DNA viruses and the cellular DNA-damage response

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It is clear that a number of host-cell factors facilitate virus replication and, conversely, a number of other factors possess inherent antiviral activity. Research, particularly over the last decade or so, has revealed that there is a complex inter-relationship between viral infection and the host-cell DNA-damage response and repair pathways. There is now a realization that viruses can selectively activate and/or repress specific components of these host-cell pathways in a temporally coordinated manner, in order to promote virus replication. Thus, some viruses, such as simian virus 40, require active DNA-repair pathways for optimal virus replication, whereas others, such as adenovirus, go to considerable lengths to inactivate some pathways. Although there is ever-increasing molecular insight into how viruses interact with host-cell damage pathways, the precise molecular roles of these pathways in virus life cycles is not well understood. The object of this review is to consider how DNA viruses have evolved to manage the function of three principal DNA damage-response pathways controlled by the three phosphoinositide 3-kinase (PI3K)-related protein kinases ATM, ATR and DNA-PK and to explore further how virus interactions with these pathways promote virus replication.

Introduction

The DNA-damage response (DDR) is a general term employed to describe a complex series of cellular pathways that detect DNA damage, initiate cell-cycle arrest so that mutated DNA is not duplicated, and then go on to repair the lesion or, if damage is too great, trigger apoptosis. Infection by many virus species is sufficient to initiate a DDR, activating some or all of the repair pathways. Simplistically, this has been seen as recognition by the host cell of viral DNA as its own damaged DNA, but it is now considered that this could, at least to some extent, be an antiviral response, aimed directly at combating infection. Viruses have a complex series of mechanisms that, in turn, have evolved to combat and inactivate the cellular damage-response pathways.

The aim of this review is to consider how and why different viruses affect the balance of these opposing pathways: for example, to what extent is an activated DDR directly required by particular virus species to facilitate or assist virus replication or, conversely, to what extent does the cellular damage response hinder replication. Additionally, it is often not clear whether activation of the DDR is a mere by-product of infection or a direct result of ‘intentional’ action of viral protein activity. If DDR activation is an unwanted result of infection, a further point of interest is to understand what measures viruses take to circumvent the deleterious effects of the cellular pathways. Past experience would suggest that viruses are so highly evolved and their primary structures so tightly constrained that the selective activation of DDR pathways by some viruses might prove advantageous to them. Whether this is the case will only become evident after considerable further investigation.

The relationship of viruses to the DDR is now of particular and increasing scientific interest. There have been a number of recent excellent reviews that have addressed this subject (Lilley et al., 2007; Weitzman et al., 2010), although many have tended to concentrate on particular aspects of the cellular response such as the effect of the infecting virus on cell-cycle checkpoints (Chaurushiya & Weitzman, 2009) or ubiquitylation (Weitzman et al., 2011). Here, we have adopted an alternative approach, dealing with the relationship of different DNA virus species to the DDR. For some of these, our knowledge is appreciable, such as human adenovirus and herpes simplex virus (HSV), but for other viruses, studies are at a very early stage. From these descriptions and a consideration of the aims mentioned above, we hope that common themes will emerge, both in the ways in which cells respond to viruses and the means by which viruses counter-attack cellular DDR pathways.

An historical perspective

Although almost all the research into the relationship between viruses and the DDR dates from the last two decades, relevant observations have been reported since the 1960s. With the growing sophistication of available technology during that decade, it became possible to visualize human chromosomes and to see that damage, in the form of
breaks and translocations, could be associated with agents such as chemicals, radiation and viruses. With relevance to this review, it became clear around this time that a large variety of virus species could damage cellular DNA. For example, adenovirus (Ad)12 induces chromosomal aberrations in human embryo kidney cells, causing breaks in chromosomes 1 and 17 (Zur Hausen, 1967; McDougall, 1970, 1971a). Numerous studies showed that other DNA viruses, such as simian virus 40 (SV40), HSV, hepatitis B virus (HBV) and Epstein–Barr virus (EBV), could also produce lesions in chromosomes of infected cells (Nichols et al., 1978; Nichols, 1983). It had been considered that these chromosome breaks occurred at random in infected cells, but for three groups of DNA viruses it became clear that they cause non-random site-specific chromosome damage. These are the group A adenoviruses (Ad12, 18 and 31), HSV strains 1 and 2 and human cytomegalovirus (HCMV) (Fortunato & Spector, 2003).

At about the same time as reports of the effects of Ad12 were published, it was shown that infection of human cells with HSV resulted in limited chromosome breaks in some cells and/or complete severing of all the chromosomes (termed ‘pulverization’) in others (Stich et al., 1964; Wahren et al., 1972). Virus strain, cell type and time of infection all play a part in determining the outcome of HSV infection. Indeed, human epithelial tumour cell lines are much more susceptible to HSV than peripheral blood leukocytes (O’Neill & Miles, 1969; Mincheva et al., 1984). The expression of HSV immediate-early (IE) and early (E) proteins is required to initiate the chromosomal damage. It has been suggested that ICPO4 is required for chromosome uncoiling and the limited breaks seen at early times, whereas chromosome pulverization is caused by viral polymerases and nucleases (Peat & Stanley, 1986; Johnson et al., 1992; Chenet-Monte et al., 1986).

The initial report of site-specific HCMV-induced chromosome breaks was relatively recent compared with those for Ad12 and HSV (Fortunato et al., 2000), although there had been earlier studies describing general damage and pulverization (Hartmann & Brunemann, 1972; Luleci et al., 1980; Sakizli et al., 1981). Of great importance for the observation of specific chromosomal breaks is the m.o.i., host-cell type and, most significantly, the stage of the cell cycle at which the virus is introduced (Fortunato & Spector, 2003). Virus entry into the cell is required to cause the breaks but, strangely, not the de novo expression of viral proteins. However, it is possible that incoming viral protein or DNA could be responsible (Fortunato et al., 2000).

The recognition that viruses interact with the cellular DDR has become apparent as our understanding of the DDR itself has increased. It is interesting to consider, with hindsight, early reports that can now be seen to point to the involvement of the DDR in viral infection. These studies focussed on the viral infection of target cells from individuals with various inherited diseases that are now known to be caused by mutations in DDR genes. For instance, infection of normal human skin fibroblasts with SV40 was shown to give rise to a limited number of transformed colonies. However, with cells from Fanconi’s anaemia (FA) patients there was a 10–20-fold increase in the number of transformants, whilst transformation of cells from ataxia telangiectasia (AT) and Bloom’s syndrome patients occurred at normal levels (Todaro et al., 1966; Kersey et al., 1972; Webb et al., 1977; Webb & Harding, 1977).

Comparable experiments were carried out with Ad12, which induced similar chromosomal damage in both normal skin fibroblasts and in those from FA patients (most obviously breaks on chromosomes 1 and 17) (Zur Hausen, 1967; McDougall, 1970, 1971b). However, it seemed that Ad12 infection in the FA fibroblasts was somewhat delayed compared with normal and did not lead to cell lysis (at least at a low m.o.i.; McDougall, 1971b). Obviously the reports of the effects of SV40 and Ad12 on FA cells are not directly comparable, but both are early indications of an involvement of DDR pathways in transformation and infection by DNA tumour viruses.

**DNA-damage pathways**

DDR signalling and repair pathways are controlled principally by the PI3K-related protein kinases ATM mutated (ATM), ATM and RAD3-related (ATR), and DNA-dependent protein kinase (DNA-PK). These Ser/Thr kinases regulate cell-cycle checkpoint control, DNA replication, DNA repair, and apoptosis in response to genotoxic stress (Fig. 1).

The ATM kinase is inactivated in AT, an autosomal recessive disorder characterized by progressive cerebellar ataxia, neurodegeneration and a predisposition to cancer (Derheimer & Kastan, 2010). It is activated in response to DNA double-strand breaks (DSBs) and coordinates DSB repair (DSBR). ATM normally exists as an inactive homodimer; autophosphorylation of S1981 in response to DSBs allows the formation of active ATM monomers, which are recruited with the MRE11–RAD50–NBS1 (MRN) complex to sites of DSBs (Derheimer & Kastan, 2010). MRN is not only a substrate for ATM kinase, but is required for full ATM activation. ATM also phosphorylates H2AX, which recruits another ATM substrate, MDC1, to DSBs which, in concert with phosphorylated H2AX (γH2AX), recruits the histone-directed ubiquitin ligases RNF8 and RNF168 (Stewart et al., 2009). ATM promotes the repair of DSBs through homologous recombination (HR) repair; ATM-dependent phosphorylation of TIF1β/KAP1 facilitates the recruitment of 53BP1 and BRCA1 to repair foci in heterochromatin (Noon et al., 2010). The role of ATM in p53-dependent G1/S cell-cycle checkpoint control, and intra-S phase and G2/M checkpoint control is also well-established (Derheimer & Kastan, 2010).

Hypomorphic mutations in ATR give rise to Seckel syndrome, an autosomal recessive disorder characterized...
by microcephaly and mental and growth retardation. ATR coordinates the cellular response to ssDNA and regulates DNA replication during unperturbed S phase, at stalled replication forks and in response to genotoxic stress (Cimprich & Cortez, 2008). ATR, like ATM, is required for the activation of both DDR and repair pathways. It is recruited to replication sites or sites of damage through ATR-interacting protein (ATRIP), which binds directly to RPA70. The RAD9–RAD1–HUS1 (9-1-1) replicative sliding-clamp complex associates with dsDNA junctions adjacent to RPA-loaded ssDNA and recruits the BRCT-repeat protein TOPBP1 to ATR–ATRIP. The ATR-activation domain of TOPBP1 facilitates substrate binding and ATR kinase activation (Cimprich & Cortez, 2008). The best-characterized ATR effector is CHK1, which regulates the G2/M checkpoint, principally by controlling the activity of the CDC25 phosphatases. Phosphorylation of CDC25 proteins inhibits CDC25 phosphatase activity against CDK1 and inhibits entry into mitosis and origin firing during S-phase in response to replication stress (Cimprich & Cortez, 2008).

DNA-PK plays a central role in DSBR, regulating the process of non-homologous end-joining (NHEJ). DNA-PK comprises a large catalytic subunit, DNA-PKcs, and two regulatory subunits, Ku70 and Ku86. The Ku complex recognizes and binds to DSBs, and then recruits, and stabilizes, the interaction of DNA-PKcs with DNA. Two DNA-PKcs molecules in concert tether DNA ends together in a synaptic complex, and recruit the DNA ligase IV–XRCC4 complex to rejoin broken DNA ends. Arrows indicate the flow of the respective DDR pathways. See text for further details.

**Fig. 1.** Roles of protein complexes in ATM, ATR and DNA-PK pathways. Schematic representation of ATM, ATR and DNA-PK signalling pathways. ATM responds to DNA double-strand breaks; phosphorylated H2AX and MDC1 localize to sites of DNA damage, whereupon the MRN complex and ATM are recruited and ATM is activated. ATM activation promotes the recruitment of repair proteins to the site of damage and regulates cell-cycle checkpoints through the activation of CHK2 and p53. ATR is activated in response to ssDNA; ATR is recruited to RPA-coated ssDNA by its cognate binding partner ATRIP and the 9-1-1 complex. ATR is activated by a number of proteins such as TOPBP1, Claspin, Tipin and Timeless and promotes cell-cycle regulation through activation of CHK1. DNA-PK regulates NHEJ. Ku regulatory proteins recruit DNA-PK to double-strand breaks; two DNA-PKcs molecules in concert tether DNA ends together in a synaptic complex, and recruit the DNA ligase IV–XRCC4 complex to rejoin broken DNA ends. See text for further details.
Adenoviruses

Adenoviruses are small DNA viruses with a linear dsDNA genome of approximately 35 kbp. Their ability to cause tumours in newborn rodents and to transform mammalian cells in culture has meant that they have been the subject of intense study for the past 40 years. Adenovirus early region 1A (AdE1A) initiates cell-cycle progression into S phase through interaction with the retinoblastoma (RB) family of proteins and/or CBP/p300 (reviewed by Berk, 2005; Frisch & Mymryk, 2002; Gallimore & Turnell, 2001). It also causes a dramatic increase in expression of p53 (Grand et al., 1994). During the first few hours of infection, the host cell responds to the virus, perhaps in recognition of viral DNA or cellular stress, by activating a classical damage response, seen as phosphorylation of, for example, H2AX, SMC1 and RPA32 (much more prominently in the case of Ad12 than of Ad5). In the case of various adenovirus early region mutants, a much more pronounced cellular response can be observed, with increased phosphorylation of DDR substrates and concatenation of viral DNA (Weiden & Ginsberg, 1994; Stracker et al., 2002; Carson et al., 2003; Blackford et al., 2008). Importantly, after infection with wild-type (WT) group A and group C viruses, a number of cellular proteins such as p53, MRE11, DNA ligase IV and BLM are degraded (Querido et al., 2001; Carson et al., 2003; Stracker et al., 2002; Baker et al., 2007; Cheng et al., 2011; Forrester et al., 2011; Orazio et al., 2011), ensuring that the HR and NHEJ pathways are incapacitated (Figs 2 and 3).

Initial indication that there might be a relationship between adenoviruses and the cellular DDR dates from the observation that Ad12 can cause specific chromosomal breaks (Zur Hausen, 1967; Stich et al., 1964; McDougall, 1969).
1970, 1971a). Significantly, in later studies, p53 was shown to be degraded rapidly by the proteasome following Ad5 and Ad12 infection (Querido et al., 1997, 2001; Steegenga et al., 1998). This degradation requires the AdE1B55K and AdE4orf6 proteins acting in combination. After Ad5 infection the E1B55K–E4orf6 complex, together with cellular proteins Cullin 5 (Cul5), RING-box 1 (Rbx1) and elongins B and C, forms an E3 ligase that ubiquitylates p53 (Querido et al., 2001; Harada et al., 2002). Ad5E4orf6 contains at least two conserved BC box motifs that are similar to sequences in other elongin C-interacting proteins (Blanchette et al., 2004; Luo et al., 2007a). These sequences are necessary for the formation of the active Ad E3 ligase and p53 degradation (Blanchette et al., 2004; Luo et al., 2007a). In the case of Ad12, Cul2 rather than Cul5 is recruited to the E3 ligase (Blackford et al., 2010; Forrester et al., 2011; Cheng et al., 2011).

Substrates amongst the DDR proteins vary with different adenovirus serotypes. Thus p53, BLM and MRE11 are not degraded by the group B and group D viruses (Forrester et al., 2011; Cheng et al., 2011; Fig. 2) and TOPBP1 appears to be degraded by only the group A viruses (Blackford et al., 2010; Forrester et al., 2011; Fig. 2). Although Cul5 has been identified as the ligase recruited by Ad5 for the degradation of p53 and Cul2 by Ad12 for the degradation of p53 and TOPBP1, there is some, as yet unresolved, dispute about the composition of the E3 ligase involved in the Ad5- and Ad12-mediated degradation of MRE11 (Forrester et al., 2011; Blackford et al., 2010; Cheng et al., 2011; Carson et al., 2003).

Proteins not involved directly in the DDR are also degraded during adenovirus infection (Schreiner et al., 2012); the Ad-mediated degradation of the integrin α3 subunit and transcriptional repressors DAXX and TIF1γ facilitates the production of progeny virus (Dallaire et al., 2009; Schreiner et al., 2010; Forrester et al., 2012). Interestingly, whilst degradation of p53, MRE11 and DNA ligase IV requires AdE1B55K and AdE4orf6, TOPBP1 degradation needs only the expression of Ad12 E4orf6 (Blackford et al., 2010). DAXX degradation requires only Ad5E1B55K (Schreiner et al., 2010) and TIF1γ requires neither E1B55K nor E4orf6, but only Ad E4orf3 (Forrester et al., 2012). The TIF1 family member TIF1β/KAP1 is also targeted by AdE1B55K during infection (Forrester et al., 2012), although whether Ad modulates TIF1β/KAP1 DDR function is not known. Mdm2 is also reduced after infection with all Ad serotypes examined, although this is probably due to the inactivation of p53 (Forrester et al., 2011).

It is possible that adenoviruses can inhibit the DDR independently of protein degradation. Ad5E4orf6 and Ad5E4orf3 have been shown to bind directly to DNA-PK, although they did not appear to inhibit its kinase activity against heterologous substrates (Boyer et al., 1999). However, autophosphorylation of DNA-PKcs (at T2609) was reduced during DSBR (Hart et al., 2005; Fig. 3). Ad5E4orf6 also enhances the DDR by inhibiting protein phosphatase 2A, which leads to prolonged phosphorylation of H2AX, activation of PARP and apoptosis (Hart et al., 2007).

Although adenoviruses inhibit the DDR by promoting the rapid degradation of key components, they are also able to affect the localization of various DDR proteins. During infection, a number of DDR proteins are recruited to viral replication centres (VRGs; Fig. 2). RPA32 is recruited to these sites after infection with both WT and mutant viruses (Stracker et al., 2005) and this has been used as a diagnostic marker for other adenoviruses. Other DDR proteins

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Fig. 3. Regulation of DNA-PK by human DNA viruses. Schematic representation of the role of DNA-PK and associated proteins in NHEJ. The schematic depicts how viral proteins from the DNA viruses considered in this review modulate DNA-PK function by targeting DNA-PK and other proteins involved in NHEJ. See text for further details.
recruited to VRCs after WT infection include ATR, ATRIP, Rad9, TOPBP1, Rad17 and hnRNPU1 (Blackford et al., 2008; Carson et al., 2003, 2009). It has been suggested that relocation to VRCs inhibits the functions of these DDR proteins, although this awaits confirmation.

As well as initiating protein degradation and localization to VRCs, adenoviruses can also promote relocation to other sites. Promelocytic leukaemia (PML) bodies play a role in sensing DNA damage, and a number of DDR proteins localize to them (Lombard & Guarente, 2000). Following Ad infection, PML bodies are disrupted and the PML protein is relocalized into ‘track-like’ structures (Fig. 2); this is dependent on the activity of the AdE4orf3 protein (Carvalho et al., 1995; Doucas et al., 1996; Leppard & Everett, 1999). AdE1B55K binds transiently to E4orf3 at PML-tracks and this interaction is necessary for AdE1B55K localization. In the absence of AdE1B55K and AdE4orf6, a mutant Ad5 virus is still able to inactivate the DDR by relocating the MRN complex to ‘nuclear tracks’ through the action of Ad5E4orf3, although this does not occur with Ad4 or Ad12E4orf3 (Stracker et al., 2005). Relocalization of MRN by Ad5E4orf3 has been proposed to inhibit the activation of ATR (Carson et al., 2009) and Ad5E4orf3 has also been shown to repress downstream DDR responses by promoting epigenetic silencing of p53 transcription (Soria et al., 2010).

As well as the ‘nuclear tracks’, Ad infection (and Ad5E1-mediated transformation) results in the formation of large cytoplasmic bodies that have been shown to be aggresomes (Liu et al., 2005; Zantema et al., 1985; Araujo et al., 2005). It has long been recognized that Ad5E1B55K localizes to the aggresomes, but it is now apparent that E4orf3, E4orf6, Cul5 and the MRN complex are also present (Liu et al., 2005; Zantema et al., 1985; Araujo et al., 2005; Fig. 2). It has been suggested that, during Ad5 infection, the MRN complex is initially localized to ‘nuclear tracks’ by Ad5E4orf3, where it binds to the E1B55K protein. Protein complexes containing Ad5E1B55K, Ad5E4orf3, Ad5E4orf6 and MRN are then transported to the aggresomes, where MRE11 undergoes rapid degradation (Evans & Hearing, 2005; Liu et al., 2005; Fig. 2). For some Ad types, p53 and the MRN complex are not recruited to nuclear tracks, but are instead recruited to VRCs (Forrester et al., 2011; Fig. 2). The reasons for these differences await investigation.

ATR pathways are selectively regulated during Ad infection. Thus Ad12, and to a lesser extent Ad5, infection promotes the ATR-dependent phosphorylation of RPA32, whilst Ad12 promotes the Ad12 E4orf6-mediated degradation of TOPBP1, and prevents ATR activation of CHK1 (Blackford et al., 2008, 2010; Fig. 2). The AdE1B55K associated protein hnRNPU1 (E1B-AP5) is required for ATR activation during infection, and has recently been shown to interact with BLM and the MRN complex to promote 3’ DNA end resection (Blackford et al., 2008; Polo et al., 2012).

It appears, therefore, that adenoviruses go to considerable lengths, seen as protein degradation and mislocalization, to disable the DDR and yet still recruit DDR proteins to VRCs, suggesting that certain components might be required for viral replication.

The family Polyomaviridae

JC virus (JCV) and BK virus (BKV) are, together with the mouse polyomavirus and SV40, members of the family Polyomaviridae. They are non-enveloped DNA viruses with a small circular dsDNA genome. Polyomavirus appears to make use of the ATM pathway for optimal virus replication (Dahl et al., 2005). Infection of mouse cells results in activation of the S and G2 checkpoints, presumably to allow the synthesis of viral DNA. Importantly, ATM is activated following infection, and SMC1, H2AX and p53 are all phosphorylated (Dahl et al., 2005; Dey et al., 2002). Inhibition of ATM or infection in ATM−/− cells results in markedly reduced virus yields, as does substitution of a non-phosphorylatable form of SMC1 (Dahl et al., 2005). It is considered that activation of ATM results from the interaction of polyomavirus large T antigen (LT) with RB, leading to E2F activation and the subsequent formation of viral initiation complexes (Dey et al., 2002). As a result of infection, p53 levels are markedly increased, with a concomitant increase in the level of p53 downstream targets such as p21CIP1/WAF1 and Bax (Dey et al., 2002). Deleterious effects of p53 are neutralized by the actions of polyomavirus LT and middle T antigens (Dahl et al., 1998; Dey et al., 2002; Doherty & Freund, 1997; Li et al., 2004).

Studies of the closely related human virus JCV have shown phosphorylation of H2AX following infection and an increase in the levels of p53 and Rad51 (Darbinyan et al., 2007). Significantly, increased expression of Rad51 has also been observed in astrocytes from patients suffering from progressive multifocal leukoencephalopathy, which is caused by the virus (Darbinyan et al., 2007). Two JCV proteins have been shown to have an effect on DNA repair in transfected cells. LT antigen inhibits HR, resulting in the accumulation of mutations and restricted cell growth after DNA damage (Trojanek et al., 2002). As a result of infection, p53 levels are markedly increased, with a concomitant increase in the level of p53 downstream targets such as p21CIP1/WAF1 and Bax (Dey et al., 2002). Deleterious effects of p53 are neutralized by the actions of polyomavirus LT and middle T antigens (Dahl et al., 1998; Dey et al., 2002; Doherty & Freund, 1997; Li et al., 2004).

Expression of agnoprotein sensitizes cells to DNA-damaging agents, inhibiting DSBR (Darbinyan et al., 2004). The protein reduces expression of Ku70 and Ku86, but also binds to Ku70, relocalizing it to the perinuclear space (Darbinyan et al., 2004; Fig. 3). In addition, agnoprotein causes G2/M arrest (Darbinyan et al., 2002). Whether as a result of expression of LT, agnoprotein or other viral proteins, JCV is able to induce genome instability in human cells (Ricciardiello et al., 2003; Theile & Grabowski, 1990; Neel et al., 1996; Darbinyan et al., 2007).
SV40 has a genome of 5.2 kbp. Its natural host is the rhesus macaque, but it is able to transform non-permissive cells, such as those of rodents, in vitro. The major early protein, LT antigen, is responsible for cellular transformation and is essential for virus replication (reviewed by Cheng et al., 2009; Fanning & Zhao, 2009). Simplicistically, SV40 LT duplicates the functions of the AdE1 region or HPV E6 and E7, inactivating p53 and the RB family of proteins. This has the effect of creating a favourable environment for virus replication as well as deregulating growth control, leading to proliferation and transformation.

There have been a number of studies examining the relationship of SV40 virus, and LT in isolation, to the DDR. During viral infection of CV1 cells and baby mouse kidney cells, ATM is activated and phosphorylated, in addition to its usual endogenous substrates, LT on S120 (Shi et al., 2005; Dahl et al., 2005). This phosphorylation is contemporaneous with, and essential for, optimal virus replication. Mutation of LT S120 or ablation of ATM function results in markedly reduced levels of infection (Shi et al., 2005). The effects on ATM appear to be directly attributable to LT expression (Shi et al., 2005; Dahl et al., 2005; Hein et al., 2009). Thus, LT is able to induce accumulation of γH2AX and 53BP1 in damage foci as well as phosphorylation of CHK1, CHK2, ATM, RPA32 and p53 (Shi et al., 2005; Hein et al., 2009). It has been suggested that activation of the DDR is dependent on the binding of LT to Bub1; this interaction is necessary for LT-mediated p53 stabilization and the induction of tetraploidy seen following SV40 infection (Hein et al., 2009).

Activation of both ATM and ATR signalling pathways occurs following SV40 infection, with γH2AX, ATM, MRN, Rad51 and FANCD2 co-localizing with LT to VRCs (Zhao et al., 2008; Boichuk et al., 2010; Shi et al., 2005; Hein et al., 2009). There is also evidence to suggest that, like adenovirus, SV40 promotes the proteasome-mediated degradation of MRN components (Zhao et al., 2008; Stracker et al., 2002; Carson et al., 2003). LT is thought to promote MRN degradation through interaction with the Cul7/p185 component of the Rbx4 and F-box protein F-box E3 ligase (Ali et al., 2004; Zhao et al., 2008). Indeed, mutation of the Cul7-binding site on LT stabilizes the MRN complex and reduces the level of virus replication and LT-mediated transformation (Ali et al., 2004; Zhao et al., 2008). Interestingly, SV40 LT also binds directly to NBS1 (Wu et al., 2004); whether this interaction is required for NBS1 degradation is not clear at present. It has been suggested, as a consequence of this interaction, that SV40 induces endoreduplication following infection (Wu et al., 2004). Thus, LT may be responsible, through binding to NBS1, for inactivating the cellular control mechanisms that guarantee a single round of cellular DNA replication in S phase (Wu et al., 2004). If inactivation of NBS1 occurs through LT binding, presumably the eventual degradation of the MRN complex would enhance these effects. It is now very well established that SV40 LT also binds to the RPA complex, interacting directly with RPA70 (Dornreiter et al., 1992; Melendy & Stillman, 1993). This association is necessary for the initiation of replication of the viral genome, but is probably quite distinct from the role of RPA in single-strand break repair (reviewed by Fanning et al., 2006).

The relationship of viruses in the family Polyomaviridae to the damage response seems rather more complex than is the case for adenoviruses. Whilst the MRN complex is degraded during SV40 infection, it is not clear whether similar events occur with mouse polyomavirus, JCV or BKV. Activation of ATM is required for optimal replication of SV40 but probably not for JCV, which adopts the novel strategy of inhibiting HR by recruitment of Rad51 to IRS-1.

**Human papillomavirus (HPV)**

HPVs are members of the family *Papillomaviridae* of non-enveloped dsDNA viruses with a short circular genome of approximately 8 kbp that infect the epithelium of skin or mucosa; high-risk HPV types 16 and 18 are responsible for over two-thirds of cervical cancers (Chow et al., 2010; Moody & Laimins, 2010). HPV infects undifferentiated cells in the basal layer of stratified epithelium, where the genome is maintained in episomal form. The HPV reproductive life cycle is intimately linked to the differentiation status of the epithelium, such that viral genome amplification, late gene expression and virus production occur in differentiated suprabasal epithelial cells, which are prevented from exiting the cell cycle by the concerted actions of E6 and E7. The ability of E6 and E7 to allow cell-cycle progression resides in their respective capacities to target p53 and RB for proteasome-dependent degradation, and to allow infected cells to bypass G1 checkpoint control and enter S phase (reviewed by Moody & Laimins, 2010). Recent evidence suggests that viral genome amplification in the suprabasal layer is dependent upon activation of the ATM pathway (Moody & Laimins, 2009).

The ATM pathway is constitutively activated in undifferentiated human keratinocyte cell lines that maintain high-risk HPV31 episomes (HFK-31), such that phosphorylated (p)-ATM-S1981 and p-CHK2-T68 can be detected in undifferentiated HPV31 lines, but not in HFK cells (Moody & Laimins, 2009). Studies with ATM and CHK2 inhibitors suggest, however, that the constitutive activation of the ATM pathway is not required for HPV episomal genome maintenance in HPV31-positive cells. When HFK-31 cells are induced to differentiate in the presence of high calcium, the ATM pathway remains activated, despite an apparent reduction in the levels of the ATM protein. Interestingly, CHK2 is phosphorylated to a greater extent upon differentiation of HFK-31 cells, and NBS1 is phosphorylated in an exclusively HPV- and differentiation-dependent manner (Moody & Laimins, 2009). Consistent with ATM activation, MRN, p-ATM, p-CHK2 and γH2AX accumulate within nuclear foci that are reminiscent of sites of DNA damage in both undifferentiated and differentiated HPV-31 cells. Interestingly, ATM and CHK2 inhibitor studies indicate that HPV genome amplification in
differentiated cells is dependent on ATM and CHK2; inhibition of ATM impairs the formation of HPV replication foci in differentiated cells (Moody & Laimins, 2009). It has been determined that HPV E7 binds directly to ATM through its LXCXE motif and promotes the CHK2-regulated, caspase-dependent activation of the HPV E1 replication protein in differentiated cells (Moody & Laimins, 2009). Interestingly, it has previously been proposed that the switch from viral genome maintenance to viral genome amplification is accompanied by a change from bidirectional DNA replication to unidirectional, rolling-circle DNA replication and the formation of viral genome concatemers (Flores & Lambert, 1997). It will consequently be important in future to establish the molecular role of the ATM pathway in facilitating rolling-circle DNA replication and processing of viral genome concatemers.

The HPV E1 DNA helicase associates specifically with HPV origins of replication through an origin-binding domain. HPV E1 recruitment to viral origins of replication is dependent upon the HPV E2 DNA-binding protein (McBride, 2008). It has been determined that nuclear expression of a number of evolutionarily divergent HPV E1 types can induce cell-cycle arrest in early S phase through their ability to activate ATM and CHK2 (Sakakibara et al., 2011; Fradet-Turcotte et al., 2011). It is apparent that, for at least HPV16 and HPV31, E2 attenuates both CHK2 and H2AX phosphorylation, but retains its ability to induce cell-cycle arrest (Sakakibara et al., 2011; Fradet-Turcotte et al., 2011). Given these findings, it has been suggested that HPV16 and HPV31 E2 do not inhibit E1-induced H2AX and CHK2 phosphorylation fully, such that low-level phosphorylation might be sufficient to promote cell-cycle arrest. Interestingly, for HPV16 at least, co-expression studies have revealed that, in dividing cells, E1 and E2 partially co-localize at sites of viral DNA replication with γH2AX, p-ATM and p-p53; E1 and E2 also co-localize with HPV genomes and the MRN component NBS1 (Sakakibara et al., 2011). It is well-established that HPV16 E2 interacts with the ATR activator TOPBP1 (Donaldson et al., 2007). E2 co-localizes at centrosomes with TOPBP1 in mitosis, suggesting that TOPBP1 might be the chromatin receptor for HPV16 E2 during HPV genome segregation at mitosis (Donaldson et al., 2007). There is also evidence that TOPBP1 regulates E2 association with chromatin, but that it is not required for E2 transcription function (Donaldson et al., 2007). Whether E2 interaction with TOPBP1 affects ATR damage signalling directly in either undifferentiated or differentiated cells infected with HPV has yet to be considered. Likewise, whether E2 interaction with TOPBP1 modulates E1-induced damage signalling pathways awaits investigation. It has been established, however, that HPV16 E1/E2-mediated DNA replication occurs in the presence of the topoisomerase inhibitor etoposide, which activates both the ATM and ATR pathways (King et al., 2010).

The ability of the HPV E6 and E7 oncoproteins to induce cell-cycle re-entry, subvert cell-cycle checkpoints, promote genomic instability and cellular immortalization, inhibit apoptosis and inactivate host interferon responses underlines their transforming potential and highlights their fundamental role in HPV oncogenesis (Chow et al., 2010; Moody & Laimins, 2010). Early studies suggested that HPV16 E6 and E7 could promote genomic instability, such that misaligned chromosomes at metaphase and anaphase bridges are observed during mitosis in both HPV16 E6- and E7-expressing cells (Duensing & Münger, 2002). E6 and E7 expression also promotes centrosome amplification and the presence of giant metaphases with increased chromosomal material, supernumerary spindle poles and misaligned chromosomes (Duensing & Münger, 2002). Furthermore, E6 and E7 can also induce DNA damage and promote γH2AX focus formation (Duensing & Münger, 2002). Consistent with these studies, there is a significant increase in γH2AX foci in mitosis from biopsy samples from high-risk HPV-positive carcinomas relative to non-malignant tissue, and that an increase in γH2AX focus formation is also observed upon expression of HPV16 E7 in primary human foreskin keratinocytes (Spardy et al., 2009). HPV16 E7 appears to promote mitotic entry in the presence of DNA damage by causing accelerated proteolytic turnover of the ATR activator claspin and overriding recovery from the ATR-regulated G2/M checkpoint (Spardy et al., 2009).

The ability of high-risk HPV18 E7 to activate DDR pathways has also been considered in suprabasal, differentiated cells (Banerjee et al., 2011). Consistent with the earlier studies using HPV31, both HPV18 genomes and HPV18 E7 promote ATM and CHK2 phosphorylation; p-ATM can be detected in the majority of suprabasal cells transfected with HPV18 genomes or HPV18 E7 (Banerjee et al., 2011). Perhaps surprisingly, there is no apparent positive correlation between the distribution of p-ATM and HPV18 viral DNA in the suprabasal layers, although the relative relationship of HPV18 genomes to p-CHK2 has not been considered. HPV18 genomes and HPV18 E7 also induce CHK1 S345 phosphorylation in differentiated cells; CHK1 activation is RB-independent (Banerjee et al., 2011). Based on these data, it has been suggested that HPV18 E7 not only promotes S-phase re-entry in suprabasal cells, but also activates ATM and ATR DNA-damage cell-cycle checkpoints to prolong the G2 phase of the cell cycle and allow viral DNA replication. Consistent with the proposed requirement for ATM and ATR in promoting E7-mediated cell-cycle arrest in G2, the CDC25C phosphatase is inactivated by phosphorylation on S216 (Banerjee et al., 2011). In contrast to HPV18 E7, expression of HPV16 E6 does not induce CHK1 phosphorylation (Chen et al., 2009). It does, however, upregulate CHK1 (and CHK2) expression, and has also been shown to enhance CHK1 activation in response to UV irradiation or treatment with benz[α]pyrene diol epoxide (BPDE; Chen et al., 2009). E6 expression also sensitizes fibroblasts to increased DNA damage, as judged by the enhanced accumulation of γH2AX. Consistent with these observations, E6 promotes a pronounced cell-cycle arrest in early S phase in response to
UV and BPDE treatment, whilst colony-survival assays indicate that E6-expressing fibroblasts are also hypersensitive to UV and BPDE treatment (Chen et al., 2009).

It has been proposed that high-risk HPV types might activate the FA pathway, such that cervical carcinoma tissue exhibits enhanced nuclear FANC2D focus formation (Spardy et al., 2007). HPV16 E7 also promotes the formation of large nuclear FANC2D foci in primary human keratinocytes, whilst low-risk HPV6 E7 does not; HPV16 E6 enhances the ability of E7 to promote FANC2D focus formation (Spardy et al., 2007). It has been suggested that HPV16 E7 activates the FA pathway by both RB-dependent and -independent mechanisms (Spardy et al., 2007). In line with these findings, expression of HPV16 E7 accelerates chromosomal instability and promotes apoptosis in FA-deficient cells, whilst metaphase spreads reveal a significant increase in chromatid breaks and chromosome fusions in FA-deficient cells expressing HPV16 E7 (Spardy et al., 2007). As FA patients have increased susceptibility to squamous cell carcinoma (SCC), a recent study has addressed whether there is a direct association between HPV, the FA pathway and SCC tumour susceptibility in a mouse model of FA (Park et al., 2010). These studies showed that the FA pathway suppresses HPV-induced oncogenesis and that the FA pathway is normally activated in response to HPV16 E7-induced DNA damage in order to repair HPV-induced DNA damage (Park et al., 2010); FANCA protein deficiency also stimulates HPV-associated hyperplastic growth in organotypic epithelial raft culture (Hoskins et al., 2009).

As integration of the HPV genome into the host genome is a common event in HPV-mediated tumorigenesis, it could be reasoned that host-cell genomic instability and/or direct deregulation of DDR and DSBR pathways by the high-risk HPV E6 and E7 proteins might promote the generation, and/or repair, of DNA DSBs that would facilitate viral genome integration. Indeed, persistent knockdown of the Ku70 regulatory subunit of DNA-PK by RNA interference (RNAi) in the cervical keratinocyte cell line W12 leads to the loss of episomal HPV16 genomes and the integration of HPV16 into the host genome (Winder et al., 2007; Fig. 3). Interestingly, the integration of HPV16 is not preceded by any alteration in genomic stability, suggesting that HPV-induced genomic instability might not be a prerequisite for integration (Winder et al., 2007). Consistent with the model of cervical neoplastic progression, it is interesting that, during the long-term culture of W12 cells, there is a loss of episomally maintained HPV16 genomes and an increase in HPV16 genome integration (Pett et al., 2006). Indeed, W12 transformants can be isolated that harbour both episomes and integrated DNA (Pett et al., 2006). It has been proposed that, under such circumstances, episomally expressed E1 and E2 can drive the replication of integrated HPV genomes (Kadaja et al., 2009). In support of this idea, expression of HPV18 E1 and E2 in HeLa cells drives the replication of integrated HPV18 genomes and results in the production of HPV replication intermediates that activate DDR repair and recombination pathways. As such, E1 and E2 co-localize with ATM, ATRIP, MRN, Ku70/86, CHK2 and CHK1 at integrated HPV18 genome replication centres (Kadaja et al., 2009).

As for other viruses, it therefore appears that HPV infection allows the selective activation or repression of DDR pathways to promote virus replication. Indeed, it could be reasoned that DDR proteins in the ATM and ATR pathways are activated selectively and specifically in response to the expression of HPV proteins and the production of viral DNA during infection, to facilitate both vegetative virus replication in the basal layer and viral genome amplification in the suprabasal layers, and are not merely unavoidable consequences of infection.

**Adeno-associated virus (AAV)**

AAV is an ssDNA virus that belongs to the family Parvoviridae and the genus Dependovirus. AAV possesses inverted terminal repeats (ITRs) that form double-stranded T-shaped hairpin structures at each end of the genome and these are required for replication, integration and packaging (Linden & Berns, 2000). AAV expresses four replication (Rep) proteins required for replication and packaging, and three structural, capsid (Cap) proteins required for virion assembly. AAV replication requires the cellular replication machinery and those supplied by helper viruses; AAV can also replicate when infected cells are treated with UV radiation or genotoxic drugs that facilitate integration. A minimal requirement for Ad5 early region proteins E1A, E1B55K, E4orf6 and E2–DNA-binding protein (DBP) in AAV replication has been established; E1A drives transcription of AAV genes and DBP plays a role in AAV replication (Geoffroy & Salvetti, 2005).

As Ad E1B55K and E4orf6 inactivate DNA-damage signalling pathways in Ad-infected cells through the degradation of MRE11 and p53, the requirement for their degradation in AAV replication has been considered (Schwartz et al., 2007). Using Ad E1B55K mutants that selectively target p53 or MRE11, studies with recombinant (r)AAV have indicated that MRE11 degradation, but not p53 degradation, enhances rAAV transduction; MRE11 degradation also correlates positively with an increase in second-strand viral DNA synthesis following rAAV infection (Schwartz et al., 2007). Furthermore, the Ad-induced degradation of MRE11 enhances the ability of WT AAV-1 to synthesize Rep proteins and undergo viral DNA replication. Interestingly, when an infectious AAV plasmid was transfected into cells with Ad DBP alone, MRE11 localized to AAV replication compartments (Schwartz et al., 2007). These data suggest that the MRN complex suppresses AAV replication by recognizing AAV ITRs as DNA damage and initiating DDR signalling pathways. It is not surprising, therefore, that AAV has evolved to replicate with Ad types that promote the degradation of MRE11. It would be interesting to see whether Ad types that do not promote MRE11 degradation also support AAV replication.
Other studies have considered the individual contribution of damage kinases to AAV transduction and replication (Collaco et al., 2009; Schwartz et al., 2009). In the absence of a functional MRN complex, AAV co-infection with Ad5 activates ATM. AAV and Ad5 co-infection also promotes the phosphorylation of CHK2, NBS1, SMC1, RPA32, CHK1 and H2AX (Collaco et al., 2009; Schwartz et al., 2009). Studies with rAAV and an infectious AAV plasmid suggest that AAV replication is required to induce a DDR. Interestingly, DNA-PK is the kinase shown to be principally required for activating the DDR following AAV and Ad co-infection (Collaco et al., 2009; Schwartz et al., 2009). Indeed, DNA-PKcs and regulatory subunits Ku70 and Ku86 co-localize to AAV VRCs with Rep in AAV and Ad co-infected cells (Fig. 3). Furthermore, DNA-PK activation is detrimental to AAV replication, whilst knockdown of ATM or ATR reduces the ability of AAV to replicate under these circumstances (Collaco et al., 2009; Schwartz et al., 2009). It has also been determined that DNA-PKcs and the endonuclease Artemis cooperate to open rAAV ITR hairpin loops and promote genome recombination in vivo (Inagaki et al., 2007; Fig. 3). Interestingly, however, DNA-PK also reduces the efficacy of rAAV persistence by preventing rAAV integration into host genomes, and rAAV transduction is also increased in Ku86-defective cells (Song et al., 2004).

Early studies established that Rep78 expression alone was able to induce a DDR and promote cell-cycle arrest (Berthet et al., 2005). Rep78 promotes ATM, CHK2 and H2AX phosphorylation in the absence of other AAV genes or helper viruses and induces cell-cycle arrest in G1, S and G2/M. It is suspected that Rep78, and to a lesser extent Rep68, activate ATM-signalling pathways in AAV-infected cells by inducing DNA nicks in the host-cell chromatin that, through processing, result in DSBs (Berthet et al., 2005). Rep78 also binds to CDC25A, inhibits its phosphatase activity and negates CDK activation and cell-cycle progression (Berthet et al., 2005). It is thought that AAV DNA itself also contributes to activation of a DDR and G2/M arrest, which is mediated by the ATR/CHK1 pathway (Fragkos et al., 2009). Studies using UV-inactivated AAV have demonstrated that infected cells display upregulated, pan-nuclear expression of γH2AX; H2AX activation correlates positively with upregulation of p53 and p21CIP1/WAF1 (Fragkos et al., 2009). Interestingly, in the absence of H2AX or p53, the DDR elicited by UV-AAV induces caspase-dependent mitotic catastrophe that is dependent upon ATR, CHK1 and CDK kinases (Fragkos et al., 2009). Taken in their entirety, these data suggest that, like a number of viruses considered in this review, AAV can selectively activate or repress components of DDR pathways in order to promote viral DNA replication or viral DNA integration.

**HSV**

HSVVs are large, linear dsDNA viruses from the subfamily *Alphaherpesvirinae* of the family *Herpesviridae*; they replicate in the mucosal epithelium of the host cell (Roizman & Knipe, 2007). Lytic infection necessitates circularization of the linear genome in the nucleus, where it is incorporated into euchromatin to allow viral gene expression and DNA replication in discrete HSV replication compartments. It is proposed that HSV replicates its DNA by a rolling-circle mechanism that results in large, linear dsDNA concatemers that are subsequently processed and packaged into nascent virions. Latency is associated with HSV spread and infection of sensory neuronal cells, whereupon the linear HSV genome is circularized in the nucleus of the ganglion, packaged into heterochromatin and maintained in episomal form (Knipe & Cliffe, 2008).

The relationship between HSV and the DDR pathway is complex (Fig. 4). A productive, lytic infection of primary human fibroblasts with HSV-1 or HSV-2 results in the activation of ATM and the subsequent activation of CHK2 and p53 (Shirata et al., 2005). The viral DNA polymerase inhibitor phosphonoacetic acid inhibits the HSV-mediated activation of ATM, particularly at low m.o.i., suggesting a link between the initiation of viral DNA synthesis and ATM activation (Shirata et al., 2005). Indeed, ATM, MRE11 and NBS1 accumulate at sites of virus replication with the viral replication protein UL42 during HSV-2 infection (Shirata et al., 2005; Fig. 4). Interestingly, however, it appears that ATM recruitment to viral replication compartments is not dependent upon a functional MRN complex and, moreover, that NBS1 recruitment to viral replication compartments is not dependent upon ATM activation (Shirata et al., 2005). These studies also determined that ATM knockdown has no effect upon the ability of HSV-2 to replicate (Shirata et al., 2005). Unfortunately, these analyses were performed in 293T cells, where AdE1B55K or SV40LT might mask any requirements for the ATM pathway. A separate study has also established that HSV-1 infection activates ATM and promotes ATM and MRN recruitment to replication compartments (Lilley et al., 2005). Using human cell lines that lack functional ATM and MRE11, these researchers also determined that the DDR to HSV-1 is mediated by ATM and the MRN complex and, in contrast to others, that an intact ATM pathway is required for efficient HSV-1 replication. Indeed, HSV-1 replication was severely impaired in AT and ATLD cell lines, relative to AT and ATLD cell lines where ATM or MRE11 expression was restored by complementation (Lilley et al., 2005).

Roles for HSV proteins in the DDR have been established. UL29 associates with NBS1, RPA and RAD51 in pre-replicative microfoci at stage IIIb and in mature, stage IV replication compartments (Wilkinson & Weller, 2004; Fig. 4). It has been determined that the recruitment of these proteins to stage IIIb foci correlates positively with the HSV-1-dependent activation of the host-cell DDR. The HSV-1 UL12 gene product functions in concert with ICP8 as a recombinase and promotes viral recombination-dependent replication. UL12 associates strongly and directly with the MRN complex, independently of DNA, in HSV-1-infected Vero cells (Balasubramanian et al., 2010). It has
been proposed that UL12 is required for production of viral DNA that can be packaged into virions (Balasubramanian et al., 2010). HSV-1 viral DNA forms large concatemers prior to processing and packaging into virions; packaged HSV-1 genomes also possess nicks and gaps that could initiate DSBR (Balasubramanian et al., 2010). Given these phenotypes, it has been proposed that UL12 and ICP8 cooperate with MRN to generate resected 3'-viral DNA tails that participate in strand invasion or strand annealing and consequently promote HR and the production of viral DNA concatemers that can be subsequently processed and packaged (Balasubramanian et al., 2010).

Although there is a general consensus that the ATM pathway is activated during HSV infection and that MRN is recruited to viral replication compartments, there is some difference of opinion as to how MRE11 is regulated during infection. Most researchers suggest that MRE11 expression is not reduced during HSV-1 infection, although one report suggests that levels are reduced significantly (Gregory & Bachenheimer, 2008). Given that the ATM pathway is activated during HSV-1 infection and that the MRN complex is recruited to replication compartments to facilitate replication, it is not clear why HSV-1 would also promote the loss of the protein. In support of the notion that MRE11 expression might be reduced following HSV infection in some cell types, data from one of the original reports establishing ATM activation following HSV infection suggested that MRE11 levels are reduced to some extent following HSV-1 and HSV-2 infection, though this result was not discussed explicitly (Shirata et al., 2005). Whether MRE11 degradation is a general phenomenon or reflects the
cell type used is not clear, but it is apparent that more work is needed to understand the role of MRE11 in HSV replication.

The IE gene product ICP0 is important for the switch from latency to lytic infection, and its deletion impairs lytic replication (Everett, 2000). ICP0 is a RING-finger-containing E3 ubiquitin ligase that promotes the proteasome-mediated degradation of PML isoforms during infection (Everett et al., 1998). Recent work suggests that although HSV-1 infection promotes the activation of ATM and CHK2, ICP0 prevents full activation of the ATM pathway by promoting the degradation of the histone-directed ubiquitin ligases RNF8 and RNF168; ICP0 phosphorylated on T67 by casein kinase I binds to the FHA domain of RNF8 and promotes its targeted polyubiquitylation (Lilley et al., 2010; Chaurushiya et al., 2012; Fig. 4).

DDR proteins activated following HSV-1 infection accumulate at the sites of viral genome entry into the nucleus; sensors and mediators of DNA damage, γH2AX and MDC1, co-localize with ICP4 in numerous foci at the nuclear periphery with incoming viral genomes (Lilley et al., 2011; Fig. 4). Components of PML nuclear bodies that accumulate predominantly at sites adjacent to incoming HSV-1 genomes partially localize with γH2AX and MDC1 at sites of viral genome entry, suggesting that DNA-damage proteins and PML bodies have discrete, separable roles during viral infection. Interestingly, RNF8 and RNF168 also accumulate at sites of incoming viral genomes when cells are infected with an ICP0-null virus. Downstream damage proteins such as 53BP1 are recruited to viral genomes in an RNF8/RNF168-dependent manner in the absence of ICP0 (Lilley et al., 2011). Consistent with the beneficial role of ATM activation in HSV-1 replication, cells depleted of H2AX are severely defective in their ability to generate replication plaques during infection.

Early studies with ICP0 indicated that it targets DNA-PKcs for degradation in a RING-finger-dependent manner (Parkinson et al., 1999). Further analysis revealed that ICP0 was solely responsible for promoting DNA-PKcs degradation, and that virus yield was enhanced 50- to 100-fold following infection of cells that lacked DNA-PKcs (Parkinson et al., 1999). It is likely that the potent antiviral activity of DNA-PK resides in its ability to promote NHEJ and HR repair pathways and, as such, ICP0 inactivates these processes, in part by targeting DNA-PKcs for degradation. It is apparent that HSV, like many DNA viruses, targets the DNA-PK NHEJ pathway specifically during infection (Fig. 3).

In order to facilitate virus replication, HSV infection activates a G2/M checkpoint in the host cell. In a mode of action that is similar to that of HPV E1, HSV-1 ICP0 induces cell-cycle arrest at the G2/M border by promoting the ATM-dependent and CHK2-targeted phosphorylation of CDC25C-S216 (Fig. 4); inhibition of ATM or infection of cells lacking CHK2 severely limits virus yield (Li et al., 2008). HSV-1 also disables ATR signalling during infection, ATRIP and RPA are recruited, along with ICP8, to pre-replicative stage II microfoci during infection (Fig. 4), although RPA that is phosphorylated, and hence activated, by ATR in response to HU treatment is excluded from these sites (Mohni et al., 2010). These data suggest that ATR signalling is inactivated specifically in these pre-replicative sites. Interestingly, this study also revealed that ATR recruitment to HSV-1 replication compartments is not dependent upon its kinase activity, suggesting that ATR recruitment is independent of DNA damage (Mohni et al., 2010). Consistent with studies using adenovirus, HSV-1 infection attenuates the ATR-dependent activation of CHK1 in response to replication stress (Mohni et al., 2010). Taken together, these data confirm that, although ATR/ATRIP are recruited to replication compartments during infection, ATR signalling is inactivated in the infected cell (Mohni et al., 2010).

It appears that HSV, like adenovirus, inactivates DDR pathways during infection by ubiquitylation or protein sequestration. It is also apparent that, although it disables full ATM activation and the activation of ATM effector proteins, HSV does require ATM and the MRN complex for virus replication. Given these observations, it is clear that HSV has evolved to modulate components of the same pathway selectively and differentially in order to promote replication.

**EBV and Kaposi’s sarcoma-associated herpesvirus (KSHV)**

EBV and KSHV are members of the subfamily *Gammaherpesvirinae* and each is considered to be a primary causative agent of human cancers. The γ-herpesviruses have large genomes, encoding up to 100 proteins as well as assorted microRNAs. The infectious cycles of EBV and KSHV are complex, involving latent and lytic infectious stages. Infection of B-cells by EBV is primarily latent; *in vivo*, resting B-cells express only the small non-coding RNA transcripts (EBERs). Infection of resting B-cells *in vitro* results in transformation into a lymphoblastic cell line (LCL) expressing the nuclear antigens EBNA1, 2, 3a, 3b, 3c and -LP, and latent membrane proteins LMP1, 2a and 2b. This expression pattern is only seen *in vivo* either during infectious mononucleosis or in post-transplant lymphoproliferative disease (PTLD). Furthermore, different variants of EBV latency are observed in other EBV-associated malignancies, including Burkitt’s lymphoma (EBNA-1), Hodgkin’s lymphoma (EBNA-1, LMP2a and b, LMP1) and in epithelial cell carcinomas (EBNA-1, LMP2a and b, LMP1). However, the virus can be reactivated periodically through the action of the IE lytic transactivator BLZF1 (Rooney et al., 1989), leading to replication and virus propagation.

Despite the complexity of their genomes and patterns of protein expression, it is becoming apparent that both EBV and KSHV interact with the cellular DDR. In a manner analogous to that of certain adenoviruses, EBV causes the
rapid degradation of p53 during lytic infection, independently of Mdm2 (Sato et al., 2009a, b); the IE lytic transactivator BZLF1 recruits functional Cul2- and/or Cul5- CRIs, through its N-terminal Cul box, to p53 and promotes its ubiquitination and proteasome-mediated degradation (Sato et al., 2009b).

Whilst it is not clear how certain viruses activate the DDR, there is now considerable evidence to show that EBV, through the actions of a number of viral proteins associated with latent infection, is able to induce genomic instability. This has the effect of activating DNA-repair pathways that are, in turn, inhibited by the virus (Kamranvar et al., 2007; Gruhne et al., 2009a, b; Lacoste et al., 2010). For example, it has been shown that EBNA-1 promotes the generation of reactive oxygen species that cause DNA damage. DNA repair is inhibited by LMP1 through downregulation of ATM and subsequent inhibition of CHK2 phosphorylation and inactivation of the G2 checkpoint. Furthermore, LMP1 is able to inhibit repair by its ability to inactivate FOXO3a through activation of the PI3K/Akt signalling pathway (Chen et al., 2008). In addition, EBNA-3C causes downregulation of BubR1 and inactivation of the mitotic spindle checkpoint (Gruhne et al., 2009a, b). The early lytic protein EBV DNase BGLF5 is able to induce genomic instability in human epithelial cells by direct damage to the DNA and by inhibiting the expression of a range of DNA-repair genes (Wu et al., 2010). This is probably a function of BGLF5’s ability to shut off host mRNA in expressing cells (Rowe et al., 2007). BGLF5 is also involved in the generation of linear viral genomes (Feederle et al., 2009a, b) and so is likely to induce genomic instability in the host cell during lytic replication.

EBNA-3C binds directly to CHK2 and by this interaction is able to release cells from mitotic arrest induced by nocodazole (Choudhuri et al., 2007). EBNA-3C is also able to disrupt other cell-cycle checkpoints, presumably helping to maintain the virus in its latent phase (Parker et al., 2000; Wade & Allday, 2000). Following the switch from the latent to lytic phase of the EBV life cycle, an ATM-dependent DDR is induced (Kudoh et al., 2005). The MRN complex, p-p53 and p-ATM are recruited to VRCs and it has been suggested that this is as a result of the recognition of linear viral DNA as damaged DNA by the cell (Kudoh et al., 2005). By inactivation of p53, EBV is able to evade ATM-mediated checkpoints, leaving the host cell in S phase and thus facilitating virus replication (Kudoh et al., 2005). Other studies suggest that activation of the DDR in EBV-infected B-cells is caused by a period of hyperproliferation and is quite independent of virus replication (Nikitin et al., 2010). In complementary experiments, it has been shown that inhibition of ATM and CHK2 activity enhances EBV-induced B-cell transformation (Nikitin et al., 2010). In further analysis, it has been shown that EBNA proteins, and in particular EBNA-3C, play a significant role in inhibition of DDR in normally proliferating lymphoblastoid cell lines (Nikitin et al., 2010). Interestingly, it has recently been reported that EBV, through the actions of EBNA-3A and EBNA-3C, can protect Burkitt’s lymphoma-derived B-cells from apoptosis induced following DNA damage by reducing BIM and NOXA expression (Yee et al., 2011). This might suggest that the virus requires some aspects of the cellular damage-response pathways, but not those associated with apoptosis. As well as the MRN complex and ATM, other proteins involved in HR locate to EBV VRCs. Thus RPA32, which is heavily phosphorylated, Rad51 and Rad52 co-localize with EBV BMRF1 and BALF2 in lytic replication compartments (Kudoh et al., 2009). It has been suggested that the HR proteins are recruited to sites of DSBs in the viral DNA and may be utilized by the virus to facilitate viral genome production (Kudoh et al., 2009). In support of this argument, it has been shown that depletion of RPA32 and Rad51 inhibits viral DNA synthesis. MRE11 and NBS1 have also been shown to be recruited to the EBV origin of plasmid replication (OrIP) in mid-S phase during viral episome replication (Dheekollu et al., 2007). It has been proposed that NBS1 and MRE11 are necessary for the formation of replication-associated recombination junctions, which are required for the maintenance of EBV episomes. It seems likely that the cellular proteins are not involved in a strict DNA damage role in this case, but contribute to replication initiation and/or reinitiation at sites of stalled replication forks (Maser & DePinho, 2004).

Two further interactions of EBV proteins with DDR components have been reported. DNA-PK and HA95 were identified as co-immunoprecipitating proteins with EBNA-LP (Han et al., 2001). EBNA-LP appears to be a substrate for DNA-PK, although the biological significance of this association remains unclear (Fig. 3). More recently, EBV BGLF1 has been shown to bind directly to 53BP1, which is required for optimal virus replication (Bailey et al., 2009). It is possible that 53BP1 is recruited to VRCs together with the MRN complex and ATM, although this has not been confirmed (Kudoh et al., 2005). Probably more significantly, the EBV kinase BGLF4 interacts with, and activates, the histone acetyltransferase TIP60 (Li et al., 2011). This is believed to be a major factor in triggering EBV-induced DDR. TIP60 is also necessary for the expression of EBV lytic genes (Li et al., 2011). Extending the study to other herpesviruses, it was demonstrated that TIP60 co-immunoprecipitates with KSHV ORF36, HCMV UL97 and HSV1 UL13, suggesting strongly that it is a common cellular target for the viruses in the family Herpesviridae and that its activation may be responsible for effects on the DDR seen following herpesvirus infection. Interestingly, an appreciable number of DDR proteins are commonly phosphorylated by the conserved kinases from HSV, HCMV, EBV and KSHV (Li et al., 2011).

KSHV also initiates a DDR during infection. Studies of the DDR in relation to KSHV have tended to concentrate on the effect of individual viral genes. For example, it has been shown that KSHV v-cyclin expression leads to activation of the DDR, seen as phosphorylation of H2AX, CHK2 and p53, and S-phase arrest (Koopal et al., 2007). In contrast, the KSHV v-interferon regulatory factor 1 (v-IRF1) inhibits
ATM signalling by direct interaction with the kinase (Shin et al., 2006). It has been proposed that inhibition of ATM by v-IRF1 reduces p53-S15 phosphorylation and promotes p53 ubiquitylation and proteasome-mediated degradation (Shin et al., 2006). v-IRF1 also binds directly to p53, inhibiting its transcriptional activity and inhibiting apoptosis (Seo et al., 2001; Nakamura et al., 2001). Latency-associated nuclear antigen (LANA) interacts with p53 in co-transfection experiments and in primary effusion lymphomas (Friberg et al., 1999; Chen et al., 2010). LANA represses p53 transcriptional activity, inhibiting its ability to induce apoptosis. Interestingly, infection with the related murine γ-herpesvirus 68 (γHV68) also results in phosphorylation of H2AX and this has been attributed to the activity of the orf36 kinase together with ATM (Tarakanova et al., 2007). γHV68 orf36 and the EBV homologue BGL4 can phosphorylate H2AX in vitro and it has been shown that ATM and H2AX, as well as orf36, are required for optimal γHV68 replication in mouse macrophages.

EBV and KSHV both activate a DDR that is then inhibited by the virus. A number of DNA-damage proteins are recruited during EBV lytic infection to VRCs, where they appear to be required for viral genome production. Interactions between multiple EBV proteins and cellular DDR proteins have been reported, although the consequences of this are not clear at present.

**HCMV**

HCMV is the largest member of the subfamily **Betaherpesvirinae**, with a genome of approximately 230 kbp. It is a major cause of birth defects and is also a serious health risk in immunocompromised individuals. HCMV has a large linear dsDNA genome containing well over 200 ORFs. As with most viruses, HCMV is able to modulate the cycle of the infected cell to produce an environment favouring virus replication. This is achieved through degradation of the RB family of proteins by the action of HCMV pp71 (Kalejta et al., 2003; Kalejta & Shenk, 2003) and inhibition of MCM loading onto host-cell chromatin, preventing replication licensing (Wiebusch et al., 2003). HCMV replication occurs in a biphasic manner from the circularized genome. Initially, origin-specific single-copy replication takes place, followed by a rolling-circle mechanism that gives rise to DNA concatemers that may be branched, with multiple exposed double-strand ends. It has been suggested that these structures could be recognized by the infected cell as broken DNA, as appears to be the case during adenovirus infection. Thus, it seems that the DDR is activated following HCMV infection, but then is inhibited at later times by the virus (Shen et al., 2004; Luo et al., 2007b; Gaspar & Shenk, 2006; Li et al., 2011). At early times post-infection, ATM is activated and phosphorylates p53 and NBS1 (Luo et al., 2007b). There is an increase in p53 level and the protein colocalizes with HCMV UL112/113 (Jault et al., 1995; Luo et al., 2007b). At later times, considerable phosphorylation of ATM and ATR substrates can be observed, as well as an apparent increase in overall level of a number of DDR proteins such as ATM, MRE11, RAD51 and ATRIP (Shen et al., 2004; Gaspar & Shenk, 2006; Luo et al., 2007b). Activation of ATM signalling and increase in p53 expression have been attributed to HCMV IE1-72 expression, although it should be borne in mind that ectopic expression of the viral protein itself has been reported to damage DNA (Castillo et al., 2005; Shen et al., 1997; Gaspar & Shenk, 2006). The recent observation that HCMV UL97 binds to TIP60 and phosphorylates a number of DDR proteins suggests that it may also be involved in ATM activation (Li et al., 2011). However, the importance of ATM is confirmed by the fact that HCMV replication is markedly reduced by an ATM inhibitor (Li et al., 2011). At later times of HCMV infection, the DDR is inhibited and ATM, CHK1, CHK2, the MRN complex and H2AX are relocated to VRCs (Luo et al., 2007b; Gaspar & Shenk, 2006). It is not clear which viral proteins are responsible for the relocation of the DDR components, although it has been suggested that HCMV UL-84 could be a candidate (Gaspar & Shenk, 2006; Lischka et al., 2003). Activation of the ATM signalling pathway by HCMV suggests that this activity is required by the virus. A recent study has suggested that ATM knockdown by RNAi results in reduced virus replication and numbers of mature VRCs, and reduced levels of expression of HCMV IE2, pp65 and gB55 but not IE1 (E et al., 2011). These observations may, however, be contrasted with a previous study which suggested that HCMV replicated almost as well in ATM+/− and MRE11+− fibroblasts as in WT cells (Luo et al., 2007b). It has been suggested that IE1 and IE2 promote ATM-dependent activation through the activation of E2F1 (Ren et al., 2002; Rogoff & Kowalk, 2004; Wade et al., 1992; McElroy et al., 2000; Poma et al., 1996). Indeed, depletion of E2F1, but not of E2F2 or E2F3, before HCMV infection reduces the phosphorylation of H2AX, the expression of HCMV proteins and HCMV replication (E et al., 2011). It has been determined that DNA-repair activity, more specifically HR, increases following HCMV infection; the increase in HR activity is stimulated by HCMVIE1-72 expression, and accompanied by elevated levels of RAD51C and FANC G (Kulkarni & Fortunato, 2011).

As with many viruses discussed here, HCMV initially activates the DDR and then inhibits it. However, an increase in expression of several DDR proteins and their relocation to VRCs appears to be necessary for optimal virus replication, as is activity of the ATM kinase.

**HBV**

HBV has a partially dsDNA genome of 3.2 kbp. It is a member of the family **Hepadnaviridae**, predominantly infects hepatocytes and is associated with the development of hepatocellular carcinoma. Most of the effects of HBV on hepatocytes are attributable to the action of the HBX oncoprotein. The relationship of HBX to the DDR has been
reviewed quite recently (Matsuda & Ichida, 2009), so here we will give a brief overview of our current understanding.

It is now clear that HBV, probably through HBX, potentiates damage to DNA in infected cells, probably by inhibiting various aspects of the DDR. As with many other viruses, HBV inactivates p53 following infection. HBX binds directly to p53 and inhibits its transcriptional activation properties (Feitelson et al., 1993; Lee & Rho, 2000; Wang et al., 1994). It also inhibits the association of p53 with transcription factors such as ERCC3/XPD and ERCC2/XPB (Wang et al., 1994, 1995; Qadri et al., 1996) and, as a consequence, abrogates p53-induced apoptosis (Wang et al., 1995). HBV is involved directly in the inactivation of various DDRs. HBX interacts directly with DDB1 (ZAP-1/UVDDR), inhibiting nucleotide excision–repair (NER) (Lee et al., 1995; Becker et al., 1998; Sitterlin et al., 1997; Jaitovich-Groisman et al., 1999; Martin-Lluesma et al., 2008). It also binds to DDB2 and these interactions have the effect of stabilizing the viral protein and inducing its nuclear accumulation (Nag et al., 2001; Sitterlin et al., 2000a; Bergametti et al., 2002). Importantly, the ability of HBX to bind to DDB1 is essential for optimal virus replication and productive infection (Sitterlin et al., 2000b). The site of interaction on HBX for DDB1 comprises a structurally conserved α-helical region lying between aa 88 and 100 (Li et al., 2010). A similar motif has been identified in the paramyxovirus SV5 V protein and in the cellular DDB1–Cul4-associated factors (Li et al., 2010). It is not clear in what way HBV utilizes the cullin-associated E3 ligase that is bound to HBX, but obviously understanding the implications of this interaction will provide exciting new lines of research. HBX also inhibits NER by its direct interaction with components of the TFIH nucleotide basal excision repair complex (Jia et al., 1999; Jaitovich-Groisman et al., 2001; Qadri et al., 1995, 2011; Haviv et al., 1996). It has been suggested that this interaction may have the effect of specifically downregulating the level of expression of XPB and XPD (Jaitovich-Groisman et al., 2001). As a result of attenuation of NER by HBX, cells expressing the viral protein become hypersensitive to UV irradiation (Capovilla et al., 1997; Qadri et al., 2011; Jia et al., 1999). In addition to its effect on the DDR, it has been shown that HBV infection causes cell-cycle arrest in S phase, presumably to facilitate the production of viral DNA (Chen et al., 2008; Martin-Lluesma et al., 2008).

HBX is responsible for most of the reported cellular effects of HBV. With regard to this review, it inhibits p53 transcriptional activity and NER and both of these actions are required for virus replication. The relationship between HBX and components of the major DDR pathways is not clear at present.

**Conclusions**

Apart from some initial early reports that cellular DNA was subject to breaks and translocations following viral infection, our knowledge of the relationship between viruses and the DDR has tended largely to parallel (although probably a step behind) our increasing understanding of the multiple ways in which cells respond to DNA damage. With an exciting, important and relatively new area of study such as this, it would have been gratifying to have been able to set out some broad conclusions that could apply to most, if not all, DNA viruses. Ideally these would contain some unifying principles which would summarize our knowledge to date and suggest novel approaches for future investigation. However, at present it is probably easier to list those aspects of the relationship of viruses to the DDR that we do not understand, rather than those that we do.

It is clear that different virus species adopt very different strategies to the damage response. In the case of adenoviruses, where our understanding is perhaps greatest, degradation of cellular DDR components is a priority and, presumably, this has the effect of disabling the cellular response [as seen by the absence of DNA concatemer (Carson et al., 2003; Stracker et al., 2002)]. Yet, even here, there are a large number of underlying observations that we do not understand, such as why numerous damage proteins are recruited to VRCs and why different adenovirus serotypes adopt very different approaches to DDR pathways (Cheng et al., 2011; Forrester et al., 2011). Other viruses also degrade various DDR proteins, presumably with the same objective of incapacitating the pathways and stopping ligation of viral DNA. Thus, SV40 causes the degradation of MRE11, whilst p53 levels are much reduced in HPV- and EBV-infected cells (Zhao et al., 2008; Scheffner et al., 1990; Sato et al., 2009a, b). Protein degradation by HSV appears to be dependent on expression of the viral E3 ubiquitin ligase, ICP0. This is involved in degradation of DNA-PKcs, RNF8 and RNF168; the substrates for degradation seem to be quite distinct from those degraded by adenoviruses (Lilley et al., 2010).

It is likely that one of the major determining factors in the relationship of viruses to the DDR is the structure of the viral DNA and, as a consequence, how the DNA is replicated. The linear dsDNA of adenovirus is more likely to elicit an immediate DDR response, by its mere presence, than a circular genome, such as SV40, which will probably not be seen as cellular DNA. However, the herpesviruses undergo replication by a rolling-circle mechanism that generates large head-to-tail concatemeric genomes that require processing, potentially by DDR proteins, prior to packaging. Obviously the infected cell will react differently in these cases, quite apart from any deliberate action of the virus in triggering activation of the pathways.

Activation of DDR pathways seems to be a very common response to viral infection, with phosphorylation of various downstream targets being observed after infection with all of the viruses discussed here. Because of cross-talk between the ATM, ATR and DNA-PK signalling pathways, it is difficult to know which particular one is activated or inhibited at any time during the response. It is also difficult to know whether transient activation, before subsequent
inhibition, is advantageous. Thus, activation of ATM and/or ATR signalling has been observed following infection with adenovirus, SV40, polyomavirus, HPV, AAV, HSV, EBV, KSHV and HCMV. This may be a result of virus-induced cellular stress, the recognition of the viral DNA as damaged cellular DNA or, in some cases, a deliberate activation of the pathways. Recognition of to what extent these alternatives apply to different virus species will, obviously, be essential for a full understanding of the complex relationship with the DDR. However, a recent report (Li et al., 2011) demonstrating that kinases from α-, β- and γ-herpesviruses appear to have many substrates in common and these include an appreciable number of DDR proteins seems to be an excellent and exciting first step in providing a more general theory of the relationship.

A number of other features of the relationship seem to be common to many viruses. The ability to manipulate cell-cycle checkpoints, often to ensure that infected cells are in S phase, is shared by most species. This is an obvious requirement for virus replication and necessitates overriding damage checkpoints. In the case of the small DNA tumour viruses, progression into S phase for replication of viral DNA is most obviously achieved by the inactivation of the RB family, but presumably the damage-response checkpoint is activated in infected cells and this is required for virus replication.

For many viruses, there is a definite requirement for DDR proteins for efficient virus replication. For example, HSV replicates only very poorly in the absence of the ATM pathway, SV40 replication proceeds more efficiently in the presence of ATM-mediated phosphorylation of LT and, similarly, HCMV probably requires active ATM for optimal replication (Shi et al., 2005; Lilley et al., 2005; Gaspar & Shenk, 2006). In all of these cases, however, it is far from clear what precise function is served by the DDR proteins with regard to the virus. Recruitment of multiple DDR proteins to viral replication centres is very common although, again, it is not known what precise role they play there. Determination of the function of these cellular proteins during replication will be central to our understanding of the relationship between viruses and the DDR.

As we have tried to stress throughout this review, the relationship between viruses and the DDR is an exciting and rapidly expanding area of research. In spite of appreciable increases in our knowledge over the last decade, there are still many viruses for which our understanding is superficial at best. However, we believe that over the next few years this will be rectified, and concerted study by virologists on the one hand and cell biologists on the other will allow us to understand fully this very subtle relationship.

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