TABLE 1 **PECOS Criteria for Inclusion and Exclusion of Studies**

	INCLUSION CRITERIA	EXCLUSION CRITERIA
Population	Human participants >18 years old All genders and ethnicities Populations in LMIC's	Animal studies Populations from HIC's Studies only including men or women Paediatric studies Participants with concomitant disease such as cancer, CVD disease, hypertension, renal disease, neurological diseases. Pregnant or breastfeeding women
Exposure	Studies investigating gene-environment interactions on obesity risk. Exposures were defined as a combination of genetic susceptibility (e.g. genome-wide association studies, polygenic risk scores, genetic risk scores, single nucleotide polymorphisms, epigenetics, and methylation) and lifestyle and environmental factors (e.g. diet, smoking, physical activity).	Studies that did not include both exposures.
Comparison	Any or no comparators.	-
Outcome	Obesity (as a disease or risk factor) as a binary outcome, or continuous outcomes such as weight-related anthropometric measurements (BMI, weight, waist circumference, waist-to-hip ratio) or body composition indices (body fat percentage).	Studies which did not report the outcome of interest (namely studies only reporting type 2 diabetes).
Study Design	Observational studies, including case-control, cohort, or cross-sectional studies.	Randomised, non-randomised or placebo-controlled trials.

Abbreviations: BMI; body mass index, CVD; cardiovascular disease, HIC; high-income countries, LMIC; low- and middle-income countries.

TABLE 2 Summary of Included Observational Studies Investigating Gene-Environment Interactions on Obesity

AUTHORS (YEAR)	STUDY COUNTRY/ DESIGN	STUDY OBJECTIVES	SAMPLE SIZE (FEMALE %; AGE DISTRIBUTION; BMI DISTRIBUTION)	OBESITY DEFINITION	LIFESTYLE/ ENVIRONMENTAL FACTORS	GENETIC APPROACH	PRIMARY RESULTS	SECONDARY RESULTS	CONCLUSION
Muhammad et al. (2021)	Indonesia Cohort	Assess the role of *UCP2* gene variation on energy intake, PA and changes in adiposity	323 (50.8%; 42.8 ± 9.7; 25.1 ± 5.0)	–	Dietary intake (total energy, protein, fat and carbohydrate intake) and total PA (MET-min/week)	Candidate genes *UCP2* −866G/A	Changes in body weight and %BF were positively associated with total energy intake. *UCP2* gene variation was not associated with changes in energy intake, dietary composition or PA	Energy intake was positively correlated with body weight and %BF changes and PA was negatively correlated with changes in WHR for *UCP2* GG genotypes but not AA or GA genotypes.	*UCP2*-866G/A GG genotypes are more susceptible to the association between energy intake and adiposity
Hosseini-Esfahani et al. (2019)	Iran Cohort	Explore the effect of dietary patterns on *FTO* SNPs and their effect on BMI and WC change.	4292 (56.8%; M 42.6 ± 14, F 40.4 ± 13) No information on overall BMI distribution	–	Healthy (high levels of vegetables, fish, poultry, legumes, whole grains) and Western dietary patterns (high intake of fast food, sweets, sugar and red meat)	Weighted GRS of 6 SNPs (*FTO* rs1421085, rs1121980, rs17817449, rs8050136, rs9939973 and rs3751812	High Western dietary pattern score was associated with 2-fold higher BMI for carriers of risk alleles rs1121980, rs1421085, rs8050136, rs1781799 and rs3751812	Significant interaction on high Western dietary pattern score and high GRS group compared with low GRS group on BMI increase (mean BMI change: 1.04±0.34 vs 2.26±0.36).	Western dietary patterns increase the association of *FTO* SNPs genetic susceptibility with BMI or WC increase.
Wei et al. (2020)	China Case-control	Assess the relationship between 3 *MC4R* SNPs, and their interaction with environmental factors on obesity	Cases: 858 (61.5%; 56.3 ± 14.3; 27.6 ± 3.1) Controls: 978 (47.3%; 55.4 ± 15.3; 20.0 ± 1.5)	BMI ≥ 25 kg/m^2	Smoking and alcohol drinking status	Candidate genes *MC4R* rs17782313, rs476828 and rs12970134	All *MC4R* genotypes and minor allele frequencies were significantly different in obesity and control groups (P<0.05)	rs12970134 GA/AA genotypes and WC (≥90cm/≥80cm M/F) had higher obesity risk than GG genotypes and lower WC. No significant gene-smoking or -drinking interaction	MC4R SNPs were associated with the risk of obesity, but there was no significant gene-environment interactions.
Sun et al. (2022)	China Case-control	Investigate if olfactory pathway genes are related to obesity, and any interaction effects of smoking, alcohol drinking and PA	Cases: 301 (61.1%; 53.5 ± 11.1; ≥ 28 kg/m^2) Controls: 307 (39.1%; 51.2 ± 14.6; ≥ 18 kg/m^2 and <24 kg/m^2)	BMI ≥28 kg/m^2 AND WC ≥90/≥85cm M/F	Smoking (current, non-smokers), alcohol and PA (inactive, moderate, vigorous)	Candidate genes 29 SNP's from 7 olfactory pathway related genes/receptors (*OR2AK2, OR2L8, OR4D1, OR52K1, OR52K2,* CALML3 and CLCA2)	*OR4D1*, and *OR52K1* gene scores were positively correlated with obesity, and *OR2L8* and *CALML3* gene scores were negatively correlated with obesity.	Higher *OR4D1* gene score smokers were at a greater risk of obesity (OR = 2.67 [CI = 1.35, 5.30]), while high *CALML3* gene score smokers had a lower risk of obesity (OR= 0.25 [CI = 0.10, 0.62]).	Genetic variations in olfactory pathway genes were associated with obesity, while smoking modified this effect.

AUTHORS (YEAR)	STUDY COUNTRY/ DESIGN	STUDY OBJECTIVES	SAMPLE SIZE (FEMALE %; AGE DISTRIBUTION; BMI DISTRIBUTION)	OBESITY DEFINITION	LIFESTYLE/ ENVIRONMENTAL FACTORS	GENETIC APPROACH	PRIMARY RESULTS	SECONDARY RESULTS	CONCLUSION
Wang et al. (2022)	China Case-control	Explore the effects of rural-to-urban living environment transformation on MC4R gene polymorphisms and obesity	Cases: 322 (66.8%; ≥ 28 kg/m^2 Controls: 643 (66.7%; < 24 kg/m^2)	BMI ≥ 28 kg/m^2	Differences in rural-to-urban living environments (education, income, smoking and drinking status and PA)	Candidate genes *MC4R* rs17782313 and rs12970134	The rs17782313 C allele and rs12970134 A allele were significantly related to obesity in Yi people.	Yi migrants had a greater obesity risk (OR = 2.59 [CI = 1.70, 3.95]) than Yi farmers. rs17782313 (AP = 0.65, [CI = 0.22,1.09]) and rs12970134 (AP = 0.59 [CI = 0.02, 1.17]) increased obesity risk in Yi migrants	The interaction between both *MC4R* SNPs and obesity risk was modified by the urban living environment
Al-Jawadi et al. (2021)	Indonesia Case-control	Investigate association of *FTO* rs1421085 with BMI and macronutrient and fatty acid intake.	Cases: 35 (57.1%; 33 [27.5 – 39]; 31.86 [28.10 – 35.39]) Controls: 36 (86.1%; 31 [27.5 – 34.6]; 20.86 [19.48 – 21.39])	BMI ≥ 25 kg/m^2	Macronutrient (carbohydrate, protein, fat) and fatty acid (PUFA, MUFA, SFA) intake.	Candidate gene *FTO* rs1421085	Individuals with the CC genotype had a significantly higher BMI (β=12.58 [CI = 5.15, 20.01]), indicating a recessive trait	MUFA (β= 1.14 [CI = 0.02, 2.26]) and SFA (β=2.06 [CI = 0.29, 3.83]) were both positively associated with TC/CC genotypes compared to TT.	*FTO* rs1421085 CC and TC genotypes are positively associated with MUFA, SFA and increased BMI.
Daya et al. (2019)	Indonesia Case-control	Assess the interaction between *FTO* rs9939609, obesity and dietary fat intake.	Cases: 40 (85.0%; median (range) 31 (21-53) ; ≥25 kg/m^2) Controls 40 (57.9%; median (range) 33 (19-52); <23 kg/m^2)	BMI ≥ 25 kg/m^2	Daily total dietary fat intake	Candidate genes *FTO* rs9939609	The AT/AA genotypes were at higher risk of obesity (OR = 3.72 [CI = 1.19, 11.64]) and dietary fat intake (OR = 5.98 [CI = 1.22, 29.22]) compared to TT genotypes.	Obese AT/TT genotype individuals were significantly more likely to have high dietary fat intake than low fat intake compared to TT genotypes (OR = 1.40 [CI = 1.07-1.84])	*FTO* rs9939609 AT/TT genotypes are associated with increased risk of obesity and tendency towards high fat foods
Rana et al. (2021)	Pakistan Case-control	Examine the effects of gene–gene and gene–behaviour/lifestyle interactions on the risk of obesity in a Pakistani population	Cases: 290 (45.2%; 30.7 ± 9.0; ≥ 25 kg/m^2) Controls: 288 (43.8%; 28.4 ± 8.4; < 25 kg/m^2)	BMI ≥ 25 kg/m^2	Random eating patterns (REP), tendency toward fat-dense food (TFDF), sleep duration, sleep–wake cycle (SWC), shift work (SW), and PA levels	Candidate genes *MC4R* rs17782313, *BDNF* rs6265, *FTO* rs1421085, *TMEM18* rs7561317, and *NEGR1* rs2815752	Only *TMEM18* rs7561317 was significantly associated with anthropometric traits such as increased BMI (*P*=0.045) and WC (*P*=0.045)	rs17782313, rs1421085, rs7561317, and rs2815752 genetic variants were shown to interact with REP, TFDF, irregular SWC, and low PA to increase obesity-related anthropometric indices	Genetic factors are the primary determinant of obesity susceptibility, however behavioural traits are shown to significantly modify this interaction.
Isgin-Atici et al. (2021)	Turkey Case-control	Assess the role of FTO rs9939609 and rs10163409 and their interaction with dietary intake and PA on obesity outcomes	Cases: 200 (46%; 36.37 ± 7; 29.04 ± 3.38) Controls: 200 (50%; 33.29 ± 6.83; 22.56 ± 1.78)	BMI ≥ 25 kg/m^2	Dietary intake (carbohydrate, protein, fibre, fat) and PA levels (sedentary vs active)	Candidate genes *FTO* rs9939609 and rs10163409, and combined GRS	*FTO* rs9939609 and the GRS was significantly associated with higher BMI and fat mass index (*P*=0.002 and *P*=0.003 respectively)	Higher protein intake was significantly associated with increased WC for *FTO* SNP rs10163409 carriers (*P*=0.044)	The impact of *FTO* SNPs on obesity may be moderated by dietary protein intake and PA.

AUTHORS (YEAR)	STUDY COUNTRY/ DESIGN	STUDY OBJECTIVES	SAMPLE SIZE (FEMALE %; AGE DISTRIBUTION; BMI DISTRIBUTION)	OBESITY DEFINITION	LIFESTYLE/ ENVIRONMENTAL FACTORS	GENETIC APPROACH	PRIMARY RESULTS	SECONDARY RESULTS	CONCLUSION
Gong et al. (2021)	China Cross-sectional	Explore the effect of the gene–environment interaction on BMI, WC, and obesity among Chinese adults born in the 1960's.	2216 (60.3%; 49.7 [48.7 – 51.3]; 24.0 [21.9–26.4])	BMI ≥28.0 kg/m^2 OR WC ≥90/≥85cm M/F	PA (leisure-time PA, housework, transportation mode), SES (economic and education level), LTSB and dietary energy intake	Candidate genes 12 obesity-related SNPs	The effect of *MC4R* rs12970134 on BMI, and *TRHR* rs7832552 and *BCL2* rs12454712 on WC was attenuated by PA	LTSB, higher SES and higher energy intake increased the impact of SNPs on BMI and WC	High PA, low SES, reduced LTSB and low dietary intake have a negative association between SNP genetic susceptibility and obesity.
Xue et al. (2021)	China Cross-sectional	Examine the associations between types of PA and sedentary behaviours on anthropometric measures and their interaction with obesity genetic susceptibility	3976 (54.9%; median age 44.8) Overall BMI distribution unavailable.	BMI ≥ 25 kg/m^2	PA (moderate to vigorous) and sedentary behaviours (time spent watching television, computer/ phone screen use)	Weighted GRS of 9 SNPs	For individuals with high GRS, there was a significant negative association between moderate to vigorous PA and WC and %BF	For those with high GRS, time spent watching TV was associated with high BMI: for every 1hr of TV watching, BMI, WC and %BF increased by 0.2kg/m^2, 0.9cm and 0.3% respectively (P<0.02)	In those with high genetic risk of obesity, moderate to vigorous PA may reduce the risk of obesity, whilst prolonged TV watching may accentuate.
Alsulami et al. (2020)	Ghana Cross-sectional	Investigate the effect of GRS on obesity-related traits and any modifying effects by dietary intake and PA levels.	302 (58.3%; 38.17 ± 9.64; 26.6 ± 5.0)	BMI ≥ 25 kg/m^2	Dietary protein, fibre and fat intake (SFA, MUFA, PUFA) and PA levels.	Unweighted GRS of 4 SNPs (*TCF7L2* rs12255372, rs7903146, *MC4R* rs17782313, *FTO* rs9939609)	No association between GRS and any obesity-related traits.	Significant interaction between GRS ≥ 3 risk alleles and high total fat intake (>47g/day) on WC (β= 71.28 ± 23.68). SFA, MUFA, PUFA intake on WC significant but not PA.	Higher consumption of total fat, SFA, MUFA and PUFA can increase genetic susceptibility to obesity.
Moore et al. (2012)	India Cross-sectional	Evaluate the association between 16 obesity-related SNPs and BMI and WC and moderating effects of PA levels.	New Delhi: 511 (54%; 47.1 ± 9.9; 19.6% obese) Trivandrum: 618 (48.7 ± 9.2; 17.5% obese)	BMI ≥30 kg/m^2 OR WC ≥90/≥80cm M/F	PA level (<81, 81-143, 144-211, >212 MET-h/wk)	Candidate genes 16 SNPs in or near *FTO, MC4R, G6PC2, GCKR, TCF7L2*, and *SLC30A8* genes	*FTO* rs3751812 T-allele was significantly associated with increased WC (1.58cm [CI = 0.60, 2.56] waist size increase per allele)	In participants with low PA (<81 MET–h/wk), T-allele was associated with increased WC (+2.68 cm [CI = 1.24, 4.12]) while high PA (>212 MET–h/wk had no association.	*FTO* rs3751812 genetic susceptibility to obesity could be attenuated by high levels of PA
Wuni et al. (2022)	India Cross-sectional	Investigate the effect of a GRS on obesity-related traits and any moderating effects of dietary intake	497 (54.7%; 44 ± 10; 24.6 ± 4.5)	BMI ≥ 25 kg/m^2	Dietary protein, carbohydrate, fibre and fat intake (SFA, MUFA, PUFA) and total energy intake	Unweighted GRS of 3 SNPs (*LPL* rs327, rs3200218 and *CETP* rs4783961)	No association between the GRS and obesity related traits (HDL, LDL, TG, total cholesterol, SBP, DBP, BMI, WC, WHR)	In individuals with high GRS (>2 risk alleles) high SFA intake was associated with increased WC compared to low SFA intake (β = 0.02, P=0.02)	SFA intake may modify the genetic risk of lipid-pathway genes SNPs on obesity

AUTHORS (YEAR)	STUDY COUNTRY/ DESIGN	STUDY OBJECTIVES	SAMPLE SIZE (FEMALE %; AGE DISTRIBUTION; BMI DISTRIBUTION)	OBESITY DEFINITION	LIFESTYLE/ ENVIRONMENTAL FACTORS	GENETIC APPROACH	PRIMARY RESULTS	SECONDARY RESULTS	CONCLUSION
Mahmoudi-Nezhad et al. (2020)	Iran Cross-sectional	Assess the interaction of *CARTPT* rs2239670 genotypes and dietary indices on anthropometric measures in obese individuals.	287 (51.1%; M: 38.44 ± 6.86, F: 37.81 ± 8.25; M: 33.90 ± 3.41, F: 35.61 ± 4.31)	BMI 30–40 kg/m^2	Dietary indices (healthy eating index (HEI) and diet quality index – international (DQI-I)	Candidate genes *CARTPT* rs2239670	Significant *CARTPT*–HEI interactions for BMR, serum glucose and HDL concentrations. HEI could not modify adverse effects of *CARTPT* rs2239670 AA genotype	*CARTPT*–DQI-I interactions were more pronounced compared to *CARTPT*–HEI interactions for fat mass (*P*=0.02), WC (*P*=<0.001), and BMR (*P*=<0.001).	*CARTPT* rs2239670 genotype was significantly associated with HEI and particularly DQI-I scores for BMR, WC and FM
Rahati et al. (2022)	Iran Cross-sectional	Investigate the impact of behavioural characteristics on the association between near *CLOCK* rs1801260 and obesity	403 (36.5 ± 8.7; 30.2 ± 3.1) No information on gender distribution	Overweight + obese: BMI 25–40 kg/m^2 No individual classification	Energy and macronutrient intake, circadian rhythm, sleep duration and food timing	Candidate genes *CLOCK* 3111 T / C	Significant difference between *CLOCK* rs1801260 genotype study groups for energy and macronutrient intake, food timing, sleep and PA	Eating lunch after 3pm significantly increased obesity susceptibility (OR= 2.95 [CI = 1.77, 4.90]) in CT + CC *CLOCK* rs1801260 genotype carriers	*CLOCK* C allele carries are more likely to experience higher energy intake, reduced sleep and later meal timings, and are more genetically susceptible to obesity if eating lunch after 3pm.
Ahmad et al. (2016)	Pakistan Cross-sectional	Use genome wide approaches to conduct gene-lifestyle interaction analyses for smoking and PA in relation to obesity.	GWAS: 14,131 (17.7%; 53.8 ± 9.6; 25.7 ± 4.2) Interaction analysis: 8,193, age: 30-80 No further distribution information	–	Tobacco smoking (never, ever, current) and PA (light, moderate, heavy)	vGWAS *FLJ33544* rs140133294	Lead variant identified (*FLJ33534*; rs140133294); with strong association on BMI phenotypic variance ($P=3.1 \times 10^{-8}$)	Association of rs140133294 (*FLJ33534*) with BMI stratified by smoking status: never smokers (β=0.90 ± 0.36); current smokers (β=−1.51 ± 0.52). No significant association for PA.	Single *FLJ33534* locus significantly modifies the relationship of smoking and BMI
Illangasekera et al. (2016)	Sri Lanka Cross-sectional	Investigate the role of *FTO* and near *MC4R* SNPs on obesity measures and the moderating effects of urban and rural living	528 (60.9%; M 47.2 ± 11.6, F 47.5 ± 11.5) No information on overall BMI distribution	BMI ≥ 25 kg/m^2 and ≥ 27.5 kg/m^2	Urban vs rural living	Candidate genes *FTO* rs9939609 and near *MC4R* rs17782313	FTO rs9939609 (AA +TT) carriers and near MC4R rs17782313 (CC+TT) had a significantly higher BMI, and were associated with categorial obesity.	FTO rs9939609 (AA +AT) was associated with significantly greater mean BMI in urban populations vs rural (M(SE) = 1.20(0.53), *P* = 0.02)	*FTO* and *MC4R* SNPs are associated with obesity, and urban living may accentuate the obesogenic effect of the *FTO* SNP.

Abbreviations: BCL2; B-cell lymphoma-2, BDNF; brain-derived neurotrophic factor, BMI; body mass index, BMR; basal metabolic rate, CALML3; calmodulin like 3, CARTPT; cocaine and amphetamine-regulated transcript prepropeptide, CETP; cholesteryl ester transfer protein, CI; confidence interval, CLCA2; chloride channel accessory 2, CLOCK; circadian locomotor output cycles kaput, DBP; diastolic blood pressure, DQI-I; diet quality index – international, F; female, FLJ33534; putative uncharacterized protein, FM; fat mass, FTO; fat mass and obesity-associated, GCKR; glucokinase regulatory protein, GRS; genetic risk score, GWAS; genome wide association study, G6PC2; glucose-6-phosphatase catalytic 2, HDL; high density lipoprotein, HEI; healthy eating index, LDL; low density lipoprotein, LTSB; leisure time sedentary behaviour, M; male, MC4R; melanocortin 4 receptor, MET; metabolic equivalent of task, MUFA; monounsaturated fatty acids, NEGR1; neuronal growth regulator 1, OR; odds ratio, OR2AK2; olfactory receptor family 2 subfamily AK member 2, OR2L8; olfactory receptor family 2 subfamily L member 8, OR4D1; olfactory receptor family 4 subfamily D member 1, OR52K1; olfactory receptor family 52 subfamily K member 1, OR52K2; olfactory receptor family 52 subfamily K member 2, PA; physical activity, PUFA; polyunsaturated fatty acids, REP; random eating patterns, SBP; systolic blood pressure, SES; socioeconomic status, SFA; saturated fatty acid, SLC30A8; solute carrier family 30 member 8, SNP; single nucleotide polymorphism, SW; shift work, SWC; sleep–wake cycle, TCF7L2; transcription factor 7-like 2, TFDF; tendency toward fat-dense food, TMEM18; transmembrane protein 18, TRHR; thyrotropin-releasing hormone receptor, UCP2; uncoupling protein 2, vGWAS; variance heterogeneity genome-wide association study, WC; waist circumference, WHR; waist hip ratio, %BF; percentage body fat.
Data are expressed as mean (standard deviation) or count (%) unless otherwise specified.

FIGURE 1 **PRISMA Flow Chart for the Selection of Studies**

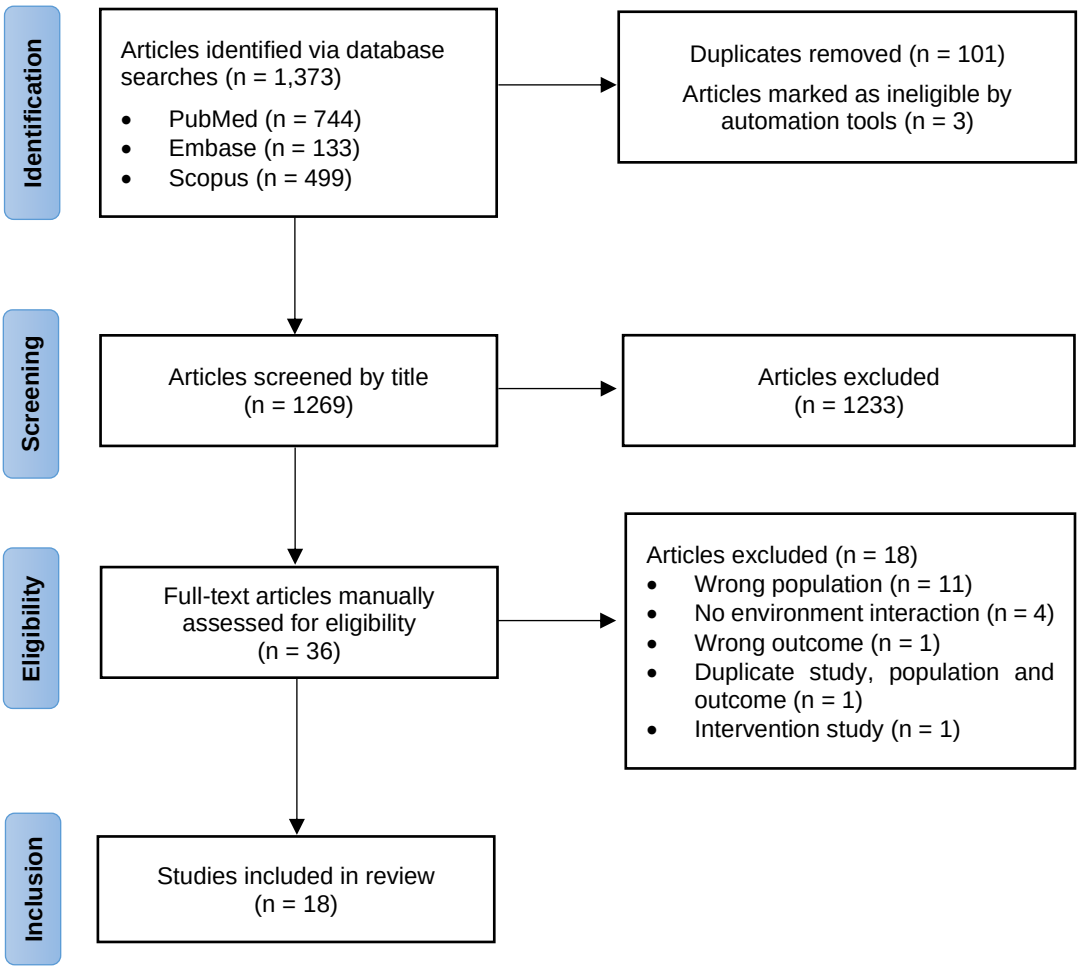

TABLE 3 **Newcastle–Ottawa Quality Assessment Scale for Observational Studies**

	SELECTION				COMPARABILITY		OUTCOME			SCORE
COHORT STUDIES	Exposed representative of average population	Selection of non-exposed from the same community	Exposure ascertained by secure record or interview	Demonstration of outcome of interest not present at start of study	Study controls for age and sex	Study controls for other variables in design or analysis	Outcome assessed by independent assessment or record linkage	Follow-up long enough for outcomes to occur	Subjects lost to follow-up unlikely to introduce bias	
Hosseini-Esfahani et al, 2019	*	*		*	*	*	*	*		7
Muhammad et al. (2021)	*	*	*	*	*	*	*			7
CASE-CONTROL STUDIES	Case definition adequate	Cases representative	Community controls	No history of outcome in controls	Study controls for age and sex	Study controls for other variables in design or analysis	Exposure ascertained by secure record or interview	Same methods of ascertainment for cases and controls	Non-response rate same for both groups	
Wei et al, 2020		*	*		*	*	*	*		6
Sun et al, 2022	*		*	*	*	*	*	*	*	8
Wang et al, 2022	*	*	*		*	*	*	*	*	8
Al-Jawadi et al, 2021	*			*	*		*	*	*	6
Daya et al, 2019	*			*		*	*	*		5
Rana et al, 2021	*	*	*		*		*	*		6
Isgin-Atici et al, 2021	*			*	*	*	*	*	*	7

TABLE 4 **Adapted Newcastle–Ottawa Quality Assessment Scale for Cross-Sectional Studies**

	SELECTION				COMPARABILITY		OUTCOME		SCORE
	Sample representative of average population	Sample size justified and satisfactory	Pre-specified target sample obtained or non-respondents summarised	Exposure ascertained by secure record** or interview combination*	Study controls for age and sex	Study controls for other variables in design or analysis	Outcome assessed by independent assessment or record linkage** or self-report*	Statistical test used was clearly described and appropriate	
Gong et al, 2021		*			*	*	**	*	6
Xue et al, 2021	*	*		*	*	*	**	*	8
Alsulami et al, 2020	*			*	*	*	**	*	7
Moore et al, 2012	*	*	*	*	*	*	**	*	9
Wuni et al, 2022				*	*	*	**	*	7
Mahmoudi-Nezhad et al, 2020	*			**	*		**	*	7
Rahati et al, 2022	*	*	*	*	*	*	**	*	9
Ahmad et al, 2016	*	*	*	**	*	*	**	*	10
Illangasekera et al, 2016	*			*	*		**		5

Adapted from the Newcastle-Ottawa Quality Assessment scales for cohort studies with a 10 point score system (1).

Supplementary Tables

SUPPLEMENTARY TABLE 1 PubMed Medliner Search Strategy

Database: PubMed MEDLINER <up to 24th October 2022>			Results
Population	1	"Developing Countries"[Mesh] OR "developing countr*"[tiab] OR "under developed countr*"[tiab] OR lmic*[tiab] OR "less developed"[tiab] OR "low income"[tiab] OR "lower income"[tiab] OR "low and middle income"[tiab] OR "low middle income"[tiab] OR "resource poor"[tiab] OR "resource constrained"[tiab] OR "low resource"[tiab] OR "limited resource*"[tiab] OR "resource limited"[tiab]	239,258
	2	"Africa South of the Sahara"[Mesh] OR "Central America"[Mesh] OR "South America"[Mesh] OR "Latin America"[Mesh] OR "Caribbean Region"[Mesh] OR "Mexico"[Mesh] OR "Asia"[Mesh] OR "China"[Mesh] OR "North Korea"[Title/Abstract] OR "Mongolia"[Mesh]	1,516,222
	3	#1 OR #2	1,658,799
Determinant	4	"Gene-Environment Interaction"[Mesh] OR "Gene X environment"[Title/Abstract] OR "gene-by-environment" [Title/Abstract] OR "g x e" [Title/Abstract] OR GxE [Title/Abstract] "gene-environment" [Title/Abstract] OR "gene environment"[Title/Abstract] OR "gene-lifestyle interaction" [Title/Abstract] OR "gene lifestyle interaction" [Title/Abstract]	8,807
	5	"Genome-Wide Association Study"[Mesh] OR GWA[Title/Abstract] OR "Genome-Wide Association"[Title/Abstract] OR "Polygenic score" [Title/Abstract] OR "polygenic risk score"[Title/Abstract] OR "PGS" [Title/Abstract] OR "PRS" [Title/Abstract] OR "Polymorphism, Single Nucleotide"[Mesh] OR SNP [Title/Abstract] OR "single nucleotide polymorphisms"[Title/Abstract] OR "gene variant"[Title/Abstract] OR "genotype"[Title/Abstract] OR "genetics" [Title/Abstract] OR "obesity-associated gene*" [Title/Abstract] OR "epigenetic"[Title/Abstract] OR "methylation"[Title/Abstract]	683,962
	6	Environment [Title/Abstract] OR obesogenic[Title/Abstract] OR lifestyle[Title/Abstract] OR "physical activity"[Title/Abstract] OR "physical inactivity" [Title/Abstract] OR exercise*[Title/Abstract] OR diet*[Title/Abstract] OR smok* [Title/Abstract] OR alcohol [Title/Abstract] OR sleep* [Title/Abstract]	2,408,124
	7	#5 AND #6	69,164
	8	#7 OR #4	73,166
Outcome	9	"Obesity" [MeSH] OR Obesit*[Title/Abstract] OR "abdominal fat" [MeSH] OR "body weight" [Title/Abstract] OR "overweight" [Title/Abstract] OR adiposity[Title/Abstract] OR BMI[Title/Abstract] OR "body mass index" [Title/Abstract] OR weight[Title/Abstract] OR "waist circumference" [Title/Abstract]	1,381,403
	10	#3 AND #8 AND #9	1,325
Exclusion	11	"Adolescent"[Mesh] OR "child"[Mesh] OR adolescent*[Title/Abstract] OR child*[Title/Abstract] OR "infant*"[Title/Abstract] OR "teen*"[Title/Abstract] OR "pediatr*" [Title/Abstract] OR "paediatr*"[Title/Abstract] OR "birth" [Title/Abstract]	4,343,961

	12	“Randomized Controlled Trial”[Publication Type] OR “controlled clinical trial”[Publication Type] OR randomized[Title/Abstract] OR randomised[Title/Abstract] OR placebo[Title/Abstract]	1,109,309
	13	"animals"[mesh] NOT "humans"[mesh]	5,065,614
	14	"Neoplasms"[Mesh] OR "Hypertension"[Mesh]	4,059,674
	15	#11 OR #12 OR #13	13,323,044
	16	#10 NOT #14	744

SUPPLEMENTARY TABLE 2 EMBASE Search Strategy

Database: EMBASE <up to 24th October 2022>			Results
Population	1	(“Developing countr*” or “under developed countr*” or lmic* or “less developed” or “low income” or “lower income” or “low and middle income” or “low middle income” or “resource poor” or “resource constrained” or “low resource” or “limited resource?” or “resource limited”):ti,ab	219,543
	2	(“Africa South of the Sahara” or “Central America” or “South America” or “Latin America” or “Caribbean” or “Mexico” or “Asia” or “China” or “North Korea” or “Mongolia”):ti,ab	512,579
	3	#1 OR #2	715,200
Determinant	4	(“Gene-environment interaction" or “Gene X environment” or “gene-by-environment” or “g x e” or gxe or “gene-environment” or “gene environment” or “gene-lifestyle interaction” or “gene lifestyle interaction”):ti,ab	11,446
	5	("Genome-wide association" or GWA or “polygenic score” or “polygenic risk score” or PGS or PRS or “single nucleotide polymorphism?” or SNP or “gene variant” or genotype or genetics OR “obesity-associated gene?” or genotype or epigenetic? or methylation):ti,ab	724,373
	6	(Environment or obesogenic or lifestyle or “physical activity” or “physical inactivity” or exercise? or exercising or diet? or dietary or smoking or smoke or alcohol or sleep?):ti,ab	2,177,846
	7	#5 AND #6	63,888
	8	#4 OR #7	69,946
Outcome	9	(obesity or “abdominal fat” or “visceral fat” or “body weight” or overweight or adiposity or BMI or “body mass index” or weight or “waist circumference”):ti,ab,kw	1,915,847
	10	#3 AND #8 AND #9	496
Exclusion	11	(Adolescent or child or children or infant or infancy or teen or teenager or pediatric or paediatric or birth):ti,ab	2,764,505
	12	‘Animal model’/exp or ‘animal experiment’/exp or (mice or mouse or pig or primate or fish or rat or rats or rabbit or rabbits or monkey or monkeys or cat or cats or dog or dogs). ti,ab,kw.	5,447,938
	13	'clinical trial'/de OR 'randomized controlled trial'/de	1,483,375
	14	11 OR 12 OR 13	9,375,128
	15	10 NOT 14	133

SUPPLEMENTARY TABLE 3 Scopus Search Strategy

Database: Scopus <up to 24th October 2022>			Results
Population	1	TITLE-ABS-KEY (“Developing countr*” OR “under developed countr*” OR lmic* OR “low* income” OR “low middle income” or “resource poor” OR “low resource” OR “limited resource*” OR Africa OR “Central America” OR “South America” OR “Latin America” OR Caribbean OR Mexico OR Asia OR China OR “North Korea” OR Mongolia	2,769,140
Determinant	2	TITLE-ABS-KEY (“Gene-environment” OR “Gene X environment” OR “gene-by-environment” OR gxe OR “gene lifestyle interaction”)	17,352
	3	TITLE-ABS-KEY ("Genome-wide association" OR GWA OR polygenic OR PGS OR PRS OR polymorphism* OR SNP OR “gene variant” OR genotype OR genetics OR “obesity-associated gene?” OR epigenetic*)	3,185,743
	4	TITLE-ABS-KEY (Environment OR obesogenic OR lifestyle OR “physical activity” OR “physical inactivity” OR exercise* OR diet* OR smok* OR alcohol OR sleep*)	7,366,799
	5	#3 AND #4	335,069
	6	#2 OR #5	337,526
Outcome	7	TITLE-ABS-KEY (Obesity OR overweight OR adiposity OR BMI OR “waist circumference”)	710,542
	8	#1 AND #6 AND #7	1,474
Exclusion	9	TITLE-ABS-KEY (Adolescent OR child* OR infan* OR teen* OR pediatric OR paediatric OR birth OR “animal model” OR “animal experiment” OR mice OR mouse OR pig* OR primate OR fish OR rat* OR rabbit* OR monkey* OR cat* OR dog* OR “clinical trial” OR “randomized controlled trial”)	28,611,345
	10	#8 AND NOT #9	499

REFERENCES

1. Herzog R, Álvarez-Pasquin MJ, Díaz C, Del Barrio JL, Estrada JM, Gil Á. Are healthcare workers’ intentions to vaccinate related to their knowledge, beliefs and attitudes? a systematic review. BMC Public Health. 2013 Dec 19;13(1):154.