
Biological Mechanisms for the Effect of Obesity on Cancer Risk: Experimental Evidence

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Abstract

Multiple epidemiological studies demonstrated that overweight and obesity significantly increase the risk of several types of cancer. As the prevalence of obesity is dramatically rising, it is expected that it will represent one of the major lifestyle-associated risk factors for cancer development in the near future. Numerous recent studies expanded knowledge about key players and pathways, which are deregulated in the obese state and potentially promote cancer initiation, progression and aggressiveness via remote and local effects. These players include (but are not limited to) insulin/IGF, adipokines and inflammatory signaling molecules as well as metabolites. Nevertheless, the detailed mechanisms linking obesity and malignant transformation at the systemic, cellular and molecular level still demand further investigation. Additionally, dysfunctional molecular metabolic pathways appear to be specific for distinct cancer entities, thereby yet precluding definition of a common principle. This chapter will present an overview of the current knowledge of molecular nodes linking obesity and cancer and will briefly touch upon potential therapy options addressing metabolic cancer etiologies.

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1 Introduction

The worldwide prevalence of overweight and its severe form obesity has reached pandemic dimensions with nowadays 500 million people being obese. In addition to its negative impact on quality of life and physical fitness, obesity commonly progresses into deleterious and often fatal pathologies, including type 2 diabetes, cardiovascular diseases and several types of cancer [1–3].

A causal connection between adiposity and increased cancer risk has been hypothesized based on obvious evidence from multiple epidemiological studies [4]. Notably, the tumor-promoting effects of excess body weight vary between distinct cancer entities and genders [4]. Additionally, several components of obesity might be independent risk factors, including elevated body weight per se as indicated by the BMI, but also weight gain and body fat distribution [5–8]. Thus, multiple mechanisms appear to be involved in obesity-associated cancer development.

Already in the early 1950s, first experimental evidence for an obesity-driven promotion of breast cancer appearance resulted from animal studies [9]. Numerous studies have since then been performed, which contributed significantly to understanding the risk connection between increased body weight and tumor development. However, a universal concept mechanistically defining the metabolic etiology of cancer still seems to be far from being achieved. As numerous players have been identified to date, it is questionable that a general mechanism exists which can explain the interconnection of obesity and cancer. It is rather very likely that the collective of pathophysiological changes in body homeostasis that occur during obesity cumulatively increase cancer risk. In essence, these changes can be grouped into altered inter-tissue cross talk on the one and generation of a tumor-promoting metabolic profile on the other hand. As a consequence, several hormones and metabolites display abnormal levels in the circulation and in the tumor microenvironment during obesity, eventually promoting tumor cell growth and invasiveness.

In this chapter, we will review the current state of the art, concerning the pathophysiological alterations caused by adiposity, which are potential molecular mediators of metabolic tumor promotion.

2 Tissue Communication

Communication between tissues and cells in our bodies occurs via hormones, cytokines and metabolites that are sensed through a variety of cellular mechanisms. Inter-tissue cross talk is vital for proper function of a biological system. As a consequence, dysfunction of tissue communication precipitates into various diseases.

Obesity primarily affects the white adipose tissue, which faces the challenge of dealing with a constant energy surplus and thus lipid overload of the adipocytes and eventually pathological expansion and cell death. Beside the adipocyte fraction, the tissue consists of several cell types with distinctive functions, as a whole summarized as stromal vascular fraction (SVF). The SVF, which contains, e.g., progenitor cells as well as cells of the immune system, has specific functions for adipose tissue integrity and thus is crucial for energy homeostasis. Dysfunctional adipocytes exert effects on cells of the SVF, such that the function of both adipose tissue fractions is compromised during obesity. The pathological consequences of adipose tissue dysfunction and their implications for cancer are outlined below.

2.1 Adipose Tissue

2.1.1 Endocrine Effects of Adipose Tissue

Adipose tissue is not considered being solely a calorie-storing depot. Nowadays it is seen as a huge endocrine organ that secretes a multitude of bioactive factors (adipokines), thereby locally and remotely regulating energy homeostasis on multiple levels [10]. In an obese setting, the body fat mass is not only markedly increased, but adipose tissue becomes also functionally impaired upon overloading of adipocytes with lipids and massive invasion of immune cells. As a result, adipose tissue dysfunction manifests in an altered signature of adipokines, particularly in visceral adipose tissue. Changes in the adipokine profile during obesity are exemplified by elevated release of leptin, resistin and pro-inflammatory cytokines, as well as reduced secretion of adiponectin [11]. Strikingly, certain cancer cells express adipokine receptors in high amounts and are therefore particularly responsive to an altered adipose secretome. The molecular pathways affected by adipokine signaling and their implications for tumor development, progression and metastasis thus required further discussion.

Leptin

Leptin is a 167 amino acid peptide hormone that activates anorexigenic and inhibits orexigenic neurons in the hypothalamus, and increases the sympathetic tone, thereby controlling food intake and energy expenditure, respectively [12]. Loss-of-function of one of the genes encoding either leptin (*OB*) or its receptor (*LEPR*, *OB-R*) results in severe hyperphagia in mice and men, and consequently leads to development of extreme obesity [13]. Leptin levels in the blood are

proportional to the amount of (visceral) adipose tissue. As a consequence of leptin resistance during obesity, the production and secretion of leptin are disproportionately increased, thereby precipitating in a vicious circle of progressively aggravating hyperleptinemia.

The leptin receptor is abundant in a number of peripheral tissues. Notably, malignant cells frequently express particularly high levels of OB-R. In line with this, specific SNPs in the leptin receptor gene were linked to an enlarged risk of certain cancers [14], altogether highlighting the significance of leptin signaling for tumor development. Despite being obese, leptin-deficient *ob/ob* mice were protected from developing specific types of cancer, whereas other tumors occurred more frequently, indicating that leptin has a role in a specific subset of obesity-associated cancer entities [15].

Epidemiologic studies indicate a connection between elevated circulating leptin levels and occurrence of (postmenopausal) breast cancer [16]. Furthermore, plasma leptin concentration is significantly correlated with poor clinical outcome in breast cancer [17]. Importantly, leptin plays a role in development of the mammary gland and the leptin receptor is thus highly expressed in mammary epithelia [18]. In the majority of human mammary tumors, leptin as well as leptin receptors is overexpressed, which provides an explanation for the increased breast cancer risk in obese women [18, 19]. Concordantly, ablation of leptin signaling suppressed tumor development in murine breast cancer models [20–22]. Given that obesity is a risk factor mainly for postmenopausal breast cancer, whereas obese young women seem rather to be protected from malignancies of the breast, increased leptin signaling is unlikely to be the sole reason for risk enhancement. At least in specific subtypes of mammary tumors in elderly women, leptin might work in synergy with estrogen, which is produced in high amounts by adipose tissue after menopause (see below). Notably, leptin potentially induces adipose tissue aromatase activity, resulting in an increased production of estrogen [17].

A connection between leptin and cancers of the gastrointestinal tract has been proposed based on several studies involving human samples. Specifically, leptin receptor expression has been observed in human colon cancer cell lines as well as colon biopsies and resected colonic adenocarcinomas [23, 24]. Besides promoting proliferation and migration/invasion, leptin-induced metabolic reprogramming by inhibition of mitochondrial respiration has been observed in human colon cancer cell lines [25], which is in accordance with observations that have been made earlier in a breast cancer mouse model [26]. Notably, whereas circulating leptin levels were found to be decreased in colon cancer patients, they were negatively correlated with tumor aggressiveness [27]. It is unclear though if decreased serum leptin levels in patients with aggressive colon cancer were secondary effects caused by the tumor disease, e.g., upon cancer-associated weight loss.

More recently, leptin signaling has been shown to be involved in pancreatic cancer by *in vitro* and *in vivo* studies. While pancreatic tumor cells were shown to express distinct isoforms of the leptin receptor, leptin accordingly stimulated tumor growth, migration and metastasis formation [28, 29]. Clinical relevance of these observations still needs to be demonstrated.

Evidence exists that leptin also promotes growth and invasiveness of cholangiocarcinomas, gliomas and thyroid tumors [30–32]. However, epidemiological data supporting an association between obesity and these tumor entities are yet lacking.

Leptin signaling has been recently reported to be centrally involved in the development of chemotherapy resistance in glioblastoma, gastrointestinal- and breast cancer [33–35], thereby worsening the clinical outcome of anticancer therapies in obese subjects. Importantly though, a present study provides evidence for an increased response of colon cancer patients with high circulating leptin to treatment with Vascular Endothelial Growth Factor (VEGF) inhibitors [36]. Altogether, these data indicate that leptin levels might be an indicator for therapeutic responsiveness, thereby representing a potential biomarker for patient stratification.

Leptin acts via a group of signal transduction pathways that have been shown previously to have tumor-promoting effects [32, 37]. Upon binding by its ligand, OB-R induces several intracellular signaling pathways through interaction with the cytoplasmic kinase janus kinase (JAK) 2. Whereas the short receptor isoforms activate PI3K-Akt signaling via phosphorylation of insulin receptor substrates (IRS), the long isoform (OB-Rb) induces phosphorylation of the mitogenic transcription factor signal transducer and activator of transcription (STAT) 3. In addition, leptin induces MAP kinase signaling pathways and promotes neovascularization through activation of angiogenetic factors. In colonic epithelial cells, leptin treatment resulted in p42/44 MAP kinase activation, thereby inducing their proliferation *in vitro* and *in vivo* [23]. Furthermore, migration and invasiveness of colon cancer cell lines derived from particularly aggressive human tumors were potentiated by leptin-dependent stimulation of PI3K and Src signaling pathways, which subsequently activated Rho GTPases, Cdc42 and Rac1 [24]. In pancreatic cancer cells, leptin was able to promote proliferation and migration through activation of PI3K-AKT signaling and enhanced expression of matrix metalloproteinase-13 [28, 29].

Altogether, clinical and experimental evidence exists that leptin signaling affects a large number of distinct tumor entities, thus being one of the foremost links between obesity and cancer risk. On a cellular level, leptin promotes signaling pathways involved in proliferation, survival, migration and angiogenesis, as well as inhibition of apoptosis, all of which are key determinants of tumor development and progression.

Adiponectin

Adiponectin is a 244 amino acid peptide secreted by adipocytes. It exists in several multimeric forms and induces signaling via its two receptor isoforms [38]. By augmenting the insulin response, adiponectin contributes to coordination of glucose and lipid metabolism [39]. Adiponectin secretion is induced by oxidation of fatty acids. In line with this, obese adipose tissue usually displays a markedly reduced adiponectin production [40]. Given its beneficial effects on insulin sensitivity and its inverse correlation with body weight, adiponectin is considered the “good guy” among the adipokines.

Several epidemiological studies provide evidence for a tumor-suppressing action of adiponectin, since its levels inversely correlate with cancers of the colon, mammary gland, endometrium and kidneys [41–43]. Accordingly, a high leptin/adiponectin ratio has been associated with poor survival in colorectal cancer patients [44]. Kaklamani et al. [45] found specific SNPs in the adiponectin and adiponectin receptor gene loci to be associated with either increased or decreased colorectal cancer risk in Caucasians. A recent meta-analysis provided evidence for an association of three SNP in the adiponectin gene with colorectal cancer in Asians, whereas there was no evidence for a significant correlation in the white ethnicity [46]. Overall, efforts to identify adiponectin SNPs associated with increases colorectal cancer risk provided inconsistent results to some degree [47]. Thus, significance of the proposed association remains a matter of debate.

Epidemiological evidence is supported by *in vitro* studies, demonstrating that adiponectin has anti-proliferative effects on distinct cancer cell lines [48, 49]. These data were confirmed by observations obtained *in vivo* using tumor mouse models. Growth of various subcutaneous and chemically induced tumors was promoted in adiponectin knockout mice, which particularly was observed under high-fat diet feeding [50, 51]. In line with this finding, adiponectin administration inhibited epithelial proliferation and development of neoplastic foci in colons of obese adiponectin-deficient mice [51]. In breast cancer mouse models, adiponectin haploinsufficiency resulted in early onset of mammary tumors as well as faster progression and enhanced metastasis formation compared to control animals [52].

Although the exact mechanisms underlying its protective function are still a matter of investigation, several mechanisms of anti-carcinogenic action of adiponectin have been convincingly demonstrated, including but not limited to restriction of macrophage recruitment [50], AMPK and LKB1 activation [49, 53], as well as inhibition of mTOR, STAT3 and AKT pathways [51, 52, 54]. Overall, the biological functions of adiponectin antagonize specific aspects of leptin action.

Others

The *VEGF* family controls development of the vascular system during embryogenesis and induces angiogenesis in response to hypoxia. In solid cancers, VEGF is frequently highly expressed to promote vascularization, thereby ensuring nutrient and oxygen supply, which is vital for tumor growth. Consequently, the VEGF pathway is one of the most promising therapeutic targets in oncology. VEGF- and VEGF-receptor-directed therapies are available on the market and approved for treatment of renal, prostate, pancreatic and gastrointestinal tumors. Treatment of further cancer entities is currently being tested in phase II and III studies [55].

Adipose tissue is an important source for circulating VEGF, and leptin activates VEGF expression (see above). As hypoxia occurs in obese adipose tissue, neo-vascularization is required, resulting in enhanced VEGF expression [56]. In consistency with this, circulating VEGF levels were twofold elevated in centrally obese versus normal weight subjects and VEGF expression was significantly upregulated in visceral compared to subcutaneous adipose tissue in the obese group [6]. Furthermore, VEGF serum levels were elevated in a mouse model of postmenopausal

obesity concomitant with enhanced growth of orthotopically implanted breast tumors compared to lean controls. Notably, in this study, VEGF expression in the subcutaneous adipose tissue was found to be higher than in visceral fat [57]. Conditioned media from visceral adipose tissue obtained from obese donors significantly promoted proliferation of esophageal adenocarcinoma and colorectal carcinoma cell lines, which was rescued by neutralization of VEGF using a specific antibody [6]. In genetically obese mice, VEGF signaling is involved in adipose tissue inflammation, which has additional implications for obesity-linked tumor promotion [58]. Altogether, these data suggest tumor-promoting actions of adipose tissue-derived VEGF through angiogenesis induction and beyond.

In summary, adipose tissue secretes a pattern of bioactive molecules, with implications for tumor development and/or progression as they control signaling pathways involved in cell proliferation, angiogenesis and migration. The composition of the adipose tissue secretome depends on the metabolic health of the adipose organ. A considerable number of studies have revealed potential molecular mechanisms that could explain how alterations in leptin and/or adiponectin levels might increase cancer risk in an obese setting. As these adipokines have basically antagonistic functions, not only their absolute levels might be of relevance for tumor development, but also their ratio should be taken into account. It should be noted that adipose tissue secretes a number of further molecules (e.g., resistin, visfatin, nesfatin, lipocalin-2 and others). Although they have not yet been as intensively investigated with respect to cancer as the above described factors, changes in their serum levels have been associated with cancer development. For example, high levels of resistin have been observed to correlate with tumor and inflammatory markers, but not with anthropometric variables in a breast cancer cohort [59]. Moreover, adipocytes secrete pro-inflammatory cytokines, which are discussed in detail below. Altogether, it might be worth considering the entire adipokine signature of an individual as prognostic factor to assess cancer risk and the clinical outcome [60]. In addition, obesity and insulin resistance are associated with increased circulating levels of adipose tissue-derived fatty acids and other lipid species, which can serve as substrates for enhanced tumor growth (see below).

2.1.2 Cancer-Associated Adipocytes (CAAs)

Besides the role of adipose tissue as an endocrine organ exerting systemic effects, adipocytes are increasingly recognized as important component of the tumor microenvironment, particularly in tumors growing in close proximity to adipocytes [61]. For instance, human and murine breast cancer cells showed increased invasive capacity when co-cultivated with mature adipocytes [62]. Conversely, the adipocytes exposed to the tumor cells exhibited a modified phenotype favoring delipidation and overexpression of proteases, including matrix metalloproteinases 11 and proinflammatory cytokines such as interleukin (IL)-1 β and IL-6, the latter of which was shown to contribute to the proinvasive effects in tumor cells. Importantly, the presence of such modified adipocytes was shown in human breast tumors and tumor size was associated with increased IL-6 expression in the surrounding adipocytes [62]. In a recent study, the secretion of the chemokine CCL7 by

periprostatic adipose tissue was found to be enhanced during obesity. Elevated CCL7 levels stimulated directed migration of CCR3-positive prostate cancer cells. As a result, obese individuals are at higher risk of particularly aggressive forms of prostate cancer [63]. Notably, CCR3 expression was associated with poor prognosis in human patients [63]. Thus, even in tumor entities without an obvious correlation between obesity and tumor risk, exemplified by prostate cancer, adipocytes in the tumor microenvironment potentially affect disease progression by secretion of pro-inflammatory mediators.

2.2 Other Tissues

2.2.1 Insulin and IGF Signaling

Constantly elevated levels of circulating insulin as a consequence of the development of insulin resistance, which can be observed in the majority of obese individuals, are associated with progression and aggressiveness of several types of cancer [64, 65]. This relationship has been validated in a vast number of studies using animal models of hyperinsulinemia and insulin resistance [66]. Likewise, levels of the insulin-related peptide hormone insulin-like growth factor (IGF) 1 were interpreted as biomarkers for cancer development [67]. Notably, insulin induces hepatic IGF1 expression in a growth hormone-dependent manner, and enhances IGF1 bioavailability by repression of IGF binding proteins [4, 64]. Thus, hyperinsulinemia goes hand in hand with elevated circulating IGF1 levels.

Insulin and IGFs activate heterotetrameric tyrosine kinase receptor complexes, namely insulin receptor (IR) and IGF1 receptor (IGF1R), respectively. Whereas IGF1R is ubiquitously expressed and activates proliferative and anti-apoptotic pathways, IR expression is mainly found in rapidly dividing cells (isoform A) as well as metabolically active tissues, including liver, muscle and adipose tissues (isoform B). Thus, IR-B mediates the metabolic functions of insulin. Importantly, the mitogenic IR-A and IGF1R were found to be highly expressed in tumor cells [68]. Due to their high homology, IR and IGF1R potentially form hybrid receptors. Notably, IGFs have a substantially higher affinity to IR/IGF1R hybrids than insulin, resulting in IGF1 occupation and consequently enhanced proliferation of cells expressing both receptors. Consistently, accumulation of hybrid receptors is characteristic for several cancer types [64, 68].

The major downstream effectors of IR/IGF1R are the PI3K/AKT and MAPK signaling pathways. Whereas PI3K mediates metabolic functions of insulin in liver, muscle and adipose tissue, both pathways have been linked to proliferation in various cancers [64]. As these pathways can be targeted with small molecule inhibitors, they became attractive for specific anticancer therapies. Inhibiting the PI3K/AKT/mTOR axis resulted in reduced growth of mammary tumors in hyperinsulinemic mice in a similar way as previously demonstrated for tyrosine kinase inhibitors blocking IR/IGF1R activity [69–71]. Of note, the anti-diabetic drug metformin, which among other effects activates AMPK and inhibits mTOR, and

eventually attenuates hyperinsulinemia, has been shown to suppress tumor activity [72].

2.2.2 Signaling via Sex Hormones

Sex hormones are involved in specific cancer entities, exemplified by the implications of estrogen and androgen signaling in breast and endometrial, as well as prostate cancer, respectively. Obesity increases the risk of development of postmenopausal breast cancer, whereas the risk of premenopausal breast cancer appears to be reduced [73]. It is evident that the adipokine leptin, which correlates with the grade of obesity, is involved in breast cancer development and progression. However, an exclusive role of leptin is unlikely, given the apparent protective function of obesity in the context of premenopausal breast cancer. After menopause, adipose tissue is the main source for estrogen production. Thus, circulating levels of estrogens directly correlate with the amount of body fat. Moreover, in obese adipose tissue, expression of aromatase, the enzyme that converts androgens to estrogens is further induced by excess of pro-inflammatory cytokines, thereby further promoting hyperestrogenemia [74]. Notably, obese women are at higher risk of developing mammary tumors derived from cells that express the estrogen receptor (ER-positive breast cancer), which applies to a high number of postmenopausal breast cancers [75]. Estrogens have many modes of action, which could contribute to tumor promotion, including mitogenic effects, mediation of genetic instability and inhibition of apoptosis [76].

Androgens play a key role in prostate cancer development and progression. According to epidemiological studies, there is no significant increase in relative prostate cancer risk in obese men [4]. This is in line with the observation that obesity correlates with low testosterone and sex hormone-binding globulin levels [77]. However, disease progression and mortality are significantly enhanced in obese patients [4]. In this context, a recent study has demonstrated that periprostatic adipose tissue-derived inflammatory signals might determine aggressiveness and invasiveness of prostate tumors under obese conditions (see above and [63]).

2.2.3 Immune Cells and Pro-inflammatory Signaling

Whereas the immune system has significant tumor-suppressing functions, cancer often develops in local environments where persistent inflammation occurs [78]. Chronic inflammatory states generally have pro-tumorigenic potential as they promote proliferation and cell survival by inducing mitotic and anti-apoptotic pathways [79]. Moreover, tumors frequently exhibit characteristics that are typically associated with inflammatory processes including activation of pro-inflammatory signaling pathways, angiogenesis and tissue remodeling [79].

Obese adipose tissue undergoes a substantial remodeling process. In this context, massive infiltration of adipose tissue by cells of the innate immune system takes place. Indeed, formation of distinctive “crown-like structures” by macrophages surrounding dying adipocytes is a hallmark of adipose tissue inflammation during obesity [80, 81]. Moreover, whereas adipose tissue-resident macrophages predominantly exhibit an anti-inflammatory M2 phenotype under lean conditions,

pro-inflammatory M1 polarized macrophages become more abundant during obesity. Macrophage reprogramming might be driven by free fatty acids and inflammatory mediators released from dysfunctional adipocytes [82]. Enhanced secretion of an array of pro-inflammatory cytokines by immune cells and adipocytes can be observed in an obese setting. Specifically, release of tumor necrosis factor (TNF) α , interleukin (IL)-1 β and IL-6, as well as CC-chemokine ligands (CCL), is markedly increased during obesity, thereby aggravating adipocyte dysfunction and promoting systemic insulin resistance [82–84]. Altogether, under obese conditions, infiltration of adipose tissue by macrophages, mast cells and lymphocytes, as well as alterations in the adipose tissue secretome, precipitates into a persistent local and systemic subclinical inflammatory state.

Pro-inflammatory cytokines have been shown to be involved in tumor development and/or progression, thus providing a possible direct link between adipose tissue inflammation and cancer. Notably, they also induce expression of chemokines and prostaglandins, resulting in recruitment and activation of immune cells, ultimately establishing an inflammatory feed-forward mechanism [78]. TNF α promotes tumor progression through activation of transcription factors controlling proliferative and anti-apoptotic pathways, particularly NF- κ B and AP-1 [78, 85]. It has been also shown to be involved in mutagenesis and epithelial to mesenchymal transition, the latter of which is a critical event in metastasis formation [86]. IL-6 promotes expression of genes involved in oncogenic pathways, mainly via Jak-STAT activation [85]. In this context, the Karin laboratory demonstrated that TNF α and IL-6 directly promote tumor growth in a STAT3-dependent manner in a carcinogen-induced liver cancer mouse model. Notably, the tumor-promoting effect of pro-inflammatory signaling was amplified in obese animals. Accordingly, loss of either the IL-6 receptor or TNF receptor 1 largely prevented tumor development even under obese conditions [87]. A more recent study demonstrated that under obese conditions, HCC was promoted through stabilization of the E3 ligase Mcl-1. Of note, IL-6 regulates Mcl-1 turnover, which was disrupted during obesity, resulting in an IL-6 independent HCC promotion in obese mice [88]. TNF α signaling was found to be central for progression of PanIN lesions toward pancreatic cancer in obese mice, supporting a general role of pro-inflammatory signaling in obesity-associated tumor development [89].

Specific tumor-suppressing immune cells are quantitatively reduced during obesity, which has implications for cancer risk. In mice and men, obesity is associated with dysfunction of the innate and adaptive immune system, which manifests for instance in reduced numbers of natural killer (NK) and cytotoxic CD8⁺ T cells [86]. These cells have direct antitumor effects as they mediate cytotoxicity to cancer cells [78]. In line with this, exercise was shown to induce infiltration of distinct tumors by NK cells, thereby inhibiting tumor growth [90]. Additionally, a reduction in regulatory T (Treg) cells could be observed in the abdominal fat of obese mice and humans [91]. Whereas Treg cells play a role in immune evasion of tumor cells, they probably have antitumor function as well as suppressive effects on chronic inflammatory states.

Several other types of immune cells have tumor-promoting or tumor-suppressing activities, including neutrophils, B-lymphocytes and T-helper cells [78]. It still needs to be shown in detail if and how these cells are affected by obesity and may link metabolic dysfunction to cancer manifestation.

3 The Gut Microbiome

Microorganisms have been threatening human health at all times. While bacteria-associated infectious diseases have mostly lost their terror due to the discovery of vaccination and antibiotics, microbes have gained attention as pathogens also in non-communicable diseases. In this context, a number of bacterial species have been designated as carcinogenic [92].

The vast majority of the human microbiota resides in the digestive tract, which provides optimal growth conditions for various bacterial species, e.g., constant temperature and availability of nutrients. Actually, the gastrointestinal tract of an average healthy adult contains more than 1 kg of bacterial mass [93]. Metagenomic analyses based on 16S rRNA sequences have revealed an unexpectedly high complexity of gut bacterial communities and that their composition depends on several parameters [94]. The symbiotic relationship between the intestinal microflora and its host results in mutual benefits for both organisms.

As gut-resident bacteria are involved in digestion and absorption of macronutrients, they have a key function in regulating metabolism of their host. However, despite being generally advantageous and health promoting for the host, the gut microbiota might as well contribute to several pathologies. In the other direction, metabolic status and diet composition potentially have significant impact on the composition of the intestinal microflora [95–97]. While Firmicutes and Bacteroidetes are the most abundant bacterial phylae under healthy conditions, Enterobacteriaceae were found to be enriched in the intestinal tracts of obese humans and rodents [98]. This family of Proteobacteria, which is hardly detectable in healthy microbiomes, is known to release large amounts of lipopolysaccharide (LPS), thereby locally and systemically leading to a pro-inflammatory milieu [99]. Accordingly, circulating LPS levels were found to be 2–3 times elevated in obese mice compared to lean controls [100]. Thus, by constantly triggering an innate immune response, a modified gut microbial community potentially might contribute to the low-grade chronic inflammatory state that is observed under obese conditions.

Obesogenic diets that contain high amounts of fat while being poor in fiber were reported to cause lowering of microbial diversity (dysbiosis) in the gut, which has been linked to cancer [101, 102]. In line with this, transfer of wild-type microbiota to dysbiotic mice reduced tumor burden in a colorectal cancer model [102]. Notably, eradication of the microbiota through germ-free housing or antibiotic treatment resulted in tumor reduction in various rodent models of colorectal cancer, leading to the assumption that no microflora at all might be better than dysbiosis

[101]. As inhibitory effects of gut microbiota elimination could be observed on tumors of the liver, the lung and the mammary gland, it is plausible that intestinal bacteria also potentially promote remote oncogenesis [101].

Specific gut-resident microbes break down dietary fiber into bioactive short-chain fatty acids (SCFA), mainly acetic, propionic and butyric acid. Whereas butyrate can be used by colonocytes as an energy substrate, SCFA are generally known to have anti-inflammatory effects [103, 104]. Moreover, butyrate was shown to have tumor-suppressing functions in neoplastic colon cells under defined dietary and microbial conditions [105]. By contrast, in colonocytes with mutations in the *Msh2* and *Apc* genes, butyrate production by microbes resulted in enhanced proliferation [106]. Furthermore, gut bacteria have important functions in bile acid metabolism. It has been recently demonstrated that mice fed a high-fat diet exhibited elevated levels of the secondary bile acid deoxycholic acid (DCA), concomitant with significant alterations of the gut microbiota [107]. It has been shown in the same study that DCA promotes development of hepatocellular carcinomas through induction of DNA damage, which could be prevented by antibiotic elimination of gut bacteria [107]. The carcinogenic effect of DCA can be at least partially explained by its cytotoxic and genotoxic potential [108]. Thus, disrupted bile acid homeostasis provides another connection between obesity, gut microbiota and cancer.

It is accepted that the connection between dysbiosis and cancer is caused not only by toxic actions of specific pathogens, but also by an impaired host–microbe interaction. However, the underlying molecular mechanisms are only partially resolved. Dysbiosis potentially results in barrier failure of the intestinal mucosa and subsequent inflammatory response. It has been hypothesized that a healthy microflora (eubiosis) might at a low-level activate receptors of the innate immune system, which are presently in the focus of tumor-suppressing immune therapies [109]. It is questionable though, if the degree of activation of the innate immune response is sufficient to induce anti-tumor effects [101]. Also, this is somewhat counterintuitive and contradictory to the tumor-promoting effects of LPS, which acts through stimulation of the innate immune system. Also, in disagreement with the hypothesis that induction of a (low level) innate immune system response could exert anti-tumorigenic effects, activation of Toll-like receptors resulted in pancreatic inflammation and subsequent carcinogenesis [110].

There is consensus that the gut microbiota contributes to health and disease in many respects. By mediating inflammatory responses, accumulation of toxic compounds, and/or provoking barrier failure, a dysbalanced microbiota might link obesity to certain cancers. Regardless of whether alterations of the microbiota are cause or consequence of obesity, promoting a healthy microbiome composition in the gut might not only help to maintain general wellbeing, but also could provide to a certain degree protection from cancer. Thus, diets rich in fiber as well as pre- and probiotic nutritional supplementation should always be taken into account when we think about lifestyle modifications aiming toward cancer prevention.

4 Tumor Cell Metabolism

Already in the 1920s, the German biochemist Otto Warburg hypothesized that a metabolic switch from respiration to increased glucose consumption for lactic acid fermentation (a process termed aerobic glycolysis or the Warburg effect) represents a main event in the transformation of a normal to a tumor cell and that cancer cells could be defeated by targeting their energetic requirements [111]. Although widely neglected for a long period of time, the field of cancer metabolism achieved enormous attention by researchers in the past decade. Consequently, Warburg's concept mainly focused on increased glucose consumption has been extended by the definition of a plethora of specific changes referred to as the metabolic reprogramming of cancer cells [112]. As both direct and indirect consequence of oncogenic mutations, cancer cell metabolism is considered a prerequisite for maintaining viability and fulfilling the biosynthetic demands associated with cell proliferation. However, the precise metabolic program of cancer cells might depend on their specific oncogenic mutations, the tissue context and other factors, including macro- and microenvironmental components. Nevertheless, most cancer cells display several of the six hallmarks of cancer metabolism, which have been defined in a recent review based on known cancer-associated metabolic changes [112]. Some of the metabolic features of cancer cells might contribute to the risk association between obesity and cancer. These include (1) the increased uptake of glucose, which might be favored by hyperglycemia under diabetic conditions, (2) the opportunistic modes of nutrient acquisition enabling tumor cells to benefit from increased lipid availability under obesity conditions and, at least in part related to the latter, (3) the metabolic interactions with the environment, e.g., neighboring adipocytes.

4.1 Hyperglycemia

As a central component of metabolic reprogramming, cancer cells take up high amounts of glucose, which is utilized for ATP production by aerobic glycolysis and generation of building blocks for nucleotide, amino acid and lipid biosynthesis. This suggests that increased concentrations of glucose in the circulation (hyperglycemia), as a hallmark of type 1 and type 2 diabetes mellitus (DM) could contribute to tumorigenesis. Indeed, a number of epidemiological studies suggest that DM is associated with higher prevalence as well as increased mortality for certain types of cancer, including liver, pancreas, colorectal, kidney, bladder, endometrial and breast cancers [113, 114]. Notably, type 2 diabetes represents approximately 90 % of total diabetes cases and arises from insulin resistance under obesity conditions. Therefore, given that cancer occurs preferentially in the older population, in which type 1 diabetes is less frequent, it can be assumed that the increased cancer risk associated with DM refers to mainly to type 2 diabetes [114]. Like for obesity, the risk connection between DM and cancer is complex and might be based on

various mechanisms including increased levels of pro-inflammatory cytokines as well as oncogenic effects of hyperglycemia which are not directly linked to glucose as an energy substrate, e.g., anti-apoptosis, induced cell migration and invasion as well as hyperglycemic memory effects [115]. However, hyperglycemic conditions *in vitro* have been shown to trigger increased glucose uptake in choriocarcinoma cells by inducing expression of the glucose transporter isoforms GLUT1 and GLUT3 [116]. Also, hyperglycemia has been shown to contribute to hypoxia-inducible factor (HIF)-1 alpha stabilization [117], which in turn can induce the expression of glycolytic enzymes further enhancing glucose utilization. However, the direct effects of hyperglycemia on cancer development are widely unexplored, also due to technical difficulties in studying the effects of high glucose levels on cancer *in vivo* without interfering with the effects of absence or induction of insulin signaling.

4.2 Lipid Metabolism

As part of the metabolic reprogramming of cancer cells, fatty acids are generally considered to serve as building blocks for biosynthesis of membranes and signaling molecules, as well as to support other aspects of the transformed phenotype of rapidly proliferating cells [118]. Consequently, there are numerous examples showing that oncogenic pathways re-activate *de novo* lipid synthesis, in part through increased expression and activation of the required metabolic enzymes, including fatty acid synthase (FASN) [118, 119]. Along this line, inhibition of fatty acid availability by different modes could offer novel opportunities in cancer therapy [120].

Despite the observation that cancer cells acquired increased capacity for *de novo* lipid synthesis to enable proliferation, it is conceivable that under obesity conditions, the increased availability of exogenous lipids from the circulation and from cancer-associated adipocytes could promote tumor development. In support of this idea, Nomura et al. showed that inactivation of the lipolytic enzyme monoacylglycerol lipase (MAGL) markedly impaired the tumorigenic capacity of different aggressive human cancer cell lines representing melanoma, breast and ovarian cancer. They identified MAGL in a proteomic analysis in which this lipase was consistently elevated in the aggressive cell lines compared with their non-aggressive counterparts from the same cancer entity. Knockdown of MAGL in the aggressive or overexpression in the non-aggressive cell lines impaired or induced oncogenic features, respectively, including migration, invasion and *in vivo* growth. Strikingly, the reduced *in vivo* growth of xenograft tumors upon knockdown of MAGL in the implanted cells could be rescued by feeding the mice a HFD, suggesting a pro-tumorigenic effect of the availability of exogenous fatty acids [121]. Another study showed that the proliferation of breast cancer and sarcoma cells expressing Lipoprotein Lipase (LPL) and CD36 is accelerated upon treatment with triglyceride-rich lipoproteins. Since LPL and CD36 are involved in lipoprotein-associated triglyceride lipolysis and fatty acid uptake, respectively, this

suggests that these cells are capable to acquire fatty acids from the circulation or other sources to fuel their growth [122]. In addition, providing prostate cancer cells, which are characterized by high lipogenic capacity, with LPL and TG-rich lipoproteins prevented the growth inhibitory effects of fatty acid synthesis inhibition [122]. Interestingly, there is also evidence that under hypoxic conditions or Ras activation, certain cancer cells can switch from *de novo* lipogenesis to scavenging of serum fatty acids to meet their lipid requirements [123]. Similarly, another study demonstrated in a panel of cell lines and in tumors that exogenous palmitate could be incorporated into both structural and oncogenic signaling lipids [124]. Furthermore, dietary lipids potentially also act as ligands for nuclear receptor transcription factors. In this context, a recent study showed that high-fat diet promotes stemness and induced the capacity for tumor initiation of intestinal progenitor cells via activation of PPAR δ and subsequent induction of WNT/ β -catenin signaling [125].

Also, more direct interactions between adipocytes and cancer cells might contribute to metabolic adaptations promoting tumor growth and aggressiveness. For instance, co-culturing of primary adipocytes with ovarian cancer cells led to the direct transfer of lipids by induced lipolysis in the adipocytes and beta oxidation in the cancer cells, suggesting that adipocytes can act as an energy source to promote tumor growth [126]. Interestingly, ovarian cancer metastasis to the omentum, an organ primarily composed of adipocytes, was induced by adipokines characterized by induced fatty acid binding protein (FABP) 4 expression, indicating a modified lipid metabolism phenotype.

Although further research is required to elucidate the interaction between cancer cell metabolism and the altered metabolic macro and microenvironment in metabolic diseases, the described examples might point to the implication of such mechanisms in the connection between obesity and cancer and guide further studies in this direction in the future.

5 Outlook and Open Questions

Obesity increases the risk of several cancer entities by triggering multiple (patho-) physiological alterations in local and remote fashions. Given its pandemic prevalence, obesity is expected to become one of the main lifestyle-associated risk factors for cancer development in the near future. Knowledge of the underlying molecular principles will be crucial, as it will open new opportunities for “metabolocentric” cancer treatment and prevention. Such options would include targeted therapies affecting deregulated pathways under obese conditions, exemplified by inhibition of inflammatory and growth factor signaling. Importantly, interventions targeting obesity and metabolic dysfunction in a more general way might have (immediate) effects on cancer risk independent of actual weight loss: Exercise triggers the release of potentially tumor-suppressing myokines, such as oncostatin and SPARC [127, 128]. Bariatric surgery instantly results in metabolic improvements

independent of body weight loss, including elevated adiponectin levels and alleviation of hyperinsulinemia [129–131]. Pre- and probiotics could be an option for supporting a healthier intestinal microflora [132]. Noteworthy, transplantation of healthy microbiota showed antitumor effects at least in murine cancer models [102]. Major future challenges will include the tumor entity-specific definition of metabolic complications and/or obesity-associated comorbidities, including type 2 diabetes, insulin resistance and dyslipidemia that determine increased tumor progression and/or aggressiveness in affected patients. Of particular interest will be the question to which extent metabolic dysfunction cannot only trigger tumor promotion but might also serve as an initiating event in the malignant transformation of a normal to a cancer cell, independent of classical gene mutations in oncogenes or tumor suppressors. Clinical and experimental studies in this direction can be anticipated to shed light onto this exciting field of biomedicine to overcome metabolism-driven tumorigenesis in the future.

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