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Association of Genetic Polymorphisms in the Human FTO Gene and Obesity: Systematic Review and Meta-Analysis

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ABSTRACT

The aim of the study is to perform a systematic review and meta-analysis to determine whether the Fat Mass and Obesity-associated (FTO) polymorphisms influenced obesity and which Single Nucleotide Polymorphisms (SNPs) raised the risk of obesity. We used PUBMED, SCOPUS, and Web of Science to identify studies investigating the association between genetic polymorphisms in the FTO gene and obesity. We discovered 16 studies that included 4,381 obese people and 5,652 healthy control people. Five genetic polymorphisms showed significant association with increased obesity risk in the allelic model: rs9939609 (OR=1.38, 95% CI:1.27−1.50: I^2=0%, p<0.001), rs8050136 (OR=1.23, 95% CI:1.03−1.46: I^2=54%, p=0.02), rs3751812 (OR=1.31, 95% CI:1.18−1.45: I^2=4%, p<0.001), rs1421085 (OR=1.29, 95% CI: 1.14−1.46: I^2=4%, p<0.001) and rs1121980 (OR=1.45, 95% CI: 1.10−1.93: I^2=66%, p=0.009). For the allelic model, no significant correlation was identified in the rs15588902 SNP FTO gene (OR=1.24, 95% CI:0.96−1.62: I^2=62%, p=0.11). Therefore, this meta-analysis found six FTO SNPs linked to human FTO polymorphisms and the risk of obesity. Further research on the FTO gene and obesity should consider gene-gene and gene-environment interactions.

Keywords: FTO, obesity, single nucleotide polymorphisms

INTRODUCTION

Obesity prevalence increased from 15.1% in 2011 to 17.7% in 2015 and 19.9% in 2019, indicating a severe global problem (Chong *et al.* 2023). Obesity can be induced by high-calorie consumption, physical inactivity, and inherited factors (Lin & Li 2021). These conditions cause noncommunicable diseases such as hypertension, type 2 diabetes, and coronary heart disease (Rangel-Huerta *et al.* 2019).

In obesogenic genes, many Single Nucleotide Polymorphisms (SNPs) are linked to an increased risk of obesity (Velazquez-Roman *et al.* 2021). It implies that inherited traits may have a role in the onset of obesity. The Fat Mass and Obesity-Associated (FTO) gene are most linked to obesity (Ruiz-Diaz *et al.* 2022). Body Mass Index (BMI) and fat deposition have been linked to this gene (Xu *et al.* 2023). Since obesity has been demonstrated to have a high heritability, genetic variation accounts for up to 80% of interindividual variance in BMI (Ramírez *et al.* 2022). A BMI-related genetic mutation may increase calorie intake and decrease satiety (Danaher *et al.* 2019).

Although numerous studies have been conducted to investigate the association between the FTO gene and other diseases such as obesity, hypertension, and polycystic ovary syndrome (Zhao *et al.* 2019; He *et al.* 2014; Cai *et al.* 2014), little study has been conducted on the associations between genetic polymorphisms in the FTO gene and obesity. It is unclear whether the FTO gene can cause obesity in some individuals and which FTO SNPs were responsible for obesity. Therefore, this study aimed to determine whether FTO polymorphisms might affect obesity and

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which SNPs can increase the risk of obesity. These findings will help academics and healthcare professionals better understand this relationship.

METHODS

Design, location, and time

This study has been registered in PROSPERO, the International Prospective Register of Systematic Reviews, with project ID CRD42022371341. Systematic searches were conducted in October 2022 on the titles, abstracts, keywords, and full texts of documents from three online databases, including PubMed, Scopus, and Web of Science. The scope of information in genetics, FTO genes, obesity, and single nucleotide polymorphisms were chosen for this study. The research focuses on FTO polymorphisms that are linked to obesity. Obese and healthy control subjects were the target populations. There were no time constraints for publishing, study design, or subject age. Exclusion criteria included book series, conferences, manuscripts, and review articles.

Sampling

Newcastle-Ottawa Scale (NOS), a validated, easy-to-use scale of 8 items in three domains, selection, comparability, and outcome, was employed to evaluate the reliability of included study outcomes for meta-analysis. Except for comparability, studies were graded one point out of nine. The quality of studies was graded on a scale of 0−9, with 0−2 indicating poor quality, 3−5 indicating fair quality, and 6−9 indicating high quality (Forte *et al.* 2022). Studies with fair and good quality were chosen for this study to improve the review's validity. Hardy-Weinberg Equilibrium (HWE) was used to calculate the number of heterozygous and homozygous carriers of each variant using an online calculator based on allele frequency in stable populations (Abramovs *et al.* 2020). Hardy-Weinberg proportions may deviate when these assumptions are violated. This review also adhered to the "Preferred Reporting Items for Systematic Reviews and Meta-Analyses" (PRISMA) guidelines 2020 for reporting this study.

Data collection

All studies in the current analysis contributed to the human FTO gene and obesity. Keywords including "genetic polymorphisms", "SNP", "FTO gene", "overweight", "obesity" and "single nucleotide polymorphisms" were used for the search strategy. Boolean operators like "AND" and "OR" were employed to combine the keywords. Following the exclusion of duplicate records, the titles and abstracts have been examined for compliance with the inclusion criteria. When there was insufficient information in the abstracts to determine selection status, the full texts of journals were assessed. The journals were evaluated separately by at least two authors. Discrepancies were resolved through group discussion, leading to final, consistent decision-making. The following information was extracted from each study's data: FTO SNPs, the first author's name, publication year, study's location, population, definition of obesity, the number of cases and controls, the risk allele, alleles, HWE p-value, and NOS scores.

Data analysis

This study calculated the I^2 index of forest plot heterogeneity using Review Manager 5.4. If the I^2 was less than 50%, the studies were classified as having low heterogeneity and used the fixed effect model. A random effect model was used if I^2 was greater than 50%, indicating high heterogeneity. To assess the correlations between FTO polymorphisms and susceptibility to obesity, we obtained the Odds Ratios (ORs) and 95% Confidence Intervals (CIs) for dominant, recessive, and allelic models from the forest plots. Egger's tests and STATA 12 were used to investigate publication bias displayed in funnel plots.

RESULTS AND DISCUSSION

The database search found 2,148 journals: 1,247 from PubMed, 343 from Scopus, and 558 from Web of Science. Eliminating 1,511 duplicate studies (n=342) reduced the number of studies to 1,806. After excluding 233 studies, 295 were retained for title and abstract screening. The study aforementioned was excluded from the analysis because it did not meet the inclusion criteria. After assessing 62 studies for eligibility, 46 were excluded due to insufficient data reporting. The systematic review included 16 studies, 14 of which were included in the meta-analysis.

Table 1 summarised the study's characteristics. This systematic review included 16 studies that were published between 2008 and 2023. However, 14 studies were evaluated in this meta-analysis, and the remaining studies were excluded due to a lack of research supporting a relationship between SNPs and the risk of obesity.

rs9939609 and rs8050136

Figure 1(a) shows the genotypes AA/AT against TT (dominant model) in rs9939609 with OR=1.42 and 95% CI:1.27−1.58. These findings showed that the allele of A in both SNPs should be highlighted as the obesity risk factor.

rs3751812 and rs1558902

The OR and 95% CI for the TT/GT vs GG genotypes in rs3751812 were 1.38 and 1.22−1.57, respectively [Figure 2 (a)].

rs1421085 and rs1121980

The dominant model for rs1421085 (CC/TC vs TT genotypes) showed OR=1.24 with 95% CI:0.92−1.67 [Figure 3 (a)]. The C allele in rs1421085 and A allele in rs1121980 may indicate an increased likelihood of obesity.

Egger's test and funnel plots examined the studies' publication bias. Only rs9939609 was assessed for publication bias as this SNP consisted of ten studies. These plots showed symmetry for dominant, recessive, and allelic models (Figure 4), which meant there were no publication biases within these studies (p=0.164, 0.826, and 0.541, respectively).

rs9939609 was the most popular SNP that was investigated in most studies. This meta-analysis found that the A-allele was an indicator of increasing the risk of obesity. Previous meta-analyses also found the A allele in rs9939609 was strongly associated with an increased likelihood of obesity (Abd Ali *et al.* 2021; Zhao *et al.* 2019). AA genotypes were protected from weight gain in Chinese children, and children with TT genotypes were predisposed to being obese (Lubis *et al.* 2017). However, rs9939609 also did not impact obesity in Malays (Apalasamy *et al.* 2012). These might be due to racial differences or interactions with other SNPs.

In Chinese and Japanese populations, the rs8050136 SNP was significantly linked with waist circumference and BMI (Cheung *et al.* 2010; Hotta *et al.* 2008). Due to higher levels of energy intake, those with AC+AA genotypes had a higher BMI correlation than the wild CC genotype (Wu *et al.* 2014). Furthermore, people with AA genotypes who exercised were more sensitive when they had mutant alleles, indicating a significant association with twice-increased obesity susceptibility (Kanwal *et al.* 2023). The finding of this meta-analysis discovered that the A allele in rs8050136 may cause the onset of obesity. Moreover, lifestyle choices influenced the effect of FTO SNPs and increased FTO genetic susceptibility to obesity (Velazquez-Roman *et al.* 2021). Additionally, our results linked the rs8050136 polymorphism to an increased risk of obesity, consistent with previous meta-analyses (Zhao *et al.* 2019).

There was a significant association between rs3751812 polymorphism and a higher risk of obesity in several populations (Hotta *et al.* 2008; Chehadeh *et al.* 2020). Compared to wild GG genotypes, the GT+TT genotype was related to greater BMI in Chinese adolescents (Wu *et al.* 2014). The findings indicated that the risk T allele was significantly associated with obesity compared to the G allele. However, those with the TG and TT genotypes who exercised suggested that it minimized the harmful effects of BMI in Taiwanese people (Liaw *et al.* 2019).

A study found that BMI was more significant in the TA+AA genotypes at rs1558902 compared to the wild TT genotype (Wu *et al.* 2014). The results also showed that AA/AT genotypes in the dominant model were significantly linked to obesity. It suggested that these genotypes might influence the development of obesity. The FTO genotypes rs1421085 and rs1121980 were associated with uncontrollable eating behaviors (Cameron *et al.* 2019). Our meta-analysis revealed that compared to the T and G alleles, the risk C allele and risk A allele of the rs1421085 and rs1121980 were significantly associated with a higher likelihood of obesity. These three SNPs were reported to be positively related to a higher risk of obesity in a previous meta-analysis (Liu *et al.* 2013).

This study had several strengths. Firstly, this study included participants of different ages compared to the previous meta-analysis (Abd Ali *et al.* 2021). Secondly, a significant correlation between FTO polymorphisms among diverse ethnic groups was discovered in this study compared to another meta-analysis (Zhao *et al.*

Table 1. Summary of studies included in the qualitative analysis

First author, publish year	Location, population	Study design	Age group	Obesity definition	Number of cases/ controls	FTO SNP	Risk allele	Alleles	HWE (*p*)	NOS score
Albuquerque *et al.* 2018	Spain, Spanish and Portuguese	Case-control	Children	BMI≥40	270/408	rs17817449	G	T/G	0.874	5
						rs9921255	G	T/G	0.046	
Apalasamy *et al.* 2012	Malaysian, Malays	Case-control	Adults	BMI≥30	158/ 429	rs1077128	G	G/T	0.775	4
						rs3751812	T	G/T	0.351	
						rs1558902	A	T/A	0.187	
						rs8050136	A	C/A	0.351	
						rs9939609	A	T/A	0.287	
						rs7186521	A	A/G	0.364	
						rs13334933	A	A/G	0.823	
						rs16952517	A	G/A	0.347	
						rs16945088	A	A/G	0.530	
						rs17817449	G	T/G	0.351	
						rs7190492	A	G/A	0.226	
						rs17218700	G	G/A	0.935	
						rs11642841	C	C/A	0.663	
						rs1861867	T	C/T	0.169	
						rs11075994	G	G/A	0.839	
						rs6499643	T	T/C	0.492	
						rs4784323	G	G/A	0.247	
						rs7206790	G	C/G	0.733	
						rs16952522	G	C/G	0.391	
						rs17817288	G	G/A	0.870	
						rs9939973	A	A/G	0.254	
						rs1121980	A	A/G	0.003	
						rs7204609	C	C/T	0.279	
						rs11643744	G	A/G	0.711	
Apalasamy *et al.* 2012.	Malaysian, Malays	Case-control	Adults	BMI≥30	158/ 429	rs1421090	C	T/C	0.171	4
						rs1421085	C	T/C	0.187	
						rs10852521	C	C/T	0.744	
						rs9935401	G	A/G	0.315	
						rs17818902	T	T/G	0.671	
						rs7191513	A	G/A	0.470	

Continue from Table 1

First author, publish year	Location, population	Study design	Age group	Obesity definition	Number of cases/ controls	FTO SNP	Risk allele	Alleles	HWE (*p*)	NOS score
Cameron *et al.* 2019	Canada, mixed	Cross-sectional	Adults	BMI≥27	55/50	rs3751812	T	G/T	0.922	5
						rs8050136	A	C/A	0.679	
						rs9939609	A	T/A	0.679	
						rs1421085	C	T/C	0.997	
						rs1121980	A	A/G	0.253	
Chehadeh *et al.* 2020	United Arab Emirates, mixed	Case-control	Young adults	BMI≥25	318/392	rs9941349	T	G/T	0.200	6
						rs3751812	T	G/T	0.407	
Cheung *et al.* 2010	Hong Kong, Chinese	Case-control	Adults	BMI≥27	470/700	rs8050136	A	C/A	0.377	5
García-Solís *et al.* 2016	Mexico, Mexican	Cross-sectional	Children	BMI Z-score>+1	226/343	rs9939609	A	T/A	0.058	6
Huang *et al.* 2016	Taiwan, Taiwanese	Cross-sectional	Adults	BMI≥27	264/323	rs6499640	A	A/G	0.698	6
Hotta *et al.* 2008	Japan, Japanese	Case-control	Adults	BMI≥30	927/1527	rs9940128	A	A/G	0.753	5
						rs8050136	A	C/A	0.541	
						rs9939609	A	T/A	0.529	
						rs3751812	T	G/T	0.583	
						rs1421085	C	T/C	0.524	
						rs9937053	A	A/G	0.790	
						rs1121980	A	A/G	0.850	
						rs9939973	A	A/G	0.790	
						rs7204609	C	C/T	0.120	
						rs7193144	C	C/T	0.793	
Hotta *et al.* 2008	Japan, Japanese	Case-control	Adults	BMI≥30	927/1527	rs1558902	A	T/A	0.987	5
						rs7185735	G	G/A	0.751	
						rs9931494	G	G/C	0.783	
						rs17817964	T	T/C	0.648	
						rs9930506	G	G/A	0.572	
						rs9932754	C	C/T	0.868	
						rs8043757	T	T/A	0.358	
						rs9923233	C	C/G	0.613	
						rs9922619	T	T/G	0.943	

Continue from Table 1

First author, publish year	Location, population	Study design	Age group	Obesity definition	Number of cases/ controls	FTO SNP	Risk allele	Alleles	HWE (*p*)	NOS score
						rs12149832	A	A/G	0.942	
						rs9926289	A	A/G	0.246	
Kanwal *et al.* 2023	Quetta, mixed	Case-control	Adults	BMI >25	150/100	rs8050136	A	C/A	0.00	5
Lubis *et al.* 2017	Indonesia, Bataknese and Chinese	Case-control	Children	BMI >95th percentile	105/107	rs9939609	T	A/T	0.258	5
Mangge *et al.* 2011	Austria, Caucasian	Clinical	Adoles-cents	BMI ≥30, BMI >95th percentile	268/103	rs9939609	A	T/A	0.244	7
Moselhy *et al.* 2017	Saudi, mixed	Case-control	Adult	BMI> 29.9	106/106	rs17817449	G	T/G	0.0003	5
Olza *et al.* 2013	Spain, Spanish	Case–control	Children	BMI ≥25	292/242	rs10852525	A	G/A	0.974	6
						rs7194336	T	G/T	0.304	
						rs7203181	A	C/A	0.063	
						rs6499656	C	G/C	0.259	
						rs7194907	C	T/C	0.629	
						rs8056299	G	A/G	0.741	
						rs17225435	G	A/G	0.630	
						rs8049235	A	G/A	0.353	
Olza *et al.* 2013	Spain, Spanish	Case–control	Children	BMI ≥25	292/242	rs697771	T	C/T	0.812	6
						rs12596638	A	G/A	0.751	
						rs11643744	G	A/G	0.178	
						rs7200579	G	C/G	0.406	
						rs12445162	A	G/A	0.534	
						rs11075986	G	C/G	0.498	
						rs7203521	G	A/G	0.544	
						rs1861868	G	A/G	0.431	
						rs7199716	T	C/T	0.498	
						rs13334214	T	C/T	0.550	
						rs7194243	T	C/T	0.730	
						rs1136002	C	T/C	0.338	
						rs4784351	G	A/G	0.674	
						rs2540781	A	C/A	0.0004	
						rs8049933	T	C/T	0.033	
						rs9928094	G	A/G	0.862	

Continue from Table 1

First author, publish year	Location, population	Study design	Age group	Obesity definition	Number of cases/ controls	FTO SNP	Risk allele	Alleles	HWE (*p*)	NOS score
						rs9930333	G	T/G	0.857	
						rs7205986	G	A/G	0.056	
						rs3826169	C	T/C	0.562	
						rs8061518	G	A/G	0.398	
						rs16952623	C	T/C	0.035	
						rs16952624	T	C/T	0.983	
						rs2111113	C	G/C	0.556	
						rs1558687	T	C/T	0.620	
						rs2075202	G	T/G	0.247	
						rs9939609	A	T/A	0.667	
						rs9935401	A	G/A	0.505	
						rs17818902	G	A/G	0.475	
						rs7191513	C	G/C	0.604	
						rs1008400	T	C/T	0.167	
Olza *et al.* 2013	Spain, Spanish	Case–control	Children	BMI≥25	292/242	rs12932373	T	C/T	0.060	6
						rs2689248	A	C/A	0.937	
						rs17833492	A	C/A	0.303	
						rs7190053	T	C/T	0.520	
						rs2111114	G	A/G	0.199	
						rs8044353	A	G/A	0.682	
						rs10521303	A	C/A	0.038	
						rs1558756	T	C/T	0.074	
						rs10852521	T	C/T	0.465	
Prakash *et al.* 2016	India, Indian	Case-control	Adults	BMI≥30	309/333	rs9939609	A	T/A	0.023	7
Velazquez-Roman *et al.* 2021	Mexico, Mexican	Case-control	Adults	BMI ≥30	285/266	rs9939609	A	T/A	0.817	5
Wu *et al.* 2014	China, Chinese	Case-control	Adoles-cents	BMI ≥ 25	178/223	rs6499640	A	A/G	0.132	5
						rs6499640	A	A/G	0.132	
						rs3751812	T	G/T	0.544	
						rs1558902	A	T/A	0.544	
						rs8050136	A	C/A	0.548	
						rs9939609	A	T/A	0.00	

BMI: Body Mas Index: FTO: Fat Mass and Obesity-Associated; SNP: Single Nucleotide Polymorphism: HWE: Hardy-Weinberg Equilibrium; NOS: Newcastle-Ottawa Scale

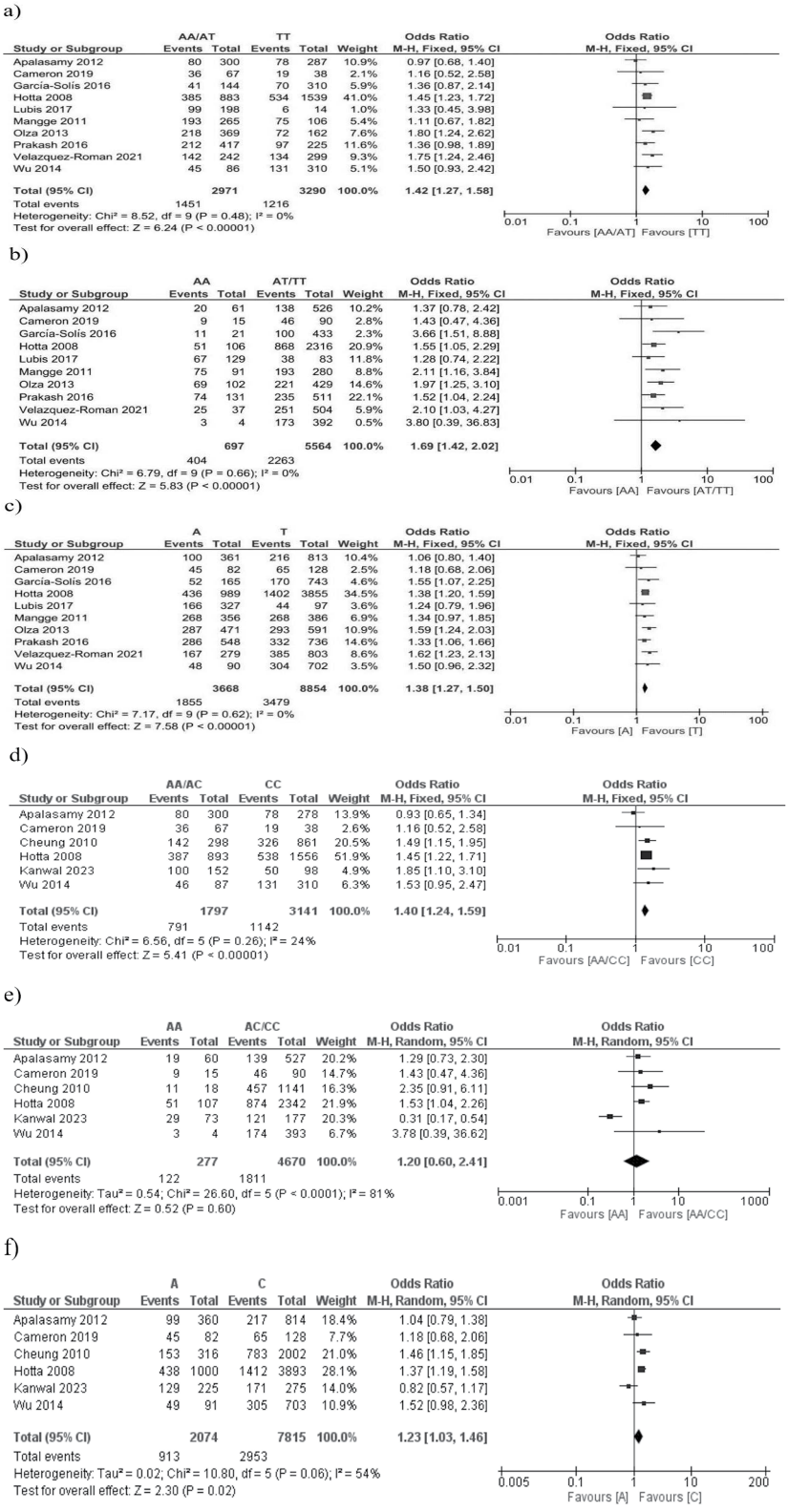
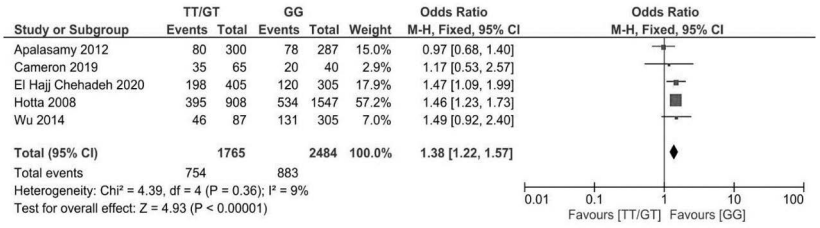


Figure 1. (a) dominant model, (b) recessive model, and (c) allelic model are forest plot in rs9939609 and (d) dominant model, (e) recessive model, and (f) allelic model are forest plot in rs8050136

a)



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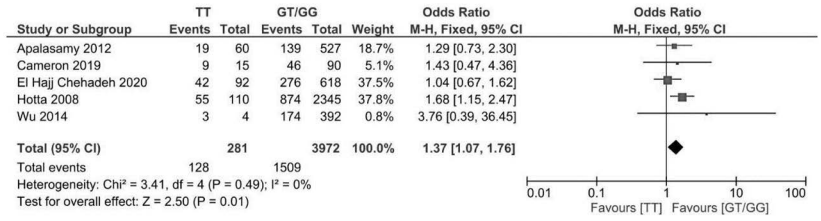

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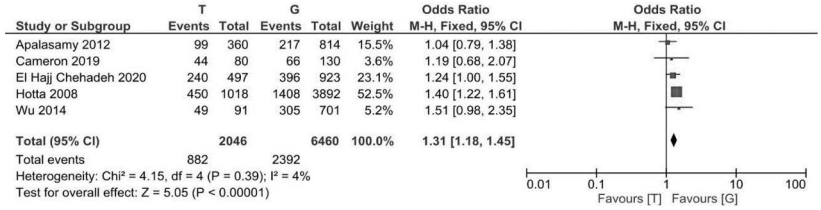
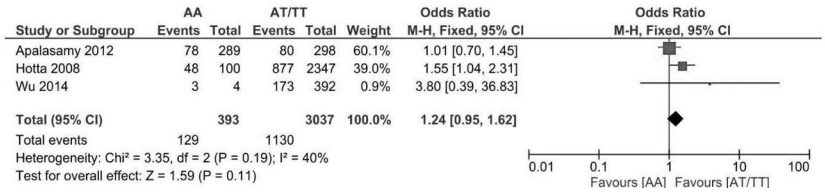


d)

e)



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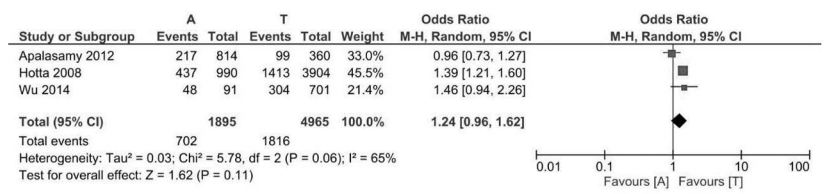

Figure 2. (a) dominant model, (b) recessive model, and (c) allelic model are forest plot in rs3751812 and (d) dominant model, (e) recessive model, and (f) allelic model are forest plot in rs1558902

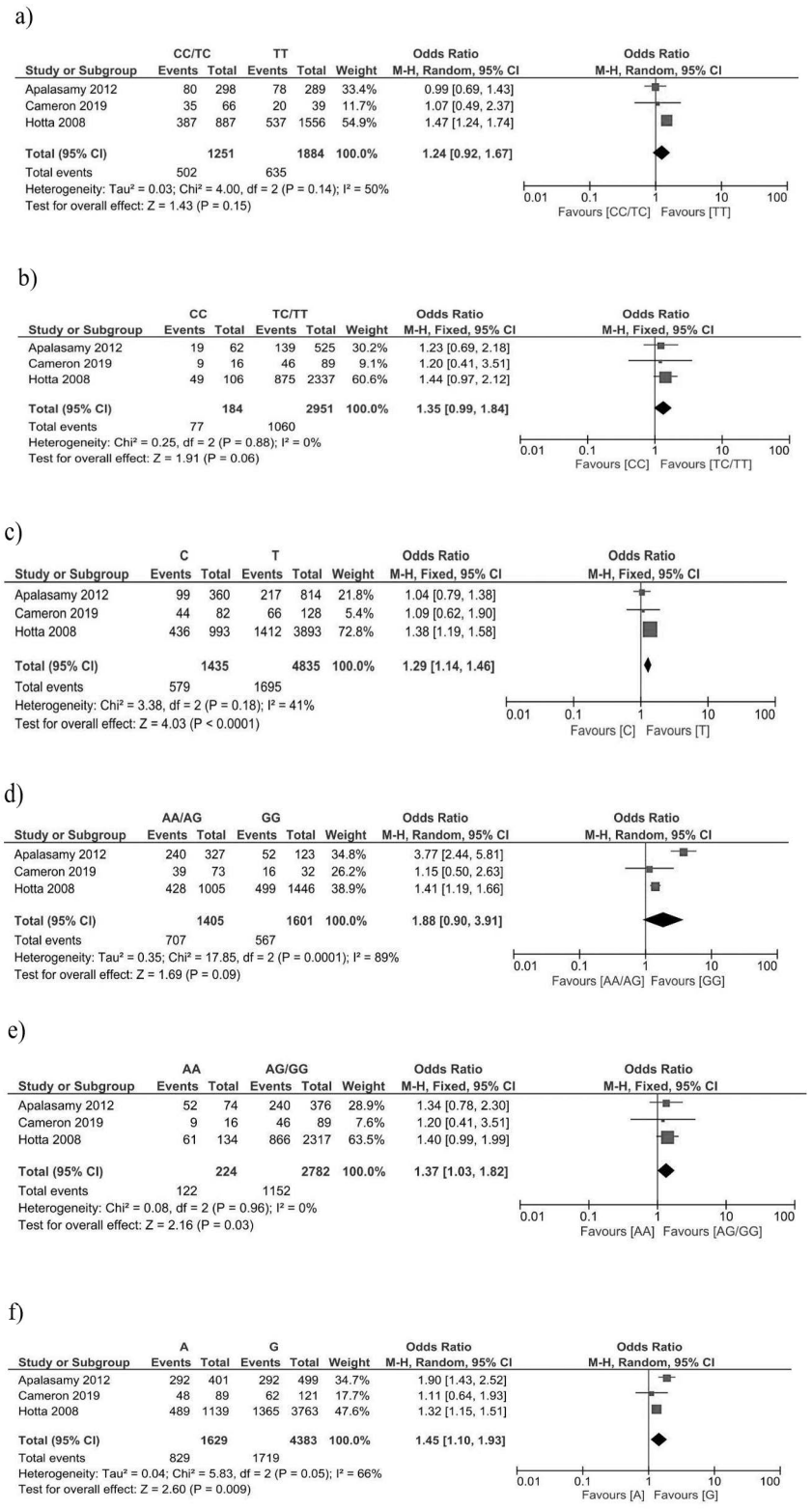

Figure 3. (a) dominant model, (b) recessive model, and (c) allelic model are forest plot in rs1421085 and (d) dominant model, (e) recessive model, and (f) allelic model are forest plot in rs1121980

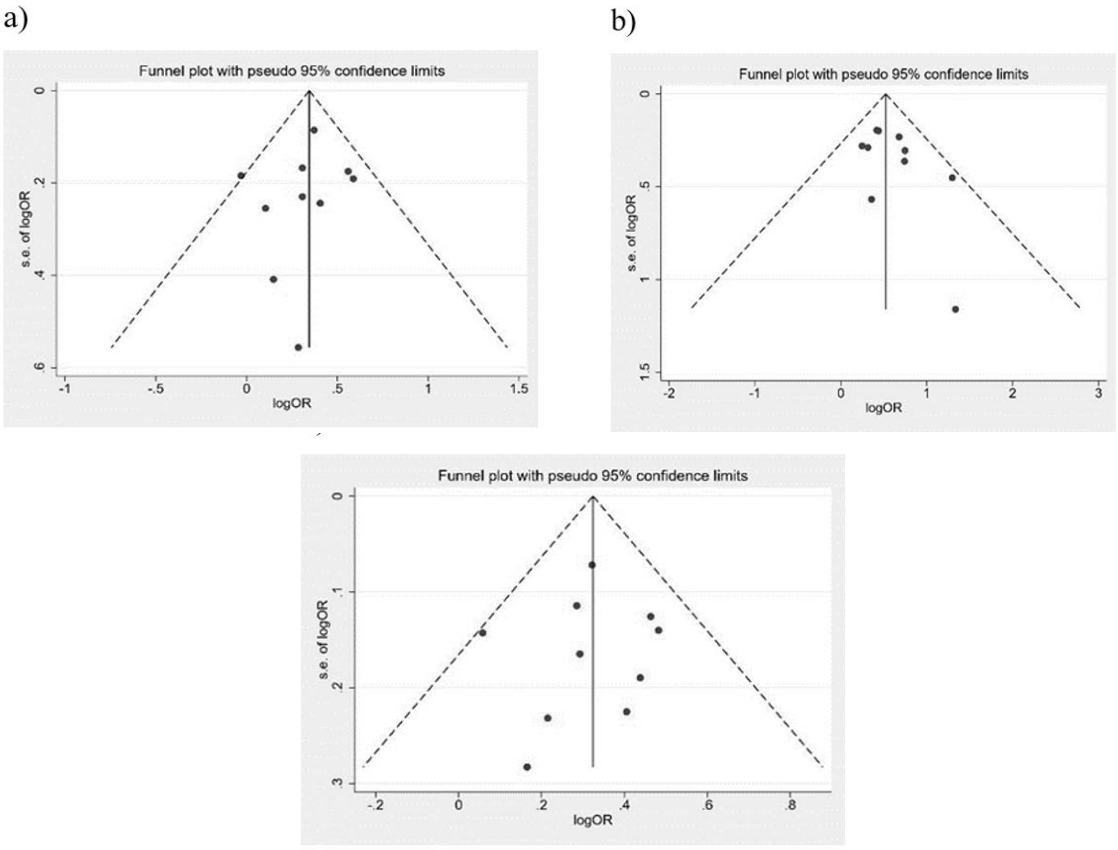

Figure 4. Egger's funnel plot for rs9939609 a) dominant model, b) recessive model, and c) allelic model

2019). Lastly, in contrast to other research, we included many FTO SNPs at increased risk of obesity in this analysis (Doaei *et al.* 2019).

CONCLUSION

In conclusion, this research showed that human FTO polymorphisms can influence the risk of obesity across a wide range of populations and age groups. A significant connection between obesity risk and six FTO SNPs were identified. Further studies should focus on gene-gene and gene-environment interactions should be conducted to gain a better understanding of the relationship.

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DECLARATION OF CONFLICT OF INTERESTS

The authors have no conflict of interest.

REFERENCES

Abramovs N, Brass A, Tassabehji M. 2020. Hardy-Weinberg Equilibrium in the largescale genomic sequencing era. Front Genet 11:210. https://doi.org/10.3389/fgene.2020.00210

Abd Ali AH, Шкурат ТП, Abbas AH. 2021. Association analysis of FTO gene polymorphisms rs9939609 and obesity risk among the adults: A systematic review and meta-analysis. Meta Gene 27:100832. https://doi.org/10.1016/j.

mgene.2020.100832
Apalasamy YD, Mao M, Rampal S, Bulgiba A, Mohamed Z. 2012. Genetic association of SNPs in the FTO gene and predisposition to obesity in Malaysian Malays. Braz J Med Bio Res 45:1119–1126. https://doi.org/10.1590/s0100-879x2012007500134
Cai X, Liu C, Mou S. 2014. Association between Fat Mass- and Obesity- Associated (FTO) gene polymorphism and polycystic ovary syndrome: A meta-analysis. Plos One 9(1):e86972. https://doi.org/10.1371/journal.pone.0086972
Cameron JD, Tasca GA, Little J, Chyurlia L, Ritchie K, Yeh E, Doucette S, Obregón AM, Bulman DE, Doucet É, Goldfield GS. 2019. Effects of Fat Mass and Obesity-Associated (FTO) gene polymorphisms on binge eating in women with binge-eating disorder: The moderating influence of attachment style. Nutrition 61:208–212. https://doi.org/10.1016/j.nut.2018.11.006
Chehadeh SEH, Osman W, Nazar S, Jerman LA, Alghafri A, Sajwani A, Alawlaqi M, AlObeidli M, Jelinek HF, AlAnouti FA, Khalaf K. 2020. Implication of genetic variants in overweight and obesity susceptibility among the young Arab population of the United Arab Emirates. Gene 739:144509. https://doi.org/10.1016/j.gene.2020.144509
Cheung CY, Tso AW, Cheung BM, Xu A, Ong KL, Fong CH, Wat NM, Janus ED, Sham PC, Lam KS. 2010. Obesity susceptibility genetic variants identified from recent genome-wide association studies: Implications in a Chinese population. J Clin Endocrinol Metab 95(3):1395–1403. https://doi.org/10.1210/jc.2009-1465
Chong CT, Lai WK, Sallehuddin SM, Ganapathy SS. 2023. Prevalence of overweight and its associated factors among Malaysian adults: Findings from a nationally representative survey. medRxi 2023-03. https://doi.org/10.1101/2023.03.06.23286889
Danaher J, Stathis CG, Cooke M. 2019. Similarities in metabolic flexibility and hunger hormone ghrelin exist between FTO gene variants in response to an acute dietary challenge. Nutrients 11(10):2518. https://doi.org/10.3390/nu11102518
Forte AJ, Guliyeva G, McLeod H, Dabrh AMA, Salinas M, Ávila FR, Perlman A. 2022. The Impact of optimism on cancer-related and postsurgical cancer pain: A systematic review. J Pain Symptom Manag 63(2):e203–e211. https://doi.org/10.1016/j.jpainsymman.2021.09.008
He D, Fu M, Song M, Hotta K, Chandak GR, Xi B. 2014. FTO gene variant and risk of hypertension: A meta-analysis of 57,464 hypertensive cases and 41,256 controls. Metabolism 63(5):633–639. https://doi.org/10.1016/j.metabol.2014.02.008
Hotta K, Nakata Y, Matsuo T, Kamohara S, Kotani K, Komatsu R, Itoh N, Mineo I, Wada J, Masuzaki H *et al.* 2008. Variations in the FTO gene are associated with severe obesity in the Japanese. J Hum Genet 53(6):546–553. https://doi.org/10.1007/s10038-008-0283-1
Kanwal S, Tariq N, Ali H, Kausar T. 2023. Role of FTO (Fat Mass and Obesity-Associated) and IRX3 (Iroquois Homeobox 3) gene variants on obesity in Quetta. Obes Med 39:100478. https://doi.org/10.1016/j.obmed.2023.100478
Liaw YC, Liaw YP, Lan TH. 2019. Physical activity might reduce the adverse impacts of the FTO gene variant rs3751812 on the body mass index of adults in Taiwan. Genes 10(5):354. https://doi.org/10.3390/genes10050354
Lin X, Li H. 2021. Obesity: Epidemiology, pathophysiology, and Therapeutics. Front Endocrinol 12: 706978. https://doi.org/10.3389/fendo.2021.706978
Liu C, Mou S, Cai Y. 2013. FTO Gene Variant and Risk of Overweight and Obesity among Children and Adolescents: A Systematic Review and Meta-Analysis. Plos One 8(11):e82133. https://doi.org/10.1371/journal.pone.0082133
Lubis SM, Fattah M, Damanik HA, Batubara JR. 2017. Association of Fat Mass and Obesity-associated Gene (FTO) rs9939609 variant with early onset obesity among Bataknese and Chinese children in Indonesia: A case-control study. Indones Biomed J 9(3):147–152. https://doi.org/10.18585/inabj.v9i3.322
Ramírez V, Robles-Aguilera V, Salcedo-Bellido I, Gálvez-Ontiveros Y, Rodrigo LS, Martínez-González LJ, Monteagudo

C, Álvarez-Cubero MJ, Rivas A. 2022. Effects of genetic polymorphisms in body mass index according to dietary exposure to bisphenols and parabens. Chemosphere 293:133421. https://doi.org/10.1016/j.chemosphere.2021.133421

Rangel-Huerta ÓD, Pastor-Villaescusa B, Gil Á. 2019. Are we close to defining a metabolomic signature of human obesity? A systematic review of metabolomics studies. Metabolomics 15:1–31. https://doi.org/10.1007/s11306-019-1553-y

Ruiz-Díaz MS, Mena-Yi D, Gómez-Camargo D, Mora-García G. 2022. Interaction analysis of FTO and IRX3 genes with obesity and related metabolic disorders in an admixed Latin American population: A possible risk increases of body weight excess. Colomb Med 53(2):e2044874. https://doi.org/10.25100/cm.v53i2.4874

Velázquez-Román J, Angulo-Zamudio UA, León-Sicairos N, Medina-Serrano J, DeLira-Bustillos N, Villamil-Ramírez H, Canizales-Quinteros S, Macías-Kauffer L, Campos-Romero A, Alcántar-Fernández J *et al.* 2021. Association of FTO, ABCA1, ADRB3, and PPARG variants with obesity, type 2 diabetes, and metabolic syndrome in a Northwest Mexican adult population. J Diabetes Complications 35(11):108025. https://doi.org/10.1016/j.jdiacomp.2021.108025

Wu J, Xu J, Zhang Z, Ren J, Li Y, Wang J, Cao Y, Rong F, Zhao R, Huang X, Du J. 2014. Association of FTO Polymorphisms with obesity and metabolic parameters in Han Chinese adolescents. Plos One 9(6):e98984. https://doi.org/10.1371/journal.pone.0098984

Xu Z, Xia J, Xiong XD. 2023. Emerging role and mechanism of the FTO gene in cardiovascular diseases. Biomolecules 13(5):850. https://doi.org/10.3390/biom13050850

Zhao N, Dong G, Wu W, Wang J, Ullah R, Fu J. 2019. FTO gene polymorphisms and obesity risk in Chinese population: A meta-analysis. World J Pediatr 15:382–389. https://doi.org/10.1007/s12519-019-00254-2