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The Role of Polyomaviruses in Human Disease

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Abstract

The human polyomaviruses, BK virus and JC virus, have long been associated with serious diseases including polyomavirus nephropathy and progressive multifocal leukoencephalopathy. Both viruses establish ubiquitous, persistent infections in healthy individuals. Reactivation can occur when the immune system is impaired, leading to disease progression. Recently, the human polyomavirus family has expanded with the identification of three new viruses (KI, WU and Merkel cell polyomavirus), all of which may prove to be involved in human disease. This review describes the general aspects of human polyomavirus infections and pathogenicity. Current topics of investigation and future directions in the field are also discussed.

Keywords

polyomavirus; JCV; BKV; PML; polyomavirus nephropathy; KI; WU; MCV

Discovery of Human Polyomaviruses

The first human polyomaviruses, BK virus (BKV) and JC virus (JCV), were coincidentally isolated in 1971 by two independent groups, BKV from the urine of a renal transplant patient who suffered from ureteral stenosis (Gardner et al., 1971) and JCV from the brain tissue of a patient with Hodgkin's lymphoma who developed progressive multifocal leukoencephalopathy (PML) (Padgett et al., 1971). Nearly four decades passed before DNA sequences representing three new members of the human polyomavirus family were discovered. Viral genomes cloned from these sequences have been designated KI polyomavirus (KI), WU polyomavirus (WU), and Merkel cell polyomavirus (MCV). KI and WU were identified from large-scale high-throughput screens of respiratory secretions from patients with respiratory tract infections (Allander et al., 2007; Gaynor et al., 2007), and MCV was identified in Merkel cell carcinomas (MCC) using digital transcriptome subtraction (Feng et al., 2008). The human polyomaviruses have a tradition of nomenclature based on the origin of the isolate: BKV and JCV take their names from the initials of the patients from whom they were isolated, while KI and WU are named after the institutions where they were discovered. Only MCV departs from this convention as it is named after the type of tumor from which it was identified. This review will focus on BKV and JCV, whose roles as human pathogens are best understood.

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General Aspects of Polyomavirus Infection

The human polyomaviruses, as with all polyomaviruses, are composed of small, non-enveloped, icosahedral virions with a supercoiled double-stranded DNA genome (Imperiale and Major, 2007). The virion consists of 72 pentamers of the major capsid protein VP1, with each pentamer associated with a single copy of the minor capsid protein VP2 or VP3 (Liddington et al., 1991; Stehle et al., 1996). The viral genome is associated with cellular histones to form a so-called minichromosome, the structure of which is similar to host chromatin (Meneguzzi et al., 1978; Muller et al., 1978). Polyomaviruses are known to have very restricted host ranges; accordingly, BKV and JCV are only known to productively infect and cause disease in humans.

The genomes of BKV and JCV are divided into three regions: the early coding region, which encodes the large tumor antigen (TAg) and small tumor antigen (tAg); the late coding region, which encodes the viral capsid proteins VP1, VP2 and VP3, and the nonstructural agnoprotein; and the non-coding control region (NCCR), which contains the viral promoters and origin of replication. These viruses also encode auxiliary T antigens that are derived from alternative splicing of the TAg transcript (Bollag et al., 1989; Trowbridge and Frisque, 1995). KI and WU share the most significant homology with BKV and JCV in regards to genome organization and amino acid sequence of predicted viral proteins (Allander et al., 2007; Gaynor et al., 2007). MCV on the other hand is most similar to the African green monkey lymphotropic polyomavirus (LPV) (Feng et al., 2008).

Route of Transmission and Seroconversion

The mode of transmission for BKV and JCV is not yet well defined, however, evidence suggesting respiratory transmission is present in the literature. A study of children with respiratory diseases showed that a high percentage of tonsillar tissues contained nonintegrated forms of BKV DNA (Goudsmit et al., 1982). Similarly, the presence of JCV DNA in B cells and stromal cells of the tonsils and oropharynx supports this hypothesis (Monaco et al., 1998a). Seroconversion for both viruses is widespread and occurs in childhood, with BKV seropositivity reaching 90% in children aged 5 to 9 and JCV seropositivity reaching 50 to 60% after the age of 10 (Knowles, 2006). Potential alternative modes of transmission for these viruses include urino-oral, transplacental, and transmission by blood transfusion, semen and organ transplantation (Bofill-Mas et al., 2001; Bofill-Mas et al., 2000; Hirsch and Steiger, 2003).

Adult seroprevalence for BKV and JCV is very high: more than 90% of the adult population is seropositive for BKV (Knowles et al., 2003), while 50 to 80% of adults have antibodies to JCV (Khalili et al., 2007; Knowles, 2006). Interestingly, the antibody titer against BKV decreases as the age increases, while that of JCV remains relatively unchanged (Knowles, 2006; Knowles et al., 2003). In addition, there is a negative association between the seropositivity of BKV and JCV, with BKV seronegative individuals more likely to be JCV seropositive, suggesting that these two viruses may either be transmitted through different mechanisms or that infection with BKV may provide some protective effects against JCV (Knowles et al., 2003; Taguchi et al., 1982).

Dissemination and Persistence

Primary infections with BKV and JCV are typically subclinical or linked to mild respiratory illness (Goudsmit et al., 1981; Goudsmit et al., 1982), and are followed by viral dissemination to the sites of lifelong persistent infection. The major sites of persistence for both BKV and JCV are the cells of the kidney and urinary tract (Chesters et al., 1983; Heritage et al., 1981). BKV DNA has been found in 30 to 50% of normal kidney tissues, with distribution patterns

of small foci throughout the cortex and medulla, and in 40% of ureters (Monini et al., 1995; Nickeleit et al., 2003). In addition, BKV-specific immunostaining analyses identified epithelial cells of the kidney, ureter and bladder as the predominant cell types that are persistently infected (Shinohara et al., 1993). JCV DNA can be detected in approximately 10 to 50% of normal kidney samples, although at lower levels than BKV DNA (Aoki et al., 1999; Chesters et al., 1983; Grinnell et al., 1983). Numerous reports of JCV DNA in lymphocytes argue for the importance of these cells in persistence and dissemination via circulatory routes (Doerries, 2006; Doerries et al., 2003; Doerries et al., 1994; Monaco et al., 1998b; Monaco et al., 1996; Tornatore et al., 1992). It is not known whether the viruses enter a latent state or maintain a low level of viral gene expression and replication at these sites, although intermittent replication must occur as evidenced by periodic excretion of virus in the urine. Approximately 5% of immunocompetent individuals have BKV viremia while 20 to 30% are actively shedding JCV (Doerries, 2001; Knowles, 2001). In addition, asymptomatic viremia has been observed in approximately 3% of pregnant women during the second and third trimesters (Arthur and Shah, 1989; Chang et al., 1996b; Coleman et al., 1980; Markowitz et al., 1991). How the host innate, humoral, and cellular immune responses control these persistent infections remains unknown.

A variety of other cell types have been reported to contain BKV and JCV sequences, and it has been suggested that infection of these cells may be involved in dissemination or persistence. BKV sequences have been detected at a high frequency in urogenital tissues and fluids including cervix, vulva, prostate, and semen, and a relatively lower frequency in brain tissues, consistent with its urotheliotropic nature (Doerries, 2006; Elsner and Dorries, 1992; Martini et al., 2004; Monini et al., 1996; Monini et al., 1995; Pietropaolo et al., 2003). Moreover, BKV DNA has been found in peripheral blood mononuclear cells and spleen (Chatterjee et al., 2000; Dorries et al., 1994; Pietropaolo et al., 2003), suggesting the involvement of the immune system in BKV spread. Additionally, endothelial cells have been shown to support BKV replication *in vitro*, raising the possibility that BKV may cross the endothelial barrier to disseminate from the periphery to its target organs via blood (Hanssen Rinaldo et al., 2005). There are rare reports of JCV sequence detection in various tissues and cells including the liver, lung, spleen, lymph nodes, and colorectal epithelium (Caldarelli-Stefano et al., 1999; Doerries, 2001; Grinnell et al., 1983; Laghi et al., 1999; Newman and Frisque, 1997; Newman and Frisque, 1999). While JCV reactivation leads primarily to infection of the brain, it is unclear whether normal brain tissue harbors the virus (Doerries, 2001). Many researchers have reported the presence (Caldarelli-Stefano et al., 1999; Elsner and Dorries, 1992; Mori et al., 1992) or absence (Chesters et al., 1983; Quinlivan et al., 1992; Stoner et al., 1988) of JCV sequences in the brains of patients without PML. Overall, however, these studies are small with significant variation in the health conditions of the individuals.

Reactivation during Immunosuppression

Human polyomaviruses cause significant disease primarily in individuals that are immunocompromised, allowing reactivation from the persistent subclinical state to a lytic infection resulting in viremia and viremia, potentially leading to severe or fatal diseases (Table 1).

For BKV, reactivation is most common in bone marrow transplant (BMT) and renal transplant patients, where BKV lytic infection results in hemorrhagic cystitis (HC) and polyomavirus nephropathy (PVN), respectively. In addition, reactivation has been observed in individuals with altered immune conditions including other solid organ transplantations, autoimmune diseases such as systemic lupus erythematosus (SLE), and patients with acquired immunodeficiency syndrome (AIDS) (Chang et al., 1996a; Munoz et al., 2005; Sundsfjord et al., 1999). The levels of BKV viremia correlate with the degree of immunosuppression, indicating that viral replication results from the reactivation of a persistent infection rather than

reinfection (Ahsan and Shah, 2006; Doerries, 2001). In patients with SLE, it has also been suggested that BKV infection might initiate autoimmunity by inducing antibodies against DNA and histones (Rekvig et al., 1997). In the context of HIV infection, BKV viremia has been shown to increase concomitantly with a decrease in CD4+ T cell counts (Gluck et al., 1994; Knowles et al., 1999). Although very rare, BKV has also been linked to meningoencephalitis, retinitis, and lung infection in AIDS patients and individuals undergoing immunosuppression (Bratt et al., 1999; Cubukcu-Dimopulo et al., 2000; Vallbracht et al., 1993).

The most common underlying cause of immunosuppression leading to JCV reactivation is AIDS. Reactivation results in the lytic infection of oligodendrocytes in the brain and the development of PML. Other immune-altering conditions in which cases of PML have been reported include lymphoproliferative diseases such as lymphomas and leukemias, myeloproliferative diseases, transplantation, chemotherapy, multiple sclerosis (MS), and inherited immunodeficiencies (Berger, 2003; Berger and Concha, 1995; Brooks and Walker, 1984). In contrast to observations with BKV, JCV viremia does not correlate with the degree of immunosuppression (Doerries, 2001), indicating the importance of other factors during reactivation.

Polyomavirus-associated Diseases

BK Virus and Polyomavirus Nephropathy

PVN, the most frequent BKV-associated disease after renal transplantation, is a form of acute interstitial nephritis (Nickeleit and Mihatsch, 2006). BKV viremia and viremia due to reactivation are found in up to 80% of renal transplant patients and 10% of patients progress to PVN, resulting in allograft loss 90% of the time (Binet et al., 1999; Bressollette-Bodin et al., 2005; Egli et al., 2007; Hirsch et al., 2002). PVN is characterized by necrosis of proximal tubules and denudation of the basement membrane as a result of BKV lytic infection in kidney epithelial cells (Nickeleit et al., 2003). Recently, the incidence of PVN has been rising with the introduction of new and more potent immunosuppressive regimens (Binet et al., 1999; Mengel et al., 2003; Nickeleit et al., 2000), indicating a relationship between BKV reactivation and the disruption of the immune system. The current standard of diagnosis of PVN includes analysis of renal biopsies using histopathology or immunohistochemistry, either to detect cytopathic changes as a result of injury or lysis of renal tubular epithelial cells, or to detect viral gene expression. In addition, urine cytology is used to detect decoy cells, which are epithelial cells with intranuclear viral inclusion bodies, and PCR to detect viral genomes and quantify viral load in blood or urine samples (Drachenberg et al., 2005; Vats et al., 2006). PCR and urine cytology may be more useful for detecting the early stages of reactivation and PVN (Hirsch et al., 2002; Ramos et al., 2002b), thus allowing for faster diagnosis and intervention, with a consequent increase in graft survival (Drachenberg et al., 2004).

There is no single risk factor associated with the development of PVN. Instead it is thought that what determines susceptibility to BKV reactivation is a combination of contributing factors from the virus, patient, and graft. The overall degree of immunosuppression, and not the particular immunosuppressive drugs employed, is suggested to be the major risk factor for PVN (Bonvoisin et al., 2008). Impairment of the immune system alone, however, is not sufficient for the development of PVN, as the disease manifestation is relatively uncommon in nonrenal solid organ transplant and other immunosuppressed patients (Hirsch, 2005; Pavlakis et al., 2006). Other suggested risk factors include donor seropositivity, specific HLA locus or HLA mismatches, anti-rejection treatment, older age, and male gender (Bohl et al., 2005; Hirsch et al., 2002; Ramos et al., 2002a; Ramos et al., 2002b).

The immune response to BKV during PVN is an active area of investigation. A critical question that arises is what facet of the immune response is important for maintaining control over

infection. The humoral response does not appear to be sufficient to restrict BKV infection, as it is reported that approximately 70% of patients are seropositive for BKV before renal transplantation (Hirsch et al., 2002) and that individuals with detectable anti-BKV antibodies still progress to PVN (Comoli et al., 2006). Instead, it seems that antibodies are more indicative of the viral load in a patient rather than protection against BKV infection, as high levels of antibodies in PVN patients correlate with high levels of viremia and low CD8⁺ T cell responses (Chen et al., 2006). The cell-mediated immune response may be more relevant to disease development: low levels of BKV-specific IFN- γ -producing T cells correlate with progression to PVN, while reconstitution of these cells correlates with resolution of PVN (Binggeli et al., 2007; Chen et al., 2006; Prosser et al., 2008). Moreover, *in vitro* studies have demonstrated that IFN- γ strongly inhibits BKV replication in kidney epithelial cells (Abend et al., 2007). Therefore, it is suspected that the effector functions and cytokines produced by T cells may be a crucial means to control BKV replication and reactivation.

At this time, effective and specific anti-viral treatments for BKV do not exist: the most common initial intervention is to decrease immunosuppression to allow the host immune system to regain control over the infection. This, however, leaves the patients at risk for acute graft rejection and is not effective in all patients. Cidofovir is an antiviral nucleoside analogue which is known to inhibit BKV DNA replication (Bernhoff et al., 2008), but can be nephrotoxic at high doses (Blanckaert and De Vriese, 2006). There are some recent indications, however, that when this drug is used at low doses and in combination with a reduction in immunosuppression, it may be effective against BKV reactivation without causing significant nephrotoxicity (Bjorang et al., 2002; Kadambi et al., 2003; Kuypers et al., 2005). In addition, there has been some limited success with leflunomide, an immunosuppressive drug (Faguer et al., 2007; Josephson et al., 2006; Williams et al., 2005). Other antiviral treatments that have been used in clinical trials include intravenous immunoglobulin (IVIG) and fluoroquinolone antibiotics (Bonvoisin et al., 2008; Rinaldo and Hirsch, 2007; Sener et al., 2006; Sessa et al., 2008). However, more systematic studies are warranted to evaluate the efficacies of these treatments. Finally, retransplantation following nephrectomy, to rapidly clear the viral source, is another therapeutic approach (Funk et al., 2006; Poduval et al., 2002).

BK Virus and Hemorrhagic Cystitis

HC is a serious BKV-associated complication characterized by dysuria and varying degrees of hematuria that affects up to 10% of BMT patients (Dropulic and Jones, 2008). The first association of BKV reactivation with HC was reported in the late 1970s and was further established in the 1980s (Arthur et al., 1985; Hashida et al., 1976; Mininberg et al., 1982). HC is likely due to viral reactivation in the uroepithelium, as BKV virions can be detected in exfoliated epithelial cells (Fogazzi et al., 2001; Hiraoka et al., 1991). Moreover, the level of viruria correlates with the development of HC (Arthur et al., 1986; Bogdanovic et al., 2004). Typically, BKV-associated HC occurs more than 10 days post-transplant (late-onset) and requires medical attention: while not usually life-threatening, HC is associated with significant morbidity (Apperley et al., 1987; Azzi et al., 1999; Bedi et al., 1995; Egli et al., 2007). Urine cytology and PCR detection of viral DNA are the most commonly used methods for diagnosis of BKV-associated HC (Dropulic and Jones, 2008). As with PVN, antivirals such as cidofovir and fluoroquinolone antibiotics are currently being tested for their effectiveness in treating BKV-associated HC (Held et al., 2000; Leung et al., 2005; Savona et al., 2007).

JC Virus and Progressive Multifocal Leukoencephalopathy

PML was originally described in 1958 as a demyelinating disease of the central nervous system (Astrom et al., 1958), and later viral particles were detected by electron microscopy in the brains of patients with PML (Silverman and Rubinstein, 1965; Zurhein and Chou, 1965). It became apparent that JCV infection is the cause of PML, as essentially all brain and

cerebrospinal fluid (CSF) samples from these affected patients have detectable levels of JCV DNA and proteins (Gibson et al., 1993; Grinnell et al., 1983; Stoner et al., 1986; Taoufik et al., 1998). Initially, PML was a fairly rare malady associated with immunosuppressed patients, primarily those with lymphomas and leukemias (Johnson, 1982; Walker, 1985). With the rise of the AIDS epidemic, however, JCV infections resulting in PML have risen dramatically. The majority (55 to 85%) of PML cases occur in patients with AIDS (Berger and Nath, 2001; Major et al., 1992), with only sporadic cases of PML developing without an underlying immune disorder (Brooks and Walker, 1984; Safak and Khalili, 2003). As such, PML is now considered an AIDS-defining illness (Stoner et al., 1986). Approximately 6% of HIV cases have JCV replication in the kidneys and approximately 5% of individuals with HIV develop PML (Berger, 2003; Berger and Concha, 1995; Boldorini et al., 2003; Stoner et al., 1986).

Clinically, PML is characterized by impaired speech and vision, dementia or confusion, and varying degrees of paralysis or akinesia, in conjunction with an immunocompromised state and a lack of increase in intracranial pressure (Berger and Concha, 1995; Brooks and Walker, 1984). The subsequent disease progression is rapid, with clinical symptoms intensifying and death of the patient within 3 to 6 months (Berger et al., 1998). At the cellular level, PML is a cytolytic infection of oligodendrocytes, the myelin producing cells of the brain. Infection results in cell death and development of lesions in the cerebrum, cerebellum and brain stem, particularly along the junction of the gray and white matter (Berger and Major, 1999; Whiteman et al., 1993). Neurons are not affected and astrocytes can be infected nonpermissively, only expressing TAg and not progressing to cell lysis (Aksamit, 1995; Berger and Concha, 1995; Johnson, 1982). In addition, JCV sequences have been detected in other cells within the brain including B cells and mononuclear cells (Hou et al., 2006; Houff et al., 1988; Major et al., 1990; von Einsiedel et al., 2004). Other characteristics of PML include enlarged JCV TAg-expressing oligodendrocytes with nuclear inclusion bodies and crystalline arrays of viral particles, an increasing presence of macrophages, and enlarged, so-called bizarre astrocytes with lobulated, hyperchromatic nuclei (Berger and Nath, 2001; Major et al., 1992). The widespread distribution of brain lesions and the high frequency of JCV-positive peripheral blood cells suggest that lymphocytes can serve as a reservoir and dissemination vehicle (Jensen and Major, 1999; Koralnik et al., 1999b; Major et al., 1992). It is not clear if JCV infection of the brain is a result of *de novo* invasion of the virus or reactivation of a persistent infection (Doerries, 2006; White et al., 1992). PML patients, however, do not have enhanced viremia and renal infection as compared to healthy controls (Arthur and Shah, 1989; Doerries, 2001; Koralnik et al., 1999a).

The underlying cause for the association between JCV-associated PML and HIV/AIDS is not fully understood. Several hypotheses may explain the link between these two virus-associated diseases (Berger, 2003; Berger et al., 2001; Khalili et al., 2006; Seth et al., 2003). First, HIV establishes a state of profound immunosuppression within the host, and specifically, a decrease in JCV-specific CD4⁺ T cells as a result of HIV infection could allow uncontested replication of JCV. More directly, HIV infection may result in breakdown of the blood-brain barrier, allowing entry of JCV-harboring B cells into the brain. Furthermore, production of certain cytokines in response to HIV infection may initiate signaling within the cell that results in activation of the JCV promoter. Finally, there is some evidence that the HIV Tat protein is able to act on JCV promoters *in vitro* and promote gene expression (Chowdhury et al., 1992; Tada et al., 1991). In support of this observation, HIV Tat and JCV VP1 expression have been detected in the same areas of the brain that are affected by PML (Del Valle et al., 2000).

The cell-mediated immune response, in particular T cells, appears to be very important for controlling JCV infections. Studies have shown that patients with higher levels of JCV-specific CD4⁺ and CD8⁺ T cells have prolonged survival (Berger et al., 1998; Gasnault et al., 2003; Koralnik, 2006). Anti-JCV antibody levels do not change during progression of PML and are

not detected in the CSF, arguing against the involvement of the humoral immune response. Early detection and various therapeutic interventions, including chemotherapy, nucleoside analogs, receptor blockers, and interferon-alpha, have not been effective at increasing survival time (Roskopf et al., 2006). Highly active antiretroviral therapy (HAART), however, has improved the survival of patients to approximately 10.5 months post-onset of clinical symptoms (Cinque et al., 2001; Clifford et al., 1999; De Luca et al., 2000).

JC Virus and Multiple Sclerosis

While MS and PML are both diseases resulting in demyelinated lesions of the brain, they are distinguished by the morphologically-distinct bizarre astrocytes, inclusion bodies within the nuclei of oligodendrocytes, and the lack of inflammatory infiltrates, which are characteristic of PML (Khalili et al., 2007). Still, the similarities between these conditions have prompted an investigation of the association of MS with JCV reactivation and PML. There are conflicting reports of JCV DNA and viremia in patients with MS: several studies report a lack of evidence for JCV infection in MS patients (Bogdanovic et al., 1998; Buckle et al., 1992), while others have found JCV DNA sequences in CSF of some MS patients but not in healthy controls (Ferrante et al., 1998; Koralnik et al., 1999a).

Recently, there have been two cases of PML in MS patients treated in the same clinical trial with a combination therapy of natalizumab (Tysabri), an $\alpha_4\beta_1$ integrin inhibitor that prevents T cell trafficking into the brain, and interferon- β -1A (Avonex) (Kleinschmidt-DeMasters and Tyler, 2005; Langer-Gould et al., 2005). A third case of PML was reported in a patient with Crohn's disease who was also treated with natalizumab (Van Assche et al., 2005). These results suggest that restricting T cell entry into the brain allows reactivation of JCV and development of PML. Further examination of patients undergoing therapy with natalizumab indicated no clear association between PML and treatment: out of 3,417 patients treated with natalizumab, only 44 were suspected of having PML and none of these cases were confirmed (Yousry et al., 2006).

Human Polyomaviruses and Cancer

There is no clear association between BKV and JCV and the development of tumors. Various reports have indicated the presence or absence of viral genomic sequences in multiple human cancers. It has been suggested that that BKV is associated with brain tumors, adenocarcinomas, prostate cancers, and bladder carcinomas, and JCV is associated with mesotheliomas, brain tumors, osteosarcomas, and lymphomas. For a more detailed discussion about the association of human polyomaviruses with cancer, refer to the following reviews (Barbanti-Brodano et al., 2006; Khalili et al., 2006; Lee and Langhoff, 2006) and this issue of *Virology*.

KI, WU, MCV, and Human Disease

Since KI and WU were first identified, viral sequences have been confirmed in respiratory specimens worldwide (Abed et al., 2007; Abedi Kiasari et al., 2008; Bialasiewicz et al., 2008; Bialasiewicz et al., 2007; Han et al., 2007; Le et al., 2007; Lin et al., 2008; Neske et al., 2008; Norja et al., 2007; Payungporn et al., 2008), suggesting both viruses are widespread among human populations. Furthermore, available data support a model in which primary infection with KI or WU occurs during childhood (Abedi Kiasari et al., 2008; Bialasiewicz et al., 2007; Gaynor et al., 2007). Despite their clear presence in specimens of patients with respiratory illnesses, the pathogenicity of KI and WU remains speculative. The proposed association of KI and WU with respiratory disease is tenuous because the majority of studies to date have not included specimens from asymptomatic patients. In the three studies that included these control groups, viral sequences were detected at similar frequencies in asymptomatic patients (Abed et al., 2007; Han et al., 2007; Norja et al., 2007). The link between KI and WU infection and respiratory disease is further complicated by the high rates of co-

infection with other respiratory viruses that were observed in these studies (Abedi Kiasari et al., 2008; Allander et al., 2007; Bialasiewicz et al., 2008; Gaynor et al., 2007; Han et al., 2007; Le et al., 2007; Neske et al., 2008). Despite the lack of evidence for KI and WU causing disease, more research is warranted to investigate this possibility, especially considering their similarities to BKV and JCV in nucleotide sequence and potential route of infection.

MCV, the most recently discovered human polyomavirus, has been implicated in the etiology of MCC (Garneski et al., 2008a; zur Hausen, 2008), a rare but aggressive form of skin cancer. Feng *et al.* (2008) identified sequences corresponding to MCV in 8 of 10 MCC tumors, as compared to 5 of 59 control tissues. Viral DNA in 6 of the 8 MCC positive tumors showed a clonal integration pattern. One tumor had similar primary and metastatic integration patterns, suggesting viral integration preceded metastasis. Interestingly, the integrated form of MCV in these tumors is predicted to encode a truncated TAg due to mutations within the second exon of the TAg gene. This truncation would result in the loss of TAg domains required for viral DNA replication and p53 binding but does not affect domains required for inducing cell-cycle progression, suggesting this predicted protein may retain its transformation capability. Subsequent studies have confirmed the presence of MCV sequences in MCC tumors at similar frequencies as the original study (Becker et al., 2008; Foulongne et al., 2008; Garneski et al., 2008b; Kassem et al., 2008). Despite the presence of MCV in significant numbers of Merkel cell tumors, the involvement of this virus in the development of MCC is still uncertain. More studies are required to determine if MCV integration or potential expression of oncogenic viral T antigens contributes to MCC.

Unanswered Questions in Human Polyomavirus Pathogenesis

While we understand much of the molecular biology of human polyomaviruses, basic questions about the viruses themselves and their interactions with the host remain unanswered. First, it is unclear how the viruses spread throughout the population. While it is apparent that BKV and JCV are shed in urine, their detection in tonsillar lymphocytes could be indicative of transmission via the respiratory route. In addition, it is curious that children seroconvert against BKV at an earlier age than against JCV. One of the most important questions is how the viruses persist in healthy individuals. The answer to this question will require more information on the biology of BKV and JCV in the urinary tract as well as a better understanding of the immune components responsible for controlling viral replication. It is not known whether the viruses undergo some low level of ongoing replication, as evidenced by periodic excretion into the urine, or establish a true latent state. It will also be important to determine whether the cells in which BKV and JCV persist are the same as or different from those in which they replicate to cause disease. To pursue studies of the immune responses to these viruses, researchers may have to rely on an animal model using mouse polyomavirus, although the genetic structure of this virus differs significantly from that of the human viruses in that it encodes a different cadre of T antigens. Lastly, the changes in the host that lead to reactivation must be uncovered in more detail. Clearly immunosuppression plays a major role in reactivation, but not all AIDS patients present with PML and not all transplant patients present with PVN, despite being on the same immunosuppressive regimen. The available evidence suggests that these differences are not due to genetic variation in the viruses themselves. Thus, one must invoke polymorphisms in the human population that affect tropism or perhaps the immune response. Rapid advances in genetics may allow the definition of host gene(s) that determine susceptibility to BKV and JCV reactivation.

For the newly discovered polyomaviruses, some very basic questions must be answered. First and foremost, can infectious MCV, WU, and KI particles be isolated and grown in the laboratory? An experimental system for the propagation of these viruses will be essential to understand their biology. It will also be important to determine if these viruses persist in the

urinary tract like JCV and BKV, or if they are only associated with acute infections or cancers. Furthermore, routes of transmission and epidemiology of KI, WU, and MCV will need to be determined. For MCV, it will be interesting to know if there is selection in MCC for variants that express truncated forms of TAg, and if there is anything unique about Merkel cells that makes them susceptible to oncogenesis by this virus. A related question in the polyomavirus field is whether SV40 is a human pathogen. This question is highly controversial and there are contradictory reports in the literature, with some groups finding viral sequences in various human tumors while other groups failed to detect sequences in the same type of tumor (Garcea and Imperiale, 2003). To date, there is no good serological evidence for SV40 in humans (Carter et al., 2003; Shah et al., 2004) although this does not prove that SV40 is not a human pathogen (Vilchez and Butel, 2004). This long-standing controversy needs resolution since a large number of people were exposed to SV40 in contaminated poliovirus vaccines, and it remains possible that the virus could spread from human to human (Stratton et al., 2002). The recent discoveries of new human polyomaviruses certainly raises the question of whether there are additional viruses in the population and has rekindled interest in previously-identified viruses. For example, there is serologic evidence for LPV infection of humans (Brade et al., 1981; Viscidi and Clayman, 2006; R. Garcea, personal communication). Although current virus discovery attempts are mainly aimed at isolating pathogens from sick individuals, it is possible that there are viruses that are not associated with disease but simply persist and spread without clinical symptoms.

Given the increasing incidence of polyomavirus-associated diseases, particularly the severe diseases in immunocompromised individuals, there is a dire need for more effective and specific antivirals. Cidofovir shows some efficacy but can be nephrotoxic, limiting its utility, especially in renal transplant patients. Candidate targets include small molecules that interfere with TAg function or virion assembly, which could be identified using high-throughput screens. One must also consider whether vaccine development is plausible; the success of the human papillomavirus vaccines, along with the fact that polyomavirus virus-like particles are easily produced, is supportive of the possibility of vaccination.

For many years, much effort was focused on SV40 as a model system for understanding basic eukaryotic processes such as transcription, DNA replication, and oncogenic transformation, while studies of the human polyomaviruses and their roles as human pathogens took a back seat. Since polyomaviruses are highly adapted to their own hosts, each virus must be studied and understood as individual entities. Future studies hold great promise for the ability to detect and combat these important and ubiquitous viruses.

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Table 1**Human Polyomaviruses and Disease**

Human Polyomavirus	Date of discovery	Major cell type infected	Associated diseases
BKV	1971 (Gardner <i>et al.</i>)	Kidney epithelium, Urothelium	Hemorrhagic cystitis (HC), Polyomavirus nephropathy (PVN)
JCV	1971 (Padgett <i>et al.</i>)	Kidney epithelium, Lymphocytes, Oligodendrocytes	Progressive multifocal leukoencephalopathy (PML)
KI	2007 (Allander <i>et al.</i>)	?	?
WU	2007 (Gaynor <i>et al.</i>)	?	?
MCV	2008 (Feng <i>et al.</i>)	Merkel cells	Merkel cell carcinoma