

Viruses Associated with Human Cancer

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1 Abstract

2 It is estimated that viral infections contribute to 15-20% of all human cancers. As 3 obligatory intracellular parasites, viruses encode proteins that reprogram host cellular signaling 4 pathways that control proliferation, differentiation, cell death, genomic integrity, and recognition 5 by the immune system. These cellular processes are governed by complex and redundant 6 regulatory networks and are surveyed by sentinel mechanisms that ensure that aberrant cells 7 are removed from the proliferative pool. Given that the genome size of a virus is highly 8 restricted to ensure packaging within an infectious structure, viruses must target cellular 9 regulatory nodes with limited redundancy and need to inactivate surveillance mechanisms that 10 would normally recognize and extinguish such abnormal cells. In many cases, key proteins in 11 these same regulatory networks are subject to mutation in non-virally associated diseases and 12 cancers. Oncogenic viruses have thus served as important experimental models to identify and 13 molecularly investigate such cellular networks. These include the discovery of oncogenes and 14 tumor suppressors, identification of regulatory networks that are critical for maintenance of 15 genomic integrity, and processes that govern immune surveillance.

1 **1.** Introduction

2 With 10.9 million new cases and 6.7 million deaths per year, cancer is a devastating 3 disease, presenting an immense disease burden to affected individuals and their families as 4 well as health care systems [1]. Development of treatment and prevention strategies to manage 5 this disease critically depends on our understanding of cancer cells and the mechanism(s) 6 through which they arise. In general terms, carcinogenesis represents a complex, multi-step 7 process. During the past 30 years it has become exceedingly apparent that several viruses play 8 significant roles in the multistage development of human neoplasms; in fact, approximately 15% 9 to 20% of cancers are associated with viral infections [2, 3]. Oncogenic viruses can contribute 10 to different steps of the carcinogenic process, and the association of a virus with a given cancer 11 can be anywhere from 15% to 100% [3]. In addition to elucidating the etiology of several human 12 cancers, the study of oncogenic viruses has been invaluable to the discovery and analysis of 13 key cellular pathways that are commonly rendered dysfunctional during carcinogenesis in 14 general.

15

16 **2. Historic Context**

17 The belief in the infectious nature of cancer originated in classical times as evidenced by 18 accounts of "cancer houses" in which many dwellers developed a certain cancer. Observations 19 that married couples sometimes could be affected by similar cancer types and that cancer 20 appeared to be transmitted from mother to child lent further support to an infectious etiology of tumors. However, during the 19th century, extensive investigations failed to demonstrate a 21 22 carcinogenic role for bacteria, fungi, or parasites leading to the belief that cancer is not caused 23 by an infectious agent. Despite the prevailing dogma, a small number of researchers 24 hypothesized that the failure to detect an infectious cause of cancer did not necessarily mean 25 that the general idea of the infectious nature of cancer was invalid. Rather, they hypothesized

1 that the causal organism had merely not yet been found and that smaller entities not detectable 2 by standard microscopy may indeed be the culprits. Despite increasing evidence to suggest 3 that infectious entities of sub-microscopic size may be associated with cancer, acceptance of 4 this hypothesis took many years. M'Fadyan and Hobday described the cell-free transmission of 5 oral dog warts with cell free extracts in 1898 [4], and Ciuffo published similar transmission 6 studies with human warts in 1907 [5]. The significance of these findings was not fully 7 appreciated since warts are benign hyperplasias and not malignant tumors. In 1908, Ellermann 8 and Bang demonstrated that leukemia in birds could be transmitted from animal to animal via 9 extracts of leukemic cells or serum from diseased birds [6]. However, at the time it was not 10 realized that this was the first successful transmission of a naturally occurring tumor, as 11 leukemia was not yet accepted as a cancer. In 1911, Peyton Rous produced solid tumors in 12 chickens using cell-free extracts from a transplantable sarcoma [7]. This study was also met 13 with considerable skepticism due to the fact that infectious cancers of birds were not considered 14 valid models for human cancers. In fact, the importance of this study was not fully appreciated 15 until the finding that murine leukemias could be induced by viruses [8, 9]. Over the next two 16 decades numerous additional animal oncogenic viruses were isolated, Rous was awarded the 17 Noble Prize for his pioneering work in 1966, and the importance of the early work on animal 18 tumor viruses was finally recognized. In fact, the enthusiasm for these findings contributed in no 19 small part to President Nixon signing the National Cancer Act into law in 1971 and declaring the 20 "War on Cancer".

After the successes of the animal tumor virus field, scientists began the search for human tumor viruses. However, initial attempts to isolate transmissible carcinogenic viruses from human tumors proved disappointing, once again raising doubts about the existence of human cancer viruses. The discovery of Epstein-Barr virus (EBV) by electron microscopy (EM) in cells cultured from Burkitt's lymphoma (BL) in 1964 [10] and the discovery of hepatitis B virus (HBV) in human sera positive for hepatitis B surface antigen in 1970 [11], together with the

1 development of animal and cell culture model systems, resulted in a renewed interest in the 2 roles of viruses in human cancer. The search for additional human tumor viruses continued, 3 and, despite several setbacks, the ultimate acknowledgment of the causal relationship between 4 viruses and human cancer occurred during the early 1980s, due in large part to three major 5 discoveries during that time. In 1983 and 1984, human papillomavirus (HPV) 16 and 18 were 6 isolated from human cervical cancer specimens [12, 13]. Additionally, although the link between 7 HBV and liver cancer had been suspected for decades, the results of a large-scale 8 epidemiological study provided a compelling link between persistent HBV infection and liver 9 carcinogenesis [14]. The third major discovery was the isolation of the human T-cell leukemia 10 virus (HTLV-I) from T-cell lymphoma/leukemia patients [15, 16]. Since their initial discovery, 11 associations of these viruses with cancers at other anatomical sites have been discovered. 12 Moreover, new links between viruses, most notably hepatitis C virus (HCV) [17] and human 13 herpes-virus 8 (HHV8)/Kaposi's sarcoma herpesvirus (KSHV) [18], and human cancers have 14 been discovered. Today, viruses are accepted as bona-fide causes of human cancers, and it 15 has been estimated that between 15 and 20% of all human cancers may have a viral etiology [2, 16 3].

17

18 **3.** General Aspects of Viral Carcinogenesis

The infectious nature of oncogenic viruses sets them apart from other carcinogenic agents. As such, a thorough study of both the pathogenesis of viral infection and the host response is crucial to a full understanding of the resulting cancers. Such an understanding, in turn, has increased our knowledge of cellular pathways involved in growth and differentiation and neoplasia as a whole.

Even though human oncogenic viruses belong to different virus families and utilize diverse strategies to contribute to cancer development, they share many common features. One key feature is their ability to infect, but not kill, their host cell. In contrast to many other

1 viruses that cause disease, oncogenic viruses have the tendency to establish long-term 2 persistent infections. Consequently, they have evolved strategies for evading the host immune 3 response, which would otherwise clear the virus during these persistent infections. Despite the 4 viral etiology of several cancers, it appears that the viruses often may contribute to, but are not 5 sufficient for, carcinogenesis; in fact, the majority of tumor virus infected individuals do not 6 develop cancer, and in those patients that do develop cancer many years may pass between 7 initial infection and tumor appearance. Additional co-factors, such as host immunity and chronic 8 inflammation, as well as additional host cellular mutations, must therefore also play an important 9 role in the transformation process. Additionally, there is an obvious geographical distribution of 10 many virus-associated cancers, which is possibly due to either geographical restriction of the 11 virus or access to essential cofactors. Thus, the long-term interactions between virus and host 12 are key features of the oncogenic viruses, as they set the stage for a variety of molecular events 13 that may contribute to eventual virus-mediated tumorigenesis [19].

14

15 4. Criteria for Defining an Etiologic Role for Viruses in Cancer

16 In many cases, viral carcinogenesis is associated with an abortive, non-productive 17 infection. Hence, the original Koch postulate for the infectious etiology of disease [20] cannot 18 be applied, as oftentimes no disease causing infectious entity can be isolated from a tumor. 19 Therefore, it is often difficult to establish a viral cause for a human cancer. As a result, different 20 guidelines have been proposed to aid in establishing a causal relationship between viruses and 21 human cancers (Tables 1 and 2) [21-23]. Although some of the guidelines are difficult to meet 22 and others are not applicable to all viruses, the guidelines are nonetheless guite useful when 23 evaluating a putative association between a virus and a human malignancy.

24

25 **5.** Human Oncogenic Viruses

1 Human tumor viruses belong to a number of virus families, including the RNA virus 2 families Retroviridae and Flaviviridae and the DNA virus families Hepadnaviridae, 3 Herpesviridae, and Papillomaviridae. To date, viruses that are compellingly associated with 4 human malignancies include; (i) HTLV-1 (adult T-cell leukemia (ATL)) [15], (reviewed in [24]); (ii) 5 HPV (cervical cancer, skin cancer in patients with epidermodysplasia verruciformis (EV), head 6 and neck cancers, and other anogenital cancers) [12, 13], (reviewed in [25-28]); iii) HHV-8 7 (Kaposi's sarcoma (KS), primary effusion lymphoma, and Castleman's disease) [18], (reviewed 8 (iv) EBV (Burkitt's Lymphoma (BL), nasopharyngeal carcinoma (NPC), postin [29, 30]) 9 transplant lymphomas, and Hodgkin's disease) [10], (reviewed in [31-33]); and (v) HBV and 10 HCV (hepatocellular carcinoma (HCC)) [11, 17], (reviewed in [34-38]). Viruses with potential 11 roles in human malignancies include; (i) simian vacuolating virus 40 (SV40) (brain cancer, bone 12 cancer, and mesothelioma) [39]; (ii) BK virus (BKV) (prostate cancer) [40], (reviewed in [41]); (iii) 13 JC virus (JCV) (brain cancer) [42], (reviewed in [41]); (iv) human endogenous retroviruses 14 (HERVs) (germ cell tumors, breast cancer, ovarian cancer, and melanoma) [43, 44]; (v) human 15 mammary tumor virus (HMTV) (breast cancer) (reviewed in [45]; and (vi) Torque teno virus 16 (TTV) (gastrointestinal cancer, lung cancer, breast cancer, and myeloma) [46]. General 17 information about viruses with known and potential associations with human cancer is provided in Tables 3 and 4, respectively. Studies of the RNA and DNA tumor viruses has led to the 18 19 discovery of oncogenes and tumor suppressors and has greatly added to our understanding of 20 the etiology of carcinogenesis, both virally and non-virally induced.

- 21
- 22 5.1. RNA Tumor Viruses

Although retroviruses have been associated with many animal tumors, to date, only one human retrovirus, HTLV-1, has been associated with human cancers. The biology of HTLV-1 will be discussed in more detail in the next section. Studies with animal retroviruses have been

instrumental establishing the concept of oncogenic viruses and led to the discovery of
 oncogenes and tumor suppressors as well as other key regulators of cellular signal transduction
 pathways. Hence, animal retroviruses warrant some discussion in this review.

4 The advent of modern tumor virology came about with the development of an in vitro 5 transformation assay for Rous Sarcoma Virus (RSV) [47]. This assay allowed for the genetic 6 analysis of the retroviral life cycle and retrovirus-induced transformation in cell culture (reviewed 7 Retroviruses are classified as either simple or complex viruses based on the in [48-52]). 8 organization of their genomes. Shortly after infection, the viral RNA genome is reverse-9 transcribed by the virally encoded reverse transcriptase into a double-stranded DNA copy, 10 which then integrates into the host chromosome and is expressed under the control of viral 11 transcriptional regulatory sequences. Once integrated, proviruses are rarely lost from the host 12 chromosome. As a consequence of integration, and of particular relevance when considering 13 oncogenesis, is the ability of simple retroviruses to acquire and transduce cellular genetic 14 material or to activate or inactivate cellular genes via provirus insertion. It was the analysis of 15 this group, the transducing retroviruses, that led to the finding that the RSV transforming gene, 16 v-src, hybridized to cellular sequences; ultimately this finding led to the discovery of proto-17 oncogenes, a group of cellular genes that mediate viral carcinogenesis and have critical roles in 18 the control of cell growth and differentiation (reviewed in [48-52]). Since this initial discovery, 19 numerous animal retroviruses with oncogenic properties have been discovered, and, as is the 20 case with src, the transduced retroviral oncogenes are derived from cellular sequences and are 21 not necessary for viral replication [50, 52].

The erroneous recombination events that allow for acquisition of host cell derived coding sequences often leave viral genomes mutated and the virus defective for replication. As such, these viruses are dependent on replication competent helper viruses to provide the necessary replication functions in trans. Normal cellular transcriptional and translational controls are lost once an acquired cellular sequence is incorporated into the viral genome, and the over-

1 expression of a proto-oncogene under the control of strong viral promoters can cause malignant 2 transformation. Moreover, since the acquired proto-oncogene is not necessary for viral 3 replication but is replicated through the same error prone mechanisms as the viral genome, 4 retrovirally acquired proto-oncogenes are subject to frequent mutation and some "activating" 5 proto-oncogene mutations endow the infected cell with a growth advantage and hence are 6 selected for over time. Such oncogene transducing retroviruses efficiently transform cells in 7 culture and cause tumors in experimental animals with very short latency periods. However, 8 this mechanism is relatively rarely seen in animals in the wild and has not been documented in 9 humans. Nonetheless, this 'oncogene piracy' has proven to be quite useful in laboratory studies 10 of the actions of oncogenes in cancer. Most remarkably, mutations in cellular oncogenes that 11 arise in human tumors as a consequence of mutagenic insults are often similar or identical to 12 those discovered in transducing carcinogenic retroviruses [53].

13 A second group, the cis-acting retroviruses, does not contain host cell derived 14 sequences but transforms cells by integrating in the vicinity of a cellular proto-oncogene or 15 tumor suppressor. Unlike the transducing retroviruses, the cis-acting retroviruses retain all of 16 their viral genes and thus can replicate without the aid of a helper virus. Cis-acting retroviruses 17 cause malignancy in only a percentage of infected animals after a longer latency period than 18 that required for transducing retroviruses, and they generally do not efficiently transform cells in 19 culture. Insertional mutagenesis is a common mechanism observed for rodent, feline, and avian 20 retroviruses, such as avian leukosis virus and mouse mammary tumor virus (MMTV). Whereas 21 there is no compelling evidence that such a mechanism significantly contributes to human 22 carcinogenesis, cloning of affected genes led to the discovery of numerous oncogenes, such as 23 int-1 [54, 55], int-2 [55], Pim-1 [56], bmi-1 [57], Tpl-1 [58], and Tpl-2 [59], that importantly 24 contribute to the development of human neoplasms. Moreover, the finding that the Friend murine leukemia virus had integrated into both alleles of the p53 gene in an erythroleukemic cell 25

line provided critical evidence that p53 was a tumor suppressor rather than an oncogene as was
 originally suspected [60].

3

4 5.1.1. Human T-Cell Leukemia Virus (HTLV-1)

5 Of more significance to human carcinogenesis, the third mechanism of retroviral 6 oncogenesis does not involve transmission of a mutated version of a cellular proto-oncogene or 7 dysregulated expression of proto-oncogenes or tumor suppressor genes near or at the 8 integration site. The latency period between the initial infection and development of a neoplasm 9 with this group of viruses is often in the range of several years to several decades. The best-10 studied example of these viruses is HTLV-1, the first human retrovirus to be discovered that is 11 clearly associated with a human malignancy [15, 16]. HTLV-1 is delta-type complex retrovirus 12 and is the etiologic agent of ATL and tropical spastic paraparesis/HTLV-1-associated 13 myelopathy (TSP/HAM). HTLV-1 is endemic to Japan, South America, Africa, and the 14 Caribbean [61, 62]. While it is estimated that approximately 20 million people worldwide are infected with HTLV-1 [63], only a small percentage (2-6%) will develop ATL [64]. The long 15 16 clinical latency, together with the relatively low cumulative lifetime risk of a carrier developing 17 ATL, indicates that HTLV-1 infection is not sufficient to elicit T-cell transformation. While the 18 exact cellular events remain unclear, a variety of steps, including virus, host cell, and immune 19 factors, are implicated in the leukemogenesis of ATL [65] (Figure 1).

A number of studies indicate that the multifunctional viral accessory protein Tax is the major transforming protein of HTLV-1 [66-73]. Tax modulates expression of viral genes though the viral long terminal repeats (LTRs), and also dysregulates multiple cellular transcriptional signaling pathways including nuclear factor kappa B (NF- κ B) [74-85], serum responsive factor (SRF) [86-90], cyclic AMP response element-binding protein (CREB) [91-94], and activator protein 1 (AP-1) [95, 96]. Rather than binding to promoter or enhancer sequences directly, Tax

interacts with cellular transcriptional co-activators such as p300/CBP [94, 97-104], and P/CAF [105]. In addition to its role in transcriptional regulation, Tax is also able to functionally inactivate p53 [106, 107], p16^{INK4A} [108, 109], and the mitotic checkpoint protein, Mitotic Arrest Deficient (MAD) 1 [110-112]. Additionally, the C-terminal PDZ domain-binding motif of Tax, which interacts with the tumor suppressor hDLG [113], is important for transformation of rat fibroblasts [114] and inducing interleukin-2-independent growth of mouse T-cells [115].

Unlike other well-established DNA tumor viruses, which generally require continuous 7 8 expression of viral oncoproteins to sustain transformation (reviewed in [116]), tax transcripts are 9 detected in only 40% of ATLs [117], suggesting that Tax may be needed to initiate 10 transformation, but may not be necessary for maintenance of the transformed phenotype. Tax 11 is the main target of the host's cytotoxic T lymphocyte (CTL) response; therefore, the repression 12 of Tax expression allows infected host cells to evade immunesurveillance and allows for the 13 preferential selection of these cells during the progression of ATL [117]. There are several 14 mechanisms by which ATL cells lose Tax expression, including the loss of the viral promoter for 15 tax transcription, the 5'-LTR [117], mutation of the tax gene [118], and epigenetic changes in the 16 5'-LTR [119, 120].

Tax has also been implicated in inducing genomic instability, most prominently 17 18 aneuploidy, which, as is the case in many cancers, is a hallmark of ATL [112]. Recent studies 19 have shown that HTLV-1 Tax expression causes multipolar mitoses, from which aneuploidy can 20 arise, in two ways [121-123]. First, Tax targets the cellular TAX1BP2 protein, which normally 21 blocks centriole replication, thus causing numerical centrosome aberrations [121]. Second, it 22 has been proposed that Tax engages RANBP1 during mitosis and fragments spindle poles, 23 thereby provoking multipolar, asymmetrical chromosome segregation. Together, these 24 mechanisms help explain the long-standing observations of an uploidy and multipolar spindles in ATL cells ("flower cells") [124]. In addition, several ATL cell lines have been demonstrated to 25 26 lack an intact mitotic spindle assembly checkpoint [112], which may be related to binding to

1 MAD1 [110, 111]. Evidence that Tax may act as a mitotic mutator gene, greatly increasing the 2 incidence of mitotic abnormalities, is consistent with reports that Tax binds to and activates the 3 anaphase-promoting complex/cyclosome (APC/C), thereby promoting premature securin 4 degradation and mitotic exit, thus contributing to aneuploidy [125-127]. However, this concept is 5 not fully accepted as a recent study found that Tax did not increase securin degradation [128].

6 As mentioned previously, alterations of the 5'-LTR, such as deletions or 7 hypermethylation, are common in ATL cells. As a result, the transcription of viral genes 8 encoded on the plus strand is often repressed. On the other hand, the 3'-LTR is conserved and 9 hypomethylated in all ATLs [120]. The HBZ mRNA is transcribed from the 3'-LTR [129, 130] 10 and is expressed in all ATL cells [131]. Suppression of HBZ gene transcription inhibits the 11 proliferation of ATL cells; additionally HBZ gene expression promotes the proliferation of a 12 human T-cell line [131]. It appears that HBZ may have a bimodal function at the mRNA and protein levels, as the RNA form of HBZ supports T cell proliferation through regulation of the 13 14 E2F1 pathway, whereas HBZ protein suppresses Tax-mediated viral transcription through the 15 5'-LTR [129].

16

17 5.1.2. Hepatitis C Virus (HCV)

HCV is the etiologic agent of posttransfusion and sporadic non-A, non-B hepatitis [17] 18 19 and infects approximately 2% of the population worldwide, although the prevalence of HCV 20 infection varies by geographical location [132]. Persistent infection with HCV is associated with 21 hepatitis, hepatic steatosis, cirrhosis, and hepatocellular carcinoma (HCC) [133-137]. HCV is a 22 single stranded RNA virus of the Hepacivirus genus in the Flaviviridae family and is the only 23 positive-stranded RNA virus among the human oncogenic viruses. Its approximately 9.6 kb 24 genome contains an open reading frame (ORF) that codes for a 3000 amino acid residue 25 polyprotein precursor [17] that is cleaved by cellular and viral proteases into three structural

proteins (core, E1, E2) and seven nonstructural proteins (p7, NS2, NS3, NS4a, NS4B, NS5A,
 and NS5B) [138].

3 In the vast majority of infected individuals, HCV establishes a persistent and life-long 4 infection via highly effective viral immune evasion strategies [139-143]. The formation of double 5 stranded RNA (dsRNA) intermediates during HCV genome replication induces cellular dsRNA-6 sensing machinery, which in turn leads to the activation of proteins involved in antiviral 7 response, including interferons (IFNs), interferon regulatory factors (IRFs), signal transducers 8 and activators of transcription (STATs), interferon stimulated genes (ISGs) and NF-kB [144]. 9 The HCV core, E2, NS3, and NS5A proteins counteract this cellular response through a variety 10 of mechanisms, including NS5A and E2 mediated suppression of dsRNA-activated kinase PKR 11 [139, 142]. HCV is also very effective in subverting T-cell mediated adaptive immunity [140, 12 141]. Although the underlying mechanisms are still unclear, it is believed that the persistence of 13 HCV infection is due in part to the selection of quasispecies that have escaped the host immune 14 response [139].

Infection with HCV causes active inflammation and fibrosis, which can progress to 15 16 cirrhosis and ultimately lead to tumor development. Numerous co-factors for the development 17 of HCV-associated HCC exist, including co-infection with HBV and excessive alcohol 18 consumption [145]. While it is currently thought that chronic inflammation and cirrhosis play key 19 roles in HCV-induced carcinogenesis, the exact underlying mechanisms are not fully understood 20 [146]. Moreover, the multiple functions of HCV proteins and their impact on cell signaling have 21 led to the idea that both viral and host factors also play a role in HCC. Core, NS3, NS4B, and 22 NS5A have each been shown to be transforming in murine fibroblasts [147] and transgenic mice 23 expressing HCV core protein develop HCC [148, 149]. In addition, HCV proteins have also 24 been reported to activate cellular oncoproteins and inactivate tumor suppressors, such as p53 25 [150], CREB2/LZIP [151], and the retinoblastoma protein (pRB) [152]. Finally, HCV causes

- genome instability, suggesting that certain HCV proteins may have a mutator function [153]. A
 summary of the role of HCV in hepatocellular carcinogenesis is depicted on Figure 2.
- 3

4 5.2. DNA Tumor Viruses

5 The human DNA tumor viruses are a diverse group with varied structures, genome 6 organizations, and replication strategies. Certain DNA tumor viruses, such as HPV, EBV, HBV, 7 and KSHV, cause malignancies in their natural hosts, whereas other DNA tumor viruses, such 8 as human adenoviruses, can transform cultured cells and only cause tumors in heterologous 9 animal models. Unlike oncogenes encoded by animal retroviruses, DNA tumor virus oncogenes 10 are of viral, not cellular, origin and are necessary for replication of the virus (reviewed in [154]). 11 In addition to elucidating the etiology of several human diseases, analysis of the DNA tumor 12 virus oncoproteins has revealed mechanisms controlling mammalian cell growth, ultimately 13 leading to the discovery of cellular tumor suppressor genes.

14 Studies on the small DNA tumor viruses, which include the adenoviruses, 15 polyomaviruses, and papillomaviruses, have been instrumental in elucidating the underlying 16 molecular mechanisms of virus-induced cell transformation. Although these viruses are 17 evolutionarily distinct, the striking similarities in their transforming functions emphasize the 18 mutual need of these viruses to utilize the host cell's replication machinery for efficient viral 19 replication. Much of the understanding of the actions of the small DNA tumor virus oncoproteins 20 has been derived from the study of the physical associations of the viral oncoproteins with a 21 variety of cellular tumor suppressors, most notably the associations of adenovirus E1A (Ad 22 E1A), SV40 large T antigen (TAg) and HPV E7 with the pRB family and adenovirus E1B (Ad 23 E1B), SV40 TAg, and HPV E6 with p53 (reviewed in [27, 155, 156]).

The first major cellular tumor suppressor that was found to be targeted by small DNA tumor virus oncoproteins is pRB, which was identified as the 105 kDa protein associated with Ad E1A in adenovirus-transformed cells [157, 158], and has subsequently been identified as a

1 cellular target for SV40 Tag [159] and HPV16 E7 [160]. The binding of Ad E1A, SV40 TAg, or HPV E7 to pRB results in the disruption or alteration of cellular complexes that normally contain 2 3 pRB, resulting in inactivation of growth regulatory functions [161-164]. Cells expressing E1A, 4 SV40 TAg, or HPV E7 display increased levels of free E2F with associated loss of cell-cycle 5 dependent regulation of E2F responsive genes [165, 166]. E2F responsive genes play key 6 roles in cell cycle progression, and thus the association of small DNA tumor virus oncoproteins 7 with pRB ultimately results in S-phase induction, an essential aspect of these viruses' life 8 cycles. Despite the fact that the core pRB binding sites of SV40 TAg, HPV E7, and Ad E1A are 9 similar, the functional consequences of viral oncoprotein association are different. Whereas Ad E1A inactivates pRB by binding both hypo- and hyper- phosphorylated forms [163], SV40 TAg 10 11 specifically interacts with G1-specific, growth suppressive hypophosphorylated form [167] and 12 HPV16 E7 preferentially binds hypophosphorylated pRB [168, 169] and targets pRB for 13 proteasome mediated degradation [170-172]. The second major cellular tumor suppressor that 14 is targeted by small DNA tumor virus oncoproteins is p53, which was originally detected as a 15 cellular protein complexed with SV40 TAg in SV40-transformed cells [173, 174], and has since 16 been shown to also complex with high-risk HPV E6 and Ad E1B [175, 176]. The p53 protein was initially classified as an oncogene because it was cloned from a cancer cell line and contained a 17 18 point mutation, and it was only later discovered that the wild type form has tumor suppressor 19 activity [177, 178].

The interaction between SV40 TAg, HPV E6, and Ad E1B with p53 results in the inhibition of p53's tumor suppressor activities [179-181]. p53 is a sequence specific, DNA binding transcriptional activator [182, 183]. It is not required for normal cellular proliferation, but rather integrates signal transduction pathways that sense cellular stress, and thus has been referred to as a "guardian of the genome" [184]. Unlike the case with SV40 TAg, HPV E7, and Ad E1A, there is no structural similarity between SV40 TAg, HPV E6, and Ad E1B; this lack of structural similarity is reflected in the differences between their interactions with p53. The

metabolic half-life of p53 is extended in cells that express SV40 TAg or Ad E1B; consequently
p53 levels are higher in these cells than in normal cells [185, 186]. On the other hand, p53
levels in high-risk HPV E6 expressing cells are lower than in their normal counterparts [187, 188], due to induction of p53 degradation through ubiquitin-mediated proteolysis [189].

5

6 5.2.1. Human Papillomavirus (HPV)

Papillomaviruses (PVs) are a group of small, non-enveloped, double-stranded DNA viruses that constitute the Papillomaviridae family. These viruses infect squamous epithelia of a variety of species [190]; to date, approximately 200 human papillomavirus (HPV) types have been described [191]. HPVs cause a range of epithelial hyperplastic lesions and can be classified into two groups: mucosal and cutaneous. These groups can be further divided into low- and high-risk, depending on the associated lesion's propensity for malignant progression.

The cutaneous HPVs 5 and 8 may be considered high-risk, as they are associated with 13 14 a rare, genetically determined skin disease, epidermodysplasia verruciformis (EV). These 15 lesions can progress to skin cancers particularly in sun-exposed areas of the body. Skin cancer 16 in EV patients was the first HPV cancer type that was associated with HPV infections [192-196]; 17 More recent studies have revealed that HPV5 and 8 as well as related cutaneous HPVs may 18 contribute to the development of non-melanoma skin cancers (NMSC), particularly in 19 immunecompromised patients [197, 198]. Infections with cutaneous HPVs appear extremely 20 frequently in the general population and some of these viruses, even the presumed high-risk 21 HPV5, may be part of the normal "flora" of the skin as they can be detected in follicles of 22 plucked hair [199, 200]. The mechanistic contributions of cutaneous HPVs and their interplay 23 with other co-factors that may result in NMSC development remains the subject of intense study 24 (reviewed in [201]). It has been shown that E6 proteins of cutaneous HPVs can target the 25 proapoptotic Bcl-2 family member, Bak, for degradation. Bak plays an important role in signaling 26 apoptosis in response the UV irradiation and hence it has been postulated that cutaneous HPV

1 expressing cells may be less prone to undergo apoptosis after UV induced DNA damage [202]. 2 This may lead to survival and expansion of HPV containing cells with extensive genomic 3 aberrations, which may contribute to transformation. Some cutaneous HPVs exhibit bona fide 4 transforming activities in cultured cells [203-206]. Moreover, skin hyperplasia and skin tumors 5 develop in transgenic mice that express early region genes of cutaneous HPVs [207, 208]. HPV 6 genomes are often found in only a subset of the cancer cells suggesting that either cutaneous 7 HPVs may contribute to initiation of carcinogenesis but are not be required for maintenance of 8 the transformed phenotype, or that they contribute to transformation through non cell 9 autonomous mechanisms (reviewed in [201]).

10 The concept of low-risk and high-risk HPVs has been most clearly established with the 11 mucosal HPVs. The low-risk mucosal HPVs, such as HPV6 and 11, cause genital warts, 12 whereas the high-risk mucosal HPVs, such as HPV16 and 18, cause squamous intraepithelial 13 lesions that can progress to invasive squamous cell carcinoma. HPV is also associated with 14 oral and other anogenital malignancies, however, it is most commonly associated with cervical 15 cancer; in fact, over 99% of all cervical cancers are associated with high-risk HPV infections. 16 Both epidemiological and molecular evidence strongly supports the link between infection with high-risk HPVs and the development of cervical cancer. 17 Nonetheless, the incidence of 18 malignant progression of high-risk HPV associated lesions is relatively low; malignant 19 progression usually occurs with other risk factors, such as decreased immune function, and/or 20 after a long latency period after other genomic alterations in the host cell DNA have occurred. 21 Smoking and prolonged use of birth control pills have also been implicated as risk factors for 22 progression (reviewed in [209]). Maybe most intriguing, Fanconi anemia (FA) patients often 23 develop squamous cell carcinomas at anatomical sites that are susceptible to HPV infections. It 24 has been reported that oral carcinomas in FA patients are more frequently HPV positive than in the general population [210]. Hence, certain aberrations in the FA pathway may predispose to 25 26 malignant progression of HPV associated lesions. Interestingly, the ability of HPV E7 to induce

genomic instability is increased in FA derived cells, thus providing a potential mechanistic
 rationalization for these findings [211]. The molecular mechanisms by which high-risk HPV
 causes cervical cancer have been studied extensively, and numerous viral and host interactions
 that may contribute to transformation and malignancy have been described (reviewed in [27]).

5 During carcinogenic progression the HPV genome frequently integrates into a host cell 6 chromosome and, as a result, the viral oncoproteins, E6 and E7, are the only viral proteins that 7 are consistently expressed in HPV positive cervical carcinomas. Viral genome integration is a 8 terminal event for the viral life cycle and often results in deletion and/or mutation of other viral 9 genes. Most significantly, expression of the transcriptional repressor E2 is often lost during 10 integration. Moreover, the viral E6/E7 genes are expressed from spliced mRNAs that contain 11 cellular sequences which results in increased mRNA stability. Hence, HPV genome integration 12 is often associated with higher, dysregulated E6/E7 expression [212]. Persistent expression of 13 E6 and E7 is necessary for maintenance of the transformed phenotype of cervical carcinoma 14 cells [213, 214]. The expression of high-risk HPV E6 and E7 immortalizes primary human 15 keratinocytes [215, 216], and when grown as organotypic "raft" cultures these cells display 16 histopathological hallmarks of high-grade premalignant lesions [217]. However, these cells remain non-tumorigenic at low passages after immortalization; tumorigenic progression is not 17 18 observed until long-term passaging in vitro or after the transduction of an additional oncogene 19 [218-220]. Moreover, transgenic mice with expression of HPV E6 and E7 require low-dose 20 estrogen for the development of cervical cancer [221]. This situation mimics the progression of 21 high-risk HPV-positive cervical lesions, a process that occurs with a low frequency and requires 22 the acquisition of additional host cellular mutations (reviewed in [222]).

HPVs have transforming properties in a number of rodent cell lines, and the transforming potential correlates with their clinical classification as high-risk and low-risk. Mutational analyses have revealed that E7 encodes the major transforming function [223-226], while E6 does not score as a major transforming activity in most assays. High-risk HPV E7 also scores

in the classical oncogene cooperation assay in baby rat kidney cells [223, 227], whereas E6 can
cooperate with ras in baby mouse kidney cells [228]. High-risk HPVs can extend the life span of
primary human genital epithelial cells, and E6 and E7 are necessary and sufficient for this
activity [226, 229-233]

As mentioned previously, the transforming activities of the high-risk E6 and E7 oncoproteins is related to their ability to associate with and dysregulate cellular regulatory protein complexes, most notably p53 and pRB (reviewed in [155]). As p53 and pRB normally control cellular proliferation, differentiation, and apoptosis, the abrogation of their normal biological activities places such a cell at a risk of malignant progression.

In addition, high-risk HPV E6 and E7 expressing cells have a decreased ability to 10 11 maintain genomic integrity [234]. The high-risk HPV E7 oncoprotein acts as a mitotic mutator 12 and induces multiple forms of mitotic abnormalities, including anaphase bridges, unaligned or 13 lagging chromosomes, and most notably multipolar mitoses [235]. Multipolar mitoses are 14 histopathological hallmarks of high-risk HPV associated cervical lesions and cancer [236] and 15 are caused by the ability of high-risk HPV to uncouple centrosome duplication from the cell 16 division cycle [237, 238]. Hence, HPV E6/E7 oncoproteins mechanistically contribute to 17 initiation and progression of cervical cancer (Figure 3).

18

19 5.2.2. Hepatitis B Virus (HBV)

It is estimated that over 400 million people worldwide are chronic carriers of HBV [239]. The vast majority of infections are asymptomatic, and the non-cytopathic HBV [240] does not cause a significant immune response after the initial infection, presumably at least in part because HBV entry and expansion do not induce the expression of any cellular genes [142, 241]. Nonetheless, HBV is a major etiological factor in the development of HCC, as 15-40% of infected individuals will develop chronic active hepatitis (CAH) which can in turn lead to cirrhosis, liver failure, or HCC [242, 243]. This development is accelerated by the exposure to

1 environmental carcinogens including aflatoxin B, cigarette smoke, and alcohol [146]. CAH is 2 characterized by liver cell necrosis, inflammation, and fibrosis, and it is believed that the 3 resulting cirrhosis may eventually lead to HCC due to the fact that the rapid regeneration of 4 hepatocytes following constant necrosis may lead to the accumulation of mutations and the 5 subsequent selection of cells with a carcinogenic phenotype [244]. Indeed, patients with 6 cirrhosis are more likely to develop HCC than patients without cirrhosis [245, 246]. While it 7 appears that both CAH and cirrhosis contribute to the development of liver carcinogenesis, 8 there is also evidence, such as the correlation between serum HBV DNA level and risk of HCC 9 [247], suggesting a direct oncogenic contribution of HBV to the carcinogenic process. Therefore, it appears that the cause of HBV-associated HCC is a combination of HBV encoded 10 11 oncogenic activities along with the synergistic effects of chronic inflammation.

12 HBV has a circular, partially double-stranded, DNA genome with four overlapping open 13 reading frames (ORFs) that encode for the envelope (preS/S), core (preC/C), polymerase, and 14 X proteins [248]. Like retroviruses, the replication of HBV is dependent on reverse transcription; 15 unlike retroviruses, integration of the viral genome into the host chromosome is not necessary 16 for viral replication but does allow for persistence of the viral genome (reviewed in [249]). The 17 integration event precedes tumor development, as the HBV genome is often found integrated in 18 the host chromosome of patients with both CAH and HCC [250, 251]. HBV integration is a 19 dynamic process, as chronic inflammation together with increased proliferation of hepatocytes 20 may result in rearrangements of integrated viral and adjacent cellular sequences [245]. 21 Moreover, the integration event can result in chromosomal deletions and transpositions of viral 22 sequences from one chromosome to another [252, 253]; consequently, HBV integration may 23 result in genomic instability [254, 255] as well as activation of proto-oncogenes [256-260]. 24 However, integration of the HBV genome is not a necessary prerequisite for malignant 25 progression as approximately 20% of patients with HBV-associated HCC do not display 26 evidence of integration [250].

Examination of viral DNA sequences present in HCC has provided insight into additional oncogenic mechanisms of HBV. Sequences encoding the HBV X protein (HBx) and/or truncated envelope PreS2/S viral proteins are expressed in the majority of HCC tumor cells. Additionally, a novel viral hepatitis B spliced protein (HBSP) has been identified in HBV-infected patients [261]. However, the mere expression of such proteins does not confirm their role in HCC development and further studies are necessary to determine their potential contributions to HCC development.

HBx is a 154 amino acid multifunctional regulatory protein that is highly conserved 8 9 among all of the mammalian hepadnaviruses [262], indicating that it likely plays an important 10 role in the viral life cycle. The expression of HBx is maintained throughout all stages of 11 carcinogenesis, including in cells with integrated HBV genomes [263-268]. Studies of HBx in 12 cultured cells and transgenic animals support a role for HBx in transformation and have 13 demonstrated that HBx functions as a regulatory protein for viral replication and, in the case of 14 woodchuck hepatitis virus (WHV), is required for efficient infectivity [269-272]. In addition, in 15 vitro and in vivo studies indicate that HBx plays an important role in the control of cell proliferation and viability [273-275]. The findings from studies of the biological functions of HBX 16 can be summarized as follows: 1) The HBx protein acts on cellular promoters via protein-protein 17 18 interactions and exhibits pleiotropic effects that modulate various cell responses to genotoxic 19 stress, protein degradation, and signaling pathways (reviewed in [276]), ultimately affecting cell 20 proliferation and viability [277, 278]. Specifically, HBx stimulates signal transduction pathways 21 such as MAPK/ERK and can also upregulate the expression of genes such as c-Myc, c-Jun, 22 NF-kB, AP-1, Ap-2, RPB5 subunit of RNA polymerase II, TATA binding protein, and CREB 23 [279]. 2) HBx regulates proteasomal function [280-282]. 3) HBx affects mitochondrial function [283, 284]. 4) HBx protein modulates calcium homeostasis [285, 286]. 5) Expression of HBx 24 25 causes genomic instability [287].

1 In addition to HBx, the HBV genome encodes a second group of regulatory proteins: the 2 PreS2 activators [large surface proteins (LHBs) and truncated middle surface proteins (MHBs^t)] 3 [288-291]. More than one-third of HBV-integrates in HBV related HCC encode functional MHBs^t 4 transactivators [292, 293], supporting the biological significance of PreS2 activators. The PreS2 5 activators are derived from the HBV surface gene ORF, which consists of a single open reading 6 frame divided into three coding regions, preS1, preS2, and S. Large (LHBs; preS1+preS2+S), 7 middle (MHBs; preS2+S), and small (SHBs; S) envelope glycoproteins can be synthesized 8 through alternate translational initiation [288, 290, 291]. The LHBs and MHBs^t display 9 transactivation activities; their transcriptional activator function is based on the cytoplasmic 10 orientation of the PreS2 domain. PreS2 activators upregulate COX-2 and cyclin A and induce 11 cell cycle progression [294]. Consistent with this notion, transgenic mice expressing MHBs^t in 12 the liver displayed increased hepatocyte proliferation rate and an increased occurrence of liver 13 tumors [295].

In addition to sequences encoding for HBx and truncated envelope PreS2/S viral proteins, a novel viral hepatitis B spliced protein (HBSP) has been identified in HBV-infected patients [261]. The spliced HBV RNA encoding for HBSP can be reverse transcribed and encapsidated in defective HBV particles or expressed as HBSP [261]. HBSP induces apoptosis without cell-cycle block in an in vitro tissue culture model, and HBSP antibodies are present in the serum of 45% of chronic hepatitis patients [296]. Moreover, there seems to be a correlation between the presence of HBSP antibodies, viral replication and liver fibrosis [296].

HBV-associated liver carcinogenesis is viewed a multi-factorial process (Figure 4). The integration of the HBV genome into the host chromosome at early stages of clonal tumor expansion has been demonstrated to both affect a variety of cellular genes as well as exert insertional mutagenesis, while chronic liver inflammation confers the accumulation of mutations in the host genome. Additionally, HBV encoded HBx, PreS2 activators, and HBSP may exert oncogenic functions. However, exactly how these viral factors contribute to higher risks of HCC

development remains unclear. Further studies are necessary to reveal the molecular mechanisms underlying HBV-associated HCC development. Moreover, since host genomic background plays a role in the final disease outcome, an evaluation of the genetic factors in both the host and viral genome that cause a predisposition to hepatocarcinogenesis will help elucidate the carcinogenic mechanisms involved in HCC development.

6

7 5.2.3. Epstein-Barr Virus (EBV)

8 EBV is a ubiquitous double-stranded DNA virus of the γ herpesviruses subfamily of the 9 lymphocryptovirus (LCV) genus. Worldwide, more than 95% of the population is infected with EBV [297, 298]; the majority of EBV infections occurs during childhood without causing overt 10 11 symptoms. Post adolescent infection with EBV frequently results in mononucleosis, a self-12 limiting lymphoproliferative disease. EBV infects and replicates in the oral epithelium, and 13 resting B lymphocytes trafficking through the oral pharynx become latently infected. Infected B 14 lymphocytes resemble antigen activated B cells, and EBV gene expression in these cells is 15 limited to a B cell growth program, termed Latency III, that includes LMP1, LMP2a/b, EBNAs -1, 16 -2, -3a-3b, -3c, and -LP, miRNAs, BARTs, and EBERs. These cells are eliminated by a robust 17 immune response to EBNA3 proteins, resulting in Latency I, a reservoir of latently infected 18 resting memory B cells expressing only EBNA1 and LMP2. The differentiation of memory cells 19 to plasma cells results in reactivation of the replication phase of the viral life cycle that includes 20 expression of latency III gene products. In addition, there is likely another amplification step by 21 re-infection of the epithelial cells followed by shedding virus in the saliva to the next host.

All phases of the EBV life cycle are associated with human disease. In immunecompromised individuals, infected cells increase in number and eventually B-cell growth control pathways are activated, inducing transformation and leading to malignancies such as NPC, BL, post-transplant lymphomas, and gastric carcinomas [3]. EBV-associated

1 malignancies follow distinct geographical distributions and occur at particularly high frequency in certain racial groups, indicating that host genetic factors may influence disease risk [299, 300]. 2 3 EBV encodes several viral proteins that have transforming potential, including EBV latent 4 membrane protein 1 and 2 (LMP1 and LMP2) and EBV nuclear antigen 2 and 3 (EBNA2 and 5 EBNA3). LMP1 can transform a variety of cell types, including rodent fibroblasts [301], and is 6 essential for the ability of EBV to immortalize B cells [302]. The multiple transmembrane-7 spanning domains and the carboxyl terminus of LMP1 can interact with several tumor necrosis 8 factor receptor associated factors (TRAFs) [303, 304]; this interaction results in high levels of 9 activity of NF- κ B, Jun, and p38 in LMP1-expressing epithelial and B cells [305-307]. Through 10 NF-kB, LMP1 provides survival signals by inducing Bcl-2 family members, c-FLIP, c-IAPs, and 11 adhesion molecules [308]. LMP1 also upregulates the expression of numerous anti-apoptotic 12 and adhesion genes and activates the expression of IRF-7 [309], matrix metalloproteinase-9 13 (MMP-9) and fibroblast growth factor-2 (FGF-2) [310]. A second viral membrane protein, LMP2, 14 is dispensable for transformation of naïve B cells but is required for transformation of post-15 germinal center B cells. LMP2 interacts with Lyn and Syk to mimic B-cell-receptor (BCR) 16 signaling, including activation of the PI3K/AKT survival pathway [311].

Other viral genes involved in transformation include EBNA2 and EBNA3. EBNA2, one of the first latent proteins to be detected after EBV infection together with EBNA-LP, is a promiscuous transcriptional activator of both cellular and viral genes [312, 313] and is essential for B-cell transformation [314]. EBNA3A, 3B, and 3C are hydrophilic nuclear transcriptional regulators. EBNA3A and EBNA3C are essential for B-cell transformation in vitro, whereas EBNA3B is dispensable [315]. All three EBNA3 proteins can suppress EBNA2-mediated transactivation [316].

An excellent cell culture model system exists for the study of EBV. In vitro infection of human peripheral blood B cells results in the long-term growth of EBV transformed

1 lymphoblastoid cell lines (LCLs). These cell lines express Latency III gene products which co-2 opt cellular pathways to effect cell growth. LMP1 mimics CD40 to activate NF-κB, LMP2 mimics 3 the B cell antigen receptor, and EBNA-2, -LP, -3A, -3B, and -3C mimic activated Notch. These 4 pathways are constitutively active and drive proliferation through a normal cell cycle cascade. 5 Moreover, there are no additional mutations to the RB or p53 pathways. Finally, if EBV signals 6 are removed, the cells stop proliferating; when LMP1 or EBNA2 expression is restored, the cells 7 begin to proliferate again. A summary of the role of EBV in carcinogenesis is depicted on 8 Figure 5.

9

5.2.4. Kaposi's Sarcoma-associated herpesvirus (KSHV)/Human Herpes Virus 8 (HHV8)

12 HHV8, also known as KSHV, is a recently discovered [18] double-stranded human 13 rhadinovirus of the γ -herpesvirus subfamily and, like other γ -herpesviruses, establishes lifelong 14 latency in B cells. KSHV is associated with all forms of KS, primary effusion lymphomas 15 (PELs), and multicentric Castleman's disease (MCD) [18, 317-319]. The neoplastic potential of 16 KSHV, especially in immunecompromised individuals, is well established: epidemiological 17 studies link KSHV to human malignancies [3], KSHV transforms endothelial cells [320], and 18 KSHV encoded transforming genes have been identified. The current model of KSHV-induced 19 malignancy involves a combination of proliferation, survival, and transformation mediated by 20 latently expressed viral proteins together with a paracrine mechanism that is exerted directly or 21 indirectly by the lytically expressed v-cytokines and viral G-protein coupled receptor (vGPCR) 22 (Figure 6). HIV-1 infected individuals are at the highest risk for developing KS. Interestingly, KS 23 lesions and tumors appear to regress in patients who receive Highly Active Antiretroviral 24 Therapy (HAART), suggesting that KSHV gene expression may be insufficient to initiate or 25 maintain transformation [321, 322].

1 KS is an angioproliferative disease involving numerous angiogenic factors, endothelial 2 cell (EC) growth factors, and pro-inflammatory cytokines, including viral factors such as vIL-6, 3 vCCL-1, 2, and 3, and viral G protein-coupled receptor (vGPCR). VEGF is induced by vIL6 and 4 subsequently promotes angiogenesis, and mouse cell lines that stably express vIL-6 and 5 secrete high levels of VEGF and are tumorigenic in nude mice [323]. A notable property of the 6 v-chemokines are their pro-angiogenic activities [324, 325]. Finally, vGPCR may contribute to 7 KSHV-associated neoplasia by inducing and sustaining cell proliferation [326-330].

Latency expressed KSHV proteins that promote cell proliferation and survival and thus may contribute to cellular transformation include the ORF73-71 locus-encoded latency associated antigen (LANA, ORF73), viral cyclin (v-cyclin, ORF72), viral FLICE inhibitory protein (vFLIP, ORF71), viral interferon regulatory factor 1 (vIRF-1), and the Kaposin/K12 gene. LANA stimulates cellular proliferation and survival [331, 332], v-cyclin induces cell cycle progression [333], vFLIP and vIRF3 mediate pro-survival signaling [334, 335], and kaposins induce cytokine expression and cell growth [336].

15 In addition to the viral cytokines, vGPCR, and the five latency genes mentioned, there 16 are two KSHV-encoded constitutive signaling membrane proteins, variable ITAM-containing protein (VIP) and latency associated membrane protein (LAMP), that play a role in KSHV-17 18 associated malignancies. VIP is encoded by the K1 ORF and can transform rodent fibroblasts, 19 which, when injected into nude mice, induce multiple and disseminated tumors [337]. VIP can 20 also functionally substitute for the saimiri transformation protein (STP) of herpesvirus saimiri 21 (HVS) to induce lymphomas in common marmoset monkeys and transgenic animals expressing 22 VIP develop lymphomas and sarcomas [338]. In addition to its direct transforming functions, 23 VIP can induce angiogenic factors and inflammatory cytokines [116]. LAMP, which is encoded 24 by the K15 ORF, exhibits potential mitogenic and survival signaling via Src-family kinases and 25 NF-kB activation and may promote cell survival via interaction with the Bcl-2 related anti-26 apoptotic protein HAX-1 [339].

Finally, KSHV also contains several immune-evasion genes, including MIR1, MIR2, VIRFs, Orf45, and complement control protein homolog (CCPH). The KSHV K3 and K5 proteins, MIR1 and MIR2, downregulate MHC I expression, thus inhibiting viral antigen presentation. The KSHV vIRFs and Orf45 inhibit the host interferon response, while CCPH inhibits complement-mediated lysis of infected cells (reviewed in [327, 340]). Together, these immune evasion proteins ensure life-long viral persistence in the host, and consequently contribute to KSHV-associated pathogenesis.

- 8
- 9

6. Viruses Implicated in Human Cancers

In addition to the above viruses and cancers, there also exist a number of other cancers that may have an infectious etiology. A causal role for these viruses in human malignancies remains to be fully addressed; current knowledge regarding these viruses and their potential role in human cancer will be summarized in the following sections.

14

15 6.1. Polyomaviruses

16 The Polyomaviridae family is a group of non-enveloped, small double-stranded DNA 17 viruses that have been isolated from humans, monkeys, rodents, and birds. The first 18 polyomavirus to be discovered, mouse polyoma virus [9, 341], is one of the most aggressive 19 carcinogenic viruses and causes tumors in almost every tissue (poly-oma) of susceptible mouse 20 strains [342, 343]. Although it does not cause malignancies in humans, mouse polyoma virus 21 has been thoroughly studied and has been instrumental in the establishment of systems for the 22 study of numerous eukaryotic cellular processes [344]. The second polyomavirus discovered, 23 SV40, was isolated as a contaminant of early batches of the polio vaccine, which was produced 24 in African green monkey kidney cells [39]. SV40 naturally infects the rhesus monkey where it 25 establishes a low-level infection and persists in the kidneys without any noticeable affects.

1 SV40 is closely related to two human polyomaviruses, BKV and JCV, which were discovered in 2 1971 from the urine of a renal transplant patient [40] and the brain of a patient with progressive 3 multifocal leukoencephalopathy [42], respectively. Infection with BKV and JCV is widespread in 4 humans and is usually subclinical. However, in immunesuppressed patients, BKV is associated 5 with renal nephropathy [345, 346] and JCV can cause progressive multifocal 6 leukoencephalopathy (PML) [347, 348]. More recently two additional novel putative human 7 polyomaviruses, termed KI and WU, have been isolated [349, 350].

8 SV40, BKV, and JCV can all transform cells in vitro and induce tumors in rodents; 9 additionally, the injection of polyomavirus transformed cells in animal models or the ectopic 10 expression of polyomavirus regulatory proteins in transgenic animals also induces tumors 11 (reviewed in [40, 41, 351]). Together, these findings demonstrate the oncogenic potential of the 12 polyomaviruses. However, the association of these polyomaviruses with human malignancy 13 remains controversial.

14 A number of studies have implicated SV40 in a range of human cancers, including 15 mesothelioma, osteosarcoma, non-Hodgkin lymphoma (NHL), and a variety of childhood brain 16 tumors. On the other hand, other studies have failed to demonstrate an association of SV40 with human cancer, and the question of whether the release of SV40 into the human population 17 18 through the polio vaccine contributed to the development of human cancers remains a 19 contentious issue. Although in the 1950s approximately 100 million people were exposed to 20 SV40 through the polio vaccine in the US alone, there is currently no evidence to suggest that 21 SV40 infection is widespread among the population or that there is an increase in tumor burden 22 among individuals who received the contaminated vaccine. Recently, studies have suggested 23 that flawed detection methods may account for many of the positive correlations of SV40 with 24 human tumors. In summary, the studies performed to date have failed to provide conclusive 25 proof implicating SV40 as a human pathogen [352, 353].

1 Like SV40, a role for BKV and JCV in human tumors has been suggested, however, no 2 conclusive proof exists that either virus directly causes or acts as a cofactor in human cancer. 3 The search for a correlation between BKV and JCV and human cancer is complicated due to 4 the fact that both viruses are ubiquitous in the population. With respect to JCV, there have been 5 reports of JCV variants in a variety of human brain tumors; these studies have not, though, 6 demonstrated any causal effects (reviewed in [354]). There is also correlative data regarding 7 the potential role of BKV in human cancer. BKV persistently infects epithelial cells in the urinary 8 tract, and some studies have linked BK virus infections to prostate cancer [355].

9

10 6.2. Adenoviruses

11 Members of the Adenoviridae family cause lytic and persistent infection in a range of 12 mammalian and avian hosts. In humans, more than 50 different adenovirus serotypes have been described. They can be divided into six species, designated A-F [356]. Generally, 13 clinically inapparent infection with these viruses occurs during early childhood, and tonsillar 14 15 lymphocytes or peripheral blood lymphocytes remain persistently infected [357, 358]. Although 16 certain Ad serotypes are highly transforming in cell culture and in animal models, early studies 17 indicated that these viruses may not associated with human cancers [359-361]. This issue has 18 been recently readdressed, however, and one study reported detection of adenovirus DNA in 19 pediatric brain tumors [362]. However, a possible causal relationship of Ad infection with the 20 pathogenesis of malignant brain tumors still remains unclear.

The transforming and oncogenic potential of adenoviruses has been traditionally ascribed to the E1A and E1B oncoproteins, which are similar to SV40 TAg and high-risk HPV E7/E6 target pRb and p53, respectively. However, more recent studies have suggested that, at least with some serotypes, E4 ORFs may contribute to cellular transformation [363], potentially through a "hit-and-run" mechanism [364]. Hence, the possible contribution of adenovirus infections to some aspects of human tumor development may need to be carefully re-evaluated.

1

2 6.3. Human Endogenous Retroviruses (HERVs)

3 HERVs are sequences within the genome that resemble infectious retroviruses 4 (reviewed in [43, 44, 365]) that result from ancestral exogenous retroviral infections that became 5 incorporated into the germ line DNA. Today, HERVs constitute ~8% of genome [366] and 6 possess a similar genomic organization to exogenous complex retroviruses such as human 7 immunodeficiency virus (HIV) and HTLV. Evolutionary pressure has ensured the inactivation of 8 HERVs, leading to the idea that HERVs are merely "junk DNA". However, recent evidence 9 suggests that some HERVs may have both physiological and pathological roles, including roles 10 in human malignancy.

While the exact role(s) of HERVs has yet to be fully elucidated, some studies have suggested that HERVs might play a role in carcinogenesis. Specifically, some HERVs have been implicated in human malignancy, due mainly to the increased expression of the HERV mRNA [367], functional protein [368], and retrovirus-like particles [369] in certain cancers. HERVs may also be linked to the generation of new promoters [370] or the activation of protooncogenes [371].

17 Current studies focus on the association of HERV-K with a number of cancers, including 18 germ cell tumors, in particular seminomas [368, 372], breast cancer, myeloproliferative disease, 19 ovarian cancer [373], melanoma [374, 375], and prostate cancer [376]. Some seminomas have 20 been reported to express HERV-K proteins and sometimes release defective viral particles 21 [369]. HERV-K proteins Rec and Np9 can bind the promyelocytic leukemia zinc finger (PLZF) 22 protein [377], and hence it has been suggested that HERV-encoded proteins may contribute to 23 the carcinogenic process.

None of these studies, however, provides compelling evidence that HERV-K expression
 contributes to tumorigenesis and it is equally possible that HERV gene expression may merely
 represent a corollary of cell transformation.

1 Recently, it has been discovered that recurrent chromosomal translocations importantly 2 contribute to the development of human solid tumors. Interestingly, some of these translocations 3 result in HERV-K regulatory sequences being placed upstream of the coding sequences of ETS 4 transcription factor family members. Since HERV-K regulatory sequences are androgen 5 responsive, such translocations cause aberrant, androgen-induced expression of these ETS 6 transcription factors [376]. This is an exciting finding as the result of such translocations is 7 conceptually similar to insertional mutagenesis, where retroviruses contribute to carcinogenesis 8 by integrating in the vicinity of cellular proto-oncogenes, thereby causing their aberrant 9 expression.

10

11 6.4. Human Mammary Tumor Virus (HMTV)/Pogo Virus

The idea of the existence of a human breast cancer virus followed Bittner's demonstration that a virus, MMTV, can cause breast cancer in mice [378]. While studies in the last 7 decades have failed to provide compelling evidence proving this model, a possible viral etiology for some breast cancers remains an active and controversial area of research. A number of reports have suggested that an MMTV-related virus, human mammary tumor virus (HMTV), sometimes also referred to as the Pogo virus, may be associated with human breast cancers (reviewed in [45]).

A 660-bp sequence similar to the MMTV env gene was reportedly detected in 38% of American women's breast cancers [379]; subsequent polymerase chain reaction (PCR) amplifications detected other gene segments homologous to MMTV [380]. Moreover, env and LTR HMTV genes have been found inserted into several chromosomes [381], reminiscent of MMTV, which induces oncogenesis via insertional mutagenesis. The entire HMTV genome, which contains hormone response elements, has also been detected in fresh breast cancers [381]; additionally, primary breast cancer cells produce HMTV particles in vitro [382];

additionally, HMTV particles with morphogenic and molecular characteristics similar to MMTV
 were reported in primary breast cancer cells [382]. However, other groups have been unable to
 detect such sequences in breast cancers [383].

Since many HERVs are similar to MMTV, it is not clear whether HMTV represents an infectious entity, and/or if it can be acquired from infected mice as has been suggested by an epidemiological study, which reported that regions where Mus domesticus infestations are prevalent have the highest incidence of human breast cancer [384]. In possible support of an infectious etiology, human MMTV receptor-related proteins have been cloned [385]. Moreover, it has recently been reported that MMTV replicates rapidly and successfully in human breast cancer cells [386].

11 Even if HMTV-like sequences are indeed expressed in some human breast cancers, 12 there is presently no compelling evidence that unambiguously supports a mechanistic 13 contribution of such viruses to breast cancer development.

14

15 6.5. Xenotropic murine leukemia virus-related virus (XMRV)

16 The finding that the familial prostate cancer susceptibility locus Hpc1 is linked to 17 mutations in the structural gene for RNase L [387], an effector in the interferon induced innate 18 viral response [388], led to the suggestion that inherited defects in RNase L might allow for 19 infection with an oncogenic virus, thus leading to the development of PC. Xenotropic murine 20 leukemia virus-related virus (XMRV) is a recently described gamma retrovirus that was 21 discovered using PCR cloned codas from tumors from PC patients with a mutation in RNase L 22 [389]. XMRV protein was detected in the stoma and hematopoetic cells of the prostate tumors, 23 but was not detected in the actual cancer cells [389]. Therefore, it is unclear whether XMRV 24 may be causally associated with prostate cancer. However, it is possible that XMRV may 25 contribute to tumorigenesis through an indirect mechanism.

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2 6.6. Torque teno virus (TTV)

3 Torque teno virus (TTV) is a single-stranded circular DNA virus of the Circoviridae family 4 and was first found in a patient with non-A-E-hepatitis [46]. Since its initial discovery, a large 5 number of TTV types and subtypes that display substantial genomic variation have been 6 described [390-395]. TTV is acquired in early childhood [396, 397] and remains prevalent in 7 adults [391, 398, 399]. Numerous attempts to link TT viruses to pathogenicity, particularly liver 8 diseases, have thus far been unsuccessful [400-402]. However, one study did suggest that a 9 high TTV load may have prognostic significance in HCV-associated liver disease, but the issue 10 of whether high TTV load mediates HCV-associated disease progression remains to be 11 addressed. Another study demonstrated a relatively high prevalence of TTV-related DNA 12 sequences in human cancers, specifically gastrointestinal cancer, lung cancer, breast cancer, 13 and myeloma [403]. No causal relationship between TTV infection and carcinogenesis can be 14 drawn from this study, as normal control tissues were not included.

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16 7. Concluding Remarks/Perspectives

17 The study of virus-associated cancers has provided many critical insights into key 18 mechanisms of carcinogenesis. The initial work that showed that some animal cancers were 19 caused by retroviruses firmly established the concept that cancers can be caused by infectious 20 agents. Analyses of retroviral integration sites and retrovirally transmitted transforming genes 21 yielded a treasure trove of information on oncogenes and tumor suppressors that were later 22 found to be similarly mutated in human malignancies. While there is no firm evidence that 23 human tumors are caused by retroviral transmission of activated oncogenes, these studies, 24 nevertheless, provided much of the foundation of modern oncology.
The main difference between these early studies with transforming animal retroviruses and human tumor viruses is that oncogenes of human tumor viruses are viral genes, rather than mutated versions of cellular genes that were accidentally assimilated during the viral replication cycle. These human tumorvirus oncogenes play central roles in viral life cycles and their oncogenic potential is a manifestation of these activities.

6 Some viruses, most notably the high-risk HPVs, play essential roles in the initiation as 7 well as progression of cancers and continued expression of their viral transforming activities is 8 necessary for the maintenance of the transformed phenotype. This concept is supported by 9 studies that showed that the major targets of the HPV E6 and E7 oncoproteins, the p53 and pRB tumor suppressors, are retained in a dormant, yet functional state, in HPV positive cervical 10 11 cancer cell lines, whereas the pRB and p53 tumor suppressor sustained mutations in HPV 12 negative cervical carcinoma lines [188]. Hence, these proteins are predicted to be excellent 13 targets for therapy. This concept is impressively supported by numerous studies that showed 14 that cervical cancer cell lines that are manipulated to lose E6/E7 oncogene expression promptly 15 undergo growth arrest, senescence, and/or apoptosis and that this is related to reactivation of 16 the p53 and pRB tumor suppressor pathways [213].

Since HPV E6 and E7 lack intrinsic enzymatic activities, the development of E6/E7 specific antivirals is difficult. HPV E6 and E7, like many viral oncoproteins, function by associating with host cellular proteins, including enzymes such as ubiquitin ligases and histone modifying enzymes. It will be important to determine whether targeting such enzymes will have a specific therapeutic benefit [404]. Last, but not least, viral proteins that are consistently expressed in virus-associated tumors are attractive targets for development of therapeutic vaccination strategies.

It will also be interesting to explore whether the alterations in cell signaling networks due to viral oncogene expression renders infected cells uniquely dependent on ("addicted to") specific cellular signal transduction pathways. The concept of synthetic lethality in yeast predicts

that such pathways may be excellent candidates for therapeutic intervention [405]. The availability of genome wide RNAi and cDNA libraries should make such approaches feasible. Given that the pathways targeted by viral oncoproteins are often mutated in non-virus associated cancers, one might predict that such studies may reveal viable therapeutic targets for numerous malignancies.

In some cases, however, the virus may only contribute to one specific step in the 6 7 carcinogenic process and its continued expression may thus not be necessary for the 8 maintenance of the transformed state. This is sometimes referred to as "hit-and-run" 9 carcinogenesis. In these cases, it is very difficult to conclusively demonstrate that the virus 10 indeed did contribute to the development of a given tumor. The relatively recent realization that 11 some viruses encode proteins that subvert genomic stability lends some mechanistic credence 12 to this model (reviewed in [27]). Accordingly, a virus-infected cell would be significantly more 13 promiscuous for accumulation of genetic aberrations that eventually may lead to tumor 14 formation. One might also imagine that viral proteins that alter the histone code may 15 permanently modify the epigenetic imprint of a host cell and the resulting alterations in gene 16 expression may contribute to cellular transformation.

Another possibility is that viral gene expression is only maintained in some tumor cells. This has been observed with some HPV containing non-melanoma skin cancers [201]. While this is consistent with a "hit-and-run" mechanism, it may also indicate that viral oncogene expression might provide a growth promoting activity indirectly through secreted factors that are necessary for optimal tumor growth.

22 Conversely, the mere presence of viral sequences in a given cancer type does not 23 necessarily imply that the virus mechanistically contributes to the genesis of the tumor. It may 24 simply represent the fact that tumor cells represent a particularly fertile ground for viral 25 replication. Tumors often contain a larger population of proliferative cells than the surrounding 26 normal tissue and hence might be particularly permissive for viral replication. In addition, they

often are subject to decreased surveillance by the immune system. Given the availability of new
 tools to discover virus sequences in tumors, this issue will represent a major challenge for the
 future.

Host defense mechanisms play a significant role in modulating viral carcinogenesis.
Their protective role is most clearly illustrated by the fact that Epstein-Barr virus in most cases
establishes life long asymptomatic latency and tumors arise when immunesurveillance of the
host organism is weakened or fails. Similarly, non-melanoma skin cancers associated with
cutaneous HPV infections are a frequent complication in organ transplant patients.

9 However, in other cases the host response to viral infection and/or their cellular 10 consequences significantly contributes to the carcinogenic process. While infection of liver cells 11 with hepatitis viruses does not appear to cause a major immune response to the initial infection 12 it causes extensive inflammation. This causes cell damage and production of genotoxic reactive 13 oxygen species, which in concert with rapid proliferation due to regenerative processes and 14 potentially genomic destabilization due to viral gene expression, may lead to accumulation of 15 mutations that eventually lead to carcinogenic progression.

16 The infectious etiology of certain cancers affords the unique possibility for prophylactic 17 vaccination. Since vaccination with a weakened live virus is not an option for oncogene carrying 18 viruses, it is necessary to develop "subunit vaccines" consisting of immunogenic recombinant 19 viral proteins. Such a vaccine has been developed for HBV and has proven highly efficacious. 20 HBV vaccines are relatively inexpensive; consequently, they are widely used and have had a 21 remarkable public health impact. Prophylactic vaccines to prevent infections with the most 22 abundant low-risk and/or high-risk HPVs (HPV6, HPV11 and/or HPV16, HPV18) are now 23 commercially available. These vaccines consist of recombinant L1 proteins that form virus-like 24 particles (VLPs), which induce a vigorous type-specific immune response and show great promise (reviewed in [406]). Vaccination has to be before the onset of sexual activity and it will 25 26 be important to determine how long the protection will last. However, since HPV-induced

1 cervical carcinogenesis is a slow process, it will be several decades before there will be a 2 noticeable decrease in cervical cancer cases due to vaccination [407]. It will also be important to 3 determine whether other high-risk HPVs that are not targeted by the current vaccine 4 preparations will fill the void and become more abundant in the population. This would require 5 development and inclusion of VLPs corresponding to additional HPV types to the vaccine 6 preparations. Perhaps most significant, these vaccines are extraordinarily expensive to 7 produce. Since most cervical cancer cases and deaths occur in medically underserved patients, 8 it is thus unlikely that the population that would profit the most from a prophylactic approach will 9 gain access to these vaccines in the near future.

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1 Figure Legends

2

- 3 **Figure 1:** Schematic depiction of the major biological activities that contribute to the
- 4 transforming activities of HTLV-1. See text for details.

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Figure 2: Schematic depiction of the major biological activities that contribute to the
transforming activities of HCV. See text for details.

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9 Figure 3: Schematic depiction of the major biological activities that contribute to the
10 transforming activities of high-risk mucosal HPVs. See text for details.

11

12 **Figure 4:** Schematic depiction of the major biological activities that contribute to the 13 transforming activities of HBV. See text for details.

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Figure 5: Schematic depiction of the major biological activities that contribute to the
 transforming activities of EBV. See text for details.

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Figure 6: Schematic depiction of the major biological activities that contribute to the
transforming activities of HHV-8/KSHV. See text for details.

Table 1. Evans and Mueller guidelines [21]

Epidemiologic guidelines

- 1. Geographic distribution of viral infection corresponds with that of the tumor, adjusting for the presence of known cofactors
- 2. Viral markers are higher in case subjects than in matched control subjects
- 3. Viral markers precede tumor development, with a higher incidence of tumors in persons with markers than those without
- 4. Tumor incidence is decreased by viral infection prevention

Virologic guidelines

- 1. Virus can transform cells in vitro
- 2. Viral genome is present in tumor cells, but not in normal cells
- 3. Virus induces the tumor in an experimental animal

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Table 2. Hill criteria for causality [22,23]

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- 1. Strength of association (how often is the virus associated with the tumor?)
- 2. Consistency (has the association been observed repeatedly?)
- 3. Specificity of association (is the virus uniquely associated with the tumor?)
- 4. Temporal relationship (does virus infection precede tumorigenesis?)
- 5. Biologic gradient (is there a dose response with viral load?)
- 6. Biologic plausibility (is it biologically plausible that the virus could cause the tumor?)
- 7. Coherence (does the association make sense with what is known about the tumor?)
- 8. Experimental evidence (is there supporting laboratory data?)

| Virus | Viral Taxonomy | Genome | Cell Tropism | Human Cancers |
|--------|-----------------|--------------------------|--|---|
| EBV | Herpesviridae | dsDNA 172 kb ~90 ORFs | Oropharyngeal epithelial cells, B- cells | BL, NPC, lymphomas |
| HBV | Hepadnoviridae | dsDNA 3.2 kb 4 ORFs | Hepatocytes, white blood cells | HCC |
| HCV | Flaviviridae | dsRNA 9.4 kb 9 ORFs | Hepatocytes | HCC |
| HPV | Papillomavirdae | dsDNA 8 kb 8-10 ORFs | Squamous epithelial cells | Cervical, oral, and anogenital cancer |
| HTLV-1 | Retroviridae | dsRNA 9.0 kb 6 ORFs | T-cells | ATL |
| KSHV | Herpesviridae | dsDNA 165 kb ~90ORFs | B-cells | Kaposi sarcoma, primary effusion lymphoma |

Table 3. Properties of human tumor viruses

ATL, adult T-cell leukemia; BL, Burkitt's lymphoma; EBV, Epstein-Barr virus; HBV, hepatitis B virus; HCC, hepatocellular carcinoma; HCV, hepatitis C virus; HPV, human papillomavirus; HTLV-1, human T-cell leukemia virus; KSHV, Kaposi's sarcoma-associated herpesvirus; NPC, nasopharyngeal carcinoma

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- 2

| Virus | Viral Taxonomy | Genome | Human Cancers | | | |
|-------|----------------|---------------|--|--|--|--|
| BKV | Polyomaviridae | dsDNA ~5.2 kb | Prostate? | | | |
| JCV | Polyomaviridae | dsDNA ~5.2 kb | Brain? | | | |
| SV40 | Polyomaviridae | dsDNA ~5.2 kb | Brain, bone, mesothelioma? | | | |
| HERVs | Retroviridae | dsRNA/DNA? | Seminomas, breast, ovarian, melanoma? | | | |
| HMTV | Retroviridae | dsRNA/DNA? | Breast? | | | |
| TTV | Circoviridae | ssDNA 3.8 kb | Gastrointestinal, lung, breast, and myleoma? | | | |

| Table 4. | Properties | of viruses | implicated | in | human | cancers |
|----------|------------|------------|------------|----|-------|---------|
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BKV, BK virus; HERVs, human endogenous retroviruses; HMTV, human mammary tumor virus; JCV, JC virus; SV40, simian virus 40; TTV, Torque Teno virus

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