Chapter 16 Interplay Between Microenvironmental Abnormalities and Infectious Agents in Tumorigenesis

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Abstract Emerging evidence has shown that the cell of microenvironmental abnormalities is a key factor that controls many cellular physiological processes including cellular communication, homing, proliferation, and survival. Given its central regulatory role, it is therefore not surprising that it is widely exploited by infectious agents for inducing pathogenesis. In the past decade, a number of oncogenic pathogens including viruses, bacteria, and parasites are demonstrated to take advantage of the tumor microenvironmental factors including hypoxia, oxidative stress, and cytokines, to create an extracellular environment more favorable for pathogen survival and propagation and escape from the host immune surveillance. Here we summarize and highlight the current understanding of the interplay between common tumor microenvironmental factors and oncogenic pathogens in promoting tumorigenesis.

Keywords Tumor microenvironment • Pathogen • Oncogenesis

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16.1 Introduction

Oxygen and glucose are not only essential nutrients but also key microenvironment factors to maintain cell survival. Imbalance between nutrients supply and demand can lead to nutrient stress within regions of tumor tissues. The growth of solid tumors, which are significantly different from the normal tissues, possesses the characteristic of rapid expansion of tumor mass and chaotic growth of tumor vasculature [1, 2]. Thus, excessive metabolism rate of tumor cells and insufficient blood supply could profoundly influence the tumor microenvironment where forms hypoxia and glucose starvation. To survive in hypoxia and glucose starvation stress, tumor cells have evolved strategies of adaptive cellular response by acting on various signaling pathways that are responsible for angiogenesis, glucose metabolism, cell proliferation, and apoptosis [3, 4]. Importantly, increasing evidence suggests that these adaptive strategies in cancer cells profoundly drive tumor growth and aggressive progression [1, 4, 5]. In addition, the consequence of limitation on the uptake of oxygen and glucose has also been shown to associate with the physiochemistry change within tumor microenvironment such as increase of acidic (H⁺) concentration and ROS production [6]. Conversely, these physiochemistry changes acting as a selective stress influence cellular signaling pathways and can be exploited in tumorigenesis. Together, nutrient stress (hypoxia or glucose starvation) in synergizing with the accompanied production of metabolites constitutes a unique tumor microenvironment where it produces a potent selective stress in driving carcinogenesis.

Distinct from noninfectious agent-associated cancer, pathogen-host interaction has been causally demonstrated in the carcinogenesis of pathogen-associated cancer [7]. The hemostasis of both extracellular and intracellular metabolic environment is equally essential for oncogenic pathogen survival, especially for virus that absolutely relied on cells for living. Whether these oncogenic pathogens are directly capable of sensing changes in extracellular or intracellular microenvironment remains to be exploited. However, the factors including low oxygen and ROS generation have been indicated to influence virus replication and virions production [8]. On the other hand, emerging evidence has also suggested that many oncogenic pathogens participate in modulating key signaling pathways and gene expression that triggered cellular response to metabolic stress. The adaptive genetic alteration of signaling pathways by oncogenic pathogens may reflect the interaction between pathogen-associated cancer cells and tumor microenvironment. Therefore, it is highly possible that some of these oncogenic pathogens have evolved their own unique adaptive mechanisms. The pathogen-specific subversion response of signaling pathway not only facilitates the survival of infected cells under stress but also promotes pathogen-mediated oncogenesis. Hence, the understandings of these pathogen-associated critical signaling pathways in adaption to hypoxia and glucose starvation stress will not only expand the oncogenesis mechanism induced by pathogen in a microenvironment base but will also favor the identification of both



Fig. 16.1 Schematic representation of microenvironmental abnormalities including immune (immune cells, cytokines, and chemokines) and nonimmune (extracellular matrix, stromal cells, blood vessels) components associated with infectious agents (virus, bacterium, and parasite)

pathogen and microenvironment based on potential therapeutic targets for the treatment of pathogen-associated cancer (Fig. 16.1).

In this review, we summarize the key cellular adaptive signaling pathways that are modified by oncogenic pathogens and highlight the common or unique mechanisms utilized by these oncogenic pathogens for oncogenesis.

16.2 Pathogen-Mediated Alteration of Hypoxic Signaling and Response to Hypoxic Stress

Cellular oxygen homeostasis is highly dependent on the regulation of oxygensensitive signaling pathway. Accumulated evidence has strongly shown the activated oxygen-sensitive signaling is the first line to respond to hypoxic stress within tumor microenvironment [9–11]. Activations of hypoxia-inducible factor 1 (HIF-1) and HIF-dependent downstream gene are the master regulatory pathway during hypoxia. In addition, mTOR kinase signaling pathway and unfolded protein response (UPR) are another two oxygen-sensitive signaling that are individually activated under the condition of severe and durative hypoxia stress [11]. Therefore, it is not surprising that most oncogenic pathogens are involved in the deregulation of key molecules in controlling these hypoxic signaling pathways.

16.2.1 Deregulation of HIF-Dependent Hypoxic Signaling

HIF-1, which consists of a constitutively expressed β -subunit and an inducible α -subunit, is a central transcriptional factor of HIF-dependent signaling in response to hypoxia stress [12]. The modulation of HIF-1 is mainly through the stability and availability of the inducible subunit HIF-1 α . The stabilization of HIF-1 α is oxygen-dependent and is tightly regulated in the presence of oxygen [13]. More recently, it has been proven that many oncogenic viruses can directly enhance the accumulation of HIF-1 α and promote its transcriptional activity through various mechanisms even in normoxia [14]. Given the role of HIF-1 α in inducing the expression of proangiogenic factors, the subversion of HIF-1-dependent angiogenesis has been deeply involved in oncoprotein-stimulated tumor angiogenesis.

16.2.1.1 Synthesis of HIF-1α Protein

Activation of growth factor signaling pathways including MAPK signaling, PI3K/ Akt signaling, and TSC/mTOR signaling has been indicated to be involved in the synthesis of HIF-1 α protein [15]. Several oncogenic viruses have been found to hijack these signaling pathways to enhance the synthesis of HIF-1 α protein in hypoxia or normoxia. For instance, KSHV vGPCR-mediated paracrine secretion can activate TSC/mTOR signaling and mTOR-dependent upregulation of HIF-1 α / HIF-2 α [16]. Similarly, EBV-encoded latent membrane protein LMP-1 is also shown to induce the activation of p42/p44 MAPK signaling pathway to promote the synthesis of HIF-1 α proteins [17], and HPV16-encoded E6 associate with ERK1/2 signaling pathway to enhance HIF-1 α accumulation [18]. In addition, some viral oncoproteins are shown to regulate HIF-1 α at a transcription level. For example, HTLV encodes Tax to promote the expression and DNA-binding activity of HIF-1 α by means of activating PI3K/Akt signaling [19]. EBV-encoded LMP-1 is also shown to enhance the stability of HIF-1 α RNA transcripts through ERK1/2 and STAT3 signaling targeting the expression of RNA-destabilizing proteins TTP and PUM2 [20].

16.2.1.2 Stability of HIF-1α Protein

The accumulation of HIF-1 α protein not only depends on the constitutive synthesis of HIF-1 α but also requires the modulation of HIF-1 α degradation. The degradation of HIF-1 α is primarily induced by PHD/HIF/VHL pathway in an oxygen-dependent manner [21, 22]. The tumor suppressor VHL acts as an E3 ubiquitin ligase to induce prolyl-hydroxylated HIF-1 α for ubiquitylation and in turn proteasomal degradation. The hydroxylation of HIF-1 α in the specific proline residue is mediated by oxygen-sensor prolyl hydroxylase (PHD) enzymes. Interestingly, increasing evidences have shown that oncogenic viruses have exploited diverse strategies to interfere PHD/

HIF/VHL pathway. For instance, both KSHV-encoded LANA and EBV-encoded LMP-1 have been demonstrated to induce the proteasome-mediated degradation of HIF-1 α suppressor. LANA can stimulate the degradation of HIF-suppressor VHL and p53, which is dependent on the recruitment of Cul5-Elongin BC complex by the cytokine signaling-box motif within LANA [23]. In contrast, LMP-1 can induce the degradation of oxygen-sensor PHD1 and PHD3 via recruitment of Siah1 E3 ubiquitin ligase [24]. Distinct from LANA and LMP-1, KSHV-encoded IFN-regulatory factor 3 (vIRF3), a viral homologue of cellular IRF gene, can stabilize HIF-1 α protein through forming a complex with HIF-1 α , although the machinery of the inhibition of HIF-1 α degradation remains unclear [25]. The EBV oncoproteins EBNA3 and EBNA5 are shown to bind to PHD1 and PHD2 for blocking the hydroxylation of HIF-1 α [26]. Interestingly, in order to stabilize HIF-1 α , the HBV-encoded HBx not only blocks the formation of VHL-HIF complex but also induces interaction between MTA1/HDAC and HIF-1 α to promote the deacetylation of HIF-1 α within the oxygen-sensitive domain [27, 28].

16.2.1.3 Transcriptional Activity of HIF-1α

In addition to the accumulation of HIF-1 α protein, the regulators of HIF-1 α transcriptional activity including nuclear translocation, and interaction with coactivators, DNA-binding capacity also plays a critical role in activating HIF signaling, which is targeted by different viral proteins [29]. For example, KSHV-encoded LANA and vIRF3 have been reported to promote nuclear accumulation of HIF-1 α [23]. EBV oncoprotein LMP-1 enhances DNA-binding ability of HIF-1 α to hypoxiaresponsive DNA elements within the VEGF promoter [17], while HBx enhances the transcriptional activity of HIF-1 α through the activation of p42/p44 MAPK signaling, leading to the interaction between HIF-1 α and coactivator CREB-binding protein [30]. In addition, some viral oncoproteins are also involved in stimulating HIF-1 α activity through posttranslational modification. For instance, the p38/MAPK signaling activated by KSHV vGPCR can phosphorylate HIF-1 α and enhance its transcriptional activity [31], and HPV E7 prevents deacetylation of HIF-1 α through dissociation with histone deacetylases HDAC1, HDAC4, and HDAC7 [32].

16.2.2 Deregulation of HIF-Independent mTOR Signaling

It has been demonstrated that the adaptive response to hypoxia stress involves not only stimulation of angiogenesis but also inhibition of protein synthesis [33]. mTOR kinase signaling pathway, as a central regulator of protein synthesis that integrates various physiological signals [34], has been shown to respond to hypoxia and restrain the growth of tumor [33]. mTOR-mediated protein synthesis is a process involving the phosphorylation of the eukaryotic initiation factor 4E binding protein

1 (4E-BP1) and the p70 ribosomal S6 kinase 1(S6K1) [34]. These two are critical effectors of the downstream of mTOR signaling and responsible for the initiation process of translation. It has been shown that inhibition of mTOR by hypoxia involves three hypoxia-inducible proteins REDD1, BNIP3, and PML [35-37]. Both REDD1 and BNIP3 can directly suppress mTORC1 activity by disrupting RhebmTOR interaction, whereas REDD-mediated downregulation of mTORC1 by hypoxia is dependent on TSC1/TSC2 complex (a negative regulator of mTOR). In view of the fact that the deregulation of mTOR signaling appears in many advanced cancers [38, 39], the constitutive activation of mTOR could be an adaptive strategy in response to hypoxia. Intriguingly, a growing number of evidence has shown the positive regulation of mTOR activity by several oncogenic viruses. For instance, HPV16-encoded E6 and HBV-encoded HBx are shown to target TSC1/TSC2 complex for stimulating protein synthesis. Moreover, HPV16 E6 not only induces the activation of mTOR/SK61 signaling, which is dependent on the disruption of TSC2 by E6-tuberin interaction and the proteasomal degradation of tuberin [40], but also enhances Atk/mTOR activity to initiate cap-dependent translation [41]. For HBV, the overexpression of HBx activates TSC1/mTOR/SK61 signaling by means of IKK β [42]. Meanwhile, HCV NS5A-mediated activation of mTOR presents a positive effect on two key translation initiation-associated proteins S6 K1 and 4EBP1, by which NS5A promotes the dissociation of FKBP38 from mTOR by competitive binding to mTOR [43, 44]. This indicates to some extent that activation of mTORC1 and protein synthesis could be potent strategies targeted by oncogenic viruses in response to hypoxia. Nonetheless, the increasing severity and duration of hypoxia will conversely cause the suppression of protein synthesis in most cells. Therefore, the mTOR signaling is also a critical regulator in hypoxia toleration. However, whether the subversion of mTOR signaling by oncogenic virus for carcinogenesis will still benefit to the survival of tumor cells during severe hypoxia remains elusive. It is likely that the oncogenic virus will shift the regulatory mechanism of mTOR signaling or constitutively activate mTOR-dependent protein synthesis to promote viral replication in response to sever hypoxia.

16.3 Pathogen-Mediated Alteration of ROS Signaling and Response to Oxidative Stress

Mounting evidence has indicated the excess generation of intrinsic or extrinsic ROS in cancer cells. It has been proven that several factors including mitochondrial dysfunction and oncoprotein activity contribute to the accumulation of ROS [45]. In tumor microenvironment, hypoxia stress and glucose starvation have been clearly linked to the induction of intracellular ROS production [46, 47]. The constitutive production of ROS (i.e., hydroperoxides) and the consequence of oxidative stress will cause DNA damage and genomic instability and trigger the normal cell death signaling. To date it is well known that oxidative DNA damage caused by ROS will activate p53 signaling through the enhancement of p53 stability and DNA-binding activity [48], which is tightly modulated by negative regulator MDM2 (an ubiquitin E3 ligase) and ATM (an important sensor of DNA damage) [49, 50]. Different from the effect on normal cells, it has been well established that the oxidative stress in microenvironment profoundly contributes to tumor progression by affecting cell proliferation, apoptosis sensitivity, and genome stability [45]. Therefore, adaptive genetic change to subvert the death signaling induced by oxidative stress has evolved in tumorigenesis.

Since the tumor suppressor p53 is demonstrated as a central regulator in both cell cycle arrest and apoptosis and is potently activated in response to oxidative stress [51], several viruses have been found to evolve an adaptive mechanism to directly block p53 function. For example, the expression of vIRF1 encoded by KSHV can attenuate ATM/p53-mediated DNA damage response through directly blocking ATM-mediated phosphorylation of p53 on serine 15 which in turn increases the degradation of p53 by MDM2. In addition, vIRF1 can also reduce the transcriptional activation of p53 [52]. In contrast, EBV-encoded lytic protein BZLF-1 can induce the degradation of p53 in ATM-dependent DNA damage response which is independent of MDM2 [53]. The deregulation of p53-dependent oxidative stress response is also found in HCV infection. The overexpression of DHCR24 induced by HCV infection can suppress the activation of p53 through the accumulation of p53-MDM2 complex, although the specific viral protein involved in this process remains unknown [54]. In addition, KSHV-encoded LANA and some structural proteins expressed during the late stage of lytic replication have been found to inhibit p53-mediated apoptosis [55, 56]. Both EBV nuclear antigen 3C and viral oncoprotein LMP-1 have also been shown to be involved in repressing p53-induced apoptosis and transcriptional activity [57–59]. However, despite that the activation of p53 signaling has been linked to multiple types of DNA damage, how p53 is regulated by viral oncogene and in turn responsible for oxidative DNA damage is still elusive and requires to be further investigated.

16.4 Cross Talk Between Pathogens and Cytokines in Tumor Microenvironment

Cytokines and chemokines, existing in tumor microenvironment, are a series of small proteins that exert great effects on host response to pathogen infection. Despite antiviral activity induced by cytokines and chemokines, extensive evidence demonstrates that some pathogens, especially oncogenic viruses and bacteria, utilize cytokines and chemokines to promote tumor progression [60, 61]. Here, we summarized and highlighted several cytokines and chemokines that play a vital role in tumorigenesis during infection of oncogenic pathogens (Fig. 16.1).

16.4.1 IL-6

Interleukin 6 (IL-6), secreted by a variety of host cells such as T cells, macrophages, fibroblasts, and malignant cells, is a multifunctional inflammatory cytokine, inducing various biological effects including tumorigenesis [62]. Increasing evidence indicates that IL-6 has a strong link with pathogen-mediated carcinomas. For example, it has been found that IL-6 acts as an autocrine growth factor targeted by EBV to promote immortalization of B cells and tumor growth [63–65]. In contrast, KSHV encodes viral IL-6 (vIL-6), sharing about 25% homology with human IL-6 (hIL-6). Different from hIL-6, vIL-6 stimulates almost each type of cells through directly binding to gp130 without hIL-6 receptor [66]. vIL-6 is able to promote the growth and survival of PEL cells and tumorigenesis of nude mice [67, 68]. Blockading vIL-6 expression or neutralizing antibody against gp130 could efficiently inhibit the growth of PEL cells [69, 70]. Further studies revealed that vIL-6 blocks IFN signaling, which contributes to tumor cell proliferation [71]. In addition, miRNA K12-1, a viral miRNA encoded by KSHV, was found to activate NF-KB/IL-6/STAT3 pathway to promote tumorigenesis [72]. In the HPV-associated cervical cancer, recent studies reported that IL-6/STAT3 is activated by the E6 oncoprotein encoded by high-risk HPV for tumorigenesis [73, 74], while HBV-encoded X protein modulates IL-6 to promote the progression of liver cancer [75]. In the HTLV-1-associated T-cell malignancy, the viral protein Tax is shown to enhance the expression of IL-6 receptor and leads to the malignant growth of T cells [76]. In the bacteriumassociated cancers, Helicobacter pylori, a gram-negative microaerophilic bacteria, is found to parasitize in the stomach and results in chronic gastritis that is intensely associated with gastric neoplasm [77]. Several reports indicated that the interplay between H. pylori and TLR2 induces the expression of IL-6 and subsequently activates IL-6/STAT3 signaling pathway, which strongly contributes to immortality of gastric cancer cells. Interestingly, TLR2 is also directly upregulated by STAT3 in gastric tumors [78–81]. Therefore, TLR2/IL-6/STAT3 pathway may form a positive loop to promote gastric tumorigenesis [77].

16.4.2 IL-10

Interleukin 10 (IL-10), initially identified as an inhibitor of cytokine synthesis, has been shown to play a vital role in regulating cell differentiation and immune response, including limiting inflammatory response to pathogens and thereby reducing damage to host [82, 83]. However, it is also reported that IL-10 is utilized by various viruses to favor viral survival and pathogenesis, among which some even encode IL-10 homologs. For instance, EBV encodes vIL-10, imitating biological activities of cellular IL-10, to inhibit cytokine synthesis and regulate immune response [83]. In addition, vIL-10 prevents EBV-infected B cells from being eliminated by NK cell and protects antigen-specific T-cell proliferation by

downregulating MHCII antigen on monocytes and ultimately maintains EBV latent infection [84, 85]. On the other hand, human IL-10 (hIL-10) expression is also induced in the EBV-infected B cells. Evidence shows that hIL-10 is upregulated by latent membrane protein 1(LMP-1) via p38/SAPK2 pathway [86]. Another mechanism study revealed that EBV transcription factor Zta, previously recognized as a master regulator of EBV productive cycle, is also involved in the expression of hIL-10 [87]. Furthermore, EBV-encoded small RNA, EBER, was found to induce hIL-10 through RIG-I-mediated IRF3 pathway [88]. For another herpesvirus, KSHV was found to force PEL cells to release hIL-10 into culture supernatant. Moreover, neutralizing antibodies against IL-10 and IL-10 receptor shows that IL-10 is critical for the progression of PEL [67]. In the HPV-associated malignant cervical cancer, HPV drives immune cells to produce IL-10 to facilitate viral persistence and tumorigenesis [89]. During chronic HBV infection, high production of IL-10 suppresses the biological activity of CD8+ and CD4+ T cells, which favors the progression of tumorigenesis [90, 91]. Recently, it has been found that HTLV-1 bZIP factor (HBZ) upregulates T-cell immunoglobulin and ITIM domain (TIGIT) and enhances expression of IL-10 for evading host immune response [92].

16.4.3 IL-13

Interleukin 13 (IL-13) is known as inflammation regulatory factor, mainly generated by B cells, T cells, and NK cells [93]. The main function of IL-13 is to induce IgE switching and CD23 expression in B cells, promoting antigen presentation ability of MHCII, inhibiting inflammation in human monocytes, and suppressing apoptosis [94–97]. Increasing evidence has shown that IL-13 collaborates with various viruses including EBV, KSHV, and HTLV-1 to promote tumorigenesis [61, 98–101]. In the EBV-associated Hodgkin lymphoma, the expression of IL-13 is upregulated, and the underlying molecular mechanism is that Zta serving as a EBV lytic protein elicits IL-13 production via directly binding to IL-13 promoter. Furthermore, neutralizing antibody against IL-13 suggests that IL-13 is vital for proliferation and latency of EBV-immortalized lymphoblastoid cell lines [98]. STAT6, a key downstream effector of IL-13, is a remarkable transcriptional factor whose constitutive phosphorylation has been indicated in controlling tumorigenesis [102]. Our group found that the constitutive phosphorylation of STAT6 is due to autocrine/paracrine of IL-13 and downregulation of SHP1 mediated by KSHV, which is closely associated with oncogenesis. Strikingly, neutralizing antibody against IL-13 suppresses the proliferation and survival of PEL, suggesting IL-13 plays a significant role in KSHV-associated latency and subsequent tumorigenesis [61]. Though previous studies reveal that IL-4, sharing the same receptor IL-4R α /IL-13R α 1 with IL-13, also leads to the phosphorylation of STAT6, we found that IL-4/STAT6 pathway is negatively regulated in the KSHV-infected cells through dephosphorylation of STAT6 by latency-associated nuclear antigen (LANA), an important viral oncoprotein for maintaining viral latency [103, 104]. Similar to the effect of EBV and KSHV, HTLV-1 Tax protein also induces production of IL-13, which is capable of promoting cell proliferation and anti-apoptosis of infected cells in an autocrine manner [96, 97, 99, 105]. This indicates that IL-13 is often targeted by oncogenic virus for host immune escape and cell survival.

16.4.4 IL-8

Chemokines are a large family of small proteins that regulates inflammation. The main property of chemokines is to attract immune cells to the site of inflammation, resulting from various causes including infection, autoimmune disease, and carcinomas [106]. Interleukin 8 (IL-8), a member of CXC chemokine subfamily, is responsible for recruiting neutrophils and T lymphocytes to the site of inflammation. Extensive evidence demonstrates that IL-8 is closely implicated in tumorigenesis such as breast cancer, gastric cancer, and pancreatic cancer [107–109]. Thus, it is not surprising that IL-8 was also found to participate in pathogen-related tumorigenesis. For example, EBV-encoded Zta protein activates IL-8 through binding to two elements within IL-8 promoter and subsequently upregulates IL-8 production, which is crucial for NPC development by recruiting infiltrates around infected cells [110]. In contrast to EBV, KSHV adopts different mechanisms to regulate IL-8 expression. It has been demonstrated that LANA-1 boosts IL-8 production to assist KSHV-infected cells in evading host immune response [111]. Similarly, in the context of lung adenocarcinomas, HPV16 infection upregulates IL-8 expression and in turn promotes angiogenesis and metastasis through inducing MMP2 and MMP9 [112], while the downregulation of IL-8 in the HPV-immortalized exocervical cells or primary keratinocytes could create a favorable microenvironment for HPV infection and subsequent tumorigenesis [113, 114]. In addition, previous studies showed that HCV infection could upregulate IL-8 expression and contribute to host immune tolerance and viral pathogenesis [115]. Interestingly, the similar phenomenon occurs to HBV, which was found to increase viral tolerance to IFN- α by inducing IL-8 production [116]. HTLV-1 also encodes Tax oncoprotein to activate IL-8 production and in turn contribute to HTLV-1-associated pathogenesis [117]. In bacteriaassociated cancer, the discoveries from gastric epithelial cells exposed to Helicobacter pylori indicate that bacterial infection could also upregulate the expression of IL-8. The fact that high production of IL-8 is tightly associated with tumor cell proliferation, angiogenesis, and metastasis suggests that IL-8 plays a key role in *H. pylori*-associated gastric cancer [118–121].

16.4.5 CCL20

CCL20 is a member of CC chemokine subfamily and acts as a potent chemotaxin of immature dendritic cells, B lymphocytes, and T lymphocytes [122]. The main characteristic of CCL20 is to recruit immune cells to the site of inflammation, and in turn it is also involved in host immune response and tumorigenesis, such as breast adenocarcinoma, hepatocellular carcinoma, and pancreatic cancer [123-125]. Many reports have indicated that CCL20 is connected with pathogen-related tumorigenesis. For instance, in the EBV-positive Burkitt lymphoma (BL) cells or EBV-negative cells overexpressing LMP-1, the production of CCL20 is highly upregulated, indicating viral oncoprotein LMP-1 is involved in inducing chemokine CCL20 [126]. In addition, CCL20 is also upregulated by another EBV latent antigen called EBNA1 [127]. Further studies showed that high-level CCL20 could recruit Treg and is capable of inhibiting CD4⁺ and CD8⁺ T cells [127, 128]. By which, EBV-infected cells can inhibit host immune response and may promote tumorigenesis. Similarly, overexpressions of CCL20 and its receptor CCR6 are also observed in both KSHVpositive cells and HTLV-1-infected cells, which may drive virus-infected cells to migrate in an autocrine or paracrine manner. In contrast, high-risk HPVs were also found to escape immune response by downregulating CCL20 through E6 and E7 proteins [129].

16.5 Remarks and Perspectives

It is well known that metabolic stress within solid tumors is characterized by hypoxia, nutrient deprivation, oxidative stress, and lactic acidosis as a hostile microenvironment for the survival of cancer cells. Nonetheless, these adverse microenvironments have been successfully exploited by cancer cells and have been converted as driving force in the initiation and progression of cancer. The same cases have been extended to the mechanism by which oncogenic pathogen utilized to involve in carcinogenesis. Here, we have summarized the potential roles of metabolic stress like hypoxia, glucose starvation, and ROS accumulation in promoting viral oncoprotein-induced adaptive signaling change and oncogenesis. Among these, extracellular lactic acidosis has also been confirmed as a potent metabolic stress that plays a multiple role in promoting cancer progression. However, rare information was reported about the interaction between oncogenic pathogens and lactic acidosis stress. In addition, the consequence of the interplay between oncogenic pathogen and metabolic stress microenvironment is complicated and elusive. For examples, although the metabolic stress environment could drive tolerance change of cancer cells, the adaptive response strategies exploited by virus may not stable but adjust to the severity and duration of metabolic stress. On ther other hand, the metabolic stress factors are not isolated but cross talked, which may imply a cooperative or opposed effect of these selective stress on the same viral-mediated adaptive signaling pathway. Thus, a dynamic and comprehensive perspective in understanding oncogenesis mechanism induced by microenvironment abnormalities and oncogenic pathogen interaction will facilitate the development of a precise pathogen-specific therapeutic strategy.

Cytokines and chemokines are crucial factors that benefit not only hosts but also viruses. For hosts, cytokines and chemokines play a key role in regulating immune system, in order to limit and eliminate harmful pathogens. In contrast, for pathogens, many of them would adopt various mechanisms to evade host immune response by manipulating cytokines and chemokines. Moreover, many pathogens, in particular oncogenic viruses, even utilize cytokines and chemokines to promote persistent infection, even tumorigenesis [60]. In recent years, increasing evidence demonstrates the strong relationship between pathogens and carcinoma, and more and more cytokines and chemokines are proved to participate in pathogen-associated tumorigenesis, whereas the potential related to underlying mechanisms remains to be fully understood. As research exploited, more knowledge about virus-mediated tumorigenesis by manipulating cytokines and chemokines will be unveiled, and this knowledge could potentially be utilized to design therapies to defeat pathogen-related malignancies.

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