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# Microenvironmental determinants of cancer progression during obesity: emerging evidence and novel perspectives

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**Abstract** Obesity is a global pandemic representing a significant public health threat, with a rising number of affected individuals and numerous associated co-morbidities, including cancer. In obese cancer patients, higher mortality rates are usually observed compared to normal weight/lean individuals. The imbalanced metabolic asset of obese patients fosters tumor growth and its progression by impacting not only on cancer cells, but also affecting their cross-talk with the tumor microenvironment, which represents a relevant and multifaceted player in disease progression. Herein, we deliver a detailed overview of certain peculiar players implicated in the reprogramming of the tumor microenvironment during obesity toward disease evolution. We highlight the key metabolic, molecular and cellular players that co-opt cancer cells and their microenvironment to foster disease progression. We emphasize the role of certain hormones and growth factors-dependent pathways (Insulin/IGF signaling system and VEGF/VEGFR axis) together with inflammatory pathways (RAGE signaling system) in triggering microenvironmental-dependent evolution of neoplastic disease during obesity. Finally, we underline current pitfalls and envisage innovative tools and future directions for better investigating tumor progression in obesity.

# Introduction

Obesity is a metabolic disorder arising from a chronic imbalance between energy intake and expenditure, leading to excessive fat accumulation and pathological adipose tissue expansion. This metabolic condition is currently considered as a disease [1]. In fact, in 1997 the World Health Organization, following consultation with the International Obesity Task Force, released a ground-breaking document clearly stating that obesity

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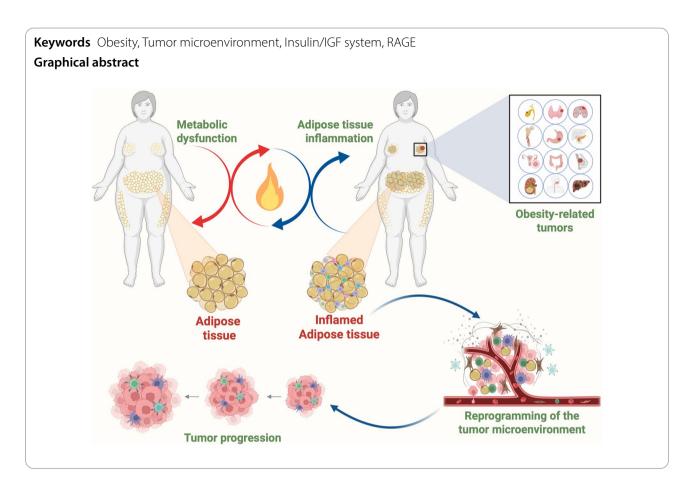
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is a chronic disease that requires the establishment of prevention and management programs at both individual and community level [2]. Subsequently, the National Institutes of Health (in 1998) and the American Obesity Society (in 2008) confirmed that obesity is a disease [3]. In 2013, the American Medical Association House of Delegates recognized obesity as a disease that requires treatment and prevention strategies [4]. In addition, in 2017, World Obesity released a similar position statement, elaborated by a group of expert advisers in the field [5].

Due to its ever-increasing incidence worldwide, obesity is currently considered as a "global pandemic" and a major risk factor for non-communicable diseases, including cardiovascular diseases (CVDs) and cancer [6]. In the latter context, obesity is a modifiable factor associated



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with increased cancer incidence and higher mortality rates. Obesity affects tumor development and progression through multiple mechanisms, such as the activation of impaired metabolic responses, the stimulation of chronic low-grade inflammation, and the aberrant activation of hormones and growth factors-dependent stimulatory pathways (Table 1).

In fact, an increased tumor risk in overweight/obese patients compared to normal weight subjects is found in colorectal, ovarian, endometrial, cervix, esophageal, pancreatic cancer, as well as in meningioma, multiple myeloma, leukemia and tumors of the stomach, liver, kidney, gallbladder and thyroid [9, 31]. A similar trend is observed for breast cancer in post-menopausal women, whereas an inverse association between cancer risk and body mass index (BMI) is detected in pre-menopausal breast cancer and in prostate cancer patients [31, 32]. Despite further investigation is needed, current literature emphasizes obesity's significant role in promoting a large subset of tumor types, accounting for nearly 40% of newly diagnosed cases [33]. Worthy, obesity impacts not only on cancer risk, but also on cancer-related mortality [34]. For instance, in obese breast cancer patients an increased risk of metastasis propagation was evidenced in a phase 3 clinical study [35]. Conversely, a lower risk of death is detected in obese patients suffering melanoma, kidney and lung cancer, indicating that tissue-dependent factors may influence cancer biology and disease evolution [36]. This phenomen, known as "obesity paradox", refers to the controversial hypothesis proposing that overweight/obese individuals could have improved outcomes and survival rates in different co-morbidities, including cancer, when compared to normal/underweight patients [37]. In cancer patients, the "obesity paradox" could be mainly attributed to methodological limitations, such as reverse causation, selection bias, confounding, and the use of BMI as a measure of adiposity [38]. In survival studies performed on obese cancer patients, reverse causation due to both weight loss or cachexia could be the main factors underlying the "obesity paradox" [38]. On the other hand, overweight and obesity could favorably impact treatment outcomes, as excess adipose tissue can alter the pharmacokinetics of anticancer therapies and offer nutritional reserves that help patients to better tolerate surgical and oncologic interventions [39]. Furthermore, there is emerging evidence of an enhanced response to immunotherapies in obese/overweight patients compared with normal weight individuals, further supporting the "obesity paradox" [40]. However, the apparent increased efficacy of immune checkpoint

Table 1 Summary table outlining key obesity-related mechanisms and their impact on specific cancer types

Obesity-related mechanisms	Key features	Associated cancer types	Effect on cancer	Ref- er- ences
Chronic low-grade inflammation	High levels of TNF- $\alpha$ , IL-6, IL-1 $\beta$ foster a pro-tumor microenvironment	Colorectal, Breast, Liver, Pancreatic	Improves proliferation, angiogenesis, and metastasis	[7, 8]
Insulin resistance / Hyperinsulinemia	Enhanced insulin and IGF-1 signaling stimulate the PI3K/ Akt/mTOR cascade	Endometrial, Colorectal, Breast, Prostate	Enhances cellular proliferation and suppresses apoptosis	[9, 10]
Adipokine imbalance	Increased leptin (which promotes tumor growth) and decreased adiponectin (which inhibits tumor development)	Breast, Ovarian, Colorectal	Promotes angiogenesis, proliferation, and immune evasion	[11, 12]
Altered sex hormone metabolism	Excess adipose tissue increases estrogen by activating aromatase	Breast (post- menopausal), Endometrial	Estrogen receptor activation drives tumor growth	[13, 14]
Gut microbiota dysbiosis	Alterations in gut microbiota linked to obesity elevate LPS levels and trigger inflammation	Colorectal, Liver	Enhances inflammation and metabolic endotoxemia	[15, 16]
Immune dysregulation	Increased M1 macrophages, Treg/Th17 imbalance, impaired NK cell function	Multiple cancers	Impairs immune surveillance, promotes tumor escape	[17, 18]
Lipid metabolism reprogramming	Elevated fatty acid availability supports membrane biosynthesis and energy production	Prostate, Breast, Liver	Enables tumor cell growth and survival	[19, 20]
Hypoxia in expanded adipose tissue	Adipocyte hypertrophy limits oxygen diffusion, leading to HIF-1α stabilization and upregulation of VEGF/VEGFR signaling; also promotes increased expression of EGFR and its ligands (e.g., amphiregulin, TGF-α)	Breast, Pancre- atic, Liver, Lung, Endometrial	Stimulates angiogenesis, vascular permeability, EMT processes, and the metastatic potential	[21– 28]
AGE/RAGE signaling	Accumulation of advanced glycation end products (AGEs) activates RAGE receptor, promoting oxidative stress and chronic inflammation	Colorectal, Pancreatic, Breast	Enhances NF-kB signaling, ROS production, and tumor-promoting inflammation	[29, 30]

inhibitors in obese cancer patients could be, also in this case, influenced by reverse causality [40]. Despite further investigations are needed to better understand the mechanisms implicated in the "obesity paradox", current literature strongly underlines the importance of avoiding misinterpretation in order to prevent the mistaken conclusion that obesity is beneficial and/or protective in cancer patients [41].

In this intricate scenario, it should be mentioned that sex-related differences may be accountable for obesity-related disparities in cancer progression. In fact, death rates from all cancers are 62% higher for obese women and 52% higher for obese men compared to the normal weight counterpart [42].

Further supporting the stimulating role of obesity in cancer, obese patients exhibit larger and higher-graded tumors, and present with lymph nodes involvement that justifies a higher metastatic propensity compared with normal weight patients [43, 44].

Of note, in animal models of breast cancer, the dietinduced obese phenotype was associated with the acquisition of several malignant features including hypoxic tumor masses, intense angiogenic responses, neutrophil infiltration and epithelial to mesenchymal transition (EMT) [45]. Interestingly, the transplantation of tumor cells isolated from obese mice within normal weight mice accelerated tumor growth and boosted metastases formation [45]. Together with enhanced metastatic dissemination, obese cancer patients fail to respond to anticancer

therapies more frequently compared with normal weight patients. This could be due to multiple factors [44].

First of all, certain chemotherapies like cisplatin and paclitaxel have altered clearance rates in patients with obesity, affecting drug concentration levels [46]. Beyond pharmacokinetics, obesity negatively affects the success of chemotherapy through the release of adipokines and inflammatory mediators [47, 48].

Moreover, in obesity an increase in saturated fatty acids within cell membranes reduces the bilayer fluidity, thus interfering with anticancer drug passive diffusion and endocytosis. Likewise, obesity-dependent alterations of the cell membrane may increase drug efflux through the activation of the ATP-binding cassette (ABC) multidrug efflux transporters [49, 50]. Worthy, the membrane abundance of saturated fatty acyls compared to polyunsaturated lipids render cancer cells less prompt to drug-dependent lipid peroxidation, with an ultimate reduction of chemotherapy efficacy [49].

Similar to standard chemotherapy, obesity jeopardizes the success of targeted therapies. For instance, a meta-analysis indicates that HER2-positive breast cancer patients receiving target therapies in neoadjuvant regimen were less likely to achieve pathologic complete response if overweight/obese [51]. Furthermore, visceral fat area (VFA) predicted poorer response to bevacizumab as a first-line treatment in metastatic colorectal cancer patients [52].

Despite these challenges, some studies suggest the previously mentioned "obesity paradox," where obese patients may experience better responses to certain immunotherapies compared to their normal-weight counterparts. This is the case for immunotherapeutic strategies, where the obese landscape may trigger PD-1 mediated T cell exhaustion and immune aging [53]. In this metabolically impaired environment, tumor progression is facilitated but, on the other hand, the efficacy of PD-1/PD-L1 blockade appears to be higher, as evidenced in both animal models and clinical samples [53]. Adding to this, immune checkpoint inhibitors have shown increased efficacy in obese patients affected by triple-negative breast cancer [54, 55]. On the other hand, these observations must take into account data coming from mice models of obesity, both genetically and dietinduced, showing that the systemic response to immunotherapy within the inflammatory-enhanced environment may lead to potentially lethal toxic responses, particularly in aged mice [56].

In this intricate scenario, survival pathways activated by hormones and growth factors elicit a stimulatory role in the obese environment, thus dampening the efficacy of anticancer strategies.

Overall, understanding the metabolic derangements that occur during obesity may help clarifying the multifaceted aspects that orchestrate disease progression. Uncovering the intricate connections between inflammatory mediators and hormones/growth factors-related pathways may contribute to the identification of more beneficial anticancer strategies, particularly in obese patients.

# Obesity shapes the tumor microenvironment

The tumor microenvironment (TME) is a complex component of the tumor mass, consisting of both cellular (adipocytes, fibroblasts, and immune cells) and non-cellular elements (blood and lymphatic vessels, cytokines, and the Extracellular Matrix—ECM) [57]. The TME coordinates a number of reciprocal and bidirectional interactions between cancer cells and their *milieu* to foster disease progression [58]. This occurs through the secretion of autocrine and paracrine molecular mediators and through the modification of the cellular and physical properties of the host tissue [58].

During obesity, most components of the TME undergo significant reprogramming due to both systemic and local factors. Solid research efforts have attempted to uncover how the re-shaping of the TME during obesity affects cancer progression, identifying the cellular and molecular players involved. Such players include stromal cells and stromal derived-factors, certain hormones and growth factors-dependent pathways, together with angiogenic and inflammatory signaling axes (Table 1).

### Stromal cells and stromal derived-factors

Adipose tissue is distributed in the body in anatomically distinct depots, each with specialized metabolic roles. The two major types of adipose tissue are brown adipose tissue (BAT) and white adipose tissue (WAT). BAT, found predominantly in the interscapular region in infants and in supraclavicular and perirenal areas in adults, is specialized for non-shivering thermogenesis and energy expenditure. In contrast, WAT primarily serves as an energy storage depot, and is further divided into subcutaneous adipose tissue (SAT) and visceral adipose tissue (VAT), each with distinct functional properties [59, 60]. VAT, located around internal organs such as the liver and intestine, is particularly metabolically active and has been strongly associated with adverse metabolic outcomes, including insulin resistance and cardiovascular disease. In contrast, SAT, found beneath the skin, is generally considered more metabolically benign [59]. In the context of obesity, WAT-especially in its visceral location-undergoes pathological remodeling. Adipocytes enlarge (hypertrophy) and may eventually die, prompting immune cell infiltration and the establishment of a chronic, low-grade inflammatory state. The inflamed microenvironment includes not only adipocytes, but also immune cells, fibroblasts, and endothelial cells, all of which interact in a dynamic and dysregulated manner. Key inflammatory mediators such as tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), interleukin-6 (IL-6), interleukin-1 $\beta$ (IL-1β) and interferon-gamma (IFN-γ) are upregulated, contributing to systemic insulin resistance, tissue fibrosis, and vascular dysfunction [61, 62].

These observations suggest that the anatomical location of adipose tissue critically determines its function, with BAT favoring energy dissipation, SAT offering relatively protective energy storage, and VAT playing a central role in metabolic disease when dysregulated.

Beyond its role in metabolic dysfunction, emerging evidence highlights that adipose tissue, particularly dysfunctional WAT, serves as a key player in cancer development and progression. The chronic inflammatory and metabolically altered state of obese adipose tissue creates a permissive TME, where adipocytes not only interact with cancer cells but actively contribute to their survival, proliferation, and metastasis [63].

This supportive environment is not homogeneous; rather, it reflects a dynamic remodeling of adipose tissue in obesity, marked by the emergence of distinct adipocyte subtypes with tumor-promoting functions.

For instance, the analysis of mouse and human WAT at the single cell level has determined that several cancer-associated adipocyte subtypes coexist in the TME, with different abilities to elicit tumor-promoting actions, thereby affecting prognosis [64].

As relevant stimulatory players, adipocytes boost the TME by (i) actively feeding tumor cells through lipid transfer; (ii) secreting inflammatory mediators; (iii) contributing to metabolic and cellular plasticity.

Balaban and co-workers demonstrated that the transferring of adipocytes-derived free fatty acids (FFAs) to breast cancer cells provides energy for their proliferation and migration [65]. Not surprisingly, FFA serum levels are higher in cancer vs non-cancer patients [66]. It is worth mentioning that FFAs function as bioactive signaling molecules mediating intercellular and intracellular communication. These signaling roles are integral to a wide range of cancer-related processes, including inflammation, immune regulation, metabolism, and cell proliferation [67, 68]. Among FFAs, polyunsaturated fatty acids (PUFAs), notably arachidonic acid, eicosapentaenoic acid (EPA), and docosahexaenoic acid (DHA), serve as precursors for lipid mediators such as prostaglandins, leukotrienes, resolvins, and protectins, which exert potent autocrine and paracrine effects on inflammation, immune function, and tissue homeostasis [69, 70]. Additionally, in cancer FFAs influence gene expression by serving as endogenous ligands for nuclear receptors such as peroxisome proliferator-activated receptors (PPARs) as well as toll-like receptors (TLRs), thereby modulating transcriptional programs central to neoplastic evolution [71, 72]. Interestingly, alterations in the composition of FFAs within membrane lipids, affects receptor distribution and signaling pathways, as well as malignant transformation [73-75].

Adding to the enormous amount of literature demonstrating the tumor-promoting role of FFAs, a recently published study has elegantly shown that removing these metabolic mediators may be a useful tool to suppress tumor growth [76]. In particular, the authors performed a CRISPRa-mediated "browning" of human adipocytes by up-regulating the genes (uncoupling protein 1 (UCP-1), peroxisome proliferator-activated receptor-gamma coactivator (PGC)-1alpha (PGC-1α), or PR domain containing 16 (PRDM16). This strategy endowed adipocytes with higher capability to uptake FFAs, which were no longer available for the energy demands of cancer cells. In fact, the in vivo implantation of engineered adipocytes, which outcompeted tumors for nutrients, was able to repress tumor growth and progression [76]. This strategy of adipose manipulation transplant supports the wise remodeling of adipocytes as a cancer therapeutic approach that warrants future investigations.

Further exploring the opportunity to manipulate the cross-talk between adipocytes and cancer cells in anti-cancer efforts, Ruiz-Vela and collaborators demonstrated that the stimulation of diverse human cancer cell lines with unsaturated fatty acids prompts certain phenotypic changes suggestive of adipogenic transdifferentiation

[77]. In fact, in hepatic, ovarian, breast and melanoma cancer cells exposed to palmitoleic, oleic and lineoleic acids a dramatic up-regulation of the adipogenic regulator PPARG was detected [77]. Furthermore, stimulated cells were subjected to an adipocyte-like phenotypic switch, as evidenced by the massive biogenesis of lipid droplets [77].

What's more, the transdifferentiation of breast cancer cells into post-mitotic and functional adipocytes represents a further mechanism for halting tumor progression [78].

In fact, breast tumor cells undergoing EMT were terminally differentiated into adipocytes using the PPARy agonist rosiglitazone in combination with the MEK inhibitor trametinib [79]. Such plasticity mechanism was exclusively shared by breast cancer cells with mesenchymal features, and not by their purely epithelial counterpart. These observations suggest that EMT may represent an efficient route through which tumor cells are transformed into adipocytes, thereby repressing primary tumor invasion and metastasis formation [78].

Additionally, in well-differentiated liposarcoma (WDLPS) and dedifferentiated liposarcoma (DDLPS) cells, the treatment with well-known adipogenic stimulators is sufficient to mount a transcriptional and translational response that sustained both maintenance of stemness and adipogenic differentiation. These molecular responses were associated with the inhibition of tumor growth in vitro and in vivo [80].

Beyond their ability to feed tumor cells and to regulate microenvironmental plasticity, adipocytes also secrete several cytokines that promote cancer cell survival. In fact, in prostate cancer, adipocytes-derived C-C motif chemokine ligand 7 (CCL7) is recruited to C-C motif chemokine receptor 3 (CCR3)-expressing tumor cells, driving their migration to survival niches present in the periprostatic fat [81]. This suggests that paracrine factors from adipocytes may contribute to cancer cell dormancy in sites commonly associated with tumor recurrence such as the periprostatic adipose tissue [81]. Additionally, obesity increases levels of many other cytokines and adipokines such as leptin, adiponectin, IL-6, TNF- $\alpha$ , and resistin that contribute to several cancer promoting events [82, 83]. For instance, high adiponectin levels (implicated in the regulation of insulin sensitivity, glucose levels, and lipid accumulation) is associated with lower body weight and reduced cancer risk, while its decline in obesity correlates with increased cancer susceptibility [84-86].

Conversely, leptin (implicated in the regulation of lipolysis and food intake) is elevated in obesity and associated with cancer cell proliferation and metastasis, especially when its receptor (Ob-R, leptin receptor) is overexpressed [87]. In this regard, in breast cancer cells,

leptin -by binding to Ob-R- enhances pro-tumorigenic responses mainly through the aberrant activation of the MAPK/ERK and PI3K/AKT signaling pathways [88].

Within the adipose stroma, adipose tissue-derived mesenchymal stromal/stem cells (ASCs/MSCs), which belong to mesenchymal stromal/stem cells (MSCs), significantly shape the TME during obesity [89]. The dynamic interaction between ASCs, immune cells, and cancer cells fosters disease progression through direct communications and chemotactic signals that recruit ASCs and MSCs to the tumor site [89–92]. Furthermore, during obesity, ASCs gain de-differentiation properties, generating cancer-associated fibroblasts (CAFs), which play a pivotal role in cancer progression and prognosis [93–95]. Accordingly, factors secreted by tumor cells, combined with direct interactions between cancer cells and ASCs/MSCs, select for a pro-tumorigenic population of MSCs, which can differentiate into CAFs and cancerassociated adipocytes (CAAs) [96].

Despite the precise mechanisms driving the de-differentiation of CA (Cancer-Associated)-MSCs are not fully understood yet, various evidence suggests that the TME is the main trigger for such process.

Together with stromal-derived factors and molecular mediators, inflammation, vascularity and fibrosis contribute to the acquisition of malignant cancer features during obesity. These events parallel adipocytes gradual enlargement toward hyperplasia and hypertrophy, leading to the compression of the vascular structure and the establishment of hypoxia. A key marker of adipose tissue fibrosis is the increased deposition of type VI collagen (Col 6), which exacerbates metabolic dysfunction and limits adipose tissue plasticity [97]. Col 6 contribution to adipose fibrosis is further amplified by endotrophin, a product derived from the carboxy-terminal cleavage of Col6 alpha 3; notably, endotrophin prompts the expansion of the fibrotic response and enhances tumor growth and metastasis in breast and lung cancer [98, 99].

# The VEGF/VEGFR axis

In the context of obesity, the changes in adipose tissue structure involve not only adipogenesis but also angiogenesis. As previously mentioned, the increase in the number and size of adipocytes during obesity induces a mild hypoxic state, which drives the adipose tissue to promote angiogenesis in order to overcome hypoxic stress [100]. Interestingly, obese patients exhibit overexpression of the active form of the transcription factor hypoxia-inducible factor 1 alpha (HIF- $1\alpha$ ), similar to tumor tissues [101, 102].

The up-regulation of HIF-1 $\alpha$  is pivotal for the transcription of HIF-1 target genes, which permit cell adaptation to hypoxic stress via activation of angiogenic programs [103]. Among the transcriptional targets of

HIF-1, the vascular endothelial growth factor-A (VEGF-A) and angiopoietin-like 4 (ANGPTL4) play a key role in tumor angiogenesis [104].

VEGF-A, secreted primarily by tumor cells, interacts with the vascular endothelial growth factor receptor 2 (VEGFR2) thus promoting endothelial cell proliferation, survival, and migration. These biological events support the formation of new blood vessels that supply nutrients and oxygen to the growing tumor mass [105]. Of note, adipocytes also produce VEGF and other angiogenic factors necessary for proper vascularization, toward the expansion of both the adipose tissue expansion and the tumor mass [106]. In this context, a positive correlation has been highlighted between the degree of microvascular invasion, an angiogenic activity marker linked to poor prognosis, and BMI in hepatocellular carcinoma patients. This indicates that in obese patients the activation of angiogenic programs may accelerate disease progression [107].

Furthermore, angiogenic factors secreted by adipose cells from obese patients activate the expression of genes involved in inflammation and lipid metabolism, including ANGPTL4, instigating a vicious cycle that fosters cancer progression [108]. Worthy, ANGPTL4 has been associated with increased proliferation and invasion of cancer cells [108]. These observations highlight the role of the adipose tissue secretome in promoting cancer cell adaptation to hypoxic stress by metabolic, angiogenic and inflammatory factors. Altogether, these mediators contribute to the aggressive phenotypes observed in obese cancer patients [108].

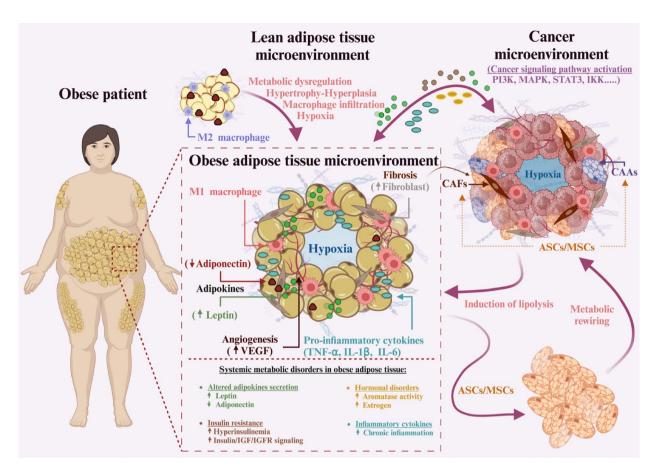
# Hormone and growth factors: the Insulin/IGF system

The cross-talk between tumor cells and adipocytes during obesity involves complex microenvironmental interactions facilitated by cytokines, adipokines, hormones, and growth factors (Fig. 1) [109].

As it concerns hormones, a paradigmatic example is the local production of 17- $\beta$  estradiol (E2) from androgens in the adipose tissue mediated by the enzyme aromatase [110]. This leads to E2-dependent activation of the estrogen receptor (ER) in cancer cells, stimulating various estrogen-sensitive tumors like breast cancer [111].

Interestingly, pro-inflammatory cytokines such as IL-6 may increase aromatase expression in obese mammary adipose tissue, further amplifying estrogen-dependent signaling pathways [112]. Adding to this, certain metabolites, like 25-hydroxycholesterol, can activate transduction cascades that promote disease progression by activating ER-dependent responses in cancer cells [113]. What's more, hypercholesterolemia, commonly observed in obesity, triggers the activation of estrogen-related

Salemi et al. Journal of Translational Medicine (2025) 23:995 Page 7 of 15



**Fig. 1** Adipocyte/cancer cell cross-talk in the obese state. Obesity increases the risk of developing cancer by promoting multiple meta-inflammatory alterations. First, an increase in body weight enlarges adipocyte size, leading to inadequate vascularization and hypoxia, combined with fibrosis and chronic inflammation. This is associated with an increase in M1 macrophages that produce various pro-inflammatory cytokines toward insulin-resistance. Second, adipocyte hypertrophy in obesity is associated with changes in adipokine secretion, reinforcing the pro-inflammatory phenotype. Third, abnormally expanded adipocytes may release hormones and growth factors that contribute to the activation of cancer-related pathways, such as the Vascular Endothelial Growth Factor (VEGF) axis, the insulin/IGF/IGFR signaling (Insulin-like Growth Factor/Insulin-like Growth Factor Receptor), and estrogen pathway. Fourth, obesity-associated metabolic disorders, initiated in the tissue and propagated systemically through autocrine and paracrine effects, increase the risk of developing cancer by promoting the activation of stimulatory signaling pathways: phosphatidylinositol 3- kinase (PI3K); mitogen-activated protein kinase (MAPK); IkB kinase (IKK); signal transducer and activator of transcription 3 (STAT3); Interleukin-1β (IL-1β); interleukin-6 (IL-6); tumor necrosis factor-α (TNF-α). Fifth, a functional cooperation between cancer cells as well as adipose tissue-derived mesenchymal stromal/stem cells (ASCs/MSCs), cancerassociated adipocytes (CAA) and cancer-associated fibroblasts (CAFs) drive obesity-dependent cancer progression. Figure created with BioRender.com

receptor  $\alpha$  toward both ER-positive and ER-negative breast cancer cell proliferation [114].

While estrogen signaling primarily contributes to neoplastic progression in estrogen-sensitive tissues, the Insulin/Insulin-like Growth Factor (IIGF) axis is hyperactivated across various cancer types, particularly in overweight and obese patients (Fig. 1) [115, 116]. Noteworthy, a cross-talk between estrogen signaling and IIGF axis has been largely demonstrated [117–120].

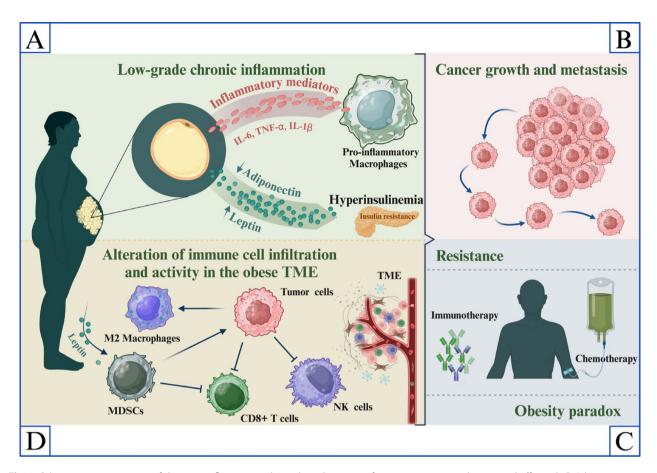
In fact, higher levels of the three ligands IGF-I, IGF-II and insulin, along with hyperactivation of their receptors (Insulin Receptor- IR, and insulin-like growth factor 1 receptor -IGFIR), are linked to increased cancer risk [115].

Extending these findings, compensatory hyperinsulinemia, consequent to insulin resistance commonly

observed in obese patients, is a strong candidate for the increased cancer risk associated with metabolic disorders [121]. Mechanisms connecting hyperinsulinemia to cancer include: 1) increased synthesis and bioavailability of IGFs leading to IGF-IR overactivation; 2) overexpression and stimulation of IR, particularly isoform A (IR-A), which mediates the non-metabolic but mitogenic effects of insulin in tumor cells. This isoform has a higher affinity for IGF-II, which in turn, stimulates a peculiar gene profile and signaling response; 3) activation of IR-mediated downstream pathways such as MAPK and PI3K/AKT/mTOR cascades, playing a role in cancer stem cell biology stem/progenitors cells differentiation [122, 123].

Additionally, in obesity the dysregulation of insulin and IGFs activity is tightly linked with the instigation of

Salemi et al. Journal of Translational Medicine (2025) 23:995 Page 8 of 15



**Fig. 2** Schematic representation of the main inflammation-dependent alterations of cancer immunity and associated effects. **A–B** Adipose tissue inflammation supported by pro-inflammatory macrophages leads to the release of inflammatory mediators, such as interleukin-6 (IL-6), Tumor Necrosis Factor-α (TNF-α), Interleukin-1β (IL-1β), toward insulin resistance and compensatory hyperinsulinemia, implicated in cancer progression. **B–D** The obese TME is primarily infiltrated by suppressive cell populations, including M2 macrophages and myeloid-derived suppressor cells (MDSCs). Leptin promotes the build-up of MDSCs in the tumor microenvironment (TME), thus inhibiting the activation of cytotoxic CD8+T cells. Obesity also results in the loss of the antitumor functions of natural killer (NK) cells, ultimately facilitating tumor burden. Although obesity can induce resistance to certain anticancer therapies, it can also elicit a positive impact on the outcomes of some of them ("obesity paradox"). Figure created with BioRender.com

chronic low-grade inflammation, thus contributing to the development and progression of cancer [109, 124–126].

In this context, obesity leads to an increase in M1 proinflammatory macrophages, resulting in adipose tissue inflammation and insulin resistance [109, 127]. In fact, FFAs released from hypertrophic adipocytes and cytokines such as IL-6, TNF-α, and C-reactive protein may directly block insulin signaling by hampering its signal transduction through IR [128-131]. This action involves the activation of inflammatory signaling pathways (JNK, IKK/NF-κB, JAK/STAT) [132]. The JNK pathway, activated by TNF-α and leukotriene B4 from immune cells, impairs IRS-1 signaling, reducing PI3K and AKT phosphorylation, which induces insulin resistance in adipose tissue, liver, and muscle. Pro-inflammatory cytokines also activate IKK kinases, facilitating NF-κB translocation into the nucleus and promoting inflammatory gene expression that contributes to insulin resistance. In addition, IL-6 activates the JAK/STAT pathway inducing suppressor of cytokine signaling 3 (SOCS-3) expression that leads to the direct degradation of insulin receptor substrate 1 (IRS-1) by proteasome, ultimately impairing insulin signaling [133].

The subsequent establishment of insulin resistance paves the way to the increased release of insulin from pancreas, which in turn determines hyperinsulinemia, associated with cancer progression [121] (Fig. 2A).

## The meta-inflammatory AGE/RAGE pathway

Among the obese individuals, certain subjects harbor metabolic imbalances typically associated with obesity, whereas others show a preserved metabolic function [134]. This observation challenges the linear relationship between BMI and adverse clinical outcomes, as metabolically healthy obese (MHO) individuals are at a lower risk of developing obesity-related morbidities compared to their metabolically unhealthy counterparts (MUO- metabolically unhealthy obese) [135].

Supporting this observation, only MUO subjects experience metabolic disorders that lead to altered glucose metabolism and insulin resistance, toward the establishment of the metabolic syndrome.

In MUO patients, glucose metabolism imbalances and insulin resistance are mainly initiated by the inflammatory state instigated within the hypertrophic adipose tissue. Therefore, inflammation is regarded as a key orchestrator of the metabolic aberrations typically observed in obesity [136].

The receptor for advanced glycation end products (RAGE) has been pointed out as an important mediator of chronic-low grade inflammation firstly initiated within the adipose tissue and then propagated systemically. Identified as a receptor for the advanced glycation end products (AGEs) generated during hyperglycemia, RAGE has been shown to mediate AGE-dependent responses that contribute to the complications of obesity and type 2 diabetes T2D through the transcriptional activation of inflammatory programs [137–140].

Beyond AGEs, several other ligands have been shown to bind to and activate RAGE, including S100 family proteins, the alarmin HMG-B1, (High Mobility Group-Box 1), Mac-1, and beta sheet fibrils [139, 141]. Of note, RAGE and its ligands accumulate in the adipose tissue during obesity, contributing to weight gain, inflammation and insulin resistance [137, 138].

In addition, RAGE expression is elevated in many cancer tissues where it supports sustained growth signals and the insensitivity to growth suppressors, immune evasion, neoangiogenesis, inflammation, the reprogramming of tumor metabolism, and the promotion of tissue invasion and metastasis [142–147]. On the basis of these observations, RAGE has been considered as a pivotal mediator in the *liaison* between inflammation and cancer [148].

Surprisingly, the cross-talk between RAGE and the IIGF axis in the establishment of metabolic-dependent inflammation has been indicated as an important player in cancer progression [142]. For instance, in breast cancer cells, IGF-1 upregulates S100A7 which binds to RAGE on endothelial cells thus triggering angiogenesis [144]. Additionally, a pharmacological inhibitor of RAGE, has been shown to blunt insulin-induced oncogenic signaling in vitro and in vivo [149]. Hence, targeting RAGE may offer a promising anticancer strategy, particularly in hyperinsulinemic conditions commonly associated with obesity.

# **Obesity impacts tumor immune infiltration**

Obesity exacerbates cancer outcomes in part due to its immunosuppressive effects [150]. Several evidence shows that adipose tissue dysfunction and excessive fat accumulation in adipocytes contribute to the development of a microenvironment in which pro-inflammatory cytokines

and dysregulated adipokines (leptin and adiponectin) impact the anti-tumor immune responses [151]. Macrophages play a fundamental role in both inflammation and insulin resistance in metabolic disorders and also exert a significant regulatory influence in cancer progression [152]. Unlike the traditional M1 macrophages activated during acute infections, macrophages in obese adipose tissue are "metabolically active" and exhibit a pro-inflammatory profile in response to obesity [153, 154]. These specialized cells produce numerous pro-inflammatory cytokines, such as TNF- $\alpha$  and IL-1 $\beta$  contributing to chronic inflammation and lipid metabolism regulation (Fig. 2A) [154].

Both obesity-dependent inflammation and immune cell dysfunctions foster cancer growth and metastasis by hampering anti-tumor immune responses [155] (Fig. 2B). Different from the adipose tissue, the obese TME is primarily infiltrated by suppressive cell populations, including M2 macrophages, T-regulatory cells, and myeloid-derived suppressor cells (MDSCs), whose accumulation is driven by immunosuppressive factors derived from cancer cells [155, 156]. In this regard, the obesity-related adipokine leptin promotes MDSCs accumulation in the TME, repressing cytotoxic T cell activation and increasing tumor burden [157] (Fig. 2D).

Similarly, obesity facilitates the exhaustion of CD8+T cells and the expression of elevated levels of the immune checkpoints PD-1, Lag3 and Tim3 [158].

Of note, tumor-associated CD8+T cells undergo a metabolic reprogramming that depends on certain energetic features and plasticity of the TME [158]. For example, in lipid-rich TME such as breast cancer, CD8+T cells stimulated by the leptin/signal transducer and activator of transcription 3 (STAT3) pathway utilize fatty acid oxidation over glycolysis, leading to diminished antitumor responses [158]. Conversely, in low-lipid TME like colorectal tumors, obesity causes fatty acid starvation in CD8+T cells due to their preferential utilization by tumor cells [158]. Obesity also reduces glutamine levels in the TME, disrupting amino acid metabolism and causing CD8+T cell dysfunction [158].

Therefore, obesity may weaken anti-tumor immunity by multiple metabolic-related mechanisms that are selected in a tissue-specific manner.

Worthy, obesity alters lipid metabolism in tumor-infiltrating natural killer (NK) cells, leading to metabolic paralysis through the mTOR-PPAR pathway, which diminishes NK cell anti-tumor functions [158].

Despite advances in understanding how metabolic factors modulate immune responses in cancer, the complex role of obesity on immune cell activity within the TME remains inadequately characterized [155, 158]. A comprehensive understanding of how obesity impacts on patients' response to anticancer therapies is still lacking,

and some controversial aspects have been reported [150, 159].

Regarding chemotherapy, obesity has been shown to hinder its efficacy through mechanisms like chronic lowgrade inflammation associated with NF-κB, and cycloxygenase 2 activation [160]. Preclinical studies indicate that obesity negatively impacts immunotherapy outcomes [161]. For instance, in murine breast cancer model, the diet-induced obese phenotype triggered higher intratumoral CXCL1, enhancing CXCR2-mediated accumulation of Fas Ligand<sup>+</sup> granulocytic MDSCs, which increases CD8+T cell apoptosis, thus fostering immunotherapy resistance [162]. On the other hand, according to the previously described phenomenon known as the "obesity paradox", obesity may positively influence the outcomes of certain anticancer therapies [161] (Fig. 2C). While immune dysfunctions associated with obesity compromise immune surveillance and tumor editing, they may also enhance the immunogenicity of tumors and their sensitivity to immune checkpoint inhibitors [163]. Likewise, a systematic review and meta-analysis demonstrates an improved Overall Survival and Progression-Free Survival in patients with high BMI after receiving immune checkpoint inhibitors treatment compared with low BMI patients [164]. Furthermore, obesity has been linked to increased expression of immune checkpoints on T cells, which correlates with enhanced sensitivity to immune checkpoint inhibitors across various cancers [165].

## **Conclusion and future perspectives**

Several mechanisms have been found to enable and facilitate cancer development and progression during obesity. Additional research efforts need to be dedicated to clarify the multifaceted aspects of cancer cells biology, as well as the mounting role of the TME in disease progression, particularly in the context of obesity. Not surprisingly, despite cancer presents as a different molecular, metabolic and biological entity in obese vs normal weight patients, the clinical approach foreseen in these two subpopulations is currently the same. This leads to poor clinical benefit and potential dispersion of healthcare resources, thus encouraging to collect further preclinical and clinical evidence that may drive decision-making processes in precision medicine strategies.

Growing epidemiological and experimental data suggest that lifestyle interventions like nutrition and diet may lower cancer risk and potentially enhance the success of anticancer therapies [166–168].

In this context, nutraceuticals and supplemental micronutrients have been recently proposed as promising potential adjunct tools in prevention and treatment of cancers for their antioxidant and anti-inflammatory actions.

For instance, oleuropein, luteolin, lycopene, and anthocyanins interfere with some TME players that prompt cancer progression, such as the IIGF axis, RAGE and PPARy pathways, exerting anti-inflammatory and antitumor effects [169–173]. Despite preliminary preclinical data suggest the usefulness of functional food and nutraceutics, their use as supplements for cancer prevention or during chemotherapy remains a controversial issue without a definitive consensus [174].

Well-designed clinical studies with long-term follow ups could shed light into this intricate topic, together with more solid preclinical evidence.

As it concerns the preclinical models, a robust research pipeline aimed at advancing knowledge in the field of cancer prevention and treatment in obesity must consider the use of proper advanced experimental systems. The ideal model should allow the simultaneous investigation of the systemic and local environmental aspects of the neoplastic disease, mimicking the multiple aberrations of the obese microenvironment. To this aim, several rodent models have been proposed: (a) genetic models obtained by mutation of a single gene (such as mutations of leptin or Ob-R) that give raise to a monogenic form of obesity; (b) polygenic obesity-prone rodent models (such as the Osborne-Mendel model); (c) diet-induced obesity (DIO) models [175, 176]. DIO models are more physiologically relevant considering that in humans the establishment of obesity mostly recognizes both genetic and environmental cues. However, BMI criteria are defined differently in rodents compared to humans; thus, specific dietary regimens, including duration of the diet, fat content and energy densities to reach the overweight/obese state have been defined in a mice strain frequently used for modelling DIO [177].

It should be mentioned that a competent immune system in rodents is necessary for the development of obesity induced by diet. On the other hand, the establishment of advanced animal models of cancer (for instance patient-derived tumor models) requires the effective suppression of the immune system in the rodent host for proper tumor take. Adding to this, mice models often fail to recapitulate the features of the human TME.

To overcome this challenge, manipulated 3D platforms (organoids and organ-on-a-chip models) for culturing freshly resected patient-derived samples across different metabolic environments provide a valuable alternative to rodent studies, facilitating the exploration of homotypic and heterotypic cell-cell interactions within the TME while accounting for metabolic imbalances [178–181].

Additional efforts should be also put in place to better assess the potential of transdifferentiation therapies, particularly in precision medicine strategies for obese breast cancer patients. In fact, inducing the adipogenic transdifferentiation of human tumor cells may represent

a promising add-on to conventional strategies, pending a deeper understanding of the molecular mechanisms that drive cancer cells conversion into adipocytes.

Overall, the use of advanced investigating tools will allow a more comprehensive understanding of the intricate cell-cell interactions and paracrine cross-talk between cancer cells and their host tissue during obesity. This approach will help identifying novel therapeutic targets and designing more effective treatments in precision-medicine strategies for cancer patients with obesity.

## **Abbreviations**

ABC ATP-binding cassette

AGEs Advanced glycation end products

ANGPTL4 Angiopoietin-like 4
ASCs Adipose-derived stem cells
BAT Brown adipose tissue
BMI Body mass index

CAAs Cancer-associated adipocytes
CAFs Cancer associated fibroblasts
CCL7 C-C motif chemokine ligand 7
CCR3 C-C motif chemokine receptor 3

COL 6 Type VI collagen
CVD Cardiovascular disease
DHA Docosahexaenoic acid
DIO Diet-induced obesity
E2 17-β Estradiol
FCM Extracellular matrix

EMT Epithelial to mesenchymal transition

EPA Eicosapentaenoic acid ER Estrogen receptor FFAs Free Fatty Acids

HIF-1α Hypoxia inducible factor 1 subunit alpha

HMG-B1 High mobility group-box 1
IFN-γ Interferon gamma
IGF Insulin-like growth factor
IIGF Insulin/Insulin-like Growth Factor
IGF-IR Insulin-like growth factor 1 receptor

IL-1β Interleukin-1βIL-6 Interleukin-6IR Insulin receptorIR-A Isoform A

IRS-1 Insulin receptor substrate 1
MAPK Mitogen-activated protein kinase
MDSCs Myeloid-derived suppressor cells
MHO Metabolically healthy obese
MSCs Mesenchymal stromal/stem cells
MUO Metabolically unhealthy obese

NK Natural killer Ob-R Leptin receptor

PPAR Peroxisome proliferator-activated receptor

PUFAs Polyunsaturated fatty acids

RAGE Receptor for advanced glycation end products

SAT Subcutaneous adipose tissue

STAT3 Signal transducer and activator of transcription 3

SOCS-3 Suppressor of cytokine signaling 3
TME Tumor microenvironment
TNF-a Tumor necrosis factor-a
VAT Visceral adipose tissue

VEGF-A Vascular endothelial growth factor-A VEGFR2 Vascular endothelial growth factor receptor 2

VFA Visceral fat area WAT White adipose tissue

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# Data availability

Not applicable.

## **Declarations**

## Ethics approval and consent to participate

Not applicable.

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Not applicable.

# Competing interest

The authors declare that they have no competing interests.

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