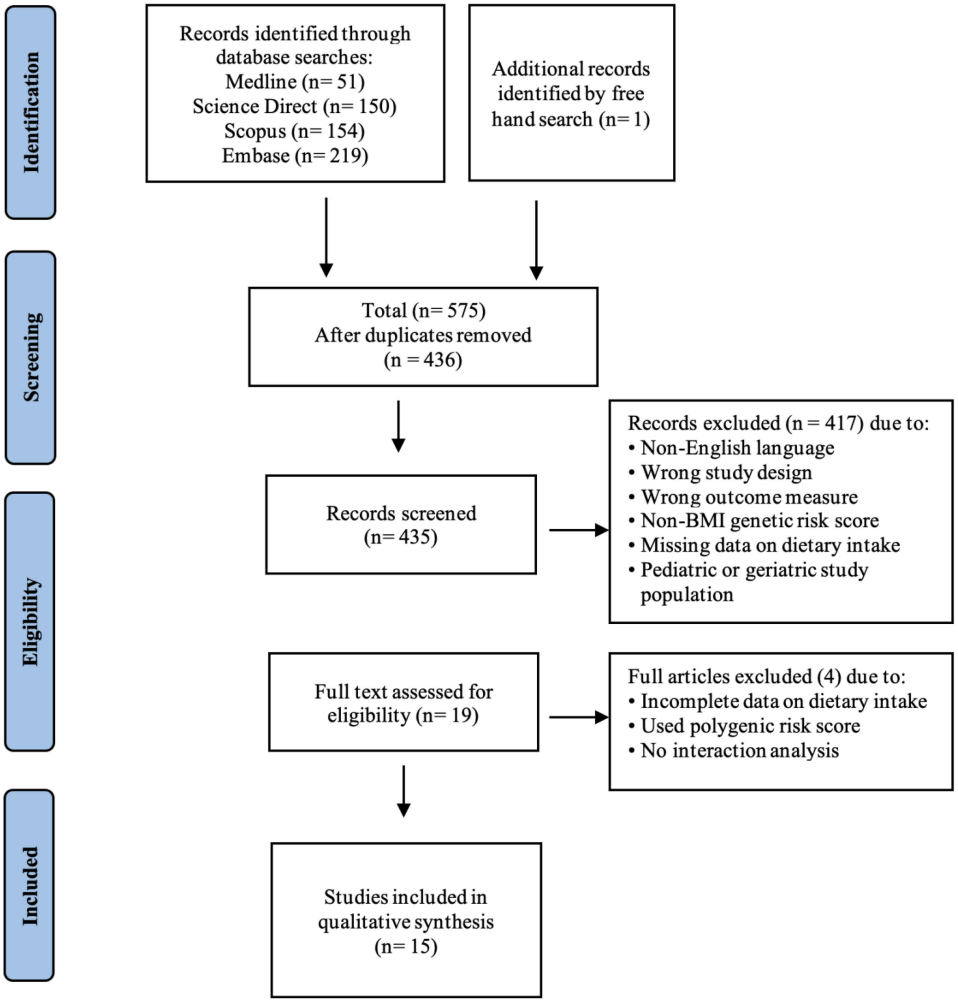

Figure 1 PRISMA flow chart for the study selection process.

Table 1 Description of the Characteristics of Studies Included in the Systematic Review

First Author, Year	Country	Population Description	Cohort Name	Number of Study Participants	Age (Range or Mean ± SD)	% Female	Outcomes
Ding et al, 2018[10]	USA	NHS: female registered nurses HPFS: male health professionals WGHS: female health professionals	Nurses' Health Study (NHS), the Health Professional Follow-up Study (HPFS), and the Women's Genome Health Study (WGHS)	NHS: 5730 HPFS: 3588 WGHS: 21,740 = 31,058 total sample	NHS: 30–55 y HPFS: 40–75 y WGHS: ≥45 y	NHS: 100% HPFS: 0% WGHS: 100%	Mean BMI
Qi et al, 2014[11]	USA	NHS: female registered nurses HPFS: male health professionals WGHS: female health professionals	Nurses' Health Study (NHS), the Health Professionals Follow-up Study (HPFS), and the Women's Genome Health Study (WGHS)	NHS: 9623 HPFS: 6379 WGHS: 21,421 = 37,423 total sample	NHS: 30–55 y HPFS: 40–75 y WGHS: ≥45 y	NHS: 100% HPFS: 0% WGHS: 100%	Mean BMI Risk of obesity
Nettleton et al, 2015[12]	USA, Sweden, Finland, Italy, The Netherlands, Greece.	Various	18 cohorts of European ancestry	68,317	Various	Various	Mean BMI
Nakamura et al, 2016[13]	Japan	Japanese adults	The Yamagata Study (Takahata)	1620	40–87	55.2%	Mean BMI at baseline and change in BMI
Tyrrell et al, 2017[14]	UK	Adults of White British descent	UK Biobank	119,733	37–73	NA	Mean BMI
Jääskeläinen et al, 2013[15]	Finland	High-risk individuals with impaired glucose tolerance and BMI over 25 kg/m2	Finnish Diabetes Prevention Study	459	40–64	66.7%	Obesity-related traits, including weight change
Svendstrup et al, 2018[16]	Denmark	Caucasian women and men with obesity	Nutrient-Gene Interactions in Human Obesity (NUGENOB)	707	20–50	75.4%	Weight change
Heianza et al, 2021[17]	UK	Adults initially free of CVD, diabetes, and cancer.	UK Biobank	121,799	40–69	57.4%	Obesity (as BMI) and untreated hypertension

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Wang et al, 2019[18]	US	NHS: female registered nurses HPFS: male health professionals	Nurses' Health Study (NHS) The Health Professional Follow-up Study (HPFS)	NHS: 8943 HPSF: 5308 Total = 14,251	NHS: 30–55 y HPFS: 40–75 y	NHS: 100% HPFS: 0%	Change in BMI and change in body weight
Lemas et al, 2018[19]	Alaska	Yup'ik people from 11 Southwest Alaskan communities	CANHR (Cultural Anthropology and Human Studies)	1073	14–94 y	52.7%	BMI, percent body fat, thigh circumference, and waist circumference
Brunkwall et al, 2016[20]	Sweden	Adults without prevalent diabetes, cardiovascular disease, and cancer	MDCS (Malmo¨ Diet and Cancer study) GLACIER (Gene-Lifestyle Interactions and Complex Traits Involved in Elevated Disease Risk Study)	MDCS: 21,824 GLACIER: 4902 = 26,726 total sample	MDCS: 57.9±7.7 GLACIER: 49.0 ±8.6	MDCS: 62.1% GLACIER: 62%	BMI
Sandholt et al, 2014[21]	Denmark	A random sample of Danish adults.	Danish Inter99 intervention study	3982	46.7±7.7	50%	Change in body weight
Lui et al, 2023[22]	UK	Adults initially free of CVD, diabetes, and cancer.	UK Biobank	26,252	37–73 y	53.0%	Primary: Obesity Secondary: Increase in BMI, Waist Circumference, and Body Fat Percentage
Hosseini-Esfahani et al, 2019[23]	Iran	Adult residents of District 13 of Tehran, the capital of Iran.	The Tehran Lipid and Glucose Study	4292	Men: 42.6±14 y Women: 40.4 ±13 y	56.8%	Changes in BMI and waist circumference
Qi et al, 2012[24]	US	NHS: female registered nurses HPFS: male health professionals WGHS: female health professionals	Nurses' Health Study (NHS), the Health Professionals Follow-up Study (HPFS), and the Women's Genome Health Study (WGHS)	NHS: 6934 HPFS: 4423 WGHS: 21,740= 33,097 total sample	NHS: 30–55 y HPFS: 40–75 y WGHS: ≥45 y	NHS: 100% HPFS: 0% WGHS: 100%	Mean BMI Risk of obesity

Abbreviations: BMI, body mass index; CVD, cardiovascular disease; NA, Not Available/Not Applicable; UK, United Kingdom; USA, United States of America.

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Table 2 Description of the Utilized Genetic Risk Score, Dietary Intakes, and Main Findings

First Author, Year	Number of SNPs Selected	GRS Computation	GRS Construction Criteria	Dietary Intervention	Dietary Assessment Method and Duration	Association Analysis Model	Non-Genetic Covariates the Model Was Adjusted for	Main Findings
Ding et al, 2018[10]	97 BMI-associated SNPs	Weighted	Each SNP is assigned a weight determined by the per-allele coefficient from a recent GWAS. The weights of total SNPs were rescaled to sum up to 194.	Alternative Healthy Eating Index 2010 (AHEI-2010), Alternative Mediterranean Diet score (AMED), and Dietary Approach to Stop Hypertension (DASH) diet score (The total score ranged from 0 (nonadherence) to 110 (perfect adherence)	Validated 131-item food-frequency questionnaire to obtain usual diet NHS and HPFS: baseline and every 4 y until 2008 WGHS: baseline only	NHS and HPFS: generalized estimation equations WGHS: linear model (diet was only assessed at baseline) Findings across cohorts were pooled using fixed-effects model.	Age, level of physical activity, smoking status, total energy intake, and history of hypertension and hypercholesterolemia +case-control data sets (NHS and HPFS) +geographic region and population structure (WGHS).	Significant interactions observed between total GRS and all 3 diet scores on BMI. • AHEI: P-interaction = 0.003. • AMED: P-interaction = 0.001. • DASH: P-interaction = 0.004. BMI difference per 10-allele increment in GRS: • AHEI: 0.84 (highest tertile), 1.14 (lowest tertile) • AMED: 0.83 (highest tertile), 1.17 (lowest tertile) • DASH: 0.78 (highest tertile), 1.09 (lowest tertile) ↑ red/processed meat, SSBs, and trans-fat = ↑ genetic effect on BMI ↑ fruit and moderate alcohol = ↓ genetic effects on BMI.
Qi et al, 2014[11]	32 BMI-associated SNPs	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	Frequency of fried food consumption, Alternative	Validated 131-item food-frequency questionnaire to obtain usual diet. NHS and HPFS: baseline and every 4 y until 2008 WGHS: baseline only	General linear models, logistic regression models	Age, physical activity, television watching, smoking, alcohol intake, intake of sugar sweetened beverages, alternative healthy eating index, total energy intake, and more (varied among cohorts)	Difference in BMI of highest GRS tertile consuming fried food >4 times/week compared to <1 time/week is 1.0 kg/m² (NHS), 0.7 kg/m² (HPFS). BMI of lowest GRS tertile consuming fried food >4 times/week compared to <1 time/week is 0.5 kg/m² (NHS), 0.4 kg/m² (HPFS). BMI per increment of 10 risk alleles were NHS: 1.3, 1.8 and 2.3 kg/m² HPFS: 0.7, 0.9, and 1.2 kg/m² WGHS: 1.4, 2.0, and 3.1 kg/m² For participants consuming fried food <1, 1–3 times, and ≥4 times/week, respectively. From all 3 cohorts: odds ratios for obesity per 10 risk alleles were 1.61, 2.12, and 2.72 for total fried food consumption of <1, 1–3 times, and ≥4 times/week, respectively.

Nettleton et al, 2015[12]	32 SNPs for BMI and 14 SNPs for WHR	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	"CHARGE" diet score (Based on intakes of whole grains, fish, fruits, vegetables, nuts/seeds (favorable) and red/ processed meats, sweets, sugar-sweetened beverages and fried potatoes (unfavorable)) Score range: 0–27	Self-reported food frequency questionnaire and/or diet records.	Multivariable adjusted, linear regression model followed by inverse variance-weighted, fixed-effects meta-analysis	Age, sex, energy intake, and study center, Additionally for education, physical activity, smoking, and alcohol intake.	Each additional 10 risk alleles in the BMI-GRS = 1.16 kg/m^2 higher BMI (p-value = 1.97×10^{-124}) Diet score did not modify the association between the BMI-GRS and BMI (Pinteraction = 0.79) ↑ diet score = ↑ association of WHR-GRS with BMI-adjusted WHR (Pinteraction = 0.04).
Nakamura et al, 2016[13]	29 BMI-associated SNPs	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	Nutritional intake in grams, including macronutrients (carbohydrates, fats, proteins), and fiber intake.	Brief self-administered diet history questionnaire.	Multivariate linear regression models	Age, sex, metabolic equivalents-hours per day, energy intake, homeostasis model assessment ratio (HOMA-R), Brinkman index, alcohol intake, carbohydrate intake, fat intake, protein intake, and fiber intake.	↑ GRS = ↑ baseline BMI with ↑ fiber intakes (+0.15 kg/m^2 per g, p=0.01). ↑ GRS = ↓ baseline BMI with ↑ Vegetable fat (−0.05 kg/m^2 per g; P=0.004) and ↑ animal protein intakes (−0.05 kg/m^2 per g; P=0.005).
Tyrrell et al, 2017[14]	69 BMI-associated SNPs	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	Using the food frequency questionnaires data, Fizzy-drink consumption, fried-food intake, percentage protein, percentage fat, and calorie-dense 'Western' diet were assessed.	24-h food frequency questionnaires. At least once and up to 5 times.	Linear regression models	Age, sex, five ancestry principal components, assessment center location, and genotyping platform.	No significant association was found between any dietary component and weight outcomes at different GRS.
Jääskeläinen et al, 2013[15]	26 SNPs for BMI and 14 SNPs for WHR	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	Total energy, macronutrients, and fiber	3-day food record, at baseline, 1-year, and 3-year	Univariate general linear model analyses and multiple linear regression analyses	Age, sex, and intervention success scores	↓ fiber intake and ↑ BMI GRS tertile groups = ↑ BMI (P = 0.051) Saturated fatty acids intake modified the association between GRS and BMI (P for interaction = 0.004) No significant interaction between carbohydrate/ high fiber/ energy intake and GRS on BMI

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Table 2 (Continued).

First Author, Year	Number of SNPs Selected	GRS Computation	GRS Construction Criteria	Dietary Intervention	Dietary Assessment Method and Duration	Association Analysis Model	Non-Genetic Covariates the Model Was Adjusted for	Main Findings
Svendstrup et al, 2018[16]	47 SNPs associated with waist-hip-ratio adjusted for body mass index (WHRadjBMI)	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	Hypocaloric low-fat/high-carbohydrate diet and a hypocaloric high-fat/low-carbohydrate diet.	Weekly visits to dietitian throughout the 10-week intervention	Linear mixed model	Age, sex, and diet adherence	The type of intervention diet did not have a significant interaction with the GRS in relation to weight loss
Heianza et al, 2021[17]	75 SNPs associated with BMI	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	Healthful plant-based diet index (hPDI)	At least one web-based 24-hour dietary assessment (Oxford WebQ questionnaire) during 2009–2012.	General linear models and logistic regression	Age, sex, and the top 5 principal components of ancestry, demographic, lifestyle, and other dietary factors.	↑ hPDI and ↑ GRS = stronger association with lower (↓) BMI (P for interaction <0.0001)
Wang et al, 2019[18]	77 BMI-associated SNPs	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	Total fruits, total vegetables, in addition to subgroups of fruits and vegetables categorized by nutritional components, fiber content, and glycemic load.	Validated 131-item semiquantitative food frequency questionnaire administered every 4 years.	Multivariable generalized linear models with repeated-measures analyses. results for the 2 cohorts were pooled by means of inverse-variance-weighted fixed-effects meta-analysis.	Demographics, lifestyle factors, medical history, total energy intake, diet quality (Alternative Healthy Eating Index), and physical activity.	↓ fruits and vegetables intake with ↑ GRS = ↑ BMI (p = 0.001) Each increased daily serving of fruits and vegetables attenuated BMI change by 0.053 kg/m^2 and 0.024 kg/m^2 per 10-risk allele increment, respectively (P-interaction <0.001 for both). Berries, citrus fruits, and green leafy vegetables showed interactions with genetic risk score on BMI change (all negatively associated, all P-interaction ≤0.04).

Lemas et al, 2018[19]	10 SNPs associated with high BMI (>25 kg/m^2)	Unweighted	Summing BMI-increasing alleles across the 10 SNPs	Intake of n-3 PUFAs (EPA and DHA).	Nitrogen stable isotope ratio (d15N) of red blood cells (Validated biomarker for EPA and DHA intake)	Linear models	Demographic covariates (age, sex, community group), environmental covariate (d15N) as an estimate of n-3 PUFA intake Sensitivity analysis: total energy and total fat (% kcal)	GRS interactions with n-3 PUFA intake were significant for BMI ($p = 0.011$), PBF ($p = 0.025$), and WC ($p = 0.018$). ↑ n-3 PUFA intake (Q4) with ↑ GRS (T3) = ↑ BMI ↑ n-3 PUFA intake (Q4) with ↓ GRS (T1) = lower BMI
Brunkwall et al, 2016[20]	30 BMI-associated SNPs	Unweighted	The unweighted GRS was generated by summing up the risk alleles at each of the 30 loci assuming an equal magnitude of effect at each locus. A weighted GRS was then generated, each locus was weighted by its previously reported main effect on BMI. Then, the weighted GRS was transformed back to the same scale as the unweighted GRS and used in reporting the results.	Sugar-sweetened beverages (SSBs) intake. Artificially sweetened beverages (ASB) intake (only in MDCS)	MDCS: 1) a 7-d menu booklet. 2) a 168-item food-frequency questionnaire. 3) a 45-min interview. GLACIER: self-administered validated semiquantitative food-frequency questionnaire.	Generalized linear equations	Age, sex, and cohort-specific covariates. A second model was included that additionally adjusted for physical activity, smoking, alcohol consumption, and total energy intake.	• Significant interaction between GRS and SSB intake on BMI in pooled analysis (P-interaction = 0.02), slightly reduced with lifestyle adjustment (P-interaction = 0.03). Lifestyle-adjusted analysis with dichotomized SSB intake: • Each 10-unit ↑ GRS associated with mean ↑ 1.31 BMI (SE = 0.11) for medium-to-high SSB intake ($P = 1.2\times10^{-33}$) ○ Equivalent to 3.8 kg in weight for a person 1.70 m tall • Each 10-unit ↑ GRS associated with mean ↑ 0.83 BMI (SE = 0.09) For seldom/low SSB intake ($P = 6.0\times10^{-21}$) ○ Equivalent to 2.4 kg in weight for a person 1.70 m tall SSB intake-BMI association ↑ by GRS quartile: • ↑ 0.15 BMI in lowest GRS quartile compared to ↑ 0.24 BMI in highest GRS quartile ($P = 2.9\times10^{-28}$). No GRS and BMI association modification by ASB intake observed in MDCS. Consistent results in weighted and unweighted GRS analyses.

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Table 2 (Continued).

First Author, Year	Number of SNPs Selected	GRS Computation	GRS Construction Criteria	Dietary Intervention	Dietary Assessment Method and Duration	Association Analysis Model	Non-Genetic Covariates the Model Was Adjusted for	Main Findings
Sandholt et al, 2014[21]	30 BMI-associated SNPs	Unweighted and weighted	Unweighted: Sum of the BMI increasing alleles for each individual Weighted: not mentioned.	Three-point dietary score (1- unhealthy, 2-moderate, and 3-healthy) Fruits, raw and boiled vegetables, vegetarian dishes, fish, fat, alcohol	Food frequency questionnaire, done both at baseline and follow-up	Linear regression models	Age, sex, baseline levels of the trait of interest, lifestyle factors (physical activity, diet intake, alcohol consumption, smoking habits, educational level)	• No association between GRS and changes in body weight over five years (p = 0.49) • Healthier diet associated with decreased body weight gain (p = 0.00029) • Less alcohol consumption associated with decreased body weight gain (p = 0.01 • No significant interactions between GRS and changes in lifestyle factors for body weight changes (including dietary habits)
Lui et al, 2023[22]	940 SNPs associated with BMI	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size	Sulfur microbial diet score (seven food groups, including foods with positive associations (Processed meats, liquor, and low-calorie drinks) and those with negative associations (beer, fruit juice, legumes, other vegetables, and sweets or desserts) score was calculated based on summing weighted food intake.	Oxford WebQ (online 24-h diet recall) on five separate occasions between 2009 and 2012	Cox proportional hazards models	Age, sex, race, centers, education level, TDI, household income, alcohol consumption, physical activity, sleep quality, and total energy intake, initial BMI, WC, or BF%. Sensitivity analysis: further adjusted for history of hypertension or diabetes, vitamin or mineral supplements, sedentary time, and Western dietary score.	• Both sulfur microbial diet score and overall GRS were independently and positively associated with the risk of obesity (all P-interaction >0.05). • Highest risk of obesity and abdominal obesity observed among individuals with high GRS and highest quartile of sulfur microbial diet score (HR: 1.74 for obesity; HR: 1.41 for abdominal obesity). • Sulfur microbial diet score showed significant positive association with BMI, WC, and BF% at the last assessment across all levels of genetic risk (all P < 0.001).
Hosseini-Esfahani et al, 2019[23]	6 BMI-associated SNPs	Weighted	Each SNP was coded 0, 1 or 2 based on the number of effect alleles and weighted based on its effect size. Divided into two groups based on the median GRS	Healthy dietary pattern score vs Western dietary pattern score.	A valid and reliable 168-item semi-quantitative food-frequency questionnaire	General linear models	Sex, age, education levels, smoking status, baseline physical activity, BMI, and energy intake.	↑ GRS + ↑ Western diet (WD) = ↑ BMI and WC compared to low GRS. BMI change in high GRS individuals; Q1 WD: 1.04 vs Q4 WD: 2.26 kg/m^2) (P-interaction = 0.04) WC change in high GRS individuals; Q1 WD: 0.47 vs Q4 WD: 0.95 cm) (P-interaction = 0.01)

Abbreviations: BMI, body mass index; DHA, docosahexaenoic acid; EPA, eicosapentaenoic acid; GRS, genetic risk score; GWAS, genome wide association studies; HR, hazard ratio; PUFA, poly unsaturated fatty acids; SNP, single nucleotide polymorphism; WHR, waist to hip ratio.

in the NOS tool, where 6–7 stars indicate high quality, 3–5 stars indicate moderate quality, and 0–2 stars indicate poor quality. The details of the quality assessment are shown in Table 1.

Results

Search Outcome

The results of the initial screening of abstracts and of full texts with reasons for exclusion are shown in the PRISMA flow chart in Figure 1. The extensive search of multiple databases resulted in the identification of 575 records. An additional study was identified although a free-hand search. After removal of duplicates, 436 records remained and were evaluated against our inclusion criteria, which resulted in the exclusion of 417 records. The remaining 19 studies were assessed by their full texts, resulting in the exclusion of 3 articles for either using a polygenic risk score, having incomplete or missing data on dietary intake, or not conducting an interaction analysis. This resulted in a total of 15 studies being included in the qualitative synthesis of this review, all of which were cross-sectional studies.

Quality of Selected Studies

The quality assessment of included studies, shown in Table 3, was completed using the NOS tool modified for cross-sectional design.[25] Out of the 15 studies, only one study received the full 7 stars, indicating a high quality and low risk of bias.[17] Additionally, ten studies received a 6-star rating, also indicating high quality and low risk of bias in these studies.[12–16,19–23] The remaining four studies received an overall rating of 5 stars, indicating a moderate quality and

Table 3 Quality Assessment of Included Studies Using Newcastle-Ottawa Quality Assessment Scale Criteria for Cross-Sectional Studies

Study	Selection			Comparability	Outcome		Final Quality Score
	Representativeness of the Sample	Non-Respondents	Ascertainment of the Exposure (Risk Factor)	The Potential Confounders Were Investigated by Subgroup Analysis or Multivariable Analysis	Assessment of the Outcome	Statistical Test	
[10]	*	–	*	**	–	*	5 - Moderate
[11]	*	–	*	**	–	*	5 - Moderate
[12]	*	–	*	**	*	*	6 - High
[13]	*	–	-	**	*	*	6 - High
[14]	*	–	*	**	*	*	6 - High
[15]	*	–	*	**	*	*	6 - High
[16]	*	–	*	**	*	*	6 - High
[17]	*	*	*	**	*	*	7 - High
[18]	*	–	*	**	–	*	5 - Moderate
[19]	*	–	*	**	*	*	6 - High
[20]	*	–	*	**	*	*	6 - High
[21]	*	–	*	**	*	*	6 - High
[22]	*	–	*	**	*	*	6 - High
[23]	*	–	*	**	*	*	6 - High
[24]	*	–	*	**	–	*	5 - Moderate

Notes: (*)Reflects one point awarded; (–)Reflects no points awarded..

moderate risk of bias.[10,11,18,24] The quality of the included studies was high overall, and the risk of bias was low. Most studies lost stars due to not reporting the characteristics of nonrespondents, which is not crucial for our systematic review, as most studies included participants with available data from large cohorts to conduct analyses.

Characteristics of Included Studies

The key characteristics of the included studies are shown in Table 2. The studies are published over the period of 11 years, between 2012 and 2023, with the majority being published between 2013 and 2019 (80%). The studies were conducted on various study populations; 4 studies included cohorts from the US, while seven others included cohorts from European populations such as the UK, Sweden, Denmark, and Finland. The remaining studies were conducted in Japan (n=1), Alaska (n=1), Iran (n=1), and one large study including populations from the US, Sweden, Finland, Italy, The Netherlands, and Greece. Most studies included a large number of participants, ranging from 84 to 121,799 participants. The ages of the participants were mostly in their 30s and 40s, and only one study[19] included participants aged 14 to 94 years. Participants were mainly healthy individuals free of disease, but one study included overweight people with impaired glucose tolerance.[15] The main outcomes of the included studies were mostly mean BMI or other body fatness indicators, such as risk of obesity, weight change, BMI change, percent body fat (%BF), thigh circumference, waist circumference (WC), total abdominal fat, visceral fat, and subcutaneous fat.

Genetic Risk Score Characteristics

The number of SNPs used in the generation of the GRSs ranged from 6 to 940 SNPs. To include the genetic variation in the prediction models, the weighted method was used by the majority of the studies (n= 12), and the remaining studies used the unweighted method (n= 1) or both methods (n= 2). Most of the included studies selected the SNPs they included from previously published genome-wide association studies (GWAS) or from other published association studies that showed a high correlation between chosen SNPs and BMI.

The Influence of Comprehensive Dietary Interventions

The influence of dietary interventions was assessed in the included studies in two different approaches; 11 studies tested the effect of dietary patterns or whole diet interventions out of the 15 studies included in this systematic review. Ding et al[10] obtained dietary information using a validated food frequency questionnaire (FFQ) from 31,058 participants living in the US. The authors generated scores for the Alternative Healthy Eating Index 2010 (AHEI), Alternative Mediterranean Diet (AMED), and Dietary Approach to Stop Hypertension (DASH). The weighted GRS used was computed based on 97 BMI-associated SNPs. The study found that the difference in BMI per 10-allele increment of the GRS was smaller among participants with higher diet scores, reflecting higher adherence, than among those with lower scores. This indicates that adhering to healthier diets may attenuate the genetic predisposition to body adiposity. This was consistent for the three cohorts included in the study (NHS, HPFS, and WGHS). Another study by Nettleton et al[12] assessed the healthfulness of dietary intake of participants in 18 cohorts by the "CHARGE diet" score, where a higher score reflects a healthier eating pattern. The study included 68,317 participants of European ancestry and constructed a weighted GRS based on 32 SNPs associated with BMI and 14 SNPs associated with waist-to-hip ratio (WHR). The results showed that a higher GRS resulted in a higher mean BMI (1.16 kg/m^2 increase for each additional 10-risk allele); however, CHARGE diet scores did not modify this association ($P_{interaction}$ = 0.79). In the Danish population, 707 Caucasian participants in the Nutrient-Gene Interactions in Human Obesity (NUGENOB) cohort were assigned to either a hypocaloric low-fat/high-carbohydrate diet or a hypocaloric high-fat/low-carbohydrate diet.[16] The weighted GRS used was based on 47 SNPs associated with WHR adjusted for BMI. Adhering to either of the diets did not have a significant interaction with the GRS in relation to weight change/loss. Additionally, in the Danish population, Sandholt et al[21] included a random sample of 3982 healthy adults from the Danish Inter99 intervention study and obtained their dietary information using an FFQ at baseline and at follow-up. The GRS used was computed as both weighted and unweighted and was based on 30 BMI-associated SNPs. A three-point dietary score (1- unhealthy, 2- moderate, and 3- healthy) was generated. No interaction was observed between GRS and any lifestyle change, including dietary intake, in relation to body weight change. A similar diet score was generated by Hosseini et al[23] using semiqualitative FFQ data for 4292 Iranian adults. However, the participants' intake was categorized into either a healthy dietary pattern or a Western dietary pattern score. The GRS used was based on 6 SNPs associated with BMI. The study found that individuals with a higher genetic predisposition to obesity and consuming a Western diet

experienced higher BMI and waist circumference (WC) changes at follow-up than individuals with a lower GRS. Specifically, individuals with high GRS who were in the first quartile of the Western diet score had a higher BMI by 1.04 kg/m^2, while those in the fourth quartile had a 2.26 kg/m^2 higher BMI ($P_{interaction}$ = 0.04). Similarly, WC increased by 0.47 cm vs 0.95 cm in individuals in the Q1 and Q4 western diet scores, respectively, and these individuals are highly genetically predisposed to obesity ($P_{interaction}$ = 0.01).[23] Thus far, the results are pointing at either the weight gain accelerating effect or the absence of an effect of adhering to an unhealthy eating pattern such as a Western diet while having high genetic susceptibility to obesity. To investigate the effect of following a healthy eating pattern such as a healthy plant-based diet, Heianza et al[17] used the genetic, anthropometric and dietary information of 121,799 participants in the UK Biobank cohort to investigate this interaction. The weighted GRS computed in this study was based on 75 BMI-associated SNPs. The study found that a higher healthy plant-based diet index and having high GRS increased the strength of association with a lower BMI ($P_{interaction}$ < 0.0001). An interesting study on the same British cohort investigated the influence of adhering to a sulfur microbial diet on obesity, BMI, WC, and body fat percentage (BF%) at varying GRSs.[22] The analysis revealed that the highest risk of obesity and high abdominal obesity was observed among individuals with high GRS and the highest quartile of sulfur microbial diet score (HR: 1.74 for obesity; HR: 1.41 for abdominal obesity). In addition, regardless of the GRS, a high sulfur microbial diet score was significantly associated with higher BMI, WC, and BF% (all p < 0.001).

The Influence of Individual Foods or Nutrients

Several studies have investigated the influence of single foods or specific macronutrients on obesity outcomes in individuals with varying genetic susceptibilities, such as sugar-sweetened beverages, fried foods, fruits and vegetables, fiber, and n-3 polyunsaturated fatty acids. In the Finnish population, Jääskeläinen el al. included 459 overweight participants with impaired glucose tolerance who had records of their dietary intake for 3 days at baseline and at the 1-year and 3-year follow-ups.[15] The study computed a weighted GRS using 26 SNPs for BMI and 14 SNPs for WHR. The results showed that participants with low fiber intake and high GRS reported high BMI (p = 0.051), and saturated fatty acid intake significantly interacted with GRS and BMI ($P_{interaction}$ = 0.004). Meanwhile, consuming high or low carbohydrate, high fiber, and high or low energy intakes did not modify the association between GRS and BMI.[15] Among the Japanese population, Nakamura et al[13] found that a higher GRS was associated with a higher baseline BMI among participants with high fiber intake (0.15 kg/m² per g, p=0.01). On the other hand, a higher intake of vegetable fat and animal protein was associated with a lower baseline BMI and a higher genetic predisposition to obesity (−0.05 kg/m² per g; P=0.004 and −0.05 kg/m² per g; P=0.005, respectively). These results are controversial, as fiber intake is mainly associated with health-promoting effects and lower body weight through multiple mechanisms. Meanwhile, saturated fatty acids are considered harmful and cause weight gain and cardiovascular diseases when consumed in excess. Other results from this study were discrepant with established and previous knowledge, suggesting a potential uncontrolled confounder in the study. The authors computed a weighted GRS based on 29 BMI-associated SNPs. Qi et al[24] conducted one of the oldest studies investigating the effect of dietary intake on obesity outcomes at varying BMI GRSs. The study included 33,097 individuals from three large US cohorts, the Nurses' Health Study (NHS), the Health Professionals Follow-up Study (HPFS), and the Women's Genome Health Study (WGHS), with available data on their sugar-sweetened and artificially sweetened beverage consumption levels (SSB and ASB). Notably, NHS and WGHS are cohorts exclusively composed of females, while HPFS is a cohort exclusively composed of males. The weighted GRS in this study was computed based on 32 SNPs associated with BMI. After pooling the results from the three cohorts, the study found that for each 10 risk alleles, the increment increase in BMI was higher by 1.00, 1.20, 1.37, and 1.85 kg/m2 for individuals consuming SSB at <1 serving/month and 1–4 serving/month, respectively. 2–6 servings/week, and >1 serving/day, respectively ($P_{interaction}$ <0.001). Since fat-mass and obesity (FTO)-related gene loci are well known to have a strong effect on BMI, the investigators performed a sensitivity analysis to ensure that the results were not derived only from the genetic effect of this gene and obtained similarly strong results ($P_{interaction}$ <0.001 in the pooled data). On the other hand, consumption of ASB did not influence the association between GRS and mean BMI. In addition, the pooled results from the 3 cohorts showed that consuming SSB <1 serving/month, 1–4 serving/month. 2–6 servings/week, and >1 serving/day increased the risk for obesity incidence by 1.35, 1.59, 1.56, and 3.35, respectively ($P_{interaction}$ < 0.001). The study also showed that one daily serving of SSB consistently increased the BMI across the quartiles of GRS in the three

cohorts. The pooled results showed the strongest association in individuals in the highest GRS quartile (β coefficient = 0.44, P = 0.003) compared to the lowest GRS quartile (β coefficient = −0.07, P = 0.36) ($P_{interaction}$ <0.001). The same group of researchers investigated the effect of the frequency of fried food (FF) consumption on obesity outcomes using the same 32 BMI-associated SNPs to calculate a weighted GRS.[11] The investigators found that among individuals with the highest GRS tertile, the difference in mean BMI between people consuming FF more than 4 times per week and people consuming less than once a week was 1.0 kg/m² in the NHS cohort and 0.7 kg/m² in the HPFS cohort. These results were also significant in the WGHS cohort. In addition, the association between FF and BMI became stronger with each additional 10-risk allele in the GRS, and BMI increased by 1.1, 1.6, and 2.2 kg/m^2 for total FF consumption <1 time, 1–3 times, and ≥4 times/week, respectively, in the pooled cohorts. Finally, the researchers found an increased odds ratio (95% confidence interval) for obesity as the GRS increased in 10-risk allele increments. Total FF consumption of <1, 1–3, and ≥4 times/week was associated with 1.61 (1.40–1.87), 2.12 (1.73–2.59), and 2.72 (2.12–3.48) increased odds for obesity, respectively.[11] Brunkwall et al[20] sought to replicate the study by Qi et al among 26,726 individuals from two Swedish cohorts. The authors computed both a weighted and unweighted GRS based on 30 SNPs associated with BMI. Similarly, the study found a significant interaction between SSB intake and GRS on BMI outcomes in the pooled analysis ($P_{interaction}$ = 0.02). When SSB intake was categorized into either seldom to low or medium to high intake, each 10-risk allele increase in the GRS corresponded to a mean BMI increase of 1.31 kg/m^2 for medium-to-high SSB intake ($p = 1.2\times10^{-33}$) and 0.83 kg/m^2 for seldom/low intake ($p = 6.0\times10^{-21}$). This is equivalent to 3.8 kg and 2.4 kg in weight for a person 1.70 m tall, respectively. In addition, the association between SSB intake and BMI became stronger at higher GRS quartiles, where 1 increment of SSB intake caused a 0.15 kg/m^2 (95% CI: 0.08, 0.24) increase in BMI for individuals in the lowest quartile of GRS compared to 0.24 kg/m^2 (95% CI: 0.15, 0.32) for individuals in the highest quartile, according to the pooled analysis (all p < 0.01). Artificially sweetened beverage intake was assessed in one of the cohorts only (ie, Malmo¨ Diet and Cancer Study), and it did not affect the association between GRS and BMI outcome.[20] An interesting study by Lemas et al[19] aimed to assess the influence of n-3 polyunsaturated fatty acids (PUFAs) on body fatness indicators at varying GRSs for BMI. The study included 1073 Yup'ik adults, one of the indigenous groups in southwestern Alaska, and n-3 PUFA intake was assessed using the nitrogen stable isotope ratio (δ15 N) of red blood cells, which is a validated biomarker for EPA (eicosapentaenoic acid) and DHA (docosahexaenoic acid). The fatty acids EPA and DHA are two specific types of n-3 PUFA involved in multiple anti-inflammatory and developmental functions. The analysis used an unweighted GRS based on 10 SNPs associated with high BMI (>25 kg/m^2) and found a significant interaction between GRS, n-3 PUFAs and BMI (p = 0.011), percentage body fat (p = 0.025), and WC (p = 0.018). Statistical analysis also showed that individual intake of n-3 PUFAs significantly modified the association between GRS and BMI outcome. At high n-3 PUFA intake levels (Q4), individuals with high GRS (T3) had the highest BMI (~ 34.8 kg/m^2), while high n-3 PUFA intake levels (Q4), while having low GRS levels, resulted in lower BMI outcomes (~ 31 kg/m^2). These associations remained consistent even after adjusting for total fat intake or total energy intake in a sensitivity analysis. To assess the effect of healthy dietary components, Wang et al[18] used two US cohorts (NHS and HPFS) and included 14,251 total participants to assess the effect of fruit and vegetable consumption on BMI change and body weight change. The weighted GRS was computed based on 77 BMI-associated SNPs derived from a genome-wide association study (GWAS). The results from the combined cohorts showed that individuals with the highest genetic risk and who consumed low fruits and vegetables showed the highest increase in BMI every 4 years over a 20-year follow-up period. In addition, individuals with high GRS were most sensitive to the influence of fruit and vegetable intake; as a result, people with the highest fruit and vegetable intake experienced a decrease in BMI or no weight gain over the follow-up period. Specifically, per 10-risk allele increment, each additional daily serving of fruits attenuated 0.053 kg/m^2 of BMI change, while an extra daily serving of vegetables attenuated 0.024 kg/m^2 of BMI change, corresponding to 0.13 kg and 0.05 kg weight loss. ($P_{interaction}$ <0.001 for both). Analysis of certain groups of fruits and vegetables revealed that berries, citrus fruits, and green leafy vegetables significantly interacted with genetic risk score on BMI change, all of which were negatively associated with BMI change (all $P_{interaction} \leq 0.005$). Last, Tyrell et al[14] assessed the influence of 12 measures of an obesogenic environment, including frizzy drink consumption, fried food intake, percentage protein, percentage fat, and a calorie-dense Western diet score, on weight outcomes at different GRSs. The study used a weighted

GRS computed based on 69 BMI-associated SNPs. The analysis included 119,733 British adults from the UK Biobank and revealed no significant association between any dietary component and mean BMI at various GRSs.

Discussion

Given the global obesity epidemic and the growing interest in personalized medicine approaches, there is a pressing need to comprehensively evaluate the interplay between GRSs and dietary intake in shaping weight status. This systematic review demonstrated the influence of dietary patterns and individual foods or macronutrients. The genetic predisposition to higher BMI and obesity was exacerbated by following certain unhealthy eating patterns and individual foods. The differential effect was significant in multiple studies, and individuals genetically predisposed to obesity were affected more severely by these unhealthy eating patterns. This effect was observed after consuming a western diet[23] and a sulfur microbial diet.[22] The Western diet is characterized by a high intake of processed and fast foods rich in sugars, unhealthy fats, and red meats. It typically includes low consumption of fruits, vegetables, whole grains, and dietary fiber.[26] The link between this dietary pattern and health issues such as obesity, cardiovascular diseases, and diabetes is well established.[26] A sulfur microbial diet is composed of foods that promote the production of sulfur by sulfur-reducing bacteria present in the human gut microbiome. Examples of these foods are red meats, seafood, garlic, onions, leeks, and cruciferous vegetables, which are rich in sulfur-containing amino acids.[27] This diet is biologically known to potentially induce obesity due to high production of sulfur, which disrupts gut permeability, allows more nutrients to pass into the bloodstream and therefore more energy uptake, and promotes absorption of lipopolysaccharides into the bloodstream, which further worsens body inflammation.[28,29] On the other hand, following a healthy eating pattern attenuated the impact of genetic predisposition in multiple studies, such as following AHEI, AMED and DASH diets[10] and consuming a healthy plant-based diet.[17]

Individual foods were also found to have a particular weight-gaining effect on highly genetically predisposed individuals compared to those less genetically predisposed. This includes the consumption of sugar-sweetened beverages[20,24] and fried foods,[11] both of which increased BMI in a dose-dependent manner. In addition, fiber,[13,15] saturated fatty acids,[15] animal protein and vegetable fat[13] showed conflicting results in the two studies. In addition, n-3 PUFAs were found to have an anti-obesogenic effect in individuals with a low genetic predisposition to obesity, and this association was determined to be derived mainly from n-3 PUFA intake rather than the consumption of a traditional dietary pattern high in fat and/or calories.[19] Consuming fruits and vegetables was also shown to attenuate weight gain in individuals with high GRS.[18] In contrast, no influence was observed for the consumption of artificially sweetened beverages on body weight status at varying GRSs in the American population[24] or in the Swedish population.[20] Additionally, energy and carbohydrate intake did not affect the association between GRS and BMI.[15] Multiple studies testing the influence of dietary patterns found no interaction between genetic predisposition and body weight outcomes.[12,16,21]

It is important to point out that systematic errors are specifically relevant biases in obesity-related research. These biases can occur when individuals either overreport or underreport their dietary intake, especially in overweight or underweight participants. This bias may also arise due to participants often being well informed about the connections between lifestyle choices and body weight, which could influence how they respond to questions about their habits. All studies included in the systematic review used data from large cohorts, and evaluating lifestyle accurately in large study populations is challenging, but differentiating the effect of perceived lifestyle factors from the unmeasured factors associated with genetic susceptibility is another important challenge yet to be overcome. These aspects warrant using more precise tools to assess diet, especially in gene-diet interaction studies. In addition, possible reverse causation is that food-related behavioral responses such as appetite, energy intake levels and macronutrient preferences may be influenced by adiposity-associated genetic variants.[30–32] Accordingly, food preferences have been recently shown to be partially genetically determined, such as a high consumption of sugar and carbohydrates.[33,34] The findings of this research suggest the potential application of the GRS in preventive medicine. Integrating the domain of gene–environment interactions in preventive medicine involves assessing how genetic factors alter the impact of lifestyle elements on obesity within intervention strategies.[35,36]

Strengths and Limitations

There are multiple strengths in this systematic review. To our knowledge, this is the first systematic review to evaluate the interaction between GRS and dietary intake on weight status and summarize almost all the available evidence regarding this

association. In addition, a rigorous systematic approach was followed to develop this review, such as the PRISMA guidelines and the Rayyan application, which was used to perform initial screening and enabled the research team to conduct blind review that would enhance the credibility of the findings. Additionally, the studies included were conducted on a large number of participants, which were relatively homogenous for their age (30s and 40s) and their health status (all were healthy at baseline except one study). Additionally, the studies included in this systematic review were conducted in various countries, which allows us to see the influence of dietary intake on body weight in individuals with various genetic backgrounds. Furthermore, the quality of the included studies was mainly high, and only four out of fifteen studies were of moderate quality, which indicates that the evidence drawn from these studies is unlikely to be biased or the result of other uncontrolled confounding factors. On the other hand, this systematic review has a few limitations, such as including only cross-sectional studies, which are observational in design. This gives rise to the need for clinical controlled trials with strong methodologies to be able to extract robust conclusions about the association between GRS and dietary intake and their effect on weight outcomes. Moreover, selected studies were heterogeneous for the number of selected SNPs and method of GRS calculation. Finally, our review exclusively incorporated English-language articles while excluding all papers written in foreign languages, thus limiting the available evidence to English literature only.

Conclusion

This systematic review explored the interplay between GRSs, dietary intake, and weight outcomes, and the synthesis of evidence from diverse studies revealed that dietary patterns and individual foods exert differential effects on individuals with varying genetic predispositions to higher BMI and obesity. Unhealthy dietary patterns such as Western diet and sulfur microbial diet exacerbated genetic predisposition to obesity and accelerated weight gain, while healthy diets and individual foods known to promote health mitigate the impact of genetics, including fruits, vegetables and n-3 PUFA. Multiple limitations related to study designs, collection of dietary data and possible systematic error warrant more controlled clinical trials with large sample sizes to be able to draw robust conclusions. Therefore, personalized nutrition and nutrigenetics can be incorporated in the design of interventions for obesity prevention and management.

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Disclosure

All authors declare no conflicts of interest in this work.

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