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MULTIFACTORIAL DETERMINANTS OF OBESITY: THE ROLES OF HORMONES, GENETICS, INFLAMMATION AND GUT MICROBIOTA – REVIEW

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ABSTRACT

Obesity is a multifactorial chronic disease resulting from the interaction of genetic, hormonal, inflammatory, and microbial factors. While caloric imbalance contributes to its pathogenesis, pathways involving molecular mechanisms—such as leptin–melanocortin pathway dysfunction, adipokine dysregulation, and microbiota-induced inflammation—are also significant. Adipose tissue inflammation is characterized by macrophage infiltration, activation of MAPK and NF-κB pathways, and abnormal adipokine secretion, all of which lead to insulin resistance and metabolic dysfunction. Genetic factors, including mutations in the LEP, LEPR, POMC, and MC4R genes, can disrupt appetite regulation and predispose individuals to early-onset obesity. Syndromic forms of obesity, such as Prader–Willi and Bardet–Biedl syndromes, further highlight chromosomal influences. Hormonal imbalances, including those involving ghrelin, GLP-1, and CCK, also affect energy expenditure and appetite regulation. Additionally, gut dysbiosis contributes to systemic inflammation through increased levels of lipopolysaccharides (LPS) and decreased production of short-chain fatty acids, which maintain metabolic endotoxemia. These patterns of evidence underscore the need for integrative interventions targeting endocrine, inflammatory, and microbial pathways. Further research is required to clarify gene– microbiota–hormone interactions and to develop personalized therapeutic intervention.

KEYWORDS

Obesity, Hormones, Gut Microbiota, Inflammation, Treatment

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1. Introduction

1.1 Pathogenesis of obesity

Obesity is classified as a disease characterized by a body mass index (BMI) of 30 or greater, calculated as weight in kilograms divided by height in meters squared (kg/m²) (X. Lin & Li, 2021). Excessive calorie intake relative to energy expenditure is a primary contributing factor (Schwartz et al., 2017). Nevertheless, obesity results from a complex interplay of factors, including genetics, hormonal regulation, epigenetic modifications, the gut microbiome, and environmental influences (Kaila & Raman, 2008). Genetic contributions often involve single-gene mutations, particularly within the leptin-melanocortin pathway, which regulate appetite. The accumulation of multiple genetic variants increases the risk of overeating, delayed satiety, and enhanced fat storage (X. Lin & Li, 2021). Gut hormones such as ghrelin, as well as anorectic hormones including peptide YY (PYY), cholecystokinin (CCK), and oxyntomodulin, play significant roles in the pathophysiology of obesity (Kaila & Raman, 2008). Adipose tissue secretes adipokines, including tumor necrosis factor alpha (TNF-α), interleukin 6 (IL-6), leptin, and adiponectin (Kaila & Raman, 2008). Recent research demonstrates that both gut microbiota and epigenetic mechanisms substantially influence the development of obesity.

1.2 Chronic inflammation linked to obesity

Obesity is closely associated with persistent, low-grade inflammation. Excessive nutrient intake results in adipocyte hypertrophy, which induces hypoxia and cellular stress. These conditions stimulate the release of pro-inflammatory cytokines, including tumor necrosis factor α (TNF-α), interleukin-6 (IL-6), monocyte chemotactic protein-1 (MCP-1), and interleukin-1β (IL-1β) (Wu & Ballantyne, 2020; Ellulu et al., 2017).

Multiple inflammation-related transcription factors contribute to adipose tissue inflammation (ATI). The mitogen-activated protein kinase (MAPK) pathway, which includes JNK, p38, and ERK, mediates extracellular stress signals and promotes inflammation, cell differentiation, and apoptosis. In the context of

obesity, MAPK activation induces ATI and insulin resistance by inactivating insulin receptor substrate-1 (IRS-1) and decreasing PPAR-γ expression (Aruwa & Sabiu, 2024).

Immune cells, such as macrophages, are recruited to adipose tissue by chemokines including MCP-1/CCL2. The accumulation of these cells correlates with adipocyte size and overall body mass (Weisberg et al., 2003). This infiltration is characterized by a shift from anti-inflammatory M2 cells (Th2, Treg, M2 macrophages) to pro-inflammatory M1 cells (Th1 cells, neutrophils, and antibody-producing B cells), (Khanna et al., 2022).

Adipose tissue secretes more than 500 bioactive substances known as adipokines, such as leptin, adiponectin, resistin, and visfatin. These adipokines regulate insulin sensitivity, lipid metabolism, and inflammatory responses (Aruwa & Sabiu, 2024). In obesity, dysregulated adipokine secretion intensifies inflammation, oxidative stress, and endoplasmic reticulum stress. This dysregulation also activates inflammasomes, including NLRP3, resulting in elevated IL-1β production and activation of proapoptotic caspase-1 (Rohm et al., 2022). These molecular events establish a self-perpetuating cycle of "meta-inflammation," linking local adipose inflammation to systemic metabolic dysfunction, insulin resistance, and type 2 diabetes (Ngamsamer et al., 2022; Wu & Ballantyne, 2020).

The inflammatory effects of obesity extend beyond metabolic tissues. For example, maternal obesity is associated with increased placental oxidative stress, altered fatty acid metabolism, and elevated inflammatory markers in the fetus. These alterations may negatively impact neonatal immune function (Zhang et al., 2024). Figure 1 illustrates a potential mechanism linking obesity to chronic low-grade inflammation.

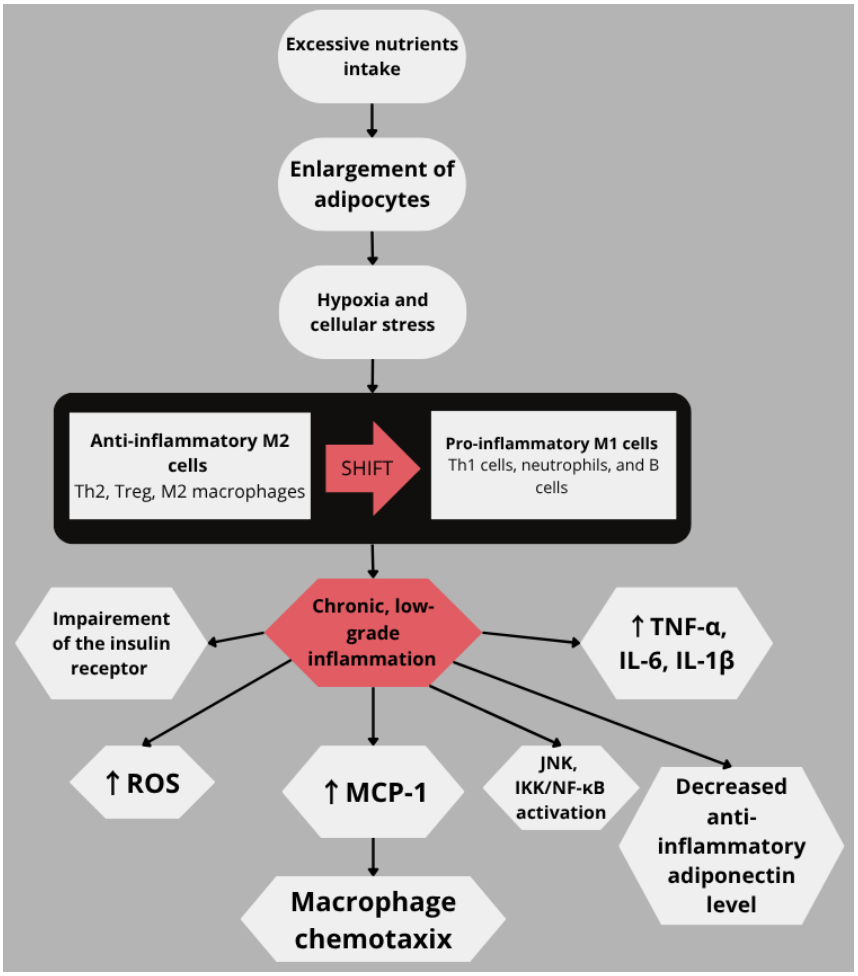

Fig. 1.

Figure 1 displays the possible mechanism which connects inflammation and obesity. In obese adipose tissue (AT), TNF-α is produced by hypertrophic adipocytes and macrophages, contributing to local inflammation and systemic insulin resistance (Ellulu et al., 2017). IL-6 is secreted from AT and stimulates hepatic CRP production, linking local inflammation to systemic responses. IL-1β is also upregulated in

inflamed AT following inflammasome activation, amplifying cytokine production and insulin signaling defects. MCP-1 drives monocyte chemotaxis into AT, significantly increasing adipose tissue macrophage (ATM) content; reducing MCP-1 signaling decreases ATM accumulation (Aruwa & Sabiu, 2024). The rise in Th1-type activity enhances AT inflammation and macrophage M1 polarization, while anti-inflammatory substances like adiponectin in obesity, promoting inflammation and insulin resistance.Kinases and transcription factors (JNK, IKK/NF-κB) in adipocytes, impair insulin signaling and maintain chronic inflammation characteristic of obesity (Ellulu et al., 2017). ROS-reactive oxygen species, MCP1- monocyte chemotactic protein-1, TNF α- tumor necrosis factor α, IL-interleukin, JNK/IKK- JNK-c-Jun N-terminal kinase

1.3 Hormonal imbalance linked to obesity

Gut hormones and peptides derived from adipose tissue are critical for maintaining body mass homeostasis. These molecules regulate food intake and energy expenditure (Sam et al., 2012). Their effects are mediated either directly on brain regions lacking a blood–brain barrier or indirectly through activation of vagal afferent neurons (Marić et al., 2014). Single-nucleotide variants in genes encoding anorexigenic hormones such as glucagon-like peptide-1 receptor (GLP-1R) and cholecystokinin (CCK) are significantly overrepresented in metabolically unhealthy obese individuals (Nikulina et al., 2024). Ghrelin dysregulation contributes substantially to this inflammatory state, as circulating levels of this orexigenic peptide influence both appetite regulation and systemic inflammation patterns (Młynarska et al., 2025).The dysregulation of these gut-derived hormones—including ghrelin, GLP-1, and CCK—disrupts the balance between orexigenic and anorexigenic signaling, leading to hyperphagia and weigt gain while simultaneously promoting low-grade systemic inflammation (Skoracka et al., 2025).

Table 1

Hormone group	Hormone	Site of secretion	Target receptor/s	Main stimuli on secretion	Primary function	Effect on appetite
Pancreatic Polipeptide Family (PP-fold)	Peptide YY (PYY)	L-cells (distal part of ileum and colon)	Y1R Y4R Y5R Y6R Y2R (highest affinity)	Food intake (especially food high in protein)	↓gastric motility and emptying. ↓pancreatic secretion. ↑satiety. ↑hypothalamic activation of POMC neurons.	Anorexigenic
	Pancreatic Polypeptide (PP)	PP cells (Langerhans islets in pancreas)	All Y receptors (mainly Y4R)	Food intake (especially food high in fat)	↓gastric motility and emptying. ↓pancreatic secretion.	Anorexigenic
	Neuropeptide Y (NPY)	-	-	-	Promotes feeding behavior and energy storage.	Orexigenic

Proglucagon-Derived Peptides	Glucagon	α-cells (Langerhans islets in pancreas)	GCGR	↓blood glucose levels	↑hepatic glucose production, ↑blood glucose level, ↓food intake in some contexts	Anorexigenic
	Glucagon like peptide 1 (GLP-1)	L-cells (small intestine), Brainstem neurons	GLP-1R	Food intake (carbohydrates, fats, proteins)	↑insulin secretion (incretin effect), ↓glucagon release, ↓gastric emptying,	Anorexigenic
	Glucagonlike peptide 2 (GLP-2)	L-cells (small intestine),	GLP-2R	Food ingestion	Stimulates process of crypt cells proliferation in the intestine.	Neutral
	Oxyntomodulin (OXM)	L-cells (small intestine), Brainstem neurons	GLP-1R, GCGR	Food intake (proportional to caloric content)	Reduces appetite, increases energy expenditure, regulates weight through dual receptor activity	Anorexigenic
Cholecystokinin (CCK)	CCK	L-cells (small intestine)	CCK-A receptor,	Food ingestion (mainly fat and protein)	↑ bile and pancreatic secretion, ↑ GLP-1 secretion, ↑ PYY secretion, ↓gastric emptying, ↓Ghrelin secretion,	Anorexigenic
Ghrelin	Ghrelin	P/D1 enteroendocrine cells in gastric fundus	GHS	Fasting, ↓blood glucose levels	↑appetite, activates NPY/AgRP neurons, inhibits POMC neurons, ↑fat storage.	Orexigenic

Table 1 presents the division of various gut hormone groups involved in regulating human appetite, thereby influencing food intake and energy expenditure. It also includes their site of secretion, target receptors,

main stimuli on secretion, primary functions, and their effect on appetite. Orexigenic- stimulating appetite, anorexigenic- decreasing appetite, ↑ - increase, ↓- decrease, PYY- Peptide YY (also known as Peptide Tyrosine Tyrosine), Y2R- neuropeptide Y receptor Y2, POMC- proopiomelanocortin, PP- pancreatic polypeptyde, Y4R- neuropeptide Y receptor Y4, NPY- Neuropeptide Y, CNS- central nervous system, Y1R- Neuropeptide Y receptor Y1, Y5R- Neuropeptide Y receptor Y5, GCGR- Glucagon receptor, GLP-1- Glucagon-like Peptide 1, GLP-1R- Glucagon-like peptide 1 receptor, GLP-2- Glucagon-like Peptide 2, GLP-2R- Glucagon-like peptide 2 receptor, OXM- Oxyntomodulin, CCK- Cholecystokinin, CCKAR- Cholecystokinin A receptor, GHS-R1a- Growth Hormone Secretagogue Receptor Type 1, AgRP - Agouti-Related Protein. (Alhabeeb et al., 2021; Suzuki et al., 2010)

1.4 Connection between genetic factors and obesity

Genetic factors contribute to the development of obesity through several biological pathways. These mainly involve dysregulation of hypothalamic function and impaired energy expenditure control. Obesity arises from the interaction of multiple genes and environmental influences rather than a single gene mutation (Mahmoud et al., 2022). Genetic factors interact with environmental influences, especially in obesogenic environments, to cause excessive weight gain and metabolic dysregulation (Hastuti, 2022; Mahmoud et al., 2022).

Researchers have identified more than 1,100 independent genetic loci associated with obesity-related traits. This discovery has sparked strong interest in understanding the biological functions involved and the nature of gene–environment interactions (Vourdoumpa et al., 2023).

Individuals with a positive family history have a much higher risk of childhood obesity. Concordance rates for obesity are much higher in monozygotic twins than in dizygotic twins. Twin-based research estimates obesity heritability at about 40–75% (Mahmoud et al., 2022).

Monogenic obesity results from a single gene mutation. Examples are LEP (Leptin), LEPR (leptin receptor), POMC (pro-opiomelanocortin), MC4R (Melanocortin-4 receptor), and PCSK1 (proprotein convertase subtilisin/kexin type 1). Polygenic obesity, which accounts for about 95% of cases, involves many genetic variants. These often cluster within related gene families (Mahmoud et al., 2022).

Table 2.

Obesity-related genes	Defect Location (mutation type)	Role in the body	Consequences of deficiency/mutation.	Citation
Leptin	chromosome 7 in humans, (homozygous frameshift mutation in the leptin gene (a G133 deletion).	Leptin crosses the blood–brain barrier and binds to presynaptic GABA-ergic neurons within the hypothalamus, where it suppresses appetite and enhances energy expenditure.	Inherited leptin deficiency leads to severe early-onset obesity (e.g., 8 years and 86 kg, or 2 years and 29 kg). Obese individuals have significantly higher leptin levels than controls, a condition known as leptin resistance.	(Mahmoud et al., 2022)
Proopiomelanocortin (POMC) Deficiency	Chromosome 2 in humans.	An appetite-suppressing gene involved in the leptin–melanocortin pathway, serving as a precursor to ACTH and MSH.	POMC protein deficiency leads to absence of ACTH and MSH, resulting in hyperphagia, lower metabolic rate, severe obesity, and often red hair with pale skin.	(Mahmoud et al., 2022).
Melanocortin-4 Receptor	Chromosome 18 in humans.	MC4R in the hypothalamus is activated by MSH, which suppresses appetite, increases energy use, and regulates body weight.	Deficiency or mutation of MC4R -> severe early-onset obesity, hyperphagia, increased fat mass and altered energy expenditure.	(Mahmoud et al., 2022).

Table 2 presents examples of obesity-related genes, their roles in the organism, and the correlation of mutations with obesity((Mahmoud et al., 2022).

The genetic basis of obesity is classified as syndromic or non-syndromic. Syndromic obesity results from mutations in groups of genes. In contrast, non-syndromic obesity can be monogenic or polygenic. People with this condition typically show obesity, cognitive impairment, hyperphagia, hypothalamic dysfunction, and multiple organ abnormalities. Examples include Prader–Willi syndrome, Bardet–Biedl syndrome, Down syndrome, Cohen syndrome, Alström syndrome, and Fragile X syndrome.

Table 3.

Chromosomal Defects and Obesity-Related Syndromes:	Defect location (mutation type)	Rate of occurrence	Clinical features	Correlation with obesity
Prader-Willi Syndrome	15q11.2–q13 region of chromosome in human (The most common cause is the loss of paternal gene expression in this region due to a de novo deletion of the paternally derived 15q11.2–q13 segment. The less frequent mechanism involves maternal uniparental disomy (UPD), in which both copies of chromosome 15 are inherited from the mother).	1 in 10,000-29,000 individuals, impacting males and females equally across all racial and ethnic groups.	infancy by hypotonia, (markedly decreased muscle tone and generalized floppiness), which often causes feeding difficulties and poor weight gain. Paradoxically, as children age, PWS progresses to hyperphagia—which typically leads to childhood-onset obesity.	PWS patients with deletions are significantly heavier and have higher BMI scores than those with UPD. The hyperphagia seen in PWS is believed to originate in the hypothalamus (the brain fails to recognize feelings of fullness) - individuals experience a persistent sensation of hunger and are driven to consume excessive amounts of food. The brain misinterprets the body's energy status as starvation, leading to a reduced metabolic rate aimed at conserving energy -> rapid and severe weight gain and ultimately morbid obesity.
Alstrom Syndrome	Chromosome 2p13 (mutations in the ALMS1 gene).	1 in 500,000 to 1 in 1,000,000 individuals.	Clinical manifestations typically appear during infancy. The earliest signs include visual impairment, nystagmus, and early-onset blindness caused by cone-rod dystrophy.	A wide range of endocrine abnormalities have been documented in Alström syndrome, such as hypothyroidism, hypogonadotropic hypogonadism in males, hyperandrogenism in females, childhood-onset truncal obesity, hypertriglyceridemia, and insulin resistance leading to type 2 diabetes mellitus.
Fragile X Syndrome (FXS)	Chromosome X (mutation at the FMR1 gene).	the most common inherited cause of intellectual disability in males (1 in 4000-7000 live births).	Approximately 10% of individuals with FXS exhibit features such as severe obesity, hyperphagia, hypogonadism or delayed puberty.	FXS patients generally have higher body weights compared with population averages. In a longitudinal study with FXS patients across various age groups, scientists observed a progressive increase in BMI with age and elevated BMI Z-scores in adulthood, reinforcing the notion that obesity is a recognized feature of FXS.

Down Syndrome (DS)	Chromosome 21 (trisomy of 21 chromosome).	the most prevalent chromosomal disorder in humans (1 in 700 live births).	-facial features (palpebral fissures, flattened facial profile, nose bridge, epicanthal folds, small, low-set ears), -physical features (hypotonia, short stature, single transverse palmar crease, short fingers and broad hands, sandal gap), -developmental features (delayed developmental milestones -> moderate intellectual disability), -medical associations (especially AV septal defect, hypothyroidism, hearing and vision problems).	Elevated serum leptin levels -> increased appetite. Leptin acts on the hypothalamic centers regulating hunger and satiety -> reduced energy expenditure and lower physical activity levels. The high prevalence of obesity in DS is likely multifactorial (genetic predisposition, hypothyroidism, limited physical activity, elevated serum cholesterol and triglyceride levels, and unhealthy dietary habits).
Bardet-Biedl Syndrome (BBS)	Over 25 genes (BBS1-BBS22) have been identified so far (autosomal recessive inheritance).	1 in 100 000-160 000 live births.	Central obesity, retinal cone–rod dystrophy, postaxial polydactyly, learning disabilities, hearing impairment, hypogonadism, and genitourinary anomalies, renal complications (polycystic kidney disease).	Early age (2-3 years) obesity occurring in approximately 89% of affected individuals. The development of obesity in BBS results from gene mutations that reduce the number and function of cilia, thereby disrupting neuroendocrine signaling between ciliated neurons and adipose tissues -> dysregulated appetite control, characterized by leptin resistance and defective leptin receptor signaling.
WAGR Syndrome	Chromosome 11 in human (deletion at 11p13).	1 in 500 000-1 000 000 individuals.	Predisposition to Wilms tumor, aniridia, genital anomalies, and intellectual disability (WAGR syndrome).	Associated with a deletion involving the brain-derived neurotrophic factor (BDNF) gene within the same 11p13 chromosomal region. Loss of BDNF function contributes to the development of an obesity phenotype, likely through its role in energy balance and appetite regulation.

Table 3 presents examples of obesity-related syndromes caused by chromosomal defects (type of mutation, rate of occurrence, clinical features, and specific correlation with obesity characteristic of those syndromes (Mahmoud et al., 2022).

1.5 The connection between obesity and weight loss by nutritional interventions and gut microbiota

The gut microbiota includes all microorganisms that inhabit the gastrointestinal tract, most present in the large intestine (Baothman et al., 2016). Dysbiosis disturbs the balance of pro-inflammatory and anti-inflammatory bacterial species in the gastrointestinal tract, resulting in a pro-inflammatory microbial profile (Pelc, 2025). Moreover, dysbiotic microbiota are frequently colonized with more gram-negative bacteria producing lipopolysaccharides (LPS), a pro-inflammatory molecule (Gaber, 2024). This is particularly notable when intestinal permeability increases due to barrier dysfunction, thus allowing LPS to enter the circulation and activate toll-like receptor 4 (TLR4) on immune cells. Such activation perpetuates the low-grade systemic inflammation characteristic of obesity (Huang, 2025).

This imbalance is reflected in the loss of beneficial bacteria (Akkermansia muciniphila and Faecalibacterium prausnitzii), which are significantly depleted in obesity and usually produce anti-inflammatory signals (Valls, 2024). The lack of these organisms causes signaling to turn to pro-inflammatory cytokines such as IL-1, IL-6, and TNF-α, which starts chronic low-grade systemic inflammation (Randeni, 2024). Supplementation of probiotic with certain bacterial strains has been proposed as an efficient means of improving barrier function and decreasing metabolic endotoxemia (Amabebe et al., 2020).

Beyond inflammatory circuits, changes in gut microbiota modulate luminal content levels in a metabolomic manner, including declines in bile acid concentrations (Ridlon et al., 2006). Lower concentrations of bile acid are known to depress energy expenditure via blockade of TGR5/FXR signaling on adipose tissue (Broeders et al., 2015; Fang et al., 2015). Additionally, low bile acid concentrations enhance de novo lipogenesis in the liver. Together, these pathways suggest that gut dysbiosis plays a major role in obesity related lipid storage. The microbiota acts by diverse mechanisms to promote lipid synthesis and storage (Cheng et al., 2022).

Research indicates that obese subjects usually have markedly lower concentrations of SCFA (short-chain fatty acids) and a reduced number of SCFA generating bacteria when compared to their lean counterpart (Ecklu-Mensah et al., 2023). SCFAs counter obesity via several mechanisms, including activation of G protein-coupled receptors that decrease appetite and promote energy expenditure (Kimura et al., 2014), fortification of gut barrier function to mitigate metabolic endotoxemia (Chakraborti, 2015), and controlling epigenetic changes in metabolic gene expression (Kopczynska & Kowalczyk, 2024). According to clinical evidence, increasing SCFA concentrations correlate with increased insulin sensitivity, less visceral fat deposition, and improved glucose homeostasis (Zhang et al., 2024), indicating that techniques such as increases in SCFA production through dietary fiber intake or probiotic supplementation is one of the promising strategies to prevent and treat obesity (Coppola et al., 2021).

Dietary habits can affect the microbiome composition, as well as concentration of SCFAs (see Table 4) (Attaye et al., 2022, L. Li et al., 2024, Muscogiuri et al., 2022, Cheng et al., 2022).

Table 4.

Nutrition style	Increasing part of gut microbiota or SCFAs	Deacreasing part of gut microbiota	Source
Ketogenic diet	↑ Bacteroidetes SCFAs	↓ Firmicutes, Bifidobacterium	(Attaye et al., 2022)
Low-carbon diet	↑ Bacteroidetes, Parabacteroides	↓ Firmicutes, Acinetobacter, Ruminococcus, Agathobacter, Streptococcus, Bifidobacterium	(L. Li et al., 2024).
Meditarrean diet	↑ Lactobacillus, Bifidobacterium, Prevotella SCFAs	↓ Clostridium	(Muscogiuri et al., 2022).
Obesity	↑ Firmicutes	↓ Bacteroidetes	(Cheng et al., 2022).

Table 4 shows the corelation between different styles of nutrition and shape of gut microbiota
↑ Increase, ↓ deacrease

Metabolite profiling and evaluation of gut microbiota composition may provide a more systematic way to discover predictors for obesity control that are easier to quantify than traditional approaches. The tools could also ascertain the most effective nutritional interventions to manage obesity on an individual basis. Nevertheless, the lack of adequately powered randomized trials limits the translation of these results into clinical settings (Puljiz et al., 2023). More studies are needed to clarify the mechanisms under which gut microbiota is related to obesity, the specific role of the microbiota, and whether dietary interventions, with or without additional prebiotics or probiotics, offer viable therapeutic options for obesity prevention (Zsálig et al., 2023).

4. Summary

Obesity is a multi-factorial, complex chronic disease with genetic, hormonal, inflammatory, and gut microbial aspects. Although an overintake of calories is a common etiology, more complicated mechanisms at the molecular level, including leptin-melanocortin pathway dysfunction, adipokine dysregulation, and gut microbiota-mediated inflammation are also critical for the etiology. Chronic low-grade inflammation of the adipose tissue, mediated by macrophage infiltration and activation of pathways such as MAPK and NF-κB, contributes to insulin resistance and metabolic dysfunction. Genetic factors (such as mutations in genes responsible for appetite regulation and energy balance (for instance, LEP, LEPR, POMC, MC4R) have been implicated in early-onset obesity, and syndromic obesity (e.g., Prader–Willi and Bardet–Biedl syndromes) emphasizes chromosomal disorders that contribute to more severe forms of obesity. Hormonal imbalances involving ghrelin, GLP-1, and CCK also lead to loss of appetite stability, overeating, and systemic inflammation. Dysbiosis of the gut microbiota involving diminished beneficial bacteria and enriched pro-inflammatory species producing lipopolysaccharides (LPS) disrupts the integrity of the intestinal barrier thereby driving chronic inflammation and metabolic endotoxemia. Such a malaise affects metabolism since it reduces short-chain fatty acids (SCFAs) and bile acids, reducing energy expenditure and promoting fat storage. Food habits such as ketogenic, low-carbohydrate, and Mediterranean diets may have a positive influence on gut microbiota and SCFA levels. Obesity is produced when combined with the endocrine, immune, genetic, and microbial systems of an organism. The integration and personalized treatment of these pathways require effective, integrated approaches tailored to individuals. Further studies have to understand more precise gene–microbiota–hormone interactions to develop better obesity therapies.

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All authors contributed to the article.

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