Contribution of Human Papillomavirus E6 PDZ-Binding Activity to Virus-Induced Pathogenesis

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Contribution of Human Papillomavirus E6 PDZ-binding Activity to
Virus-induced Pathogenesis

Christian Kranjec

This thesis is submitted for the degree Doctor of Philosophy in the faculty of Life Sciences of the
Open University, UK

International Centre for Genetic Engineering and Biotechnology (ICGEB), Trieste-Italy

Director of Studies: Lawrence Banks, PhD

Second Supervisor: Sally Roberts, PhD

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Abstract

It is clear that the targeting of PDZ-containing substrates by E6 is important for the normal viral life cycle and for the progression to malignancy. However, which of these PDZ domain-containing proteins is relevant for HPV pathology is still elusive. In this study, we provide the evidence that different PDZ domain-containing proteins are differentially targeted by E6. With these experiments, we identified MAGI-1 as a sensitive proteolytic substrate for both the HPV-16 and HPV-18 E6 oncoproteins. We show that E6 promotes the degradation of membrane-bound and nuclear pools of MAGI-1, and the silencing of E6 expression resulted in the MAGI-1-mediated junctional recruitment of ZO-1. Using a mutant MAGI-1, resistant to E6-mediated degradation, we also show that its expression in HeLa cells also promotes membrane recruitment of the tight junction-associated proteins ZO-1 and PAR3, represses cell proliferation and promotes apoptosis. These findings suggest that E6-mediated inhibition of MAGI-1 function perturbs tight junction assembly, with concomitant stimulation of proliferation and inhibition of apoptosis. We also found that the cell polarity regulator hScrib is differentially targeted by HPV-16 and HPV-18 E6-mediated degradation. Surprisingly, we found that residual levels of hScrib expression are required for the maintenance of high levels of HPV-18 E6 expression in HeLa cells. This is not due to an effect on E6 stability or transcription, but rather is due to an effect upon E6 translation. We provide evidence that hScrib and E6 both regulate the PI3K/mTORC1 pathway, and that hScrib might regulate cap-dependent translation through the modulation of the mTORC1 effector S6 kinase. This provides an unexpected role for hScrib in the regulation of tissue homeostasis, and provides further evidence that E6, by fine-tuning the levels of expression of its different cellular substrates, can impact upon a wide range of biological processes implicated in the pathogenesis of cervical cancer.
**Introduction**

**Oncogenic viruses: proto-oncogenes and tumor suppressors**

The term oncogenic virus, or oncovirus, refers to a virus with a DNA or RNA genome whose infection is associated with cancer. This terminology originated from studies of acutely transforming retroviruses in the 1950–60s, however the notion that tumor development could have a viral etiologic origin was postulated at the dawn of the 20th century. The first suggestions that human and animal tumors could be transmitted by viruses came from the observations made by Giuseppe Ciuffo in 1907 and Ellermann and Bang in 1908, in which human warts and chicken leukemia could be transmitted to healthy recipients of cell-free filtrates derived from diseased donors (Ciuffo, 1907; Javier and Butel, 2008). Soon after, in 1909, similar experiments led Peyton Rous to discover that avian sarcomas could be transmitted using filtered cell-free tumor extracts, suggesting that a biological agent, the Rous sarcoma virus (RSV), could transmit a genuine cancer, similar to mammalian solid malignant tumors (Rous, 1910, Rous, 1911). Nevertheless, the concept of a infection-associated origin of cancer was dismissed for long time by the scientific community, and the field of tumor virology gained new interest only between 1930s-1960s with the identification of mammalian oncogenic viruses. In 1933, Richard Shope and co-workers reported the isolation of the first mammalian DNA tumor virus. They revealed that a filterable agent, the Shope papillomavirus, could transmit cutaneous warts in cottontail rabbits (Shope and Hurst, 1933), and subsequently the Shope papillomavirus, now known as cottontail rabbit papillomavirus (CRPV), could produce skin carcinomas when inoculated in domestic rabbits (Rous and Beard, 1934; Syverton and Berry, 1935). In addition, cancer-causing CRPV infections in domestic rabbits, were associated with a failure to produce viral progeny. This observation defined a paradigm for small DNA tumor viruses in which deregulation of the viral life cycle is often the causative event associated with the malignant progression of the infection.

After the first evidence suggesting that papillomaviruses might cause malignant tumors in rabbits, an additional 40 years were necessary for the formulation of a hypothesis speculating on a possible role played by human papillomaviruses HPVs in the onset of genital cancers (zur Hausen et al.,
1974; zur Hausen, 1975). This stimulated additional interest in papillomaviruses, which ultimately led in the late 1970s to the identification of cytological changes in cervical smears as being papillomavirus-specific (Meisels and Fortin, 1976). Subsequently in the early 1980s the complete nucleotide sequence of two human papillomaviruses, HPV 1a and 6b, (Danos et al., 1982; Schwarz et al., 1983) and of one bovine papillomavirus, BPV 1 (Chen et al., 1982), were published. In the same period the genomes of two “high-risk” HPV isolates, types 16 and 18, were cloned from cervical cancer biopsies (Durst et al., 1983; Boshart, 1984), providing the first evidence for the presence of these virus types in genital cancers, unlike “low-risk” types, such as HPV-6 and 11, which are mainly associated with genital warts that do not progress to malignancy. In the following years, fundamental insights into HPV-linked carcinogenesis were provided by the demonstration that specific viral genes, such as E7 and E6, were expressed in cancer cells (Schwarz et al., 1985). The first molecular evidence for the transforming potential of papillomaviruses came from studies showing that E6 and E7 could induce immortalization of human keratinocytes (Durst et al., 1987).

Finally in 1991 at an International Agency for Research on Cancer (IARC) and World Health Organization (WHO) workshop, the causative role of HPV infection in the onset of cervical cancers was officially recognized by the scientific community (Bosch et al., 1992).

The other two families of small DNA tumor viruses are polyomaviruses and adenoviruses. Polyomaviruses were first discovered in mice (Gross, 1953; Stewart et al., 1953), and this was rapidly followed by the discovery of the simian virus 40 (SV40). SV40 is a naturally occurring infectious agent of the Rhesus macaque (Macaca mulatta) and is not associated with disease in Rhesus macaques or other monkeys. The virus was originally isolated as a contaminant of Rhesus monkey kidney cell cultures used to produce the polio vaccine (Sweet and Hilleman, 1960), and was assigned to the family Polyomaviridae, closely related to the human polyomaviruses BK polyomavirus (BKPyV or BKV), JC polyomavirus (JCPyV or JCV), KI (KIPyV), WU (WUPyV) and Merkel cell polyomavirus (MCPyV or MCV), the latter of which has been recently associated with the development of Merkel cell carcinoma (see below) (Feng et al., 2008; Jiang et al., 2009). Research on SV40 gained interest when it was found that Rhesus monkey kidney cell extracts could produce tumors when injected into newborn hamsters (Eddy et al., 1961) and that the agent
responsible for these tumors was indeed SV40 (Girardi et al., 1962; Eddy et al., 1962). Although these tumors in hamsters did not produce progeny virus, the animals were positive for antibodies against the viral protein large tumor antigen (or T-antigen). Furthermore, the small t antigen (or t-antigen) has been subsequently identified as the second SV40 oncoprotein. Small t-antigen possesses a weak transforming activity when expressed alone, but in combination with the T-antigen it cooperates in the induction of transformation (Sleigh et al., 1978; Seif and Martin, 1979). SV40 was also shown to infect human cells and to promote their transformation in tissue culture (Jensen et al., 1963; Shein, 1967). However, the possible causality between SV40 infection and cancer in humans, particularly in human mesotheliomas and brain tumors, has long been a matter of debate (Fang et al., 2011), and, at present, there is minimal evidence for SV40 implication in the etiology of these tumors. As mentioned before, MCV is the only polyomavirus associated with carcinogenesis in humans, and MCV DNA is found in about 80% of Merkel cell carcinoma (MCC). Although MCV infection of the skin is very common during childhood, MCC occurs primarily in the elderly, and is strongly associated with immunosuppression (Moore and Chang, 2010). Loss of immune control of the infection, promotes a strong reactivation of the replicative life cycle of the virus, and during progression to MCC this event is commonly followed by the viral DNA integration into the host genome (Feng et al., 2008). All MCC cells carry integrated MCV DNA molecules, suggesting that integration is a crucial event for MCC development. Viral DNA integration is believed to result from mutations in the MCV genome arising from the exposure of the skin to mutagenic agents, such as UV radiation. Integration is associated with the loss of viral replicative capacity, however, the expression of large T antigen is maintained and is required for the prolonged survival of MCC cells (Houben et al., 2010). The induction of the fully transformed phenotype is associated with additional mutations in the large T antigen ORF, which results in the loss of its ability to regulate viral DNA replication, but retains the ability to express its differentially spliced forms small and middle T antigens (Shuda et al., 2008; Shuda et al., 2009) and to interact with host cell tumor suppressors, such as pRB (see below).

The third member of small DNA tumor viruses are adenoviruses. These were first isolated in the 1950s from adenoid and tonsil explants, where these viruses were found to be responsible for acute
respiratory diseases (Rowe et al., 1953; Hilleman and Werner, 1954). A few years later, it was shown that infection with some strains of adenovirus could lead to the formation of tumors in hamsters (Trentin et al., 1962). Similar to papillomavirus- and SV40-driven tumorigenesis, tumor cells from infected hamsters did not produce viral progeny and the hamsters developed antibodies against the adenovirus oncoproteins, E1A and E1B.

A number of other viruses are also defined as cancer-causing. These include the herpesviruses Epstein-Barr virus (EBV) and Kaposi’s sarcoma herpes virus (KSHV), the hepatitis B (HBV) and C (HCV) viruses and human T-cell leukemia virus-1 (HTLV-1) (Banks et al., 2012). As will be clear from the following discussion, research on the oncoproteins expressed by DNA tumor viruses has led to the discovery of cellular pathways commonly inactivated by viral oncoproteins and deregulated in most human cancers. In addition, they have provided excellent examples of oncogene addiction, since the expression of the oncoproteins in tumor cells is continuously required to maintain the transformed phenotype.

The oncoproteins expressed by papillomaviruses, SV40 and adenoviruses act as direct carcinogens. By definition, a genomic sequence coding for a direct viral carcinogen is present in each cancer cell and expresses oncoprotein(s) that directly contribute to cell transformation. Indeed, in studies aimed at defining the viral DNA status in transformed cells, some regions or all of the SV40 DNA was found to be integrated into the host genome (Sambrook et al., 1968), whereas only a portion of the Adenovirus DNA was found integrated into host chromosomes (Sambrook et al., 1980). However, in tumors and in transformed cells in culture, the expression of selected genomic regions is maintained. For SV40, this region corresponds to the coding sequence for the large-T and small-t antigens (Huebner et al., 1963), whereas for Adenoviruses this is the early region of the genome expressing the E1A and E1B oncoproteins (Ross et al., 1980a, b). Likewise, in HPV-transformed cells the expression of E6 and E7 is responsible for the establishment and maintenance of the transformed phenotype. The functional relevance for the continued expression of viral oncoproteins became clear when they were found to interact with and inactivate important host cell tumor-suppressors, such as p53 and pRB. The first evidence for this came from the fact that hamsters
carrying SV40-induced tumors possessed high levels of antibodies against a 54 KD protein (Linzer and Levine, 1979), and that the high levels of expression of this protein, p53, in SV40 transformed cells were directly dependent on the expression of the viral T-antigen (Linzer et al., 1979), generating the mistaken concept that p53 might be a T antigen-induced oncoprotein rather than a tumor-suppressor. These observations were soon followed by one of the milestones of tumor virology: the discovery of the interaction between SV40 T-antigen and p53 (Lane and Crawford, 1979). However, the importance of this association only became clear much later, when p53 was finally recognized as a tumor-suppressor. At the time of its discovery, the hypothesis that p53 could be a putative oncoprotein was further reinforced by recent discoveries suggesting that activating mutations in cellular proto-oncogenes could be a common mechanism during cell transformation (Parada et al., 1982; Der et al., 1982; Sukumar et al., 1983). In addition, cDNA clones coding for p53 generated in the early 1980s contained a mutation at codon 135 that conferred transforming capacity on the protein (Levine et al., 2004). It was only several years later that the comparison of the transforming p53 clones with wild type mouse p53 led to the identification of the mutation, and p53 was rapidly recognized as a potent tumor suppressor by its ability to repress transformation in cultured cells (Hinds et al., 1989; Finley et al., 1989). Moreover, in the same period mutations in the p53 genomic locus were found in colon carcinoma cases (Baker et al., 1989).

Now it is clear that mutations of p53 are associated with over half of all human cancers and its tumor-suppressor potential relies on its ability to promote apoptosis, cell cycle arrest and cellular senescence in response to proto-oncogenic cues, such as oncogene-induced hyperproliferation or DNA damage (Kastan and Bartek, 2004; Bieging and Attardi, 2012). The inactivation of p53 by viral oncoproteins was suggested to be a common tumorigenic mechanism used by small DNA tumor viruses, and this was supported by the observation that adenovirus E1B was also able to form a protein complex with p53 in adenovirus-transformed cells (Sarnow et al., 1982). Subsequently, the E6 oncoproteins expressed by HPV-16 and -18 were found to complex with p53 (Werness et al., 1990), but unlike adenovirus and SV40 oncoproteins, E6 recruited a host E3-ubiquitin ligase, E6AP, to promote the proteasome-mediated degradation of p53 (Scheffner et al., 1990). The requirement by DNA tumor viruses to inactivate a potent pro-apoptotic protein such as
p53, is a direct result of their replicative life cycles, where the virus promotes S-phase re-entry and therefore stimulates high levels of DNA replication. This is accomplished through the inactivation of members of the “pocket protein” family, which includes the product of the retinoblastoma tumor susceptibility gene, pRB and its related proteins p107 and p130. The best studied functions of the pocket proteins are their abilities to repress transcription of E2F-responsive genes, through the direct association with members of the E2F family of transcription factors. Phosphorylation of pocket proteins by G1 cyclin-dependent kinases promotes the release of E2Fs, triggering the activation of genes required for cell cycle progression and proliferation (Reviewed in Manning and Dyson, 2011). The tumor suppressor activities of p53 and pRB are integrated by the expression of two other potent tumor-suppressor genes, p16\textsuperscript{INKa} and p14\textsuperscript{ARF}, both expressed by the INKa/ARF locus (Sherr and Weber, 2000). The potential genome instability originating from loss of pRB function is prevented by the activation of p53 which, in turn, leads to cell-cycle arrest through activation of the cyclin-dependent kinase (CDK) inhibitor p21\textsuperscript{cipl} and repression of cyclin B and CDK1 expression (el-Deiry et al., 1993; Smits and Medema, 2001). This is achieved by a feedback loop leading to the expression of p14\textsuperscript{ARF}, which induces the activation of p53 by inhibiting MDM2, the ubiquitin ligase responsible for the degradation of p53 (Stott et al., 1998). In addition, p14\textsuperscript{ARF} also promotes the hAda3-mediated acetylation of p53, ultimately leading to cellular senescence (Sekaric et al., 2007). On the other hand, loss of p53 function and induction of oncogenic stress triggers the expression of p16\textsuperscript{INKa}, a potent inhibitor of cyclin-D-dependent kinases that prevents the inhibitory phosphorylation of pRB (Serrano et al., 1993; Suzuki-Takahashi et al., 1995; Sherr and Weber, 2000). In agreement with these activities the INKa/ARF, p53 and pRB genomic loci are among the most commonly mutated genes in human cancers (Sherr and Weber, 2000), and DNA tumor viruses have evolved efficient mechanisms to overcome their tumor-suppressor activity (Shamanin et al., 2008). Figure 1 summarizes how the activities of p53 and pRB are interconnected and their interplay in the prevention of cancer development.

The Rb protein was shown to interact with SV-40 large T-antigen (DeCaprio et al., 1988), adenovirus E1A (Whyte et al., 1988) and HPV E7 (Dyson et al., 1989; Boyer et al., 1996). HPV E7, E1A and SV40 T-antigen share sequence homology in three regions, designated conserved
region (CR) 1, 2 and 3 (Dyson et al., 1992). Strikingly all three viral proteins harbor a short amino acid stretch (LXCXE) lying within the CR-2 region allowing for the interaction with members of the pocket protein family (Dyson et al., 1992; Helt et al., 2002). Interaction of SV40 T-antigen and adenovirus E1A with pocket proteins results in their displacement from E2F transcription factors (Bagchi et al., 1990; DeCaprio et al., 1988; Dyson et al., 1989), and possibly also in the alteration of their phosphorylation status (Wang et al., 1991; Parreno et al., 2001). Conversely, E7 oncoproteins deriving from high-risk HPV types drive the proteasome-mediated degradation of pRB, p107 and p130 (Boyer et al., 1996; Helt et al., 2001; Gonzalez et al., 2001). Whilst the pRB binding is a conserved feature among high- and low-risk E7 proteins, and all are able to interact with the pocket proteins, only those E7s derived from high-risk viruses can direct proteasome-mediated degradation of Rb. In the case of p130, this is bound and targeted for degradation by high- as well as low-risk E7 oncoproteins (Felsani et al., 2006; Klingelhutz et al., 2012), suggesting that the pocket protein-binding motif is necessary but not sufficient for the ability of E7 to drive their degradation.

In the context of HPV- and adenovirus-mediated tumorigenesis, E7 and E1A posses respectively the strongest oncogenic potential. Consistent with this, the expression of E1A alone is able to promote cellular immortalization (Houweling et al., 1980), whereas E1B lacks transformation activity (Van den elsen et al., 1983), but E1A and E1B together cooperate to transform rodent cells (Graham., 1984). Similarly, HPV E7 possesses the stronger transforming activity, but together E6 and E7 cooperate to transform human keratinocytes, the natural host of HPV infection (Barbosa and Schlegel, 1989; Hawley-Nelson et al., 1989; Münger et al., 1989a; Watanabe et al., 1989).

It is clear that inactivation of p53, pRB and pocket proteins is common in the life cycles of human tumor viruses, and that is reflected in the tumors associated with their infection. It is also clear that additional functions of viral oncoproteins, independent of the p53 and pRB targeting, are important for the regulation of viral life cycle and tumorigenesis. For instance, high-risk HPV E6, adenovirus 9 E4ORF1 and HTLV-1 Tax evolved the ability to interact with PDZ domain-containing proteins (see below), and this was shown to play crucial roles in context of the viral life cycles and oncogenic transformation (Banks et al., 2012).
Figure 1. Cartoon showing the interconnections between p53 and pRB pathways and their inactivation by small DNA tumor viruses. A. the expression of p14ARF and p16INKa is part of a feedback loop that integrates p53 and pRB tumor-suppressor pathways. The activation of either p14ARF or p16INKa following loss of pRB or p53 respectively, activates mechanisms leading to cell cycle arrest, senescence and apoptosis. B. The expression of the oncoproteins encoded by small DNA tumor viruses leads to the inactivation of both p53 and pRB, thereby inactivating the p14/p16 feedback loop.
The demonstration that certain human tumor virus oncoproteins can target PDZ domain-containing substrates provided an exciting early indication of their potential relevance in the development of human tumors. One of the first suggestions that PDZ-binding motifs (PBMs) (see below) might confer oncogenic potential and, by implication, that their PDZ domain-containing substrates might have tumor-suppressor potential, came from studies in a mouse model of mammary tumorigenesis. In this system, adenovirus 9 (Ad9) E4ORF1 protein, has potent transforming activity, and this was dependent on an intact PBM (Lee et al., 1997). The E4ORF1 oncoprotein is expressed by the E4 region of the adenovirus genome, which encodes viral proteins important for the regulation of viral DNA replication and late gene expression (Halbert et al., 1985). The Ad9 possesses a unique tumorigenic capacity, and, unlike other adenoviruses, is able to induce estrogen-dependent mammary tumors in mice (Ankerst and Jonsson, 1989; Javier et al., 1991), and this phenotype is conferred by the E4ORF1 PBM (Weiss and Javier, 1997; Thomas et al., 1999; Thomas et al., 2001). The precise contributions of specific PDZ domain-containing substrates to this activity have remained elusive, although hDlg and MAGI-1 appear to be good candidates as tumor suppressors in this system (Javier, 2008). A particularly interesting development was the realization that cancer-causing HPVs also encode a class-1 PDZ binding motif at the extreme C-terminus of the E6 oncoprotein (Kiyono et al., 1997; Lee et al., 1997; Massimi et al., 2004). This is a highly conserved feature among the high-risk mucosal HPVs, such as HPV-16 or HPV-18, and this motif is absent from those HPV E6 proteins that are only associated with benign lesions. In addition, an intact PBM on E6 is essential for many of E6’s associated activities, including the regulation of viral life cycle, induction of EMT (epithelial-to-mesenchymal transition) and induction of malignancy in transgenic mouse models (Thomas et al., 2008). Another human tumor virus, HTLV-1, the causative agent of adult T-cell leukaemia, also encodes an oncogene, Tax, which has a PBM, through which it interacts with hDlg (Lee et al., 1997). Unlike E6, Tax does not seem to be involved in the later stages of disease, but an intact PBM does seem essential for the capacity of Tax to transform cells (Tsubata et al., 2005; Higuchi et al., 2007), suggesting that PBM–PDZ interactions might contribute to tumor initiation by HTLV-1.
PDZ proteins in homeostasis and disease of epithelial tissues

PDZ domains and PDZ-binding motifs

PDZ (PSD-95, Disc-Large, Zonula-Occludens-1) domains are named based on the names of the first proteins in which the domain was recognized (Songyang et al., 1997). PDZ domains are motifs of 80-90 amino acids that form a conserved pattern of tertiary structures composed of 6 $\beta$-sheets ($\beta$A-$\beta$F) and two $\alpha$-helices ($\alpha$A-$\alpha$B). These are shown as a cartoon in Figure 2a, aligned with each of the three PDZ domains of human hDlg. Linear amino-acid stretches form joining loops that connect the different structural components of the PDZ domain. The shape of a correctly folded PDZ domain 2 of human hDlg is shown in Figure 2b. PDZ domains interact with PBMs located most commonly at the C-terminus of the target proteins, although internal PBMs also exist, and the specificity is given by the interaction between ligand side chains and the PDZ domain itself (Harris et al., 2001). Early studies identified two classes of PDZ domains based on the ligand specificity displayed: class I PDZ domains target sequence X[T/S]XOCOOH, and Class II PDZ domains target sequence $X\Phi X\Phi COOH$, where $X$ is any residue and $\Phi$ is an hydrophobic amino acid (Songyang et al., 1997; Nourry et al., 2003). Less common PDZ domain-binding specificities were also identified with the class III PDZ domains (X[ED]XOCOOH) (Stricker et al., 1997). More recent studies, however, have shown that PDZ domains can interact with up to seven residues in the PBM (Zhang et al., 2007; Thomas et al., 2008), and this elicited the further subdivision of PDZ domains into 16 different subclasses (Tonikian et al., 2008; Subbaiah et al., 2011). Therefore, a single PDZ domain can interact with a multiplicity of different PBMs, making the number of possible PDZ-ligand combinations incredibly high. Target PDZ-binding peptides lodge in a cleft between $\beta$B and $\alpha$B strands, forming a hydrogen bonding network that allows the C-termini of target proteins to interact with the carboxylate binding loop connecting the $\beta$A and $\beta$B sheets (Jemth and Gianni, 2007). This loop contains the consensus sequence R/K-X-X-X-G-$\Phi$-G-$\Phi$, also known as the GLGF repeat, that facilitates the hydrogen bonding to carboxylate groups and provides the specificity for the PDZ-binding sequence. An example of the mode of interaction of HPV-18 E6 PBM with the PDZ domain 2 of hDlg is shown in Figure 2c. The dissociation constants...
Figure 2. Structural features of PDZ domains. A. A cartoon in linear format of the structural elements that compose a PDZ domain (adapted from Junqueira et al., 2003) aligned with each of the three PDZ domains of human hDlg (hDlg). B. A cartoon showing the folding of the structural elements in Figure 2a, based on the crystal structure of hDlg PDZ2 (Zhang et al., 2007). The proximity of the N and C termini can be seen. (C) A cartoon showing the binding of a PDZ binding motif (PBM), in this case the 6 C-terminal amino acids of HPV-18 E6, to the PDZ domain of hDlg (Zhang et al., 2007). The antiparallel binding of the peptide can be seen.
(Kₘ) calculated in solution for the α1-syntrophin PDZ domain and PSD-95 PDZ domains 2 and 3 were in the low micromolar range (1-10 μM) (Niethammer et al., 1998; Harris et al., 2001). This moderate affinity places PDZ-mediated interactions in the same range as SH2 and SH3 domains, and suggests that these interactions are highly reversible in cells and are likely to be subject to regulatory mechanisms (Nguyen et al., 1998). In the case of PDZ-PMB associations, the on/off switch appears to be regulated in some cases through phosphorylation events (reviewed in Jeleń et al., 2003; Kim and Sheng, 2004). Multiple kinase pathways have been shown to regulate PBM-PDZ interactions, indicating that a variety of biological processes are mediated through PDZ domains. In most cases, phosphorylation of phospho-acceptor sites in close proximity to the PBM negatively affects the binding of the PBM to the PDZ target. For instance, phosphorylation of the high-risk E6 PBM by PKA and Akt has been shown to prevent its interaction with PDZ-containing substrates (Kühne et al., 2000; Boon and Banks, 2013), and similarly phosphorylation events within the PBMs of the inward rectifier K⁺ channel (Kir2.3), β2-adrenergic receptor and glutamate receptor (GluR2) have been shown to negatively regulate their PDZ-mediated recognition (Cao et al., 1999; Matsuda et al., 2000). However, examples exist in which the regulatory phosphorylation events occur in the PDZ domain, and in this case it promotes the interaction with the PBM (Hegedus et al., 2003). PDZ domain-containing proteins can generally be subdivided into one of three groups according to their domain composition: 1) PDZ-only proteins, containing exclusively one or multiple PDZ domains; 2) membrane associated guanylate kinases (MAGUKs) which contain one or multiple PDZ domains along with a SH3 and guanylate kinase (GUK) domains; and 3) PDZ-proteins containing additional domains (reviewed in Jeleń et al., 2003; van Ham and Hendriks, 2003).

Examples of some of the PDZ domain-containing proteins belonging to the three classes are depicted in Figure 3. Many PDZ domain-containing proteins typically function as scaffolds to recruit soluble proteins and assemble macromolecular signaling complexes at specialized cell-to-cell contact sites termed adherens junctions (AJ) and tight junctions (TJ) (Javier et al., 2008).
Epithelial polarity complexes and establishment of apico-basal cell polarity

Epithelial cell polarity can be referred as the establishment of asymmetries within a cell or a tissue. Cell polarity is required for the regulation of key biological processes and most aspects of development (i.e. organ development and function), and its loss is associated with a large proportion of late-stage cancers (Martin-Belmonte and Perez-Moreno, 2011). In complex eukaryotic tissues, such as stratified epithelia, two types of cell polarity can be distinguished: apico-basal polarity (ABP), in which functional membrane domains are set along the vertical axis of the cell through the polarized distribution of so called polarity complexes; and planar cell polarity (PCP), which refers to the coordinated positioning of cells within the plane of the epithelium. Often components of the ABP mediate pathways involved in PCP and vice versa, therefore the two types of polarity are interdependent and the maintenance of both is a requisite for regulation of cell adhesion and tissue architecture. Increasing evidence suggests that their perturbation is associated with early stages of tumorigenesis and cancer progression (McCaffrey and Macara, 2011; Martin-Belmonte and Perez-Moreno, 2011; Banks et al., 2012). For the purpose of this thesis I will focus on ABP, and in the next section I discuss how polarity proteins set ABP within cells, and provide evidence that link their loss by genetic inactivation or targeting by viral oncoproteins to tumorigenesis.

In vertebrate epithelia, three polarity complexes have been identified: the Crumbs (Crb-PALS1-PATJ) complex, the PAR (Cdc42-PAR6-PAR3-aPKC) complex, and the Scribble (Scrib-Dlg-Lgl) complex. Polarity complexes are formed by polarity determinants that were originally identified in model organisms such as worms, yeast and flies, and their high evolutionary conservation is underlined by the fact that mammalian members of the Scrib complex can complement their counterparts in Drosophila melanogaster and yeast mutant cells (Thomas et al., 1997a; Kim et al., 2002; Dow et al., 2003; Grifoni et al., 2004). Cell polarisation is a stepwise process which requires the coordinated interplay of different biological processes, including migration, cadherin-based cell adhesion (see below) and cytoskeleton remodelling.
Figure 3. Diagrammatic representation of PDZ domain-containing proteins belonging to three different groups: PDZ-only proteins, MAGUK proteins and multi-domain PDZ proteins.
Figure 4a recapitulates the basic steps leading to cell polarisation. Polarity complexes set cell polarity by distributing asymmetrically in epithelial cells, and by restricting their reciprocal pattern of localisation. In this scenario, the Crumbs complex localizes to, and identifies, the uppermost apical domain which is often associated with the formation of specialized membrane structures, such as microvilli and primary cilia which are connected to actin and spectrin filaments. Conversely, the PAR and the Scrib complexes localize respectively at TJ and AJ (Figure 4b). In vertebrate cells, TJ set the limit between the apical and lateral domains of the cell, where transmembrane proteins, such as junctional adhesion molecules (JAMs), occludin and claudins, form a semi-permeable barrier that limits the paracellular diffusion of solutes. Adherens junctions define baso-lateral membrane identity and assemble beneath the TJs; the respective localizations of these two structures set the limit between the baso-lateral and sub-apical regions of the cell. As their name suggests, AJs represent the main adhesive cellular structures, and are characterized by the presence of cadherins and adaptor proteins such as β- and α-catenin which mediate homophilic interactions between cells (St Johnston and Ahringer, 2010).

**PAR complex**

The PAR complex includes the PDZ domain-containing proteins partitioning defective (PAR) 3 and 6, the Ca^{2+} and diacglycerol-independent atypical protein kinase C (aPKC) and the cell division control protein 42 (Cdc42), and it regulates the assembly of TJs. The initial stages of polarization and TJ assembly require the formation of cadherin-based homophilic adhesive structures. These primordial adhesive structures, known as puncta, contain a mixture of AJ and TJ components, including junctional adhesion molecules (JAMs), PAR3 and zonula occludens (ZO)-1 (Suzuki *et al.*, 2002). The subsequent dissociation of AJ and TJ components, and the maturation of separated junctional complexes, requires the activation of the RAC1 GTPase and the kinase activity of aPKC (PKCζ and PKCι in humans). PAR3 directly participates in restricting the activation of RAC1 to primordial adhesion structures through the recruitment of T lymphoma invasion and metastasis-inducing protein 1 (TIAM1), a RAC1 guanine nucleotide exchange factor (GEF), and its exclusion from subapical sites (Chen and Macara, 2005). Subsequently, aPKC is directly involved
in the recruitment of the PAR complex at the TJs through the phosphorylation of PAR3, promoting its PDZ-mediated association with transmembrane TJ protein JAM-1 (Ebneth et al., 2001; Itoh et al., 2001; Hirose et al., 2002), an activity that requires PAR6 to interact with and bring together aPKC and PAR3 (Schneeberger and Lynch, 2004). In addition, PAR6 tethers the PAR complex to the Rho family GTPase, Cdc42, (Joberty et al., 2000; Lin et al., 2000), an interaction that enhances the aPKC kinase activity (Yamanaka et al., 2001), favouring the phosphorylation of additional TJ components, including occludin, claudin-1 and ZO-1, at later stages of TJ assembly (Nunbhakdi-Craig et al., 2002). The activity of aPKC is counteracted by protein phosphatase 2A (PP2A), the first serine/threonine phosphatase found to localize at the TJs, which negatively regulates TJ assembly by dephosphorylating aPKC itself and its TJ substrates (Nunbhakdi-Craig et al., 2002). Therefore, TJ assembly and initial stages of cell polarity are regulated by fine-tuning of the aPKC kinase activity, as well as that of RAC1 and Cdc42 GTPases.

Crb complex

Of the three mammalian homologs of Drosophila Crumbs, Crb3 is the one expressed at the apical compartment of epithelial cells (Roh and Margolis, 2003). Crb3 is a transmembrane protein and coordinates the formation of the Crb polarity complex through the cortical recruitment of the MAGUK protein PALS1, mediated by the interaction between the PDZ domain of the latter and the C-terminus of Crb3. In addition to a PDZ domain, PALS1 possesses additional protein-protein interaction modules, including a L27 domain, which promotes the interaction with, and the apical recruitment of, PATJ (Schneeberger and Lynch, 2004), the third component of the Crb polarity complex. The Crb complex is physically linked to TJs through the interaction of PALS1 with PAR6. This association is mediated by the PDZ domain of PAR6 and N-terminus of PALS1 and is enhanced by the GTPase activity of Cdc42 (Hurd et al., 2003). In addition, the C-terminal PBMs of the TJ proteins ZO-3 and claudin-1 bind respectively to the sixth and eighth PDZ domains of PATJ (Roh et al., 2002), strengthening the association of the Crb complex with TJs. The importance of the interaction between the Crb and the PAR complexes for the maintenance of apical polarity identity is underlined by the fact that overexpression of a dominant-negative form of PATJ in
Figure 4. Establishment of cell polarity in epithelial cells. A. Representation of the sequential events occurring during acquisition of cell polarity in epithelial cells (adapted from Ebnet et al., 2004). B. Cartoon showing the polarized distribution of components of the three polarity complexes along the apico-basal axis. The figure also shows the reciprocal inhibition between the three complexes, the key aPKC-mediated phosphorylation of Lgl (Hugl) and the interaction between the Crb and PAR complexes.
epithelial cells not only causes the mislocalization of PALS1, but also disrupts the localisation of the PAR complex and of TJ core components (Hurd et al., 2003).

Scrib complex

The scribble (Scrib) complex is composed of the leucine-rich repeats and PDZ domain (LAP) protein Scrib, the MAGUK protein Dlg and the WD40 domain-containing protein Hugl (the vertebrate homolog of Drosophila Lgl). The Scrib complex localizes at the AJs of mammalian cells, whereas in flies it associates with septate junctions, the Drosophila homologs of mammalian TJs (Bilder and Perrimon, 2000; Navarro et al., 2005). The Scrib complex co-localises with E-cadherin where it promotes the basolateral identity by preventing the basal expansion of the apical polarity complexes (Yamanaka and Ohno, 2008). This polarity complex was also shown to regulate the expansion of the apical domain at intermediate stages of polarisation. At this stage, Lgl interacts with PAR6 and aPKC, competing for their binding to PAR3 (Yamanaka et al., 2003), thereby inhibiting the PAR complex assembly and TJ maturation. In later stages of polarisation, the extensive aPKC-mediated phosphorylation of Lgl induces its dissociation from the PAR6-aPKC module (Plant et al., 2003). This is a crucial step during the acquisition of ABP, since phosphorylated Lgl is excluded from nascent TJs and is redirected to the AJ-associated hScrib complex, which in turn allows the assembly of the PAR complex and maturation of the sub-apical domain.

Assembly and signalling from junctional polarity complexes

Epithelial sheets are located at the boundaries between anatomical compartments where they strictly regulate the passage of solutes and immune cells without affecting the overall homeostasis of the tissue (Laukoetter and Nava, 2008). In this context, the polarized formation of cell junctions between neighbouring cells, maintains tissue homeostasis by i) forming spatially segregated cell compartments that respond to stimuli coming from different microenvironments, and ii) functioning as a scaffold for the recruitment of regulatory molecules. Consistent with this, loss of
components of AJs as well as of TJs is associated with loss of cell polarity, increased proliferation and acquisition of invasive capacities (reviewed in Martin-Belmonte and Perez-Moreno, 2011). In the next sections I will provide an overview on the control of cell signalling by junction-associated proteins and on how viral oncoproteins can promote tumorigenesis through their perturbation.

**Tight junctions**

Biochemical data revealed that TJs are supramolecular complexes composed of hundreds of proteins including transmembrane and scaffolding proteins, cytoskeletal components and signalling molecules (Tang, 2006). Within TJs, bundles of transmembrane proteins (such as claudins, occludin and junctional adhesion molecules (JAM1-4) protrude in the intercellular space and contact the TJs of adjacent cells, while cytoplasmic scaffolding proteins interact with the cytoplasmic domain of transmembrane proteins, to stabilize the intercellular connections, assemble signalling complexes and modulate the activity of regulatory proteins. Within the epithelial sheet, intercellular TJ interactions from adjacent cells form a selective barrier for the paracellular diffusion of solutes and macromolecules (e.g. electrolytes and growth factors) controlling normal growth rates and homeostasis of epithelial tissues by generating spatially segregated microenvironments exposed to different proliferative cues (Laukoetter et al., 2007; Tamura et al., 2008; Vetrano et al., 2008). These two functions of TJ transmembrane proteins are not mutually exclusive since controlled paracellular permeability limits cell proliferation, whereas stimulation of proliferation down-regulates adhesive structures (Farkas et al., 2012). A good example of this regulation is the control of proliferation through the segregation of EGF and EGF-like ligands from their receptors (EGFR and ErbB2-4). Epidermal growth factor receptor (EGFR) and ErbB2-4 are members of the type-1 tyrosine kinase receptor family, and are involved in the regulation of physiological processes that require the controlled activation of proliferation and cell migration, such as development, and wound healing. Activation of EGFR and ErbB receptors occurs through their interaction with EGF or EGF-like ligands, which in turn leads to the stimulation of downstream proto-oncogenic pathways (Sweeney et al., 2001). In polarized epithelial tissues, EGFR and ErbB2-4 receptors are spatially segregated from their respective ligands; receptors
localise at the basolateral domain, whereas ligands are present at the apical domain of the cells and in the extracellular fluid covering the surface of certain epithelia (Vermeer et al., 2003; Tsukita et al., 2008). In this context, intact TJs are believed to be the primary barrier to the paracellular diffusion of EGF and EGF-like ligands, and TJ disruption, for instance by mechanical injury of the epithelium, triggers epithelial proliferation and migration downstream of activated EGFR/ErbB receptors, leading to the rapid restoration of the epithelial sealing (Veemer et al., 2003). This barrier function of TJs has been recognized as a protective mechanism, ensuring a rapid restoration of the epithelial barrier function upon tissue damage (Chao et al., 2003). In addition, this also highlights that the maintenance of separated cellular compartments by junctional complexes limits the acquisition of potentially tumorigenic characteristics by epithelial cells. Figure 5 shows the basic structure of stratified epithelia and how TJs might contribute to the maintenance of tissue homeostasis.

The relevance of aberrant activation of ErbB signaling in human cancers has been provided (Hynes and Lane, 2005; Murphy and Morris, 2012), and recently a link between activated ErbB2, disruption of cell polarity and acquisition of carcinogenic properties has been reported (Aranda et al., 2006; Xue et al., 2012). In 3D breast cancer cell models, active ErbB2 mediates loss of cell polarity through the mislocalization of the PAR6-aPKC module, and cooperates with downstream activated Ras/ERK signaling to activate proliferation (Aranda et al., 2006). This is also consistent with other studies which show that mislocalization or overexpression of PAR6 and aPKC are common in many cancers (Aranda et al., 2008). Expression of a PAR6 mutant unable to bind ErbB2 prevented cell polarity alterations in mammary cells, underlining the critical role played by the PAR complex in epithelial homeostasis. Intriguingly, ablation of hScrib in mutant PAR6-expressing cells, restored the polarity defects produced by the ErbB2/PAR6-aPKC interaction (Aranda et al., 2006), suggesting that the PAR and hScrib polarity complexes can modulate cell polarity and prevent tumorigenesis through the regulation overlapping pathways. This is also supported by the observation that both PAR3 and hScrib can regulate Rac, contributing to the control of polarized cell migration by restricting Rac activity (Qin et al., 2005; Xue et al., 2012). In contrast, a pro-oncogenic activity has been indicated for PAR6, with its overexpression being
linked to increased proliferation and also to the induction of TJ breakdown. Furthermore, TGFβ (transforming growth factor β)-induced phosphorylation of PAR6 increases its interaction with the ubiquitin ligase Smurf1 (Smad ubiquitylation-regulatory factor 1), thereby resulting in RhoA degradation and the induction of a more mesenchymal phenotype (Ozdamar et al., 2005). Thus the PDZ domain-containing components of the Par complex can function as promoters and inhibitors of EMT, depending on the balance of PAR3/PAR6 activities (Aranda et al., 2008).

Components of the PAR complex belong to a large group of proteins that contributes to the assembly of a macromolecular complex on the cytosolic side of TJs, referred to as the TJ plaque. The first TJ plaque protein identified was ZO-1 (zonula occludens-1) (Stevenson et al., 1986). ZO-1, with ZO-2 and ZO-3, constitute the ZO protein family that localises at TJs of epithelial cells in a cell density-dependent manner (Gottardi et al., 1996). ZOs share common structural features that place them in the MAGUK superfamily, including multiple PDZ domains, SH3 and GUK domains and proline-rich regions variable in length, and several ZO-interacting partners have been identified (reviewed in Bauer et al., 2010). A crucial function of junctional-localised ZO-1 is the regulation of RhoA-induced proliferation. This is achieved by ZO-1 directly through the SH3-mediated membrane sequestration of the RhoA effector ZONAB/DbpA (Balda and Matter, 2000) and its associated protein CDK4 (Balda et al., 2003), or through the recruitment of cingulin, another TJ plaque protein, that in turn binds and sequesters the RhoA-specific guanine nucleotide exchange factor (GEF) GEF-H1/Lcf (Citi et al., 2009). ZONAB/DbpA is a Y-box transcription factor, whose nuclear translocation stimulates proliferation by activating the gene expression of the G1-associated cyclin D1, PCNA and ErbB2 (Balda and Matter, 2000; Sourisseau et al., 2006), in an active RhoA-dependent manner (Nie et al., 2009). In addition, ZONAB/DbpA recruits the cyclin D1-associated kinase CDK4 to the nucleus (Balda et al., 2003), thus efficiently promoting the G1-S progression through the cell cycle. In agreement with these data, ZO-1 down-regulation is observed in a large proportion of breast cancer cases (Hoover et al., 1998). The control of cell proliferation mediated by the TJ protein ZO-1 is completed by the second member of the ZO family, ZO-2, whose translocation to the nucleus of proliferating cells has been shown to inhibit the transcription of cyclin D1 (Gonzalez-Mariscal et al., 2009), whereas a role in the modulation of cell-cycle-
Figure 5. Contribution of TJs to the maintenance of epithelial tissue homeostasis. In stratified epithelia the asymmetric division of basal cells (perpendicular to the basal membrane) generate daughter cells that are pushed along the differentiating epithelium and are committed for terminal differentiation. Cells of the basal layer also maintain the ability to undergo symmetrically cell divisions (parallel to the basal membrane) in order to generate two daughter cells that maintain the stem cell phenotype. In the differentiating epithelium TJs (red squares between cells) are enriched in the granular layer (stratum granulosum) and form a barrier that blocks the paracellular diffusion of solutes and growth factors, thereby preventing the exposure of basal cells to proliferative cues. Upon mechanical injury of the epithelium and TJ disassembly, the lower epithelial layers become exposed to growth factor stimulation which ensures the rapid restoration of the epithelial sealing by promoting transient cell migration and proliferation.
dependent stability of cyclin D1 has been proposed for ZO-3 (Capaldo et al., 2011). The assembly of TJ complexes and the correct localisation of ZO proteins are mutually dependent on each other (Umeda et al., 2006). Thus, in epithelial cells MAGI (MAGUK with inverted domain structure)-1 is recruited to junctional sites by JAM-4 in a PDZ-dependent manner, and this promotes TJ stabilisation and recruitment of ZO-1 (Hirabayashi et al., 2003). MAGI-1 is a member of the MAGI protein subfamily that also comprises MAGI-2 and -3. These are defined as MAGUKs although they differ from the canonical domain composition, having a unique arrangement of protein-protein interaction domains (Dobrosotskaya et al., 1997). MAGI-1 is able to interact with PTEN and β-catenin through its PDZ domains 2 and 5 respectively (Dobrosotskaya and James, 2000; Kotelevets et al., 2005). This set of interactions stabilises β-catenin at the membrane and re-localisates PTEN to membrane bound sites, protecting it from proteasome-mediated degradation, a function also found with MAGI-2 (Valiente et al., 2005; Hu et al., 2007). The formation of a trimeric β-catenin–MAGI–PTEN complex has been shown to mediate PTEN tumor-suppressor function in the context of oncogene activation (Kotelevets et al., 2005). This is in agreement with the fact that membrane-bound PTEN down-regulates the PI3K signalling pathway (Leslie and Downes, 2002), thus inhibiting several processes related to tumor formation and cancer progression, including cell growth, survival and migration (Leslie and Downes, 2002; Salmena et al., 2008).

**Adherens junctions**

Adherens junctions mediate cell-cell adhesion through the formation of homophilic interactions between the extracellular domains of cadherins, which in epithelial cells are best represented by E-cadherin (Nagafuchi, 2001). The adhesive properties of E-cadherin are enhanced by formation of macromolecular complexes, mediated by the direct recruitment of cytosolic proteins by the intracellular domain of E-cadherin. These include β-catenin (the vertebrate homolog of Drosophila armadillo), γ-catenin and p120-catenin, which bind directly to E-cadherin and promote its localisation and stability (Reynolds et al., 1994; Yap et al., 1998; Huber and Weis, 2001; Davis et al., 2003). Engagement of cadherin-based junctions represents the basis for the induction of the
polarised epithelial phenotype (Figure 4a). Consequently E-cadherin is, perhaps, the main barrier to
the epithelial-to-mesenchymal transition in which epithelial cells lose cell polarity and acquire
migratory and invasive capacities. During development, EMT is followed by its reverse process,
MET (mesenchymal-to-epithelial transition) to regulate organ morphogenesis. Thus, during
malignant transformation in epithelial tissues, the induction of EMT correlates with increased
aggressiveness of the tumor (Thiery et al., 2009). So far, several inducers of EMT have been
identified; these include the transcription factors TWIST, SNAIL and ZEB-1/2, which directly
down-regulate E-cadherin expression through the repression of its promoter activity (Nieto, 2002;
Peinado et al., 2007). One of the best known functions of E-cadherin-based AJs in the regulation of
tumorigenesis is the control of the Wnt/β-catenin pathway through the modulation of APC
(adenomatous polyposis coli) function. APC is a tumor-suppressor and plays a fundamental role in
the regulation of the Wnt pathway, orchestrating the formation of the so-called “axin destruction
complex”, formed by axin, the kinases CK2 and GSK3β, APC and β-catenin, which leads to the
recruitment of the E3 ubiquitin-ligase β-Trcp and drives the proteasome-mediated degradation of β-
catenin (de Law et al., 2007). Activation of the Wnt pathway and stabilisation of β-catenin, leads to
the activation of a number of proto-oncogenic genes (Wnt target genes), whose expression is
deregulated in many human cancers (de Law et al., 2007). Consistent with this important tumor-
suppressor function, germline mutations in the APC gene are associated with familial adenomatous
polyposis (Kinzler and Vogelstein, 1996), a risk factor for development of colon carcinoma. APC
has multiple protein interaction sites, one of which includes a C-terminal class 1 PBM
(Morais Cabral et al., 1996; Giles et al., 2003). The PBM-dependent interactions have been shown
to be crucial for the modulation of its function, and mutations affecting the ability of APC to bind
PDZ domains have been found in human cancers (Miyoshi et al., 1992; Pedemonte et al., 1998).
The PBM-mediated interaction of APC with hDlg, appears to regulate its correct localization with
important consequences for the regulation of cell-cycle progression and cell adhesion (Matsumine
et al., 1996; Etienne-Manneville et al., 2005). The APC PBM also binds to the PDZ domain of the
FAP-1 (Fas-associated phosphatase 1) tyrosine phosphatase (Erdmann et al., 2000). FAP-1 displays
a pleiotropic behaviour in the context of the regulation of tumorigenesis. The phosphatase activity
of FAP-1 is required to inhibit the proliferation of Wnt-stimulated cells through the modulation of the APC/β-catenin complex (Erdmann et al., 2000; Welter et al., 2008); consistent with this, FAP-1 function is lost in colorectal cancers (Wang et al., 2004). On the other hand, FAP-1 had been originally identified for its antiapoptotic function through its ability to de-phosphorylate the death receptor Fas, thereby preventing Fas-ligand mediated apoptosis (Saras et al., 1997; Ungefroren et al., 2001). In addition, FAP-1 expression is progressively increased in cancer progression of the Ewing’s sarcoma family of tumors, in which FAP-1 is a direct transcriptional target for EWS-FLI1 (Ewing sarcoma breakpoint region 1/Friend leukaemia virus integration 1) fusion protein (Abaan et al., 2005). Therefore, the function of FAP-1 with respect to tumorigenesis is likely to be highly context-dependent.

As discussed above, AJs are the resident site of the hScrib polarity complex. This complex is essential for regulating cell polarity and proliferation in Drosophila, with loss of any component resulting in broadly similar and complementary phenotypes. In human tumors, loss of hScrib and hDlg is a common event in later stages of cancer progression, although at earlier stages of disease progression the two proteins are expressed at extremely high levels and often mislocalized (Watson et al., 2002; Cavatorta et al., 2004; Nakagawa et al., 2004; Gardiol et al., 2006). However, their relative contribution to tumorigenesis in higher eukaryotes has begun to be clarified only recently. Depletion of either hDlg or hScrib in human keratinocytes has opposing effects on cell adhesion, invasion and apoptosis (Massimi et al., 2012). Considering that, in human cells, the function of hDlg still remains to be determined, this study suggested that its function is highly context-dependent. Human hDlg acted as tumor-suppressor during induction of anoikis, an apoptotic pathway induced by the growth of cells in the absence of cell-substratum attachment (Massimi et al., 2012). Conversely, loss of hDlg reduced the invasive potential of human keratinocytes (Massimi et al., 2012), and in a similar study, the depletion of hDlg impaired the invasive capacity of cervical cancer-derived HPV-positive cells (Krishna Subbaiah et al., 2012), suggesting a pro-oncogenic role for hDlg in certain circumstances. This activity of hDlg, however, has been linked to its ability to activate proto-oncogenic pathways upon its mislocalization by viral oncoproteins.
hScrib is recruited to AJs and cell-cell contacts through its interaction with E-cadherin (Navarro et al., 2005) and the correct localisation of the two AJ components is mutually interdependent (Navarro et al., 2005; Qin et al., 2005). Recent studies have suggested that a central tumor-suppressor function of hScrib is its modulation of the Ras/Raf/MAPK pathway. Loss of hScrib cooperated with oncogenic Ras to promote anchorage-independent growth of breast cancer cells and invasion in organotypic 3D cultures (Dow et al., 2008), although the depletion of hScrib alone was recently shown to be sufficient to promote an invasive phenotype in human keratinocytes (Massimi et al., 2012). In addition, hScrib has been shown to reduce the levels of phosphorylated (active) ERK kinase (Dow et al., 2008; Nagasaka et al., 2010), at least in part, through the recruitment of the cellular phosphatase PP1γ (Nagasaka et al., 2013), and this activity of hScrib is required to suppress oncogenic Ras co-transforming activity (Nagasaka et al., 2010). The tumor-suppressor activity of hScrib also relies on its ability to induce pro-apoptotic pathways (Zhan et al., 2008; Liu et al., 2010). Once again, however, this activity is context-dependent, since anti-apoptotic functions for hScrib have also been reported (Massimi et al., 2012). This is also highlighted by the observation that mislocalization of hScrib is sufficient to promote carcinogenesis in breast cancer cell models through the augmentation of the activity of the Hippo transducer Taz (Cordenonsi et al., 2011).

The transcription factors Taz and Yap are the final targets of the Hippo tumor-suppressor pathway, which is highly conserved from flies to humans (Pan, 2010). The activation of this pathway leads to a signalling cascade that culminates in the sequential activation of the kinases MST1 and LATS1, which in turn leads to the inhibitory phosphorylation of Yap and Taz. The phosphorylation of Taz leads to its proteasome-mediated degradation (Pan, 2010), and in this context hScrib controls the localisation and activity of MST1, which is required for the activation of LATS1. Consistent with this, loss of hScrib expression or its membrane displacement have been shown to induce the
aberrant activation of Taz and acquisition of EMT and cancer stem cell-related traits (Cordenonsi et al., 2011). Similar effects were also mediated by Crb in mouse mammary cells. Assembly of the Crumbs complex resulted in increased Yap/Taz phosphorylation and in the inhibition of TGFβ-SMAD-mediated EMT (Varelas et al., 2010). This suggests that hScrib and Crb could have complementary tumor-suppressor effects through the regulation of the Hippo pathway. hScrib has been implicated in the induction of the c-Myc-mediated apoptotic pathway, through the formation of a ternary complex which includes hScrib, the Rac and Cdc42 GEF βPIX, and the G protein-coupled receptor kinase interactor 1 (GIT1) (Zhan et al., 2008). In polarised breast cancer cells, the c-Myc-mediated hScrib/βPIX/GIT1 complex drives apoptosis through the downstream activation of the Rac-JNK-Jun-Bim apoptotic pathway, whereas loss of hScrib function, caused by RNAi-mediated ablation or by membrane displacement of the protein, redirected c-Myc signalling from a pro-apoptotic to a pro-oncogenic pathway (Zhan et al., 2008), possibly involving an aberrant activation of the MAP kinase JNK (Wu et al., 2010). The interaction of β-PIX with hScrib has also been shown to modulate the correct localisation of the GEF at the leading edge of migrating cells, to promote directional migration by spatially restricting the activities of Rac and Cdc42 (Qin et al., 2005), and to guide epithelial morphogenesis in 3D culture systems through the control of the Cdc42 and Rac effector p21-activated kinase 1 (PAK1) (Eastburn et al., 2012). Interestingly, in the latter study hScrib has been identified as a client protein for the HSP90/sgt1 chaperone complex, and the integrity of the HSP90/sgt1/hScrib complex appears to be required to regulate hScrib stability (Eastburn et al., 2012). These data provide molecular evidence for the importance of the correct expression of hScrib for regulation of apoptosis, migration and epithelial morphogenesis.

For the other member of the hScrib polarity complex, the tumor-suppressor properties of Hugl are the least understood. Vertebrates express two homologs of the Drosophila Lgl, Hugl-1 and Hugl-2 whose expression have been shown to be deregulated in a variety of human cancers (Schimanski et al., 2005; Kuphal et al., 2006; Tsuruga et al., 2007; Lisovsky et al., 2009). Moreover, recent evidence suggests that Hugl1 and 2 are potent inhibitors of the EMT program. Consistent with this, expression of Hugl-1 and Hugl-2 has been shown to promote junctional E-cadherin localization and re-induction of the epithelial phenotype, respectively, in melanoma and breast cancer cell lines
(Kuphal et al., 2006; Kashyap et al., 2012). Therefore, Hugl proteins are strong inducers of the epithelial program and this is achieved, at least in part, through the modulation of the EMT-associated transcription factor Snail (Kashyap et al., 2012). However, recent data from a zebrafish model for epidermal carcinogenesis, suggest that Lgl2 can maintain the epithelial phenotype by regulating ErbB2-associated signalling (Kashyap et al., 2012). To date there is no evidence for direct targeting of Lgl by oncogenic viruses, however the inactivation of the PDZ-containing members of the hScrib polarity complex are likely to affect also the activity of Lgl.

**Targeting of junctional complexes by viral oncoproteins**

As noted above, although human oncogenic viruses constitute a highly heterogeneous group of viruses, their life cycles necessitate the modulation of common host cellular pathways (Moore and Chang, 2010) and these effects are reflected in the tumors they produce. One such pathway is cell polarity, and different human tumor viruses adopt overlapping strategies to perturb the expression patterns of polarity proteins, including cadherins and PDZ domain-containing proteins (Figure 6). A list of PDZ domain containing proteins known to be targets for viral oncoproteins is provided in Table 1. Human tumor viruses, including HPV, EBV, HBV, HCV, and KSHV, have all been shown to perturb the pattern of E-cadherin expression. Oncoproteins expressed by EBV, HBV and HCV have been shown to down-regulate E-cadherin expression through the methylation of its promoter or by up-regulating the expression of EMT-associated transcription factors TWIST and SNAIL (Banks et al., 2012). In contrast, KHSV promotes both the degradation and the PAK-1-mediated mis-localisation of VE-cadherin in endothelial cells (Banks et al., 2012). In the case of HPV, both E6 and E7 oncoproteins are able to repress the transcription of E-cadherin by increasing the activity of DNA methyltransferases and E-cadherin promoter methylation (Laurson et al., 2010; D'Costa et al., 2012). In addition, the perturbation of members of the hScrib complex is also likely to affect E-cadherin stability (Qin et al., 2005; Lohia et al., 2012). Thus, HPV and other human tumor viruses perform a coordinated attack aimed at perturbing the pattern of expression E-cadherin, suggesting the importance of inhibiting E-cadherin function during viral life cycles.
Figure 6. Distribution of polarity and signalling components at the AJs and TJs and their targeting by tumor-associated viruses. See the next page for the full legend.
Figure 6 (Cont.). Depicted are the transmembrane components of AJs and TJs as well as the cytosolic proteins associating with their plaques (blue boxes) and the downstream pathways that are regulated upon their assembly (green boxes) in non-infected and infected cells. The modulation of AJ- and TJ-associated components by oncogenic viruses leads to the deregulation of proto-oncogenic signalling pathways (see text) promoting cell proliferation, migration and invasion. TJ integrity creates separate microenvironments in the basal and apical compartments of polarized cells. Disruption of TJ assembly by oncogenic viruses through the inactivation of TJ-associated cytosolic proteins increases the accessibility of growth factor receptors (e.g. EGFR/ErbB) to their ligands (e.g. EGF), further promoting the activation of oncogenic pathways. Targeting of cadherin-based AJs or its associated proteins contributes to the loss of cell polarity and acquisition of a mesenchymal phenotype.
Besides induction of cell proliferation, another possible role for the perturbation of E-cadherin expression might be linked to its ability to modulate the cell-mediated immune response to viral infection. The recruitment of epidermal antigen-presenting cells to the sites of infection in the epidermis requires the expression of E-cadherin by both antigen-presenting cells and keratinocytes. Loss of E-cadherin expression leads to reduced retention of antigen-presenting cells in the infected tissue (Tang et al., 1993; Jakob and Udey, 1998), and low abundance of antigen-presenting cells at sites of viral infection has been shown to correlate with higher disease severity (Sprecher and Becker, 1983; Sprecher and Becker, 1989). Thus, the targeting of E-cadherin could contribute to the immune evasion by human tumor viruses; however, loss of E-cadherin is also strongly implicated in the process of virus-induced carcinogenesis. As mentioned above, the perturbation of E-cadherin expression is a hallmark of EMT and is invariably associated with loss of APC function and acquisition of invasive properties by tumor cells. In addition, loss of E-cadherin also results in the perturbation of hScrib complex-mediated regulation of cell polarity.

The perturbation in the pattern of hDlg expression has been shown to be associated in some cases with acquisition of tumorigenic capacity, and this, in part, is achieved through the interaction of hDlg with PBM-containing GEFs, including Net1 and SGEF (García-Mata et al., 2007; Krishna Subbaiah et al., 2012). hDlg has been reported to regulate Net1 localization and activity, conversely, oncogenic mutants of Net1 are believed to promote the hDlg sequestration and inhibition of hDlg function (García-Mata et al., 2007). Likewise, high-risk HPV E6 and E4-ORF1 tumorigenic activities have been shown to rely in part on the mislocalization of hDlg. In HPV-18 positive cervical cancer cells, E6 oncoprotein has been shown to recruit hDlg to detergent-insoluble sites where, in cooperation with SGEF, a RhoG-specific GEF, hDlg promotes the invasiveness of HeLa cells via the activation of RhoG (Krishna Subbaiah et al., 2012). The interaction of Ad9 E4-ORF1 with PDZ proteins has been shown to recruit the oncoprotein to cell-cell contact sites, where it drives the activation of the PI3-kinase, an activity that correlates with Ad9 mammary tumorigenesis in mice (Frese et al., 2003). In this context, the E4-ORF1-mediated PI3-kinase stimulation was shown to rely on the formation of a complex with hDlg, resulting in its membrane sequestration where it cooperates with the adenoviral oncoprotein to stimulate the PI3 kinase
pathway (Frese et al., 2006). Another homolog of hDlg, PSD95, has also been identified as a binding partner for high-risk E6 oncoproteins (Gewin et al., 2004). PSD95 is a preferential proteolytic substrate for HPV-18 E6 oncoprotein, and the forced expression of this PDZ protein in HPV-positive cervical cancer cells has been shown to reduce their tumorigenic potential (Handa et al., 2007).

Many PDZ domain-containing proteins of the TJ plaque are inactivated by viral oncoproteins, resulting in the loss of TJ integrity. Consistent with the importance of ZO proteins for the modulation of cell proliferation, ZO-2 was found to interact with adenoviral E4-ORF1 in a PDZ-dependent manner, leading to aberrant cytoplasmic sequestration of the PDZ protein (Glaunsinger et al., 2001). Cells that lack ZO-1 and ZO-2 fail to form TJs (Umeda et al., 2006), and although the targeting of ZO-2 by E4-ORF1 proved the importance of ZO proteins for adenovirus 9-mediated transformation, other members of the ZO family do not appear to be directly targeted by virus-encoded oncoproteins. However, indirect effects are likely, through the inactivation of factors involved in the regulation of ZO localisation/activity. The PDZ proteins MAGI-1 and PATJ, have been shown to be substrates for high-risk HPV E6 and E4-ORF1 oncoproteins (Glaunsinger et al., 2000; Latorre et al., 2005; Storrs and Silverstein 2007), and their inactivation is associated with mislocalisation of ZO-1 and other TJ components (Latorre et al., 2005; Kranjec and Banks, 2011).

In the context of HTLV-1-mediated transformation, populations with reduced expression of MAGI-1 are selected during neoplastic transformation (Makokha et al., 2012). In addition, the loss of MAGI-1 observed in acute lymphoblastic leukaemia (Kuang et al., 2008) suggests that its tumor-suppressive potential goes beyond the regulation of junctional stability. In addition, MAGI-2 and MAGI-3 have also been shown to be the target for viral oncoproteins (Thomas et al., 2002; Ohashi et al., 2004) suggesting a potential tumor-suppressor role also for these proteins.

It is interesting to note that the crystal structures of HPV-18 E6 bound to the PDZ domains of MAGI-1, MAGI-3 and hDlg have recently been solved, and this allowed us to define the relative contributions given by single amino acids within the PBM and PDZ domains to the interaction (Zhang et al., 2007; Thomas et al., 2008a). Importantly, these studies revealed that not only
residues within the HPV-18 E6 PBM (ETQV), but also those immediately upstream, contribute to the binding to PDZ proteins. The residues of the PBM specifically contributing to the binding to hDlg, MAGI-1 and -3 varied according to the PDZ substrate considered, suggesting that subtle differences within the PDZ domains of these proteins modulate the interaction with E6 PBM (Thomas et al., 2008a). Moreover, subsequent studies identified the specific residues within the PDZ domain-1 of MAGI-1 that mediate its association with the E6 PBM (Fournane et al., 2011). Within the PDZ1 the arginine residue at position 499 (K499) was shown to be crucial for the interaction with E6 PBM, and its mutation to glutamic acid (K499E) strongly reduces the strength of the interaction (Fournane et al., 2011). However, what the functional consequences are of the disruption of the interaction between MAGI-1 and E6 in context of the HPV pathology, remains an open question.

*Targeting of PDZ-dependent functions not associated with cell junctions*

Although high-risk HPV E6 targets a number of PDZ domain-containing proteins associated with junctional complexes, it has also been shown to interact with PDZ-proteins associated with other activities, and a list of the identified E6 PDZ substrates is shown in Table 1. These include the protein phosphatases PTPN3 and FAP1, the Tax-interacting proteins (TIP)-1 and -2 and CFTR (cystic fibrosis transmembrane regulator)-associated ligand (CAL) (reviewed in Thomas et al., 2008b).

TIP-1 and TIP-2 were originally discovered as HTLV-1 Tax-binding proteins in a yeast two-hybrid screen for PDZ-containing binding partners for Tax-1 (Rousset et al., 1998), and subsequently both have been shown also to interact with high-risk E6 oncoproteins (Hampson et al., 2004; Favre-Bonvin et al., 2005). TIP-2 interacts with the GTPase-activating protein (GAP) GAIP, which associating with Gα subunits of heterotrimeric G proteins, promotes their rapid cycling from GTP- to GDP-bound state, thereby accelerating their inactivation (De Vries et al., 1998). One of the functions associated with TIP-2 expression is the modulation of cell responsiveness to TGFβ, by driving the expression of type III TGFβ receptors at the cell surface through the direct interaction with its class I PBM. This results in the activation of TGFβ-responsive genes and inhibition of cell
growth (Blobe et al., 2001). HPV-18 E6 has been shown to interact with and drive the proteasome-mediated degradation of TIP-2 and, consistent with its biological function, loss of TIP-2 correlated with a decrease in TGFβ-mediated cell growth inhibition of HPV-positive cells (Favre-Bonvin et al., 2005). In marked contrast with other PDZ-containing proteins, TIP-1 activity was shown to be promoted by the presence of HPV-16 E6. Structurally the TIP-1 protein is composed almost

Table 1. Identified PDZ-containing targets for viral oncoproteins.

<table>
<thead>
<tr>
<th>Target PDZ protein</th>
<th>Targeting viral oncprotein</th>
<th>Effects on target protein</th>
<th>Target protein function</th>
<th>References</th>
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<tr>
<td>hDlg</td>
<td>HPV E6</td>
<td>Degradation/sequestration</td>
<td>Cell polarity / context dependent function (?)</td>
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<td>Sequestration</td>
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<td>Lee et al., 1997</td>
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<td></td>
<td>HTLV-1 Tax1</td>
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<td>Modulation of p38γ / context-dependent function</td>
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<td>Sequestration</td>
<td>Cell polarity/tumor suppressor</td>
<td>Glaunsinger et al., 2001</td>
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exclusively of a single PDZ domain, and it has been proposed to antagonize PDZ-mediated interactions by competing with other PDZ-proteins for the binding to target PBM (Alewine et al., 2004).
2006). A pro-oncogenic function for TIP-1 has been proposed, with the activation of Rho-dependent gene expression, exerted through the interaction with the PBM of the Rho effector rhotekin (Reynaud et al., 2000). Consistent with the latter studies, expression of TIP-1 in HPV-16 E6-expressing cells has been shown to be required to activate RhoA signaling (Hampson et al., 2004).

A contribution to the stimulatory effect of cell growth has been suggested to be given by E6 through the targeting of PDZ domain-containing cellular phosphatases. Three PDZ domain-containing protein tyrosine phosphatases (PTPs), FAP-1 (PTPN13), PTPH1 (PTPN3) and PTPMEG1 (Alonso et al., 2004), have been described, with PTPH1 and FAP-1 closely linked to tumorigenesis. Although their roles in tumorigenesis are still controversial, FAP-1 and PTPH1 have been shown to be inactivated by high-risk HPV E6 oncoproteins, supporting a tumor-suppressor function in the context of the HPV pathology. Early studies suggested a possible tumor-suppressor potential for PTPH1, since mutations were reported in some colorectal cancers (Wang et al., 2004): however, more recent studies are indicative of pro-oncogenic activity. K-Ras was shown to increase the expression levels of PTPH1 and p38γ (Hou et al., 2010), with PTPH1 and p38γ interacting in a PDZ–PBM-dependent manner. This results in dephosphorylation of phospho-p38γ and inhibition of the phospho-p38γ-mediated down-regulation of Ras signalling (Han and Sun 2007; Hou et al., 2010), thereby generating a positive-feedback loop. PTPH1 was also found to be overexpressed in a number of breast cancers, resulting in a perturbation of vitamin D receptor localization and stimulation of cell proliferation (Zhi et al., 2011). PTPH1 has been recently identified as proteolytic substrate for HPV-16 E6 oncoprotein in human keratinocytes (Jing et al., 2007; Töpffer et al., 2007). Expression of HPV-16 E6 in human immortalized keratinocytes correlated with the acquisition of cell growth capabilities with reduced nutrient requirements, in a PBM-dependent manner. Silencing of PTPH1 partially reproduced the ability of keratinocytes to grow under stringent conditions, suggesting a contribution of loss of PTPH1 toward this phenotype (Jing et al., 2007). Although FAP-1 has been reported to be regulated through its localization at AJs, it possesses a broader spectrum of biological activities. FAP-1 has been shown to be a potent negative regulator of the Src signaling, and a regulator of the Fas-
mediated apoptotic pathway (Cuppen et al., 2000; Ungefroren et al., 2001; Lai et al., 2007; Glondu-Lassis et al., 2010). Recently, HPV-16 E6, but not its PBM-deletion mutant, has been reported to promote anchorage-independent growth in tonsil epithelial cells and invasive cell growth in cooperation with activated Ras (Spanos et al., 2008a, Spanos et al., 2008b). Likewise, loss of FAP-1 was sufficient to promote anchorage-independent growth of epithelial cells, and depletion of the phosphatase cooperated with Ras to promote invasiveness (Spanos et al., 2008b). This suggest that these oncogenic activities of E6 are mediated, at least in part, through the inactivation of FAP-1.

CAL is a PDZ-containing protein associated with the Golgi apparatus. It is involved in the intracellular trafficking of different receptors (Yao et al., 2001; Hassel et al., 2003; Gentzsch et al., 2003), and it was shown to promote the lysosomal degradation of CFTR, hence reducing its exposure on the cell surface (Cheng et al., 2002; Cheng et al., 2004). Recently, CAL was described as a novel binding partner for HPV-16 E6, and is targeted for proteasome-mediated degradation by HPV-16 and -18 E6 oncoproteins, although it is a preferential substrate for 16 E6 (Jeong et al., 2007). Interestingly, CFTR expression was described as a prognostic marker for malignant progression of cervical cancer (Peng et al., 2012), hence the inactivation of CAL by E6 could significantly contribute to cervical cancer progression through the elevation of CFTR levels.

**HPV life cycle**

Papillomaviruses (PVs) are a broad group of small unenveloped DNA viruses, infecting a wide variety of vertebrates. A recent classification, listed 189 PV types in the Papillomaviridae family, organized in 29 genera according to their genetic and pathological characteristics. Of these, 5 genera include the HPVs (Bernard et al., 2010). This heterogeneity is reflected by different replicative modalities, due to differences in their gene products, sites of infection, patterns of interaction with host factors and responsiveness to external stimuli. The best studied group are the alpha papillomaviruses, which infect cutaneous and mucosal epithelia with clinical manifestations ranging from self-remissive infections associated with benign warts to persistent infections that can eventually lead to anogenital and head and neck cancer. Within the alpha PV types, 12 HPV types
have been defined as cancer-causing, with HPV-16 and -18 being predominant, accounting for about 70% of the global cervical cancer cases (zur Hausen, 2002), of which there are over 500 000 new cases every year (Forman et al., 2012).

The HPV life cycle is intimately linked to the differentiation program of the infected keratinocytes, where the expression of specific viral gene products and maturation of viral particles coincides with the induction of differentiation in the infected cells. Figure 7 shows the genomic organization of HPV-16 and the sequential activation of the HPV genome in the infected epithelium. In the generally accepted model for HPV infection, viral particles are thought to penetrate stratified epithelia through micro-lesions, resulting in the localization of the virus at the basal lamina where it can infect stem cells or transiently amplifying cells of the basal epithelial layer, the natural host cells of HPV (Stubenrauch and Laimins, 1999; Pyeon et al., 2009). The pro-inflammatory response evoked during wound-healing processes, as well as the transient elevation of growth factors at the site of infection in the basal layer, are also thought to be beneficial for successful infection through the stimulation of cell proliferation. Recent evidence suggests that the mitotic progression through the cell-cycle and nuclear membrane break-down are also required for successful viral infection, allowing nuclear entry of the viral DNA (Peyon et al., 2009). In stratified epithelia only the cells in the basal layer are mitotically active, and this might in part provide an explanation for the tropism of HPV for these cells. At initial stages of infection, viral gene expression is activated resulting in the production of 20 to 100 copies of episomal viral DNA. Episomes are stably maintained in basal layer cells (Sterling et al., 1990; De Geest et al., 1993), and induction of differentiation results in the viral DNA vegetative amplification in the suprabasal epithelial layers, where viral DNA is amplified to a high copy number and ultimately packaged in the new virions. These three phases of the viral life cycle are accomplished by the activation and sequential expression of “early” and “late” viral proteins within the differentiating epithelium.

As mentioned above, the primary function of DNA tumor virus-encoded oncoproteins is to provide an environment that can support the viral life cycle. The two major HPV oncoproteins are E6 and E7, although E5 also displays important oncogenic functions (see below). The expression of HPV-
16 E6 and E7 from the early region of the viral genome is under the control of the p97 promoter and begins at early stages after the virus entry. The expression of E6 and E7 in the basal layer clonally expands the population of infected cells that are competent to progress to the differentiation-promoted stages of viral life cycle (i.e. expression of late transcripts and release of viral particles). In stratified epithelia, the basal layer represents the reservoir of actively proliferating cells. As basal cells divide, a population of daughter cells is pushed to migrate in the suprabasal layers whilst the basal cell population is maintained as slow-cycling and self-renewing cells. In virus-free epithelia, cells that leave the basal layer exit the cell cycle, cease to replicate their DNA and, as a result of the terminal differentiation program, they lose their nuclei in the upper layers of the epithelium. Therefore, HPV needs to reprogram this process and force the cell cycle entry of differentiating cells in order to replicate the viral DNA and establish the infection; this is accomplished mainly through the expression of E6 and E7, which are expressed from initial phases of infection onwards. As mentioned above, E7 oncoproteins play an active role in the induction of cell proliferation through the inactivation of members of the pRB family, whilst E6 prevents the activation of apoptotic pathways induced by E7, through the inactivation of p53. The cell-cycle entry in the basal cell layer is mainly controlled by pRB and p107, whereas the S-phase re-entry in differentiating cells is preferentially regulated by p130, likely reflecting the availability of different E2F family members of transcription factors during different phases of epithelial differentiation (Paramio et al., 1998; Litovchick et al., 2004). Thus, E7 proteins derived from high-risk HPV types through the inactivation of all the members of the pRB protein family, drive the acquisition of a S-phase competent phenotype throughout the epithelium (Zhang et al., 2006; Zerfass et al., 1995a). This also highlights the molecular basis for the different pattern of cell-cycle activation seen in the pathology linked to low-risk HPV infection, where S-phase competent cells are present primarily in the suprabasal layers of the epithelium (Doorbar et al., 2012). In addition, the CKII-mediated phosphorylation of E7 increases the ability of E7 to bind and inactivate p130 (Genovese et al., 2008), suggesting that changes in the levels of CKII phosphorylation of E7 might affect the ability of E7 to perturb pocket protein function. Furthermore, the ability of E7 to promote the activation of E2F responsive genes depends on its ability to impair the function of cellular
Figure 7. Schematic representation of HPV-16 genome and the sequential expression of viral gene products during differentiation of the infected epithelium.

A. The ORFs encoding the different viral genes are positioned along the genome. The position of the early and late promoters, as well as of the long control region (LCR) are also depicted. B. The figure shows the presumed route of HPV infection of the epithelial mucosa basal cell layer through microtraumas. There is coordinate expression of the different viral gene products in a differentiation-regulated manner, with E6/E7 causing an expansion of S-phase competent cells. This allows viral genome amplification and, ultimately, the synthesis and shedding of new viral particles within a period of 2–3 weeks (adapted from Middleton et al., 2003).
histone deacetylases (HDACs) (Brehm et al., 1999; Longworth et al., 2005), and the activation of E2F-responsive promoters by E7 is dependent upon the integrity of both its pRB and HDAC binding sites (Zhang et al., 2004; Zhang et al., 2006). The ability of E7 to promote S-phase entry, is also aided by its interaction with cyclin-dependent kinase (CDK) inhibitors p21cip and p27kip1, leading to their inactivation (Zerfass-Thome et al., 1996; Funk et al., 1997; Jones et al., 1997b) and upregulation of the S-phase cyclins A and E (Zerfass et al., 1995b). The inhibitory effect of p21cip and p27kip1 are in part driven by E7, also through the up-regulation of Akt activity. Akt, or PKB, is a serine/threonine kinase activated upon the sequential phosphorylation by PDK1 and mammalian target of rapamycin complex 2 (mTORC2), which are downstream targets of the growth factor-responsive phosphoinositide 3-kinase (PI3K). Akt regulates several proto-oncogenic processes, including proliferation, cell survival and protein translation, the last of which is mediated through the regulation of the "nutrient sensor" mTORC1 and its associated signaling (Ma and Blenis, 2009). In the stratified epithelium the activity of proto-oncogenic pathways, such as Ras and PI3K, are restricted in the basal layer and are lost during differentiation (Dajee et al., 2002; Menges et al., 2006). The disruption of pRB-E2F complexes by viral oncoproteins has been suggested to promote the stimulation of PI3K and Akt, through the activation of the E2F-responsive gene Gab2, a positive mediator of PI3K signaling (Chaussepied and Ginsberg, 2004). The HPV-16 E7-mediated activation of Akt has been shown to promote the cytoplasmic retention of the CDK inhibitors p21cip and p27kip1 upon oncogenic insult (Westbrook et al., 2002; Charette and McCance, 2007). The E7-induced mislocalisation of p21 and p27 correlated respectively with loss of oncogene-induced cell cycle arrest and increased migration of human foreskin keratinocytes (HFKs), and both these effects could be reverted upon inhibition of Akt (Westbrook et al., 2002; Charette and McCance, 2007). Interestingly, low-risk E7 oncoproteins are also able to stimulate the activity of Akt, however this occurs through a pocket protein-independent mechanism (Pim et al., 2005). Thus, E7 induces a pseudo S-phase condition in parabasal layers of the epithelium, establishing an environment suitable for the viral genome amplification.

As mentioned above, in normal epithelia, the expression of p14ARF and activation of p53 can function as a molecular sensor of unscheduled DNA replication. However, the expression of E6
prevents the activation of these pathways by promoting the proteasome-mediated degradation of both hAda3 and p53 itself, an activity dependent upon the host E3 ubiquitin-ligase E6AP (Scheffner et al., 1990; Scheffner et al., 1993; Shamanin et al., 2008; Hu et al., 2009). Conversely, low-risk E6 proteins are thought to perturb p53 function by relieving its repression on TATA-containing promoters (Lechner et al., 1992) and hindering the activation of p53-responsive genes (Mietz et al., 1992; Pim et al., 1994). Moreover, it was shown that E6-interacting regions of p300 are necessary for E6 to inhibit p53-dependent transcription and that E6 activity can inhibit the acetylation of both p53 and nucleosomal core histones, without altering p53 and p300 recruitment to chromatin. This process is E6AP-independent and shows a unique mechanism of E6 repression of p53 activity which does not involve proteasomal degradation (Thomas and Chiang, 2005). In line with a central role for p300/CBP in the life cycle of many different viruses, several other DNA tumor viruses have also been shown to interact with p300/CBP (Goodman and Smolik, 2000; reviewed in Moore and Chang, 2010), highlighting its central role in regulating cellular homeostasis. As for other E6 targets, high-risk HPV E6 oncoproteins were reported to bind strongly to p300/CBP whereas the association with low-risk HPV-derived E6 is weaker (Patel et al., 1999). It was also shown that HPV-16 E6 inhibits the intrinsic transcriptional activity of p300/CBP on both p53 and NFκB-responsive promoter elements. In the case of p53 this is partly due to an inhibition of p300-mediated acetylation (Thomas and Chiang, 2005).

High-risk, but not low-risk, E6 proteins are able to reactivate the telomerase complex, partly in cooperation with E7, thereby contributing towards prolonging the lifespan of infected cells (Klingelhutz et al., 1994; Klingelhutz 1996; DeFilippis et al., 2003; Xuefeng et al., 2009). An interesting function of E6, shared with E7, is its ability to activate PI3K/Akt signaling. Expression of HPV-16 E6 in primary keratinocytes, has been found to be sufficient to sustain the PI3K signaling under conditions of nutrient deprivation, through the aberrant hyper-activation of growth factor receptors (Spangle and Münger, 2013). This activity of E6 correlated with the stimulation of mTORC1 and increased cap-dependent protein synthesis (Spangle and Münger, 2010). Interestingly, the effect produced by high-risk E6 oncoproteins on protein translation was shown to be dependent upon its interaction with the E6AP and, in part, on its PBM. Consistent with this,
low-risk HPV E6 oncoproteins, which are able to interact with E6AP but lack the PBM, were able to activate protein translation, albeit to a lesser extent compared with HPV-16 and -18 E6 oncoproteins (Spangle and Münger, 2012).

An important factor in the establishment of infection, is the modulation of the host immune system response. This evasion can lead to the establishment of persistent infections, the prime risk factor for malignant progression (Bodily and Laimins, 2011). HPV exerts a global effect on the innate immune response in infected keratinocytes; pro-inflammatory cytokines, including type-1 interferon, are not released and signals required for the activation and migration of intraepithelial Langerhans cells (LCs) and macrophages are inadequate (Kanodia et al., 2007). High-risk HPV E6 and E7 actively contribute to this through the deregulation of the innate immune response. They cooperate to down-regulate the expression of interferon (INF)-responsive genes, including INF-α and -β (Nees et al., 2001). The two oncoproteins also perturb the signaling pathways activated following INF stimulation; E6 interferes with the activation of Jak-STAT signaling upon INF-α treatment (Li et al., 1999), whereas E7 blocks the activity of interferon responsive element (IRF)-1 and NFκappaB following exposure of cells to interferon stimulation (Perea et al., 2000; Um et al., 2002). In addition, perturbation of cell polarity by E6 and E7 through the reduction of cell surface E-cadherin exposure contributes to impair the recruitment of LCs to infected epithelial cells, ultimately leading to the depletion of LCs from the infected epithelium and inadequate T-cell priming (Matthews et al., 2003). Recently, PDZ proteins have also been shown to contribute directly to the regulation of the interferon response (Werme et al., 2008; Kumar et al., 2012), suggesting that E6’s PDZ-binding activity could be relevant for the modulation of innate immunity, although the experimental evidence is still missing.

The viral E1 and E2 proteins are among the first viral proteins to be expressed in the infected epithelium (Longworth and Laimins, 2004b). E2 is a DNA-binding protein that recognizes multiple binding sites in the LCR (long control region) of the viral genome. The association of E2 with E1 recruits the latter to viral origins, where the recruitment of cellular polymerases begins the viral DNA replication (Sedman et al., 1997; Dixon et al., 2000). E1 possesses a helicase activity but has
a weak DNA binding activity, and it requires the interaction with E2 to mediate its association with viral origins (Sedman et al., 1997; Dixon et al., 2000). In addition, studies with the bovine papillomavirus type 1 (BPV1), revealed that E2 plays an important function in tethering the viral episomal DNA to host chromosomes, thereby ensuring an equal partitioning of replicated viral DNA to daughter cells (Skiadopoulos and McBride, 1998; Ilves et al., 2006). In BPV1, the host bromodomain protein Brd4 mediates the association of E2 with chromatin (You et al., 2004; McPhillips et al., 2006) and stimulates the E2-dependent transcription activation (Ilves et al., 2006). Conversely, HPVs rely on different cellular factors in order to mediate the tethering of viral DNA to chromatin through E2 (Parish et al., 2006), although Brd4 is required for the E2-mediated viral DNA transcription (McPhillips et al., 2006). It is important to note that intact E1 and E2 ORFs appear to be required for the stable maintenance of BPV1 viral episomes, (Sarver et al., 1984), and that the DNA-binding activity of E2 prevents the integration of HPV-31 genome into the host (Stubenrauch et al., 1998a). Viral genome integration leads to unscheduled E6 and E7 expression, and has been proposed as one of the events leading to malignant progression of HPV infections (Jeon et al., 1995b; Song et al., 2000). Moreover, binding of E2 to its DNA-binding sites in the LCR has been shown to repress the activity of the early promoter (p97) (Steger and Corbach, 1997; Stubenrauch et al., 1998a). Thus, this ability allows E2 to have an indirect inhibitory effect on cell proliferation through the repression of E6 and E7 expression (Francis et al., 2000).

The E5 protein is highly hydrophobic and interacts with the 16-kD pore-forming protein component of the vacuolar H⁺-ATPase, responsible for acidifying cellular organelles such as the Golgi apparatus (Conrad et al., 1993). E5-mutant HPV-16 and -31 genomes exhibit reduced DNA synthesis in the suprabasal layers of infected epithelia (Genther et al., 2003; Fehrmann et al., 2003a) and hence impaired expression of late viral proteins (Fehrmann et al., 2003), however E5's role in HPV genome amplification is controversial. One of the most prominent functions of E5 is its ability to potentiate EGF signaling and drive the activation of MAP kinase pathways (Conrad et al., 1994; Crusius et al., 1998; Crusius et al., 2000). Importantly, ERK kinases 1 and 2 have been show to be critical modulators of the nuclear accumulation of the viral helicase E1, where
phosphorylation by cyclin A and B/Cdk2 complexes inhibit the shuttling of E1 to the cytoplasm (Deng et al., 2004; Yu et al., 2007). However, loss of E5 function in the context of HPV-16 and -31 infection only marginally affected the viral genome amplification (Genther et al., 2003; Fehrmann et al., 2003), suggesting that host and viral DNA synthesis are uncoupled. The modulation of host mitogenic pathways, along with the ability to inhibit apoptosis (Kabsch et al., 2004), supported a possible role for E5 in cancer progression together with E6 and E7. The expression of E5 induces the potentiation of the epidermal growth factor (EGF)-mediated mitogenic signal in multiple cell lines (Pim et al., 1992; Leechanachai et al., 1992) and cooperates with E7 to transform primary rodent epithelial cells (Bouvard et al., 1994; Valle and Banks, 1995). Nevertheless, during cancerous progression in most cases large parts of the viral genome, including the E5 ORF are deleted upon integration of the viral DNA into the host genome (Schwarz et al., 1985), although the potentiation of EGFR signalling by E6 might compensate for loss of E5 (Akerman et al., 2001).

The expression of E4 is under the control of the differentiation-dependent promoter, and it is the most highly expressed of the viral proteins. Its accumulation is dependent upon the formation of amyloid-like insoluble structures driven by the C-termini of E4 proteins (McIntosh et al., 2008). High level of E4 expression is a surrogate marker for efficient viral replication (Doorbar et al., 1997), associated with productive viral life cycle and low grade lesions (Doorbar et al., 2012), whereas its expression is progressively lost during malignant progression. A role for E4 in mature virion release has been proposed, since E4 is able to interact with and reorganize cytokeratins (Doorbar et al., 1991; Wang et al., 2004). Loss of the integrity of the keratin network is thought to favor the viral egress (Doorbar et al., 1991). In addition, E4 promotes the G2 arrest of infected cells through the modulation of cyclin/Cdk complexes (Knight et al., 2004; Davy et al., 2005; Knight et al., 2006; Davy et al., 2006). This activity is thought to be important for uncoupling viral genome replication from mitosis, thus supporting HPV genome amplification while blocking progression through the cell cycle. Evidence for the relevance of E4 functions in context of the viral life cycle come from studies where loss of E4 reduced vegetative replication and expression of late
transcripts, ultimately leading to reduced virion formation (Peh et al., 2004; Nakahara et al., 2005; Wilson et al., 2005).

The viral capsid proteins L1 and L2 are expressed in the late stages of infection, after viral genome amplification. While both capsid proteins are essential for the assembly of infectious viral capsids (Zhou et al., 1993; Holmgren et al., 2005; Kämper et al., 2005), L1, the major viral capsid protein, can spontaneously assemble into VLPs (Kirnbauer et al., 1992), and this ability of L1 provides the basis for the HPV vaccine (Kirnbauer et al., 1992). Conversely, L2, the minor capsid protein, regulates the early stages of infection, promoting the shuttling of viral DNA from late endosome/lysosome compartments to the host cell nucleus. In the later stages of infection, it enhances the viral genome encapsidation, ensuring the successful completion of the productive stage of the life cycle (Holmgren et al., 2005).

From productive viral life cycle to cancer and the significance of PDZ-protein targeting

An important feature of HPV and other tumor virus life cycles, is their ability to establish long-term persistent infection in their hosts (Banks et al., 2012). In order to persist, HPV needs to evade the host immune response. This is achieved in part by the E6 and E7 through the modulation of the innate immune response, but is also aided by the peculiarities of the HPV life cycle; it is exclusively intraepithelial, there is no viraemia and it is not associated with cytolysis or inflammation (Stanley, 2012b). The steps believed to be involved in the progression from productive viral life cycle to cervical cancer are depicted in Figure 8. Nevertheless, the vast majority of HPV infections (80-90%) result in low-grade lesions, and, as suggested by animal models of HPV infection, are cleared as a result of the generation of a CD4 and CD8+ T cell-mediated immunity which leads to the regression of the lesion (Nicholls et al., 2001; Monnier-Benoit et al., 2006). However, the lack of an effective cell-mediated immune response able to control the infection can lead to persistent infection and, in the case of cancer-causing HPV types, to an increased risk of developing high-grade lesions and invasive carcinoma. Long term infections imply that the cells have to support the expression of viral oncoproteins for long periods of time, thus increasing the risk of accumulating proto-oncogenic mutations and the likelihood of
Figure 8. Schematic representation of the events believed to be involved in the progression from productive HPV infection (left-hand panel) to malignancy (right-hand panel). Upon HPV infection, the lack of immune clearance might lead to a persistent infection in which lesions are not resolved and viral DNA can be detected over extended periods of time. This ultimately predisposes the host to the development of a malignancy. This is characterized by a loss of differentiation, no viral replication and high levels of E6 and E7 oncoprotein expression (adapted from Middleton et al., 2003).
“mistakes” that eventually might lead to deregulation of the viral life cycle and/or viral DNA integration into the host genome. In HPV-infected epithelia, the viral life cycle can become deregulated as the result of the perturbation of viral gene expression, frequently leading to viral genome integration and progression to malignancy (Doorbar et al., 2012). This model appears to be confirmed by the observation that epithelia that are not permissive for the viral life cycle are sites where infection by high-risk HPV types can progress very rapidly to cancer, with high rates of viral genome integration (Herfs et al., 2012). In epithelia permissive for the viral life cycle, such as columnar and squamous cervical epithelia, where most of the research has been carried out, productive infection is primarily associated with low grade lesions, or cervical intraepithelial neoplasia grade 1 (CIN1), where tightly controlled expression of E6 and E7 sustains all the phases of productive viral life cycle. In this context, the consequences of deregulation of PDZ-containing proteins by high-risk E6 oncoproteins is still poorly understood. In stratified epithelia, symmetric divisions of basal cells occur parallel to the basal membrane axis, producing two daughter cells phenotypically identical that preserve the ability to proliferate and self-renew. Conversely, asymmetric divisions, perpendicular to the basal membrane produce a basal stem cell and an apical cell that is committed to differentiate (Muroyama and Lechler, 2012), involving the reorientation of the mitotic spindle and unequal distribution of cell fate determinants between daughter cells (Lechler and Fuchs, 2005). Although the mechanism that controls the switch from symmetric to asymmetric division in basal cells is poorly understood, compelling evidence suggests that reorientation of mitotic spindles requires components of the apico-basal polarity control (Roegiers and Jan, 2004). Therefore, HPV is potentially able to subvert the control of spindle orientation through E7’s stimulation of the cell cycle combined with the E6 perturbation of hScrib, hDlg and components of apical polarity complexes, all of which have been shown to direct the spindle orientation in epithelial cells (Knoblich, 2008; Johnson et al., 2009; Hao, 2010). This could contribute towards increasing the population of infected basal cells able to sustain viral replication and expand the area of the lesion by lateral spreading of infected cells. Although the status of most of the HPV PDZ-containing targets is still obscure in context of the viral life cycle, hDlg localization was found to be aberrantly cytoplasmic in the suprabasal layers of CIN1 lesions.
(Cavatorta et al., 2004). This was similar to the pattern of hDlg distribution in the basal epithelial layers of the cervix, suggesting that HPV infection delays differentiation of epithelial tissues. Perturbation of PDZ polarity proteins by E6 in the suprabasal layers is likely to perturb the assembly of TJs, which normally takes place in the differentiated granular layer (Brandner et al., 2002; Kirschner and Brandner, 2012). As discussed previously, assembly of TJs promotes the formation of segregated microenvironments in the cell that prevents the generation of proliferative cues. Thus, after establishment of HPV infection in wounded epithelia, the targeting of PDZ proteins and other components of the epithelial polarity machinery by HPV oncoproteins might delay the restoration of intact junctional complexes and of the epithelial barrier function. Ultimately, this would prolong the exposure of infected cells to proliferative cues, favoring the expansion of the HPV-positive cell population. A summary of the processes potentially targeted by HPV through the inactivation of PDZ domain-containing proteins is depicted in Figure 9. High-risk HPV genomes can be efficiently maintained as episomes in human keratinocytes, and episomal maintenance is dependent upon the functions of E6 and E7 and also of the viral replicative proteins E1 and E2 (reviewed in Doorbar et al., 2012). Human foreskin keratinocytes (HFKs) expressing wild type HPV-31 genomes display marked hyperplasia in suprabasal layers when cultured in organotypic raft cultures (Lee and Laimins, 2004). This effect was associated with the ability of HPV-31 E6 to interact with PDZ-containing proteins since, mutant genomes expressing a PDZ-defective E6 failed to promote the hyperplastic phenotype. HPV-31 genomes, where the E6 PBM has been mutated, provide evidence that loss of PDZ-binding activity results in the abolition of the replicative viral life cycle by the increased tendency of viral DNA to integrate into the host genome (Lee and Laimins, 2004). Recently, similar results have been obtained also with HPV-16 genomes stably expressed in immortal human keraticocytes (NIKS) (Nicolaides et al., 2011). In this study, genomes expressing a truncated form of E6, lacking its PBM, had an increased propensity to integrate in the host genome. However, this correlated with a reduced stability of PBM-defective E6 oncoproteins (Nicolaides et al., 2011).

Although the mechanism is still unknown, these studies suggest that the ability of E6 to interact with PDZ domain-containing proteins is important for the establishment of viral copy numbers in
Figure 9. Possible roles for the targeting of PDZ domain-containing proteins in the HPV pathology. Following infection of basal cells, HPV genomes are maintained as episomes (green circles in dividing cells). The expression of HPV oncoproteins in these cells might lead to the expansion of the basal cell population harboring HPV genomes. In this scenario, the targeting of PDZ domain-containing proteins by E6 might contribute through the alteration of the normal wound healing response and defects in the mitotic spindle orientation due to loss of cell polarity. In the suprabasal layers, targeting of PDZ proteins might interfere with the normal differentiation process by preventing the formation of junctional complexes. Furthermore, this could also increase the exposure of infected cells to mitogenic stimuli, further supporting viral genome amplification and the vegetative life cycle.
basal layers of infected epithelia, and is essential for the correct progression of productive life cycle. Although a subset of HPV-16-positive cervical cancers can arise from cells containing exclusively episomes (Matsukura et al., 1989; Pett and Coleman, 2007; Vinokurova et al., 2008), deregulation of the viral life cycle due to viral DNA integration, has been proposed to be a hallmark of malignant progression of HPV infection (Cullen et al., 1991; Pirami et al., 1997; Badaracco et al., 2002; Woodman et al., 2003), and is associated with transition from low grade productive lesions to higher grade lesions (CIN3), where the ability of the virus to replicate is progressively lost. This condition is believed to be associated with the elevation of E6/E7 expression, predisposing infected cells to accumulate mutations and leading to the development of overt cancer.

**HPV and cancer**

It is currently estimated that about 20% of cancer cases worldwide are caused by an infectious agent. It is important to note that infections leading to cancer in humans can have both viral and non-viral origins, and that 70% of these (about 15% of total cancer cases) are nonetheless linked to viruses. In terms of prevalence in human cancers, however, HPV-associated cancers are the most abundant, with HPV infection being responsible for approximately 5% of the cancer burden worldwide (Parkin and Bray, 2006).

Experiments in tissue culture systems and animal models showed the importance of the combined E6 and E7 activities for cellular immortalization and transformation (Hawley-Nelson et al., 1989; Matlashewski et al., 1987; Riley et al., 2003). Furthermore, in HPV-positive cells the inhibition of E6 and E7 expression, by re-expression of the HPV transcriptional repressor E2, or by siRNA ablation, results in the inhibition of cell growth and induction of cell death by apoptosis, thus highlighting the strict requirement of HPV-transformed cells for the continuous expression of E6 and E7 (Alvarez-Salas et al., 1998; Yoshinouchi et al., 2003). It is important to point out, however, that in primary keratinocytes, the natural target of HPV infection, E6 displays only weak transforming capacity in absence of E7, and that both oncoproteins are required to promote cell immortalization (Barbosa and Schlegel, 1989; Hawley-Nelson et al., 1989; Münger et al., 1989;
Watanabe et al., 1989). An interesting feature of HPV oncoproteins deriving from these assays is that only E6 and E7 oncoproteins deriving from high-risk HPV types drive immortalization, whereas those expressed by low-risk types have weak or no immortalizing capacity (Schlegel et al., 1988b; Hawley-Nelson et al., 1989). As mentioned before, p53 and pRB are major substrates for E6 and E7 in context of their immortalizing activity, however the interaction and perturbation of additional cellular factors are required for the full transforming capacity of HPV oncoproteins. For example, in tissue culture experiments E6 with mutated PBM was less efficient in conferring EMT-like characteristics and, moreover, was defective in cellular transformation and tumorigenicity (Kiyono et al., 1997; Watson et al., 2003). Furthermore, the HPV 16 E6 PBM was also shown to be required for induction of anchorage-independent growth of human tonsillar keratinocytes in cooperation with an activated Ras oncoprotein (Spanos et al., 2008a; Spanos et al., 2008b).

An important contribution towards the understanding of the relative contribution of E6 and E7 in malignant transformation has been provided by transgenic animal models mimicking the natural progression of HPV-induced tumorigenesis. In this model, transgenic mice express the K14HPV16 E6/E7 transgene, in which E6 and E7 are placed under the control of the human keratin 14 (K14) promoter, whose activity is restricted to cells occupying the basal layer of the stratified epithelium. This restricts the expression of E6 and E7 to the cell type in which the natural infection takes place. Mice expressing the entire HPV early region under the control of the K14 promoter displayed hyperplasia, dysplasia and papillomatosis in different epidermal and mucosal sites (Arbeit et al., 1994). In addition, the individual expression of E6 or E7 promoted epithelial dysplasia and skin tumors. It is interesting to note that tumors developing from E7-expressing mice were significantly different from those induced by E6 expression. The expression of E7 induced benign and well differentiated tumors, conversely those expressing E6 had a more malignant phenotype (Simonson et al., 2005; Song et al., 2000).

In contrast with animal models for skin carcinogenesis, transgenic mouse models for cervical cancer suggested that E7 can drive initial proliferation and induction of primary cervical tumors with weak invasive capacity, whilst E6, although it fails to drive the initial steps of tumorigenesis,
significantly increases the dimension as well as the invasiveness of primary tumors induced by E7 (Riley et al., 2003). These results were also supported by studies in models for head and neck squamous cell carcinoma (HNSCC) and in co-carcinogen assays, in which transgenic mice were treated with chemical carcinogens known to drive different stages of carcinogenesis. In these studies E7 was found to retain the strongest transforming potential and to drive tumorigenesis, whereas E6 had weak transforming capacity and was dispensable for initial tumor formation, although E6 contributed significantly in the later stages of tumor progression, enhancing the malignant conversion of the primary tumor (Strati and Lambert, 2007; Song et al., 2000).

Mutational analysis of E6 in the transgenic mouse models has shown that lack of p53 failed to cooperate with carcinogens to produce epidermal hyperproliferation, suggesting the existence of p53-independent tumorigenic pathways used by E6 (Song et al., 1999). In addition, mice expressing a mutant form of E6, E6I128T, unable to interact with E6AP, showed a reduced ability to overcome DNA synthesis block upon exposure to ionizing radiation, and to have a decreased propensity to develop spontaneous skin tumors compared with wild-type K14 E6 mice (Nguyen et al., 2002b). This also supports the notion that the association of E6 with E6AP is not exclusively required for the degradation of p53, but is involved in the inactivation of additional targets. Good candidates for p53-independent substrates important for E6 tumorigenic activity are the PDZ domain-containing proteins. Consistent with this, in mice expressing a PBM-defective mutant of E6 (E6Δ146-151), which retains the ability to interact with p53, but displays a reduced ability to promote hyperplasia in squamous epithelia, E6Δ146-151 still retained the capacity to promote malignant progression (Nguyen et al., 2003a; Simonson et al., 2005). This observation was also consistent with similar experiments in mouse lens epithelia, where the PBM of E6 was required to induce epithelial hyperplasia and defects in cell adhesion and differentiation (Nguyen et al., 2003a). In HPV-16 cervical cancer transgenic mouse models, expression of a PBM mutant of E6 in combination with wild type E7 led to the formation of smaller tumors characterised by a reduced invasive potential (Shai et al., 2007). Thus the interaction of E6 with PDZ-containing substrates has marked effects on the metastatic progression of HPV-related cancers in mice.
Results

Part I:

Analysis of PDZ-containing proteolytic substrates of E6 in HPV-positive cells

MAGI-1, hDlg and hScrib are degraded by E6 in HeLa and CaSKI Cells

As mentioned before, several studies have identified a number of PDZ domain-containing proteins as potential targets of the high-risk HPV E6 proteins. Many of them were analysed in ectopic overexpression systems and each study made use of different cell types, thus making it difficult to directly compare the susceptibility of these targets to E6-induced degradation in cells. In an attempt to compare directly the degree to which the various PDZ domain targets of E6 are susceptible to increased rates of degradation, we used siRNA to block E6/E7 expression in CaSKI (HPV-16 positive) and HeLa (HPV-18 positive) cells. HeLa and CaSKI are two cervical cancer-derived cell lines, hence they can reflect more closely the molecular events brought about by the expression of E6 and E7 in the context of cervical carcinogenesis. Extracts from E6/E7-silenced cells were analysed by western blot and compared with those from control cells transfected with siRNA to Luciferase, or from cells transfected with siRNA to E6AP. In the first set of assays we analysed changes in the levels of expression of hScrib and hDlg at 48h and 72h post-transfection. The results in Figure 10 show that there is a strong increase in the levels of p53 at both time points following siRNA transfection against E6/E7 and E6AP in both CaSKI and HeLa cells. This is in agreement with previous studies (Scheffner et al., 1993; Huibregtse et al., 1993) and confirms efficient ablation of E6 expression. In the case of hDlg, there is a modest increase in expression at the 48h time point in HeLa cells, and this is even more apparent at the 72h time point, thus confirming hDlg as a substrate for HPV-18 E6-induced degradation in HeLa cells (Mantovani et al., 2001a; Massimi et al., 2004; Handa et al., 2007). Interestingly there is also a slight increase in the overall level of hDlg expression in CaSKI cells. It is also noteworthy that hDlg migrates somewhat differently in the two cell lines, most likely reflecting differences in the degree of phosphorylation. This is particularly relevant, since phosphorylation events can influence the pattern of hDlg
Figure 10. hDlg and hScribble are degraded in HeLa and CaSKi cells. A. HPV-positive HeLa and CaSKi cells were transfected with siRNA Luciferase, siRNA E6/E7 or siRNA E6AP and grown for 48h prior to harvesting. The expression patterns of hDlg, hScribble, p53 and also α-actinin to monitor the protein loading, were assessed by western blot analysis. B and C. The assay was repeated as in A, but HeLa and CaSKi cells were harvested at 72h post-transfection before western blot analysis. Numbers represent the percentage of band intensity for hScribble and hDlg in comparison with the siRNA Luciferase control (100%).
localization and its susceptibility to E6-mediated degradation (Massimi et al., 2006; Narayan et al., 2009b). In the case of hScrib, there is a significant increase in its levels of expression in the E6/E7 siRNA treated CaSKi cells at both the 48h and 72h time points, whereas changes in hScrib levels in HeLa cells are minimal at both time points. E6AP ablation has only modest effects on both hDlg and hScrib, which are somewhat dependent upon the time at which the assays were performed, however there are slight increases in hDlg expression in HeLa cells (Figure 10a) and in hScrib expression in CaSKi cells (Figure 10c). Taken together, these results confirm previous studies suggesting that hDlg and hScrib are preferential proteolytic substrates of HPV-18 and HPV-16 E6 respectively (Thomas et al., 2005b).

Previous studies showed that the Dlg-related protein MAGI-1 is strongly bound by high-risk E6 oncoproteins, and is also susceptible to E6-induced degradation (Glaunsinger et al., 2000; Thomas et al., 2001). However these studies were also performed in an in vitro setting or under conditions of ectopic expression, and the effects of E6 ablation on MAGI-1 expression in HPV-positive cells were not determined. Therefore, we analysed the MAGI-1 pattern of expression in a similar series of E6/E7 and E6AP ablation experiments in HeLa and CaSKi cells. The results in Figure 11 demonstrate a strong increase in the levels of MAGI-1 expression in E6/E7-silenced HeLa cells at 24 and 48h post-transfection, and this is also observed equally well following ablation of E6AP expression. In the case of CaSKi cells, there is a modest increase in MAGI-1 levels, although not as strong as that observed in HeLa cells. Since the rescue of MAGI-1 in CaSKi was weak, we wanted to confirm that the band detected did correspond to the MAGI-1 protein. To do this, we repeated the analysis including an siRNA against MAGI-1. The results obtained are shown in Figure 11c and, as can be seen, the protein that is rescued following siRNA against E6/E7 disappears when the MAGI-1 siRNA is also included. We then extended the analysis to another HPV-16 positive cell line, SiHa, and obtained similar results (Figure 11d). Taken together, these results would suggest that whilst MAGI-1 is a good substrate of HPV-18 E6 it is also subject to HPV-16 E6-induced degradation.
We next wanted to determine whether other reported PDZ substrates of E6, such as FAP-1, TIP-2, PTPN-3 and PSD95, were also similarly targeted by E6 in cervical tumour-derived cell lines. The HeLa and CaSKi cells were transfected with siRNA against E6/E7 and changes in the PDZ protein levels ascertained by western blot analysis. The results in Figure 12 show no significant changes in the levels of expression of either PTPN3 (Figure 12a) or TIP2 (Figure 12c), following siRNA ablation of either E6/E7 or E6AP. In contrast there was a significant increase in the levels of expression of PSD95 in HeLa cells and a slight increase in CaSKi cells (Figure 12b) following E6/E7 knockdown. Removal of E6AP had no effect on PSD95 levels of expression in HeLa cells, whilst in CaSKi cells, a greater increase was obtained. These results confirm that PSD95 is a potential target for HPV-18 and HPV-16 E6-induced degradation (Handa et al., 2007). In the case of FAP1, an apparently contradictory result was obtained. Although its levels of expression in HeLa cells are very low, siRNA to E6/E7 apparently reduces FAP1 levels still further (Figure 12d). This effect is more marked in CaSKi cells, where loss of E6/E7 expression results in a dramatic decrease in the levels of FAP1 expression. In addition, removal of E6AP also results in lower levels of FAP1 expression in HeLa, with a slight decrease also evident in CaSKi cells.

Since a number of these proteins were present at quite low levels, we also verified that the correct proteins were detected by the antibodies. To do this we performed a series of western blot analyses on cell extracts following transfection with siRNAs to each of the PDZ-domain containing proteins. The results in Figure 12e (PTPN3, TIP2 and FAP1) and Figure 12b (PSD 95) show that the protein recognized by the relevant antibody also disappears following transfection with the relevant siRNA.

Taken together, these results demonstrate that PTPN3 and TIP2 are not major targets of E6-induced degradation in monolayer cultures of cells derived from cervical tumours. In contrast, PSD95 appears to be a good substrate for HPV-18 E6, in agreement with previous studies (Handa et al., 2007). Finally, it would appear that, at least in cervical tumour-derived cells in monolayer culture,
Figure 11. MAGI-1 is efficiently rescued in HPV-16- and HPV-18-positive cells upon E6/E7 ablation. A. HeLa and CaSKi cells were transfected with siRNA Luciferase, siRNA E6/E7 or siRNA E6AP and grown for 48h before harvesting. The expression patterns of MAGI-1, p53 and also α-actinin to monitor the protein loading, were assessed by western blot analysis. B. The assay was repeated as in A, but cells were grown for 72h before harvesting and western blot analysis. C. To confirm the identity of the band corresponding to MAGI-1, CaSKi cells were transfected with siRNA Luciferase, siRNA E6/E7, siRNA MAGI-1 (M-1) or a combination of siRNA E6/E7 and siRNA MAGI-1. 72h after transfection cells were harvested and western blot analysis was performed as in A and B. D. The assay was repeated in SiHa cells and processed as in panel B.
Figure 12. Analysis of PTPN3, PSD95, TIP2/GIPC and PTPN13/FAP1 susceptibility to E6 degradation in vivo. See the next page for the full legend.
Figure 12 (Cont.). HeLa and CaSk i cells were transfected with siRNA Luciferase, siRNA E6/E7 or siRNA E6AP and grown for 72h before harvesting. The expression levels of PTPN3 (A), PSD95 (B), TIP2/GIPC (C), PTPN13/FAP1 (D), p53 and α-actinin, were assessed by western blot. E. To confirm the correct identity of PTPN3, TIP2 and PTPN13, cells were transfected with siRNA Luciferase, siRNA PTPN3, siRNA TIP2/GIPC, or siRNA PTPN13/FAP1 and their expression patterns were assessed by western blot analysis. In panels A-D, numbers represent the percentage of band intensity for PTPN3, PSD95, TIP2 and FAP1 in comparison with the siRNA Luciferase control (100%).
E6/E7 might actually increase the levels of FAPl expression. Whether this is through E6’s PDZ interactions with FAPl, or through an, as yet, unknown function of E7 remains to be determined.

**HPV E6 preferentially degrades nuclear and membrane bound pools of MAGI-1**

Previous studies have shown that certain cellular pools of hDlg are more susceptible than others to E6-induced degradation (Massimi et al., 2004; Massimi et al., 2006; Narayan et al., 2009). Since MAGI-1 is a major common target for both HPV-16 and HPV-18 E6, we were interested in determining whether there are also similar cellular pools of MAGI-1 that are preferentially targeted by E6. To investigate this HeLa cells were transfected with siRNA against E6 and E7, and after 72 hours cells were harvested and subjected to differential sub-cellular fractionation. For comparison we also included H1299 cells in the analysis to determine where MAGI-1 would normally be expressed in epithelial cells in the absence of HPV sequences. The cells were fractionated into cytosolic, membrane, nuclear and cytoskeletal components, and the levels of MAGI-1 expression in each fraction were ascertained by western blot analysis. The results obtained again demonstrate that MAGI-1 is a strong substrate for HPV-18 E6 induced degradation in HeLa cells (Figure 13a). Interestingly, the bulk of MAGI-1 protein that is rescued upon ablation of E6/E7 expression resides mainly in the membrane and nuclear fractions of the cell, with the largest recovered pool actually being present within the nucleus. In contrast, a similar fractionation of H1299 cells (Figure 13b) shows that the main concentration of MAGI-1 is found at membrane sites, with slightly smaller pools in the nuclear and cytosolic fractions. These studies demonstrate that the rescue of MAGI-1 from E6-induced degradation results in a preferential restoration of MAGI-1 expression at membrane sites and also within the nucleus, suggesting that E6 targets MAGI-1 for degradation at membrane and nuclear sites.

**HPV E6-induced degradation of MAGI-1 disrupts cellular TJs**

Although there is no information on the potential function of MAGI-1 in the nucleus, previous studies have implicated the membrane-bound form of MAGI-1 in the establishment of cellular TJs (Murata et al., 2005). It has also been shown that TJs are disrupted in HPV-positive cells, and a
possible role for hScrib was suggested in this phenotype (Nakagawa and Huibregtse, 2000). However, we reasoned that MAGI-1 was also a likely candidate to explain the disruption of TJs by HPV E6, since its expression is required to promote the junctional targeting of TJ-associated proteins, including ZO-1 and occludin (Hirabayashi et al., 2003). Therefore we proceeded to investigate the TJ status in cells that had been ablated for E6/E7 expression. At the same time we performed siRNA ablation of MAGI-1 and of hScrib on a subset of cells treated with siRNA to E6/E7, to determine whether any changes in TJs were MAGI-1 or hScrib dependent. 72h and 96h post-transfection of the siRNAs, HeLa cells were fixed and analysed by immunofluorescence for MAGI-1 and a TJ marker, ZO-1 (Stevenson et al., 1986, Denker and Nigam, 1998). We focused primarily on cells that were in contact so that junctions would have the opportunity to become established, and the results for MAGI-1 are shown in Figure 14. As can be seen, there is no MAGI-1 protein detectable at sites of cell-cell contact in the siRNA Luciferase control cells and ZO-1 displays a diffused pattern of expression and is also absent at these sites. In contrast, siRNA to E6/E7 results in a very marked accumulation of MAGI-1 expression at cell-cell junctions. Interestingly, this occurs in a beaded structure at the 72h time point and there is also a perfect co-localisation with ZO-1 in these structures, suggesting the re-initiation of correct TJ formation. By the 96h time point this is even more marked and a broader junctional staining could be observed between adjacent cells. These results demonstrate that TJs can be re-established in HeLa cells when E6/E7 expression is ablated. Interestingly, a similar pattern of staining is also obtained upon ablation of E6AP expression, consistent with the results from the western blot analyses. We also analysed cells that had been co-transfected with a MAGI-1 siRNA, and, as can be seen in Figure 14, there is a failure to restore TJs in cells treated with the MAGI-1 siRNA, as determined by the pattern of ZO-1 expression, even by the 96hr time point. In contrast, ablation of hScrib (Figure 15a) has no effect upon the re-establishment of TJs upon ablation of E6/E7 expression. In addition, removal of E6/E7 expression in HeLa cells results in a marked increase in hScrib expression at the cell membrane, despite the apparent lack of significant levels of degradation seen in Figure 10. Furthermore, in control siLuciferase CaSKi cells residual hScrib is localized predominantly at cell contact sites, and a potent rescue of the cytoplasmic pool of the protein can be observed upon
Figure 13. MAGI-1 is rescued at membrane and nuclear sites upon silencing of E6 in HPV-positive cells. A. HeLa cells were transfected with siRNA Luciferase or siRNA E6/E7, and after 72h cells were fractionated into 4 subcellular compartments: cytosol (F1), membrane (F2), nucleus (F3), cytoskeleton (F4). The expression patterns of MAGI-1 or those of the four subcellular fraction markers E-cadherin, nuclear matrix protein p84, α-tubulin and vimentin were assessed by western blot analysis. B. The subcellular fractionation was repeated on HPV-negative H1299 cells and the levels of MAGI-1 and of the subcellular fraction markers were detected as in A.
Figure 14. Rescue of MAGI-1 from E6-induced degradation restores TJs. HeLa cells were seeded on glass coverslips and transfected either with siRNA Luciferase, siRNA 18E6/E7, a combination of siRNA 18E6/E7 plus siRNA MAGI-1, or with siRNA E6AP. Cells were grown for 72h or 96h before fixing and incubated with anti-MAGI-1 and anti-ZO-1 antibodies and counterstained with rhodamine-conjugated (MAGI-1) and fluorescein-conjugated (ZO-1) secondary antibodies. Confocal images were taken at 480 and 510 nm wavelengths.
Figure 15. Loss of hScrib does not affect TJ formation. See the next page for the full legend.
Figure 15 (Cont.). Loss of hScrib does not affect TJ formation. HeLa cells (panel A) and CaSKi cells (panel B) were seeded on glass coverslips and transfected with siRNA Luciferase, siRNA 18E6/E7, siRNA 18E6/E7 in combination with siRNA hScrib or siRNA 16E6/E7 as indicated. Cells were grown for 96h before fixing and staining for hScrib (red) and ZO-1 (green) in HeLa cells or for hScribble (red) and p53 (green) in CaSKi cells. White arrows indicate sites of hScrib and ZO-1 junctional accumulation.
silencing of E6 and E7 (Figure 15b), suggesting that hScrib can be differentially regulated by HPV-16 or -18 E6 oncoproteins. However, taken together, these results suggest that loss of TJs in a HPV-positive, tumour-derived cell line is, at least in part, due to the ability of E6 to induce the degradation of MAGI-1.

**Generation of an E6-resistant MAGI-1 mutant**

*The K499E mutation reduces MAGI-1 affinity for E6*

The fact that MAGI-1 is a sensitive proteolytic substrate of E6 prompted us to perform a more detailed analysis of its possible function in the context of HPV pathology. To do this, we reasoned that using a MAGI-1 mutant that was resistant to E6 targeting might by one way to address this. We made use of previous studies suggesting that E6 interacts with MAGI-1 specifically through its PDZ domain 1 (Thomas et al., 2001), and more recent structural data that identified the lysine 499 (K499) as one of the most critical residues within the PDZ1 domain mediating its interaction with E6 (Fourmane et al., 2011). Using surface plasmon resonance to measure the binding affinity between peptides encompassing the HPV-16 and -18 E6 PBMs and a purified form of MAGI-1 PDZ1, these studies suggested that the K499E mutation was indeed able to produce a dramatic decrease in the interaction between E6 and MAGI-1 (Fourmane et al., 2011). However, these results were not verified in the context of full-length E6 and MAGI-1 proteins and, importantly, the impact of the K499E mutation on the ability of E6 to degrade MAGI-1 was not assessed. In an attempt to address these points, we decided to introduce the K499E mutation into the full-length MAGI-1 cDNA. For this purpose, a FLAG-tagged wild-type MAGI-1 (M1wt) expression construct was used as a template to generate the K499E MAGI-1 mutant (M1K499E) by site-directed mutagenesis. Figure 16a shows a comparison between the protein sequence of wild-type and K499E MAGI-1 PDZ1 domain, and the structural elements of the PDZ domain that mediate the interaction of MAGI-1 to its PBM-containing partners are highlighted. Once the FLAG-tagged M1K499E was generated, we first wanted to verify that the wild-type and mutant MAGI-1 proteins were expressed at comparable levels. To assess this, 293 cells were transiently transfected with the two constructs. 24h after transfection cells were harvested and MAGI-1 expression levels were analysed by SDS-
PAGE and western blot using anti-FLAG antibody. As can be seen in Figure 16b, wt and mutant MAGI-1 proteins are expressed at comparable levels in 293 cells, suggesting that the K499E mutation does not alter the steady state levels of MAGI-1. In order to test whether the K499E mutation could indeed reduce the affinity of MAGI-1 for HPV-16 and -18E6 oncoproteins, we first performed GST pull-down assays. To do this, HPV-16 and 18 E6 were expressed as GST-fusion proteins and purified using glutathione-coated agarose beads. The beads were incubated for 1 hour at 4°C with cell extracts from 293 cells that had been transiently transfected with either the M1wt or M1K499E expression plasmids. After extensive washing, the amount of MAGI-1 bound to GST-E6 was assessed by SDS-PAGE and western blotting using anti-FLAG antibody. As can be seen in Figure 16c, GST-18 E6 bound strongly to M1wt and bound about 70% of the protein compared to the input, whereas the K499E mutation exhibited a dramatically reduced ability to interact with E6. Similar results were also obtained with GST-16 E6 (Figure 16d), although wild-type MAGI-1 was bound less efficiently compared with 18 E6, which is in agreement with previous studies (Thomas et al., 2001). Thus these results confirm that the residue K499 within the MAGI-1 PDZ1 domain is important for the recognition of MAGI-1 by both the HPV-16 and -18 E6 oncoproteins.

**MAGI-1 K499E mutant is resistant to E6-mediated degradation**

To determine whether the reduced ability of E6 to interact with the MAGI-1 K499E mutant also resulted in decreased rates of degradation, we compared the relative susceptibilities of wild-type and mutant MAGI-1 to E6-mediated degradation *in vitro*. The two MAGI-1 proteins were *in vitro* translated in the presence of $^{35}$S-labelled methionine, and then incubated at 30°C for different periods of time with *in vitro* translated and radiolabelled HPV-16 and -18 E6, and the pattern of MAGI-1 expression was assessed by SDS-PAGE and autoradiography. The results in Figure 17a show that the levels of wild-type and mutant MAGI-1 are stable over a period of 120 minutes when incubated in absence of E6. In contrast, wild-type MAGI-1 was degraded upon addition of HPV-16 or -18 E6, with HPV-18 E6 being the most efficient (Thomas et al., 2001). Consistent with the reduced level of interaction, M1K499E was also significantly more resistant to E6-mediated
Figure 16. The K499E mutation affects the E6-binding capacity of MAGI-1. See the next page for the full legend.
Figure 16 (Cont.). The K499E mutation affects the E6-binding capacity of MAGI-1.

A. diagram showing the domain composition of MAGI-1 and the location of the K499E mutation. Elements of secondary structure that compose the PDZ1 are also shown (βA-E (β-strands A to E); αA-B (α-helix A to B)), and those involved in the interaction with E6 and other target proteins are highlighted in red (adapted from Fournane et al., 2011). B. HEK 293 cells were transfected with 1μg of FLAG-tagged wild-type or mutant MAGI-1 and grown for 24h hours prior to harvesting. The levels of MAGI-1 expression were assessed by western blot. β-galactosidase was included to monitor the transfection efficiency. C and D. Extracts from HEK293 cells transfected with 3 μg of wild-type or mutant MAGI-1, were subjected to GST-pulldown reactions with the indicated GST fusion proteins, and bound MAGI-1 was detected by western blot using anti-FLAG antibody. Numbers represent the percentage of wild type and mutant MAGI-1 proteins bound to the indicated GST-fusion protein relative to the input control. The lower panel shows the Ponceau staining of the membrane, confirming the equal loading of the GST proteins.
Figure 17. The K499E mutation renders MAGI-1 resistant to E6-mediated degradation. See the next page for the full legend.
Figure 17 (Cont.). A. Wild-type and the K499E mutant, together with HPV-16 and HPV-18 E6 oncoproteins, were in vitro translated in the presence of $^{35}$S-labelled methionine or cysteine. They were then incubated together at 30°C as indicated. Residual MAGI-1 protein was detected by SDS-PAGE and autoradiography. Numbers are the band intensities expressing the percentage of residual MAGI-1 protein relative to the control (100%). B. HEK 293 cells were co-transfected with 1 μg of FLAG-tagged wild-type or K499E mutant and either 2, 5 and 10 μg of HPV-18 E6 expression plasmid. After 24 hours cells were harvested and the expression levels of MAGI-1 and β-galactosidase were detected by western blot analysis. C. HeLa cells were transfected with 3 μg of FLAG-tagged wild-type or K499E mutant MAGI-1. After 24 hours the cells were treated with MG-132 for an additional 3 hours prior to harvesting. The expression levels of MAGI-1, p53 and β-galactosidase were assessed by western blot analysis.
degradation; although low levels of degradation were observed at the later time points, which is consistent with the residual binding of E6 to the K499E mutant.

To investigate whether similar results could also be obtained in vivo, we compared the steady state levels of FLAG-tagged wild-type and mutant MAGI-1 in 293 cells when expressed alone or in combination with increasing amounts of HPV-18 E6 (Figure 17b). In good agreement with the in vitro assay, M1wt was highly susceptible to E6-induced degradation, whereas, the K499E mutant was significantly more resistant. We then proceeded to investigate whether the K499E mutant was resistant to E6 targeting in the more physiologically relevant setting of cervical cancer-derived cells that express endogenous levels of E6 oncoprotein. To do this we expressed the FLAG-tagged MAGI-1 constructs in HeLa cells. 24 hours after transfection, cells were left untreated or treated with the proteasome inhibitor MG-132 for an additional 3 hours before harvesting, in order to determine whether differences in MAGI-1 level of expression were due to proteasomal degradation. Total cell extracts were separated by SDS-PAGE and the pattern of MAGI-1 and, for comparison, of p53 expression was analysed by western blot. As can be seen in Figure 17c, MG-132 treatment produced a strong recovery in the levels of p53 expression, confirming the efficient inhibition of the proteasome. In agreement with our degradation assays in 293 cells, the expression levels of the K499E mutant in HeLa were significantly higher than the wild-type protein, again reflecting their differential susceptibility to HPV-18 E6-mediated degradation. Proteasome protection produced an increase in the levels of expression of both M1wt and M1K499E, confirming that M1K499E is nonetheless susceptible to 18 E6-mediated degradation, although to a much lesser extent than the wild-type MAGI-1.

The K499E mutation perturbs the functionality of MAGI-1 PDZ1 but does not affect its sub-cellular localization

The crystal structures of MAGI-1 PDZ1 and Dlg PDZ2 and 3 in complex with a peptide encompassing the HPV-18 E6 PBM have been solved (Zhang et al., 2007). These data suggested that, unlike most PDZ-PBM interactions, the association of 18 E6 with PDZ domains is stabilized
by non-canonical residues that extend upstream of the PBM, and make contact with β-strands B and C of PDZ domains (Zhang et al., 2007; Thomas et al., 2008a). With regard to the MAGI-1 PDZ1 domain, the K499 residue maps in its β-strand C (Figure 16a), one of the structural components in close proximity to the substrate binding groove (Doyle et al., 1996; Fournane et al., 2011), indicating that the alteration of this domain could potentially perturb the functionality of the PDZ domain rather than selectively block the interaction with E6. To date, several PBM-containing cellular proteins have been identified as potential binding partners for MAGI-1 PDZ1, including the RhoA modulators NET1 and p116Rip (Dobrosotskaya, 2001), JAM4 (Hirabayashi et al., 2003) and the zyxin family protein LPP (Fournane et al., 2011). Of these, however, only the interactions between MAGI-1 PDZ1 and the Rho GEF NET1 and JAM4 have been confirmed by biochemical analysis (Dobrosotskaya, 2001; Hirabayashi et al., 2003), although JAM4 has been shown to preferentially associate with MAGI-1 through its PDZ4 domain (Hirabayashi et al., 2003). In an attempt to define whether the K499E MAGI-1 mutant retained the overall functionality of its PDZ1 domain, we decided to monitor the interaction of M1wt and M1K499E with NET1. To do this, 293 cells were transiently transfected with the FLAG-tagged M1wt and M1K499E constructs, either alone or in combination with MYC-tagged NET1. After 24 hours, the cells were harvested and cell extracts were immunoprecipitated using anti-MYC antibody, and the co-immunoprecipitated M1wt and M1K499E were detected by western blot using anti-FLAG antibody (Figure 18a). The results of these assays demonstrate that wild-type MAGI-1 specifically co-immunoprecipitates with NET1, confirming previous results (Dobrosotskaya, 2001). In contrast, the interaction between NET1 and the K499E mutant was significantly reduced, suggesting that this mutation does introduce structural changes into the substrate binding groove of the PDZ1 domain so that the ability of MAGI-1 PDZ1 to interact with the PBM of NET1 is perturbed. It is interesting to note, however, that the PBMs of 16 and 18 E6 oncoproteins, as well as that of NET1, possess a glutamic acid at position -3 which contributes to the interaction with K499 within the MAGI-1 PDZ1 domain (Figure 18b). Therefore, we reasoned that the interaction of the MAGI-1 PDZ1 domain with PBMs that do not have a glutamic acid at the -3 position might be less susceptible to the K499E mutation. In order to test this hypothesis, we repeated the GST pull-down
Figure 18. The K499E mutation affects the interaction of MAGI-1 with NET1 but not with HPV-58 E6. A. HEK293 cells were transfected with 3μg of the FLAG-tagged MAGI-1 plasmids together with 5μg of MYC-tagged mNET1, as indicated. After 24 h cells were extracted and immunoprecipitated using anti-MYC antibody. NET1-bound MAGI-1 moieties were then detected by western blot using anti-FLAG antibody. B. Sequence alignment of the PBMs of JAM-4, NET1, HPV-16 E6, HPV-18 E6, and HPV-58 E6. C. HEK 293 cells were transfected with 3μg of the FLAG-tagged MAGI-1 constructs; after 24 h the cells were harvested and extracts were subjected to GST-pulldown reactions using the GST-HPV-58 E6 fusion protein, and bound MAGI-1 was detected by western blot using anti-FLAG antibody. Numbers represent the percentage of wild type and mutant MAGI-1 proteins bound to the indicated GST-fusion protein relative to the input control. The lower panel shows the Ponceau staining of the membrane, confirming the equal loading of the GST proteins.
assays of wild type and mutant MAGI-1 using purified GST-tagged HPV-58 E6, whose PBM is identical to HPV-18 E6 except that it has a glutamine at the -3 position (Figure 18b). As shown in Figure 18c, the amount of wild type and K499E mutant MAGI-1 pulled down by HPV-58 E6 was similar. This suggests that the K499E mutation only marginally affects the ability of HPV-58 E6 to bind to MAGI-1. Therefore, this confirms that the presence of a glutamic acid at the -3 position of the PBM of MAGI-1-binding partners makes an important contribution to the interaction, and, importantly, also suggests that the K499E mutation might affect to a lesser extent the interaction with other MAGI-1 binding partners that do not have a glutamic acid residue at the -3 position, such as for example JAM-4 (Figure 18b).

The fact that the K499E mutation might affect the functionality of the PDZ1 domain towards some MAGI-1 binding proteins, prompted us to investigate whether this might impinge on the pattern of MAGI-1 sub-cellular localization, and in particular on its membrane targeting, since the integrity of the PDZ domains has been reported to be important for this function (Dobrosotskaya and James, 2000; Laura et al., 2002). A previously identified membrane-bound interaction partner for MAGI-1 is β-catenin, and although the binding site for β-catenin is spatially segregated from the PDZ1 domain, interacting with the PDZ5 domain of MAGI-1 (Dobrosotskaya and James, 2000), we speculated that this association could be a marker to indirectly test the functionality of the K499E MAGI mutant. We repeated the co-immunoprecipitation experiments in 293 cells by overexpressing HA-tagged β-catenin alone or in combination with the FLAG-tagged M1wt or M1K499E constructs. After 24h cells were harvested and M1wt or the M1K499E were immunoprecipitated by incubating cell extracts with anti-FLAG conjugated agarose beads. Co-immunoprecipitated β-catenin was detected by western blot using anti-HA antibody, and the results of this assay are shown in Figure 19a. As can be seen, β-catenin co-immunoprecipitated with similar efficiencies with both the wild-type and mutant MAGI-1, suggesting that the membrane targeting of MAGI-1 is not affected by the K499E mutation. To confirm this, we also compared the expression pattern of wild-type and mutant MAGI-1 by immunofluorescence analysis. To do this FLAG-tagged M1wt and M1K499E were transfected into U2OS cells and, after 24 hours, the cells
were fixed and stained with anti-FLAG antibody. As can be seen from Figure 19b, and in agreement with previous studies (Dobrosotskaya and James, 2000), wild-type MAGI-1 displayed a differential pattern of sub-cellular localization, with different pools of MAGI-1 detectable in the nucleus as well as in the cytoplasm of transfected cells, whereas a prominent membrane staining was also apparent in cells forming intercellular junctions. In good agreement with the β-catenin co-immunoprecipitation experiments, the sub-cellular distribution of M1K499E was very similar to the wild-type protein, confirming that the K499E mutation does not affect the sub-cellular distribution of MAGI-1.

Taken together these data suggest that the K499E mutation which blocks HPV-16 and -18 E6 recognition, is only likely to affect the ability of MAGI-1 to interact with its cellular partners that recognize the PDZ1 domain and which have a glutamic acid residue at the -3 position of the PBM. Consistent with this, the K499E mutation does not appear to affect the sub-cellular localization of MAGI-1.

The M1K499E mutation potentiates the ability of MAGI-1 to establish tight junctions in HeLa cells

Previous studies defined an important role for MAGI-1 in the establishment of TJs, by promoting the recruitment of TJ-associated proteins such as ZO-1 and occludin (Hirabayashi et al., 2003), and recently the silencing of HPV-18 E6 in HeLa cells was shown to promote the junctional accumulation of ZO-1 through MAGI-1 (Figure 14; Kranjec and Banks, 2011). These observations, prompted us to investigate whether the expression of MAGI-1 was sufficient to promote the junctional recruitment of TJ-associated proteins in HeLa cells, and to define whether the K499E mutant could potentiate this activity of MAGI-1. To do this, we decided to monitor the expression pattern of the TJ-associated proteins ZO-1 and PAR3 (Stevenson et al., 1986; Izumi et al., 1998; Kranjec and Banks, 2011). HeLa cells were grown on glass coverslips and transfected with the FLAG-tagged MAGI-1 constructs; 24 hours after transfection cells were fixed and the expression patterns of MAGI-1, ZO-1 and PAR3 were analysed by confocal microscopy. In order to evaluate whether the expression of M1wt and M1K499E could confer an advantage in terms of junctional
Figure 19. The K499E mutation does not affect the interaction of MAGI-1 with β-catenin and does not affect its localization. A. HEK293 cells were transfected with 3μg of wild-type or mutant MAGI-1 expression plasmids together with 5μg of HA-tagged β-catenin. After 24 hours cell extracts were immunoprecipitated using anti-FLAG-antibody conjugated agarose beads, and MAGI-1-bound β-catenin was then detected by western blot using anti-HA antibody. The arrow indicates the position of HA-tagged β-catenin. B. U2OS cells were transfected with the FLAG-tagged MAGI-1 constructs, and after 24 hours the cells were fixed and incubated with anti-FLAG antibody to detect the MAGI-1 pattern of expression. White arrows indicate sites of MAGI-1 junctional accumulation.
assembly, multiple confocal fields were used to count transfected and untransfected HeLa cells until at least 100 FLAG-positive cells were analysed. Within each sample, HeLa cells were divided into subpopulations based on their positivity for the FLAG staining (MAGI-1 transfected or untransfected) and on their ability to form ZO-1 and PAR3-positive cellular junctions. As can be seen in Figure 20a, the vast majority of HeLa cells did not display junctional staining of ZO-1, and a similar pattern of staining was also observed for PAR3 (Figure 20b), suggesting that HeLa cells are largely unable to form intact cellular junctions. This was also confirmed by direct cell counting, since within the untransfected subpopulation about 10-20% of HeLa cells displayed ZO-1- and PAR3-positive junctional staining (Figure 21a). Strikingly, the expression of wild type and mutant MAGI-1 significantly increased the junctional assembly in HeLa cells, with the wild type and K499E mutant MAGI-1 proteins displaying similar efficiencies in promoting the junctional recruitment of ZO-1 and PAR3 (Figure 20 and Figure 21a). This is in agreement with the fact that the K499E mutation does not affect the ability of MAGI-1 to localize at junctional sites between contacting cells (Figure 18c), and further suggests that the mutant retains the capacity to restore junctional complexes. Furthermore, when compared with the wild type protein, the expression of the K499E mutant produced a much higher number of MAGI-1-positive cells, which is consistent with its increased resistance to E6-mediated degradation (Figure 20a and 20b, Figure 21b). In addition, this increased proportion of K499E MAGI-1-expressing cells was reflected in a corresponding increase in the number of cells showing junctional recruitment of ZO-1 and PAR3 (Figure 20a and 20b, Figure 21c).

Taken together, these data suggest that wild type and mutant MAGI proteins display comparable efficiencies in recruiting ZO-1 and PAR3 to cell contact sites, however the resistance of the K499E mutant to E6 degradation increases the number of HeLa cells with intact cell junctions, indicating that MAGI-1 expression potently enhances the ability of HeLa cells to form junctional complexes.

A well known biological effect associated with the establishment of junctional complexes is the inhibition of cell proliferation (Balda et al., 2003; Aijaz et al., 2005; Sottocornola et al., 2010).
Previous studies indicated that both ZO-1 and PAR3 can inhibit cell proliferation when localized at cell contact sites by modulating the activity of multiple proteins implicated in G1/S cell cycle transition (Balda and Matter, 2000; Sottocornola et al., 2010). Therefore, having shown that the expression of K499E mutant MAGI-1 can potently increase the junctional recruitment of ZO-1 and PAR3, we were interested in determining whether this could also correlate with an inhibition of cell proliferation in HeLa cells. In order to do this, we labeled proliferating cells with the thymidine analogue 5-ethyl-2’-deoxyuridine (EdU), which allows the visualization of proliferating cells while not affecting the overall structural integrity of the cell (Salic and Mitchison, 2008). HeLa cells were grown on glass coverslips and transfected with the FLAG-tagged M1wt and M1K499E constructs. 24h post transfection, and prior to fixation, HeLa cells were pulsed with EdU for additional 2 hours, and the pattern of MAGI-1 and ZO-1 expression and the proportion of EdU-positive cells were visualized by confocal microscopy. As can be seen in Figure 22a, a high proportion of untransfected HeLa cells display positive nuclear EdU staining, demonstrating that the HeLa cells are highly proliferative. The expression of wild type MAGI-1 led to an increase in junctional ZO-1 staining and this correlated also with the absence of EdU staining in the M1wt-expressing cells. Conversely, K499E mutant MAGI-1, which also showed high levels of ZO-1 junctional recruitment, displayed a reduced ability to block the proliferation in HeLa cells compared with the wild type protein, suggesting that the integrity of MAGI-1 PDZ1 domain increases its ability to inhibit cell proliferation. The quantification of the number of EdU-positive nuclei relative to MAGI-1 expression, confirmed that wild type MAGI-1 dramatically reduced the proliferative potential of HeLa cells, and that the K499E mutation decreases the ability of MAGI-1 to inhibit cell proliferation by about 20% (Figure 22b). Nevertheless, consistent with the ability of mutant MAGI-1 to form larger MAGI-1-positive HeLa cell populations, its expression also correlates with an increased population of EdU-negative cells compared with the wild type protein (Figure 22c). These data suggest that MAGI-1 is a negative regulator of cell proliferation and that its expression in HeLa cells is capable of reducing the proportion of proliferating cells. However this regulation of the proliferative potential appears to be independent of MAGI-1’s ability to
Figure 20. The expression of wild type and mutant MAGI-1 promotes junctional assembly in HeLa cells. A. HeLa cells were seeded on glass coverslips and transfected either with wild type or mutant MAGI-1. After 24 hours the cells were fixed and incubated with anti-FLAG and anti-ZO-1 antibodies and counterstained with rhodamine-conjugated (FLAG) and fluorescein-conjugated (ZO-1) secondary antibodies. Confocal images were taken at 480 and 510 nm wavelengths. Confocal images were taken at 480 and 510 nm wavelengths. White arrows indicate sites of MAGI-1 and ZO-1 junctional accumulation.
Figure 20 (Cont.). B. Cells were seeded and transfected as in A. After fixation, cells were incubated with anti-FLAG and anti-PAR3 antibodies and counterstained with rhodamine-conjugated (FLAG) and fluorescein-conjugated (PAR3) secondary antibodies. Confocal images were taken at 480 and 510 nm wavelengths. White arrows indicate sites of MAGI-1 and PAR3 junctional accumulation.
Figure 21. The resistance of MAGI-1 K499E to E6-mediated degradation correlates with an increased junctional assembly in HeLa cells. See the next page for the full legend.
Figure 21 (Cont.). The total number of HeLa cells showing M1- or M1K499E-positive staining were quantified within the total cell population visualized by immunofluorescence. In each experiment at least 100 wild type and mutant MAGI-1-positive cells were counted. A. The number of ZO-1 and PAR3-positive junctions formed in untransfected, wild type and mutant MAGI-1-transfected cells was calculated as the percentage of cells displaying ZO-1- and PAR3-positive junctional staining in each subpopulation (one way analysis of variance [ANOVA]). B. The total population of wild type and mutant MAGI-1-expressing cells was calculated as the percentage of FLAG-positive cells present in each sample relative to the total population of untransfected cells (P<0.0001; unpaired two-sample t-test). C. Percentage of MAGI-1-positive cells displaying ZO-1-positive (P=0.0006) and PAR3-positive (P<0.0001) junctional staining relative to the total population of untransfected cells counted in each sample (unpaired two-sample t-test). Each panel represents the mean values and standard deviations calculated from three independent experiments. The corresponding P values are: *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001.
restore TJs, since it seems to depend, in part, upon an as yet unidentified function of the MAGI-1 PDZ1 domain.

In order to assess whether the MAGI-1 is able also to mediate the inhibition of cell proliferation in HPV-negative cells, we repeated the EdU staining upon transfection of wild type and K499E mutant MAGI-1 in HaCaT cells, and the results are shown in Figure 23. As can be seen, in agreement with previous studies (Massimi et al., 2012), HaCaT cells form cellular junctions between adjacent cells, as evidenced by junctional recruitment of ZO-1 (Figure 23a). Consistent with the data obtained in HeLa cells, wild type and K499E mutant MAGI-1 proteins co-localized with ZO-1 at cellular junctions, although the expression of either construct marginally increased the ZO-1 junctional recruitment. When the two MAGI-1 constructs were expressed in HaCaT cells, the effects on cell proliferation were markedly reduced when compared to HeLa cells (Figure 23a). This was highlighted by the quantification of the cells displaying an EdU-positive nuclear staining (Figure 23b), where about the 40% of MAGI-1-expressing cells also displayed an EdU-positive staining. As expected, in the absence of E6, the two constructs displayed a similar transfection efficiency (Figure 23c), however, consistent with lower efficiency of MAGI-1 in inhibiting the proliferation of HaCaT cells, also the percentage of EdU-negative and MAGI-1-positive cells compared to the total cell population was likewise reduced compared to HeLa cells (Figure 23d).

Taken together these data indicate MAGI-1 has a strong capacity to induce the junctional recruitment of TJ-associated proteins, and that the ability of MAGI-1 to inhibit cell proliferation could be linked to the inhibition of specific functions associated to the expression of E6 and E7.

MAGI-1 is a pro-apoptotic protein

The epifluorescent examination of HeLa cells stained for wild type and mutant MAGI-1 suggested us a possible involvement of this protein in the regulation of apoptosis, since proportions of the MAGI-1-expressing cells had morphological features resembling those of cells undergoing apoptosis, including blebbing and rounding up of the cells (Taylor et al., 2008). In our opinion this
was particularly interesting since HeLa cells have been shown to be resistant to different apoptotic stimuli (Assefa et al., 1999; Eichholtz-Wirth and Sagan, 2000), and MAGI-1 had been previously implicated in the regulation of apoptosis (Ivanova et al., 2007; Gregorc et al., 2007); however its possible direct involvement in the induction of apoptosis has not been previously investigated. A well studied biochemical event associated with the induction of apoptosis is the fragmentation of genomic DNA (Williams et al., 1974; Tian et al., 1991) due to the activation of cellular nucleases (Wyllie, 1980; Nagata et al., 1998). Therefore, in order to determine whether the expression of wild type and K499E mutant MAGI-1 could promote apoptosis of HeLa cells, we decided to monitor their pattern of DNA fragmentation by performing terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) assays. In addition, we also included HaCaT cells in the analysis, in order to determine whether MAGI-1 could also induce apoptosis in HPV-negative cells. To do that, HeLa and HaCaT cells were seeded on glass coverslips and transfected either with wild type or K499E mutant MAGI-1 constructs. Since the induction of DNA fragmentation is a rather late event during induction of apoptosis (Collins et al., 1997), we decided to grow the cells for 48h after transfection. The cells were then fixed, and the pattern of wild type and K499E mutant MAGI-1 expression as well as the number of cells positive for the TUNEL reaction, were assessed by immunofluorescence and confocal microscopy. Results are shown in Figure 24 and, as can be seen, untransfected HeLa (Figure 24a) and HaCaT (Figure 24b) cells both showed a low level of apoptosis, as evidenced by the low proportion of TUNEL-positive cells. Strikingly, the expression of wild type and mutant MAGI-1 led to the appearance of MAGI-1/TUNEL-positive cell subpopulations in both cell lines, suggesting that the ability of MAGI-1 to induce apoptosis is not exclusive to HPV-positive cells. In addition, the expression of the K499E mutant in HeLa cells led to a higher number of MAGI-1-positive cells than the wild type protein, and this also correlated with an increased subpopulation of MAGI-1/TUNEL-positive cells. It is also interesting to note that in HaCaT cells the TUNEL positivity associated with the transfection of the MAGI-1 constructs was not linked to the acquisition of a clear apoptotic morphology as in the case of HeLa cells under the same experimental conditions. However, this is consistent with the fact that some cell types can acquire an apoptotic morphology rather slowly, although they are already undergoing
Figure 22. MAGI-1 inhibits cell proliferation of HeLa cells. See the next page for the full legend.
Figure 22 (Cont.). A. HeLa cells were seeded on glass coverslips and transfected either with FLAG-tagged wild type or mutant MAGI-1 constructs. After 24 hours, and prior to fixation, cells were incubated with EdU for additional 2 hours in order to allow its incorporation by proliferating cells. After fixation, cells were incubated with anti-FLAG and anti-ZO-1 antibodies and counterstained with rhodamine-conjugated (FLAG) and fluorescein-conjugated (ZO-1) secondary antibodies. After incubation with the indicated antibodies, cells were processed for the detection of EdU-labeled DNA (green nuclei). Confocal images were taken at 480 and 510 nm wavelengths. White arrows indicate sites of MAGI-1 and ZO-1 junctional accumulation. B. The percentage of EdU-positive cells was quantified by direct cell count of untransfected, wild type or K499E mutant MAGI-1-transfected cells displaying positive nuclear EdU staining within each subpopulation (one way analysis of variance [ANOVA]). C. Cells were counted as in B, and shown is the percentage of MAGI-1-positive cells displaying EdU-negative staining relative to the total population of untransfected cells counted in each sample (P=0.0008; unpaired two-sample t-test). Each panel represents the mean values and standard deviations calculated from three independent experiments. The corresponding P values are: *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001.
Figure 23. MAGI-1 is less efficient to inhibit the cell proliferation of HPV-negative cells. A. HaCaT cells were seeded on glass coverslips and transfection was carried out as in Figure 22. After 24 hours, and prior to fixation, cells were incubated with EdU for additional 2 hours in order to allow its incorporation by proliferating cells. After fixation, cells were incubated with anti-FLAG and anti-ZO-1 antibodies and counterstained with rhodamine-conjugated (FLAG) and fluorescein-conjugated (ZO-1) secondary antibodies. After incubation with the indicated antibodies, cells were processed for the detection of EdU-labeled DNA (green nuclei). Confocal images were taken at 480 and 510 nm wavelengths. White arrows indicate sites of MAGI-1 and ZO-1 junctional accumulation.
Figure 23 (Cont.). B. The percentage of EdU-positive cells was quantified by direct cell count of untransfected, wild type or K499E mutant MAGI-1-transfected cells displaying positive nuclear EdU staining within each subpopulation (one way analysis of variance [ANOVA]). C. The total population of wild type and mutant MAGI-1-expressing cells was calculated as the percentage of FLAG-positive cells (~100 cells per sample) present in each sample relative to the total population of untransfected cells. D. Cells were counted as in B, and shown is the percentage of MAGI-1-positive cells displaying EdU-negative staining relative to the total population of untransfected cells counted in each sample. Each panel represents the mean values and standard deviations calculated from three independent experiments. The corresponding P values are: *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001.
Figure 24. The expression of MAGI-1 induces apoptosis in HeLa and HaCaT cells.

A. HeLa cells were seeded on glass coverslips and transfected either with wild type or mutant MAGI-1. After 48 hours the cells were fixed and incubated with the anti-FLAG antibody and counterstained with rhodamine-conjugated secondary antibodies. After incubation with the indicated antibodies, cells were processed for the identification of TUNEL-positive cells using the In situ cell death detection kit according to the manufacturer's instructions. Confocal images were taken at 480 and 510 nm wavelengths.
Figure 24 (Cont.). B. HaCaT cells were seeded on glass coverslips, and the immunodetection of MAGI-1 and the TUNEL assay were performed as in A.
Figure 25. The expression of MAGI-1 correlates with induction of apoptosis. See the next page for the complete legend.
Figure 25 (Cont.). The expression of MAGI-1 correlates with induction of apoptosis. A. The percentage of TUNEL-positive HeLa cells was quantified by direct cell count of untransfected, wild type or K499E mutant MAGI-1-transfected cells displaying positive TUNEL staining within each subpopulation (one way analysis of variance [ANOVA]). B. The total population of wild type and mutant MAGI-1-expressing cells was calculated as the percentage of FLAG-positive cells (~100 cells per sample) present in each sample relative to the total population of untransfected cells (P=0.0002; unpaired two-sample t-test). C. Cells were counted as in A and B, and shown is the percentage of MAGI-1-positive cells displaying TUNEL-positive staining relative to the total population of untransfected cells counted in each sample (P=0.0033; unpaired two-sample t-test). D. The percentage of wild type or K499E mutant MAGI-1-transfected HaCaT cells displaying positive TUNEL staining was determined as in A (one way analysis of variance [ANOVA]). Each panel represents the mean values and standard deviations calculated from three independent experiments. The corresponding P values are: *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001.
the biochemical events associated with the apoptosis (Oberhammer et al., 1994), in addition this also suggests that the kinetics of the induction of apoptosis are different between HeLa and HaCaT cells. Therefore, these data indicate that the increased resistance of K499E mutant MAGI-1 to E6-mediated degradation also correlates with an increased induction of apoptosis. In order to gain more quantitative insights about the ability of MAGI-1 to induce apoptosis, we decided to count the cells in each sample and to correlate the number of TUNEL-positive cells to the status of MAGI-1 expression. At least 100 cells were counted per sample, and as can be seen in Figure 25a, and in good agreement with the confocal images, only a small proportion of untransfected HeLa cells displayed TUNEL-positive staining; in contrast the expression of either wild type or mutant MAGI-1 led to a strong induction of apoptosis. It is also interesting to note that the two MAGI-1 proteins displayed a similar efficiency in inducing apoptosis, suggesting that the PDZ domain 1 is probably not involved in this function of MAGI-1. In addition, the expression of the K499E mutant MAGI-1 in HeLa cells generated a larger MAGI-1-positive population than the wild type protein (Figure 25b), and, consistent with this, also the MAGI-1/TUNEL-positive subpopulation was higher upon the expression of the mutant (Figure 25c). Untransfected HaCaT cells showed a slightly higher susceptibility to apoptosis induction compared to untransfected HeLa cells, however the expression of the MAGI-1 constructs also induced a high degree of apoptosis but with similar efficiencies (Figure 25d), although the levels in HaCaT were slightly lower then in HeLa.

Taken together, these data suggest that the expression of MAGI-1 increases the rate of cell death in both HPV-positive and HPV-negative cells, and that this function of MAGI-1 is likely not to be exerted through the PDZ domain 1. Moreover, this provides an additional advantage for HPV to promote the E6-mediated degradation of MAGI-1.
Part II:

Regulation of HPV-18 E6 expression by hScrib

hScrib specifically stabilizes HPV-18E6 protein levels

It is well established that the continuous expression of E6 and E7 oncoproteins is a prerequisite for maintaining the survival and tumorigenic potential of HPV-positive cancer cells. Recent studies suggested that the interaction of high-risk HPV E6 oncoproteins with PDZ domain-containing proteins could be beneficial for the viral life cycle by maintaining high levels of E6 expression (Nicolaides et al., 2011). Furthermore, these studies also suggested that this phenomenon was linked to the direct stabilization of E6 by several different PDZ substrates rather than by one specific E6 target. However, all of these analyses were done under conditions of ectopic overexpression, and we were interested in determining whether different PDZ domain-containing substrates of E6 could likewise contribute to maintaining the steady state levels of E6 in cells derived from cervical lesions, in which E6 is expressed at endogenous levels. To do this, we decided to investigate the effect of siRNA ablation of several different PDZ domain-containing targets of E6 upon the steady state levels of E6 expression in HeLa cells, as reagents for the detection of HPV-18 E6 are readily available (Tomaić et al., 2009; Krishna Subbaiah et al., 2012). Cells were transfected with siRNA against Luciferase, hScrib, hDlg, TIP2, PSD95, MAGI-1, PTPN3 and FAP1. We also included in the analysis siRNA against HPV-18 E6/E7 as a reference for E6 downregulation. 72 hours after transfection, the cells were extracted and the expression levels of HPV-18 E6, p53 and the set of silenced PDZ proteins were monitored by western blot analysis. In addition, since recent studies had shown that the stability of HPV-18 E6 in HeLa cells is dependent upon E6AP expression (Tomaić et al., 2009), we also assessed the levels of E6AP in order to determine whether PDZ proteins might affect the expression of E6 indirectly through the modulation of E6AP levels. The results are shown in Figure 26a, and the quantifications of HPV-18 E6 levels from multiple experiments are shown in Figure 26b. As can be seen, control siLuciferase HeLa cells express readily detectable levels of endogenous HPV-18 E6, p53 and E6AP as well as of the PDZ proteins TIP2 and hScrib, whereas lower residual levels of hDlg
Figure 26. hScrib regulates the expression of HPV-18 E6 in HeLa cells.
Figure 26 (Cont.). A. HPV-positive HeLa cells were transfected with siRNA Luciferase, siRNA HPV-18 E6 or siRNA against the indicated E6 PDZ substrates. Cells were grown for 72 hours prior harvesting and the expression patterns of HPV-18 E6, hDlg, hScrib, TIP2, p53, E6AP and α-actinin, to monitor the protein loading, were assessed by western blot analysis. B. Band intensities were determined using the OptiQuant quantification program. E6 levels were normalized to 100% relative to siLuciferase-transfected HeLa cells. Histograms represent the mean values and standard deviations calculated from three independent experiments (unpaired two-sample t-test). C. The silencing of hScrib was performed as in A but using two different siRNAs specific for hScrib. The expression levels of HPV-18 E6, hScrib, p53 and α-actinin to monitor the protein loading, were assessed by western blot analysis. The corresponding P values are: *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001.
expression could be detected. Silencing of E6 and E7 produced a massive downregulation of HPV-18 E6 expression compared with control cells, and, as expected, this led to a significant increase of p53 expression levels, which is consistent with previous studies (Scheffner et al., 1993; Huibregtse et al., 1993), and with the results presented in Figures 10, 11 and 12. It is interesting to note that upon ablation of E6/E7 the expression levels of E6AP were also upregulated, and this is consistent with previous studies suggesting that high-risk HPV E6 promotes the self-ubiquitylation and increased rates of proteasome-mediated degradation of E6AP (Kao et al., 2000). In addition, in agreement with previous results (Kranjec and Banks, 2011; Figure 10b and 10c), the silencing of HPV-18 oncoproteins in HeLa cells produced a rescue of hDlg levels of expression and also hScrib levels were increased. In contrast, TIP2 levels remained relatively unchanged. Surprisingly, among the E6 PDZ targets assayed, the ablation of hScrib produced a dramatic reduction of HPV-18 E6 levels of expression, with an efficiency that was slightly lower than that obtained with the E6/E7 siRNA (Figure 26a and 26b). Consistent with this reduction in E6 levels of expression, the ablation of hScrib also resulted in increased levels of hDlg, E6AP and p53, although to a lower extent than in siE6/E7 transfected HeLa cells. Interestingly, similar levels of E6AP upregulation were also obtained upon ablation of hDlg, TIP-2, PSD95 and FAP1, and similarly p53 expression was also generally increased upon the silencing of the other E6 PDZ targets, although in this case HPV-18 E6 levels were not significantly reduced. In this context, the modulation of p53 expression has been linked so far only to the PDZ protein TIP1, which by promoting increased p53 ubiquitylation, increases its levels of proteasome-mediated degradation (Han et al., 2012), therefore loss of TIP1 would be expected to increase p53 levels. However, our data also suggest that p53 expression could, at least in part, be regulated by multiple PDZ domain-containing proteins in HeLa cells. In addition, silencing of hDlg also produced a strong upregulation in the levels of hScrib expression, which was even higher than that obtained following ablation of E6. Low levels of hScrib upregulation were also obtained by silencing MAGI-1, TIP2 and PSD95. Similarly, hDlg and TIP2 expression levels were also elevated upon silencing of the other PDZ domain-containing proteins, possibly suggesting the existence of a high level of compensation between different PDZ proteins.
In order to confirm that the maintenance of HPV-18 E6 levels in HeLa cells were indeed dependent upon the expression of hScrib, and to verify that this was not due to any off-target effects of the hScrib-specific siRNA we repeated the analysis with an alternative siRNA obtained from a different supplier. As can be seen in Figure 26c, the two hScrib siRNAs blocked the expression of hScrib, although with slightly different efficiencies. Consistent with the results in Figure 26a and 26b, the two hScrib siRNA produced a similar reduction in the HPV-18 E6 levels of expression, and this reduction correlated directly with the efficiency with which hScrib levels were reduced.

Taken together these data confirm that loss of hScrib expression in HeLa cells can directly lead to a reduction in the levels of E6 in HeLa cells, and that multiple PDZ proteins are involved in complex molecular networks that might regulate the function of p53 as well as of other PDZ proteins.

Previous studies suggested that HPV-18 E6 displays a differential subcellular localization, with protein pools localizing predominantly at membrane and nuclear sites of transfected cells (Grossman et al., 1989). In order to investigate whether loss of hScrib affected the pattern of expression of specific pools of E6 we performed fractionation experiments on HeLa cells transfected with either siRNA against Luciferase or hScrib. 72 hours post-transfection, HeLa cells were separated into four subcellular fractions and the expression pattern of HPV-18 E6, p53 and of the fraction-specific markers α-tubulin, E-cadherin, p84 and vimentin were assessed by western blot analysis. As can be seen from Figure 27, in siLuciferase transfected cells we detected the majority of E6 in the membrane fraction, with lower levels present in the nuclear and cytoplasmic fractions. In cells transfected with control siRNA, p53 was mainly expressed in the nucleus with residual levels also found in membrane and cytoskeletal fractions. Conversely, in cells transfected with hScrib siRNA, the levels of E6 are generally reduced in all three fractions. Consistent with this, p53 levels increase slightly in the same three fractions. These data suggest that silencing of hScrib in HeLa cells affects the total levels of E6 expression, rather than a specific subcellular pool.
Figure 27. Loss of hScrib does not affect specific subcellular pools of E6 in HeLa cells. HeLa cells were transfected with siRNA Luciferase or siRNA hScrib, and after 72h cells were fractionated into 4 subcellular compartments: cytosol (F1), membrane (F2), nucleus (F3), cytoskeleton (F4). The expression patterns of HPV-18 E6, p53, hScrib and those of the four subcellular fraction markers E-cadherin (membrane), p84 (nucleus), α-tubulin (cytoplasm) and vimentin (cytoskeleton) were assessed by western blot analysis.
Ablation of hScrib does not affect HPV-18 E6 turnover

Having shown that loss of hScrib results in decreased levels of HPV-18 E6, we were interested in investigating whether this was due to an increase in the rate of E6 turnover, since previous studies had shown that the lack of PDZ binding capacity affected E6 stability (Nicolaides et al., 2011). To do this, we decided to monitor the E6 half-life in HeLa cells following ablation of hScrib expression. 72 hours after transfection, the cells were treated with cycloheximide for different time-points. The cells were then harvested and the expression levels of E6 were monitored by western blotting. The results are shown in Figure 28a, with the quantifications from multiple experiments shown in Figure 28b. In agreement with previous studies, the half-life of HPV-18 E6 in control siRNA-transfected HeLa cells was between 60 and 120 minutes (Grossman et al., 1989; Tomaic et al., 2009). This is also in agreement with previous studies showing that different subcellular pools of E6 display differences in their half-life, and that the membrane pool of the protein, the predominant form of E6 found in HeLa cells, has a half-life of about 2 hours (Grossman et al., 1989). The silencing of hScrib however, did not produce any significant change in the E6 half-life, suggesting that loss of hScrib expression does not affect E6 turnover. It is interesting to note, however, that although the turnover of E6 was not affected in siScrib transfected HeLa cells, p53 was stabilized in these cells. Consistent with previous studies, in control siRNA transfected HeLa cells the half-life of p53 was between 15 and 30 minutes (Talin et al., 1998). The ablation of hScrib significantly prolonged the half-life of p53, which is consistent with the overall decrease in E6 levels, but this is not as a result of increased E6 turnover.

We were then interested in investigating whether hScrib might alter the levels of E6 gene expression. Since E6 and E7 are expressed from a bicistronic mRNA (Schneider-Gädicke and Schwarz, 1986; Smotkin and Wettstein, 1986), we reasoned that any reduction in E6 transcription in HeLa cells, would also be reflected by lower levels of E7 expression. The high-risk HPV E7 oncoprotein promotes the proteasome-mediated degradation of hypophosphorylated, E2F-binding competent forms of pRB (Boyer et al., 1996; Gonzalez et al., 2001). Therefore, the analysis of the expression pattern of differentially phosphorylated forms of pRB in HPV-positive cells can be used
as a surrogate marker to monitor the levels of E7 expression (Tang et al., 2006). HeLa cells were transfected with control siLuciferase, siRNA against hScrib or HPV-18 E6/E7 as a reference for the silencing of E7. After 72 hours, cells were harvested and the expression pattern of pRB was monitored by western blot analysis. The results of this assay are presented in Figure 28c, and the quantifications of pRB levels obtained in multiple experiments are shown in Figure 28d. In agreement with previous studies, our results demonstrate that pRb is expressed as differentially phosphorylated forms, and that HeLa cells predominantly express the hyper-phosphorylated pRB (Tang et al., 2006). Following ablation of E6 and E7, the expression of p53 and the ratio between the hypo- and hyper-phosphorylated pRB levels are significantly increased, demonstrating the efficient silencing of both oncoproteins. In contrast, whilst loss of hScrib expression led to an increase in p53 levels, the ratio between the hypo- and hyper-phosphorylated forms of pRB was comparable to that of the control siRNA-transfected HeLa cells, indicating that upon loss of hScrib the levels of E7 expression remained unaffected. Interestingly however, loss of hScrib resulted in an overall reduction of both pRB forms. This might be a reflection of a decrease in E6 levels, as previous studies suggested that E6 was able to induce high levels of expression of both hypo- and hyper-phosphorylated pRB (Malanchi et al., 2004). Taken together these data indicate that loss of hScrib does not directly affect the levels of transcription of E6 and E7 in HeLa cells.

Loss of hScrib decreases HPV-18 E6 translation

We were next interested in determining whether E6 rates of translation were affected by loss of hScrib. To do this, HeLa cells were first transfected with siLuciferase or siScrib, and after 72 hours the cells were treated for 6 hours with cycloheximide to block protein translation. Cells were then washed several times with PBS to remove the cycloheximide, and the recovery in the levels of HPV-18 E6 and p53 protein expression were monitored over time by western blot analysis. The results are shown in Figure 29a, and the quantifications of multiple experiments are shown in Figure 29b. As can be seen, the prolonged treatment with cycloheximide produced over an 80% decrease in the levels of E6 in both control and siScrib transfected HeLa cells. Even more apparent was the drop in p53 levels, which upon cycloheximide treatment became undetectable in both the
Figure 28. Loss of hScrib does not affect HPV-18 E6 protein stability nor its transcriptional rate. A. HeLa cells were transfected with siRNA against Luciferase or siRNA against hScrib, 72 hours after transfection and prior to harvesting, cells were treated with cycloheximide for 5 different time points: 0, 15, 30, 60 and 120 minutes. The expression levels of HPV-18 E6, p53, hScrib and α-actinin to monitor the protein loading, were assessed by western blot. The collated results from 3 independent experiments to measure E6 protein turnover in cells treated with siRNA Luciferase and siRNA hScrib are shown in panel B. Band intensities were determined using the OptiQuant quantification program. The E6 levels in siLuciferase and siScrib transfected cells were normalized to 100% at time 0. Shown are the mean values and standard deviations calculated from three independent experiments.
Figure 28 (Cont.). C. HeLa cells were transfected with siRNA against Luciferase or siRNA HPV-18 E6/E7 or siRNA hScrib. 72 hours after transfection, cells were harvested and the expression pattern of pRB, p53, hScrib and α-actinin, to monitor the protein loading, were assessed by western blot. D. Band intensities were quantified using the OptiQuant quantification program, and levels of of hypo-phosphorylated and hyper-phosphorylated pRB expression in control, siLuciferase-transfected cells, and siScrib-transfected cells were normalized to 100%. Differences in the expression pattern of pRB were expressed as percentage of hypo-phosphorylated and hyper-phosphorylated pRB protein relative to control cells. Histograms represent the mean values calculated from three independent experiments. Standard deviations are also shown (unpaired two-sample t-test). The corresponding P values are: *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001.
Figure 29. hScrib regulates the translation of HPV-18 E6 in HeLa cells. A. HeLa cells were transfected with siRNA against Luciferase or siRNA against hScrib. 72 hours after transfection, cells were treated with cycloheximide for an additional 6 hours. After the treatment, and prior to harvesting, cells were washed three times with PBS to remove the cycloheximide and protein translation was left to recover in complete medium for 4 different time points: 0.5, 1, 3 and 5 hours. The collated results from 3 independent experiments are shown in panel B. Band intensities were determined using the OptiQuant quantification program. The E6 levels in siLuciferase and siScrib transfected cells were normalized to 100% at time 0. Shown are the mean values and standard deviations calculated from three independent experiments.
control and siScrib transfected cells. Upon removal of cycloheximide, the levels of HPV-18 E6 expression progressively recovered after the 30 minute time point. It is interesting to note that the bulk of E6 oncoprotein was translated within 3 hours of cycloheximide wash-out, suggesting that the accumulation of E6-encoding mRNAs during translation inhibition led to the rapid synthesis of newly translated E6 upon removal of cycloheximide. In contrast, loss of hScrib in HeLa cells greatly reduced the rate of recovery in E6 protein levels upon translation re-initiation. Interestingly, the pattern of p53 recovery was opposite to that of E6, being rapidly upregulated in siScrib cells after cycloheximide wash-out, which is consistent with the lower levels of E6 expression in these cells. Taken together these data suggest that the residual expression of hScrib in HeLa cells contributes towards maintaining high levels of HPV-18 E6 expression through the modulation of its rate of translation.

**hScrib regulates the mTORC1 pathway through the modulation of S6 kinase activity**

Previous studies suggested that the E6 mRNA is translated using the canonical cap-dependent ribosome scanning model (Stacey *et al.*, 2000; Tan *et al.*, 1994). In this model, the 40S ribosome subunit contacts the 5' end of the mRNA and begins to scan the messenger until it recognizes a suitable start codon, at which the 60S ribosomal subunit is recruited to form the complete ribosome and begin the polypeptide translation (Kozak *et al.*, 1989; Pestova *et al.*, 2001; Gebauer and Hentze 2004). In this process the rate-limiting step is the translation initiation, in which the loading of the small (40S) ribosomal subunit onto the mRNA is dependent upon the recruitment of multiple translation initiation factors (eIFs), including eIF4E, eIF4A and eIF4G, to form the translation initiation factor 4F (eIF4F) complex at the 5' cap structure of the mRNA (Ma and Blenis, 2009). In this context, the mTOR complex 1 (mTORC1) is part of the molecular machinery that couples growth factor stimulation to translation initiation by promoting the assembly of the eIF4F complex and enhancing the scanning activity of the small ribosomal subunit (Martin and Blenis, 2002). Therefore, we speculated that hScrib might modulate cap-dependent protein translation through the regulation of components of the mTORC1 pathway. To assess this possibility, we decided to investigate the activity of the PDK1 and S6 kinases, two protein kinases known to modulate the
mTORC1 pathway (Pullen and Thomas; 1997; Williams et al., 2000). Figure 30a shows a cartoon of the mTORC1 pathway, and, as can be seen, the activity of PDK1 and S6 kinase is regulated by phosphorylation events. The autophosphorylation of PDK1 at serine 241 is crucial for its full activation, which is required upstream of mTOR for the activation of the pathway through the PI3K signaling (Casamayor et al., 1999). On the other hand, mTOR directly activates its effector S6 kinase through the phosphorylation of its threonine 389; in turn, activated S6 kinase promotes protein synthesis by modulating the activity of multiple proteins involved in translation. HeLa cells were transfected with either siRNA Luciferase, or siRNA hScrib and after 72 hours the cells were harvested and levels of PDK1, S6 kinase and Akt were assessed by western blot by using antibodies to detect the total as well as phosphorylated forms of the different kinases. As can be seen in Figure 30b, HeLa cells express high levels of phospho-serine 241 (pS241) PDK1, and, surprisingly, the ablation of hScrib resulted in a reduction of both the phosphorylated and total PDK1 levels, suggesting that the reduced levels of phosphorylation are a reflection of the lower total protein levels. The activation of PDK1 results in the phosphorylation of Akt at threonine 308, which for its full activity also requires the mTORC2-mediated phosphorylation of serine 472 (Alessi et al., 1996; Scheid et al., 2002). The two phosphorylation events are sequential, however which of the two sites needs to be phosphorylated first to allow the subsequent full activation is still not completely clarified. Upon reduction of PDK1 expression due to the loss of hScrib, the levels of phosphorylated T308 as well as S473 Akt were also reduced, suggesting that the PDK1-mediated phosphorylation might play a crucial role in the full activation of Akt (Toker and Newton, 2000). Furthermore, this also indicates that the expression of hScrib might positively regulate the PI3K pathway. In the case of S6 kinase, this protein is expressed as two isoforms, p70 and p85, which share the same sequence with the exception that the p85 isoform has an extended N-terminus encoding a nuclear localization signal that promotes its nuclear accumulation (Pullen and Thomas, 1997). The mTORC1-mediated phosphorylation of a threonine residue which is located at position 389 in p70 and at position 412 in p85 is most critical for their function in vivo (Weng et al., 1998); therefore we also monitored this phosphorylation event upon silencing of hScrib in HeLa cells. Similar to PDK1, the ablation of hScrib also led to the downregulation of total and phosphorylated
Figure 30. The expression of hScrib in HeLa cells maintains high levels of total PDK1 and S6 kinase levels. A. A cartoon summarizing the main components of the mTORC1 pathway is shown. The relative position of the components along the pathway as well as activating phosphorylation events are depicted. Adapted from Cheng and Force, 2010. B. HeLa cells were transfected with siRNA Luciferase or siRNA hScrib. 72 hours after transfection cells were harvested and the patterns of expression of total and phosphorylated levels of Akt, PDK1 and S6 kinase as well as those of hScrib and α-actinin as loading control, were assessed by western blot.
p70 and p85 S6 kinase. Previous studies indicated that the expression of HPV-16 E6 in human keratinocytes is sufficient to promote the activation of PDK1 and S6 kinase (Spangle and Mönger, 2010), therefore we decided to also include siRNA against HPV-18 E6 in the analysis, in order to rule out the possibility that effects on PDK1 and S6 kinase activity produced by the ablation of hScrib are indirectly linked to a reduction of E6 levels. Since previous studies suggested that E7 can also affect the levels of components of the PI3K pathway (Pim et al., 2005; Menges et al., 2006; Charette and McCance, 2007), we decided to use an siRNA that targets the intronic region of the E6 ORF. This strategy has been shown to efficiently inhibit the expression of HPV-18 E6 whilst only marginally affecting the expression of HPV-18 E7 and E6* (Butz et al., 2003), which is consistent with the fact that type-I transcripts encoding the full-length E6 and E7 proteins are expressed at significantly lower levels than type-II and III transcripts, which encode E6* and E7 (Schneider-Gädicke and Schwarz, 1986). As can be seen in Figure 31a, silencing of HPV-18 E6 produced a reduction in levels of total and phosphorylated PDK1 comparable to that obtained by the ablation of hScrib. This indicates that the effect on PDK1 expression could be, at least in part, linked to the reduction in E6 levels upon loss of hScrib in HeLa cells. Interestingly, however, the silencing of E6 did not downregulate total and phosphorylated S6 kinase protein levels compared with siScrib cells, suggesting that hScrib might be regulating protein translation through the modulation of the S6 kinase activity.

The fact that loss of hScrib expression led to a reduction of total S6 kinase levels might indicate that this is linked to increased turnover of the protein. To assess whether the reduced levels of S6 kinase might result from increased degradation, we repeated the silencing of hScrib in HeLa cells in the presence of the proteasome inhibitor MG-132. 72 hours posttransfection, siLuciferase or siScrib HeLa cells were left untreated or treated with MG-132 for an additional 3 hours prior to harvesting. The levels of total and phosphorylated forms of PDK1, S6 kinase and also HPV-18 E6 were assessed by western blotting. The results are shown in Figure 31b, and, as can be seen, the ablation of hScrib again led to the efficient reduction in the levels of E6 expression. The proteasome inhibition led to a strong accumulation of HPV-18 E6 levels in siLuciferase HeLa cells,
which is in agreement with previous studies suggesting that E6 is regulated by the proteasome in a E6AP-dependent manner (Stewart et al., 2004). Interestingly, upon silencing of hScrib the proteasome inhibition did not induce a rescue of E6 protein levels, which is consistent with the result in Figure 28 showing that loss of hScrib does not affect E6 protein stability. Upon proteasome inhibition total and phosphorylated PDK1 were upregulated in siLuciferase HeLa cells, suggesting that PDK1 is also regulated through the proteasome. In hScrib-silenced cells, however, PDK1 displayed a pattern of expression similar to E6, with the MG-132 treatment failing to rescue total and pS241 levels. Conversely, total S6 kinase levels were only marginally modified upon proteasome inhibition, both in siLuciferase and siScrib HeLa cells, indicating that its expression is most likely not regulated through the proteasome. However when the levels of phosphorylated S6 kinase were monitored upon MG-132 treatment, phospho-p85 S6 kinase levels were massively increased in both siLuciferase and siScrib transfected cells whereas phospho-p70 remained relatively unaffected. These data suggest that total and phospho-p70 are not regulated by the proteasome, whereas phospho- and total p85 display a differential mechanism of regulation and loss of hScrib might promote the proteasome-mediated degradation of phospho-p85 S6 kinase.
Figure 31. HPV-18 E6 regulates the expression levels of PDK1 but not those of S6 kinase. A. HeLa cells were transfected with siRNA Luciferase, siRNA hScrib and siRNA E6. 72 hours after transfection cells were harvested and the expression patterns of total and phosphorylated PDK1 and S6 kinase, as well as those of hScrib, HPV-18 E6 and α-actinin as loading control, were assessed by western blot.

B. The siRNA transfection was performed as in A, but cells were treated with the proteasome inhibitor MG-132 for an additional 3 h prior to harvesting. The expression pattern of total and phosphorylated PDK1 and S6 kinase, as well as those of hScrib, HPV-18 E6 and α-actinin as loading control, were assessed by western blot.
Discussion

Part I:

**E6-mediated regulation of PDZ domain-containing proteins in HPV-positive cells**

A number of PDZ domain-containing substrates of E6 have been described, and many of these proteins are involved in diverse regulatory pathways, including the assembly of cell-cell junctions and cell attachment, and in the control of cell signaling. Potential tumor suppressor activities have also been assigned to several of these proteins. An important question that remains to be answered is whether or not all of these substrates are equally susceptible to E6-induced degradation *in vivo*, and how the relevant pathways they regulate might contribute to HPV-related malignancy. In an attempt to provide an answer to that, in our analysis we used specific siRNAs to silence the expression of E6 and E7 and E6AP in HPV-16 and HPV-18 transformed cell lines with the aim of identifying potential E6 PDZ domain-containing substrates relevant for HPV carcinogenesis *in vivo*. Recent structural studies had shown that the PDZ recognition by the HPV-16 and HPV-18 E6 PBMs requires very defined structural features, and minimal variations in the sequences of either the PBM or of the target PDZ domains has dramatic effects upon the pattern of substrate selection, as well as in the recognition of specific PDZ domains within the same protein (Zhang *et al.*, 2007). This is also supported by *in vitro* studies in which hDlg, hScrib and MAGI-1 were shown to be differentially selected for degradation by HPV-16 and HPV-18 E6 oncoproteins, with the former being more efficient for binding to hScrib, whereas HPV-18 E6 displays an increased affinity for hDlg and MAGI-1 (Gardiol *et al.*, 1999; Pim *et al.*, 2000; Thomas *et al.*, 2001; Thomas *et al.*, 2005). Although residues located upstream of the canonical PBM of E6 oncoproteins have been shown to contribute to the interaction with PDZ domains (Zhang *et al.*, 2007; Thomas *et al.*, 2008a), the major contribution towards the differential selection of these PDZ proteins is brought by the last residue of their PBM; respectively V and L in HPV-18 and -16 E6. This was further underlined by recent biacore measurements of the $K_d$ values for the association of MAGI-1 PDZ domain 1 with the PBMs of HPV-16 and HPV-18 E6. These studies suggested that by mutating the HPV-16 E6 PBM into that of HPV-18 E6 (-ETQL→V ) the affinity of MAGI-1 PDZ domain 1 for
HPV-16 E6 could be increased of three folds (Fournane et al., 2011). Similarly, by swapping the two PBMs HPV-16 E6 becomes more efficient in degrading hDlg and MAGI-1, whereas HPV-18 E6 increases its efficiency in degrading hScrib (Thomas et al., 2001; Thomas et al., 2005). In agreement with all these studies, the data presented in Figures 10, 11 and 12 strongly suggest that the proteolytic degradation of PDZ proteins by E6 in HPV-transformed cells, is a highly specific process that involves the targeting of a specific subset of host-encoded PDZ domain-containing proteins.

In our study, we found that the levels of MAGI-1 expression are very low in HPV-16 and HPV-18-positive cells, and increased significantly following ablation of E6/E7 expression. As shown in Figure 11, the silencing of E6 and E7 led to a dramatic rescue of MAGI-1 protein levels in HeLa and SiHa cells, whereas the rescue in CaSKi was somewhat more marginal. However, the fact that MAGI-1 levels of expression were efficiently rescued in SiHa, but not in CaSKi, upon ablation of HPV-16 E6 and E7 suggests that the low levels of MAGI-1 expression in CaSKi cells might not be directly dependent upon HPV-16 E6 expression, and indicates that MAGI-1 is a sensitive proteolytic substrate for both HPV-18 and HPV-16 E6 oncoproteins \textit{in vivo}. A marked difference in the pattern of HPV-16 and HPV-18 E6 PDZ substrate selection appears to be particularly relevant for some other potential targets, including hDlg, hScrib and PSD95. An interesting aspect of hScrib and hDlg expression in HPV-positive cells is that their levels are readily detectable in HeLa and CaSKi cells. Upon ablation of E6 and E7, hScrib appears to be rescued more efficiently in CaSKi than in HeLa cells (Figure 10a and 10c), whereas hDlg showed the higher degree of rescue in HeLa cells at 48 and 72 hours post transfection (Figure 10a and 10b). However, an increase in hDlg levels became more apparent at 72h after transfection also in CaSKi cells (Figure 10b), suggesting that HPV-16 E6 retains the ability to promote the degradation of hDlg in HPV-transformed cells. It is also interesting to note that upon silencing of E6 and E7 the pattern of hDlg expression differed between HeLa and CaSKi cells, likely representing differentially modified forms or different isoforms of hDlg. This suggests that both HPV-16 and HPV-18 E6 target hDlg for degradation \textit{in vivo}, but they might differ in the selection of the pools of hDlg targeted for
degradation. Similarly, we found that the hDlg-related protein, PSD95, is efficiently targeted by HPV-18 E6, but less so by HPV-16 E6 (Figure 12b), and this is in agreement with previous reports (Handa et al., 2007). Silencing of E6AP largely confirmed the differential PDZ substrate selection pattern between HPV-16 and HPV-18 E6. It would be of interest to better define the contribution of E6AP towards the degradation of E6 PDZ substrates, since previous studies reported that E6 can degrade its substrates also in an E6AP-independent manner (Massimi et al., 2008b). However, in our experimental setting it is hard to obtain conclusive evidence about the involvement of E6AP in the E6-mediated degradation of its substrates, since loss of E6AP expression has been shown to greatly affect E6 stability (Tomaic et al., 2009), making it virtually impossible to differentiate their respective contribution towards the degradation of E6 substrates under these experimental conditions.

Of the remaining PDZ substrates of E6 that were analysed, we failed to obtain conclusive evidence that PTPN3 (Figure 12a) or TIP2 (Figure 12c) were targeted for degradation either by HPV-16 or HPV-18 E6 in monolayer cultures of cells derived from cervical tumors and. This is in marked contrast with previous studies suggesting that TIP2 and PTPN3 are targeted for proteasome-mediated degradation by high-risk HPV E6 oncoproteins (Favre-Bonvin et al., 2005; Töpffer et al., 2007; Jing et al., 2007). However, these studies do not rule out the possibility that these PDZ domain-containing proteins may be degradation substrates of E6 in other biological settings: during different stages of the normal viral life cycle where the cells are subject to terminal differentiation, or at an earlier stage of tumor development. This might reflect differences in the phosphorylation status of the target protein, which could influence accessibility to E6 and subsequent targeting (Massimi et al., 2006; Narayan et al., 2009). Finally, we should also emphasize that, although degradation has been proposed as a major mechanism by which E6 exerts its function, it is possible that some of these substrates may be only bound by E6, and that blocking a certain PDZ substrate-ligand interaction might be sufficient for E6 to modulate the function of that particular cellular PDZ domain-containing protein, or alternatively, E6 might also alter the localization of the substrate.
The last E6 PDZ domain-containing substrate analysed in our study was the non-receptor tyrosine phosphatase PTPN13 or FAP-1. We included this protein in our analysis since previous studies described FAP-1 as a proteolytic target for the HPV-16 E6 oncoprotein in tonsillar keratinocytes (Spanos et al., 2008b). In our analysis we detected very low levels of FAP-1 expression in HeLa cells, whereas higher FAP-1 protein levels were expressed in CaSKi cells. Surprisingly, the expression of FAP-1 was downregulated in both HPV-positive cell lines upon ablation of E6 and E7, whereas its levels were unchanged upon silencing of E6AP in CaSKi cells (Figure 12d). This pattern of expression in CaSKi cells would fit with a possible involvement of E7 in the regulation of FAP-1. This possibility is particularly intriguing since two sequences matching the putative E2F-binding site TTTSSCGC (where S is C or G) are present in the promoter region of FAP-1 (C.K. personal observation; Abaan and Toretsky, 2008). This suggests that that HPV-16 E7 could indirectly drive the expression of FAP-1 through the destabilization of E2F/pRB complexes.

Considering the differences in the regulation of FAP-1 by HPV E6 in head and neck and cervical cancer-derived cells, it is important to note that there appear to be some significant differences between HPV-mediated head and neck and cervical carcinogenesis. Recent studies in which HPV-16 E6 and E7 were expressed in head and neck tissues, under the control of the K14 promoter, suggested that in head and neck tumors the carcinogenic potential of HPV-16 is less dependent upon the ability of E6 to interact with E6AP and its PDZ domain-containing substrates (Jabbar et al., 2010) compared with models for cervical carcinogenesis (Shai et al., 2007a; Shai et al., 2010), indicating that in different tissues HPV oncoproteins might follow different routes of oncogenic transformation. In addition, these differences are also underlined by the fact that although the p16 expression is generally accepted as a surrogate marker for cervical cancer progression (Tsoumpou et al., 2009), the correlation between the p16 overexpression and HPV-positive cancers in different head and neck tissues appears not to be unequivocal (Hoffaman et al., 2012), possibly reflecting tissue specific differences.

FAP-1 function appears to be highly pleiotropic and context-dependent. Consistent with this, several reports ascribe to FAP-1 both tumor suppressive and tumor promoting functions (Abaan
A relevant aspect of FAP-1 biological activity is its effect on Fas-mediated apoptosis. The activation of the Fas (CD95/APO-1) receptor, which is exposed on the cell surface, occurs through the engagement of the Fas ligand (FasL/CD95L), a trimeric protein belonging to the tumor necrosis factor (TNF) superfamily, ultimately resulting in the induction of caspase-8-mediated apoptosis. Expression of FAP-1 has been correlated either with a decreased expression of FasR on the cell surface (Ungefroren et al., 2001; Ivanov et al., 2001) or with the deregulation of the Fas-associated pro-apoptotic signaling (Meinhold-Heerlein et al., 2001; Foehr et al., 2005; Wieckowski et al., 2007), thereby prolonging the survival of FAP-1 expressing cells. The maintenance of FAP-1 expression in the context of viral life cycle could then represent an additional strategy to escape apoptosis or evade the immune system surveillance, since the Fas-associated signaling is one of the prime mediators of T-cell-mediated cytotoxicity towards virus-infected cells (Ju et al., 1994). This hypothesis is also reinforced by the fact that HPV-16 E5 has been shown to downregulate FasR protein levels and its membrane targeting. In addition, other viruses, including adenovirus, KSHV and HTLV-1, have evolved similar mechanisms to block Fas-mediated apoptosis (Shisler et al., 1997; Tollefson et al., 1998; Belanger et al., 2001; Okamoto et al., 2006). Obviously, further studies are required to determine whether E7 can upregulate FAP-1 in an E2F-dependent manner.

Since biochemical data suggest that MAGI-1 is the strongest interacting partner of HPV E6 (Thomas et al., 2001, Zhang et al., 2007) we focused on further defining the relevance of MAGI-1 degradation in HPV-induced malignancy. MAGI-1 is a TJ-associated protein whose best understood function is its ability to promote TJ assembly (Hirabayashi et al., 2003; Murata et al., 2005). However, the sequence analysis of MAGI-1 reveals the presence of a strong bipartite nuclear localization signal in the carboxy terminus of the protein (Dobrosotskaya et al., 1997), consistent with there being a pool of MAGI-1 normally resident within the nucleus of epithelial cells (Dobrosotskaya and James, 2000; Kranjec and Banks, 2011). Thus, this complex pattern of distribution suggests that MAGI-1 is likely to be involved in additional biological processes beside its ability to promote the assembly of junctional complexes. Using differential cell fractionation we verified that the abolition of E6/E7 expression restores MAGI-1 expression at two main locations within HPV-positive cells: the cell membrane and the cell nucleus (Figure 13a). This suggests that
whatever functions these two pools of MAGI-1 perform, the removal of one or both has advantages for the virus. Fractionation experiments in HPV-negative cells, however, revealed high levels of MAGI-1 expression also in the cytoplasm (Figure 13b), suggesting that the pattern of MAGI-1 localization is likely to be dynamic and cell-type specific. There are currently no studies available that could offer an explanation for what MAGI-1’s function is in the nucleus. Further studies will aim at more fully defining the functions of this form of the protein.

In contrast, the membrane-bound form of MAGI-1 has been implicated in the control of TJs (Murata et al., 2005), which are lost in HPV-positive cells (Nakagawa and Huibregtse, 2000; Latorre et al., 2005; Storrs and Silverstein, 2007). The results reported here show that this loss is indeed a result of E6 directing the degradation of MAGI-1. Using ZO-1 as a marker of TJ integrity, we have confirmed that these junctions are largely absent in HPV-18-positive HeLa cells, and that ablation of E6 expression results in a clear re-accumulation of MAGI-1 at the cell membrane, accompanied by an accumulation of ZO-1 at the same cellular location (Figure 14). Interestingly, this appears to be a slow process, with a bead-like structure, indicative of the early stages of junction formation (Kimura et al., 2010), apparent at 72h after transfection with E6/E7 siRNA, and more complete junctions visible by 96h. To verify that restoration of TJs depends upon the rescue of MAGI-1 from E6-induced degradation, we co-transfected a MAGI-1 siRNA with the E6/E7 siRNA, and in this case there was no evidence of TJ formation (Figure 14). Recent studies suggested that hScrib is also strongly implicated in the process of epithelial TJ assembly (Nakagawa and Huibregtse, 2000; Ivanov et al., 2010; Elsum et al., 2013). However, upon silencing of hScrib in combination with E6 and E7 in HeLa cells we failed to detect any deleterious effect upon ZO-1 junctional recruitment (Figure 15a), confirming the specificity of the results with MAGI-1.

**Potential roles played by MAGI-1 in HPV-related disease**

A particularly interesting structural insight in the context of MAGI-1 regulation by E6, has been the identification of lysine 499 within the PDZ-1 domain as a crucial residue required for the interaction with the PBM of HPV-16 and HPV-18 E6 oncoproteins (Fournane et al., 2011).
Consistent with this, mutating K499 to E in the context of full length MAGI-1, we were able to dramatically decrease the affinity of MAGI-1 for HPV-18 and HPV-16 E6 oncoproteins (Figure 16c and 16d), and this also correlated with a reduced ability of E6 to induce the proteasome-mediated degradation of MAGI-1, in vitro and in vivo (Figure 17). The PDZ domain 1 of MAGI-1, has also been identified as the interacting region for the PBM of multiple cellular proteins, and one of such binding partner is NET1 (Dobrosotskaya, 2001). NET1 is a RhoA-specific guanine nucleotide exchange factor which is involved in a number of cancer-associated biological processes, including cell migration, proliferation and matrix invasion (Murray et al., 2008; Han et al., 2012). By performing co-immunoprecipitation assays we confirmed that NET1 is a binding partner for wild type MAGI-1 in vivo, and that the K499E mutation also strongly affects the interaction of MAGI-1 with NET1 (Figure 18a). However, the K499E mutation might not completely disrupt the functionality of the PDZ 1 domain, as the interaction with HPV-58 E6 was shown to be not affected by the mutation (Figure 18c). Furthermore, by performing immunofluorescence on wild type or K499E mutant MAGI-1-transfected cells, we showed that the mutation does not significantly modify the pattern of subcellular localization of MAGI-1, and also does not affect its interaction with a membrane-bound protein such as β-catenin (Figure 19).

The generation of the K499E MAGI-1 mutant provided a valuable molecular tool for exploring its role in the context of HPV-related pathology, since it allowed us to evaluate the effects of reintroducing MAGI-1 expression in HPV-positive cells without the need to silence E6 and E7 expression. By transiently expressing wild type and mutant MAGI-1 in HeLa cells, we confirmed that MAGI-1 expression alone is sufficient to drive TJ reassembly in HPV-positive cells, which was assessed by monitoring the expression of ZO-1 and another TJ marker, PAR3 (Figure 20a, 20b and Figure 21). However, both ZO-1 and PAR3 have a dynamic pattern of junctional localization, and have been shown to co-localize with AJ components during the induction of primordial AJ structures following initial cell-cell contact (Ando-Akatsuka et al., 1999; Suzuki et al., 2002). Therefore, we cannot rule out the possibility that the ZO-1- and PAR3-positive junctional structures observed in MAGI-1-expressing cells are infact primordial AJs. Nevertheless, these data strongly suggest that MAGI-1 directly participates in the establishment of macromolecular
complexes that localize at the TJ plaque in fully polarized cells. PAR3 is part of the PAR complex which localizes and controls the maturation of TJs, however PAR3 has been shown to be able to promote TJ assembly independently of PAR6 and aPKC (Chen and Macara, 2005), suggesting that PAR3 is one of the prime regulators of TJ formation. Therefore, the fact that MAGI-1 enhances PAR3 junctional localization strongly suggests the involvement of MAGI-1 in the establishment of cell polarity by inducing the formation of apical junctional structures (Murata et al., 2005). In support of this, the expression of MAGI-1 and PAR3 have been shown to have similar effects on the recruitment of occludin at TJs (Hirabayashi et al., 2003; Chen and Macara, 2005). However, so far a direct interaction of MAGI-1 with either ZO-1 or PAR3 has not been shown, suggesting that their MAGI-1-mediated junctional recruitment is likely to occur in an indirect way. MAGI-1 as well as ZO-1 and PAR3 have all been shown to interact with JAMs which are enriched at the TJs of epithelial cells (Ebnet et al., 2000; Bazzoni et al., 2000; Itoh et al., 2001; Ebnet et al., 2003; Hirabayashi et al., 2003). The interaction of the cytoplasmic domain of JAM molecules with components of the TJ plaque has been shown to promote their stabilization. Therefore it is likely that the expression of MAGI-1 might promote the initial clustering of JAM molecules at the cell membrane (Hirabayashi et al., 2003), which subsequently also drives the recruitment of ZO-1 and PAR3. Figure 32 summarizes the role of MAGI-1 in maintaining TJ integrity as well as in regulating proliferation and apoptosis, and describes the effects of E6 expression in the context of MAGI-1 activity.

These results demonstrate that the loss of TJs in HPV-18 positive HeLa cells is a direct consequence of the ability of E6 to direct the degradation of MAGI-1, and might provide a an explanation of why this protein is targeted by the virus during the life cycle and by E6 in malignancy.

TJs play an important role in differentiation where their correct assembly promotes the exit from the cell cycle and contributes to keratinocyte differentiation (Saitou et al., 2000; Bordin et al., 2004; Aijaz et al., 2005). Loss of TJs can therefore be expected to delay the differentiation process. In addition, TJs directly participate in the regulation of cell proliferation by modulating signaling
cascades such as MAPK, PKB/Akt and RhoA signaling (Li and Mrsny, 2000; Kotelevets et al., 2005; Aijaz et al., 2005). Interestingly, both ZO-1 and PAR3 are believed to be involved in controlling cell proliferation; while ZO-1 binds and sequesters the transcription factor ZONAB/DbpA at the cell membrane (Balda et al., 2003), PAR3 is believed to potentially regulate cell proliferation through the modulation of the p53-binding partner ASPP2 (Sottocornola et al., 2010). In our cell proliferation assay, we found that the expression of wild type MAGI-1 had dramatic effects upon the proliferative potential of HeLa cells (Figure 22). However this effect was shown to be largely independent of the junctional recruitment of ZO-1 and PAR3. Consistent with this, the K499E mutant MAGI-1 was less efficient than the wild type protein in inhibiting cell proliferation yet displaying the same efficiency as the wild type protein in promoting ZO-1 and PAR3 junctional recruitment. Most importantly, the effects of MAGI-1 upon cell proliferation appear to be specific for HPV-positive cells, since the transfection of wild type and mutant MAGI-1 into HaCaT cells had a much weaker effect upon cell proliferation (Figure 23).

This suggests that MAGI-1 can regulate cell proliferation through a mechanism not involving its junctional recruitment. An intriguing possibility is that MAGI-1 might regulate cell proliferation, at least in part, through the modulation of RhoA activity (Figure 32a). This is supported by the fact that MAGI-1 interacts with the RhoA-specific activator NET1, and that MAGI-1 had already been shown to modulate the activity of another small GTPase Rap1, with consequent stabilization of vascular-endothelial cell adhesion structures (Mino et al., 2000; Sakurai et al., 2006;). In addition, RhoA and NET1 have already been described as positive regulators of cell cycle progression (Leyden et al., 2006; Han et al., 2012). The decreased ability of the K499E mutant MAGI-1 to inhibit cell proliferation would then be consistent with its reduced capacity to interact with NET1. It is also interesting to note that recent studies had shown that NET1 is mainly localized in the nucleus of epithelial cells, where its activity is required to maintain RhoA in an active GTP-bound state (García-Mata et al., 2007; Dubash et al., 2011). Although the effect that the MAGI-1 could have on NET1 is still not clear, these data potentially provide a possible biological function for the nuclear pools of MAGI-1 in regulating RhoA activity, and might suggest that the targeting of
nuclear pools of MAGI-1 contributes to increase the proliferation of HPV-positive cells (Figure 32b).

Our data also suggest a new function for MAGI-1 in the induction of apoptosis of HPV-positive cells. We hypothesized a possible involvement of MAGI-1 in the regulation of apoptosis since upon expression of wild type and K499E mutant MAGI-1 in HeLa cells, we noticed that a proportion of MAGI-1-positive cells were also displaying a morphology typically associated with apoptosis. In order to determine whether MAGI-1 could indeed promote apoptosis we performed TUNEL assays on HeLa cells transiently transfected either with wild type or K499E MAGI-1 constructs (Figure 24a). Our data strongly suggest that both the wild type and mutant MAGI-1 can promote the apoptosis of HeLa cells. It is also interesting to note that the K499E mutant MAGI-1 displayed an efficiency in the induction of apoptosis that was comparable to that of the wild type protein. Therefore, this might suggest that the regulation of apoptosis by MAGI-1 is not dependent upon functions associated with the PDZ1 domain. Furthermore, as for the induction of junctional assembly in HeLa cells, the increased resistance of the K499E mutant MAGI-1 to E6-mediated degradation also correlated with an increased subpopulation of HeLa cells undergoing apoptosis (Figure 24a and Figure 25).

Therefore, taken together these data strongly indicate that the E6-mediated degradation of MAGI-1 could represent an additional mechanism evolved by high-risk HPV types to escape apoptosis.

Previous studies had suggested that TJ assembly might also be implicated in the regulation of apoptosis. It is interesting to note that the PAR3 binding partner ASPP2 has been shown to be strongly implicated in the induction of apoptosis by promoting the p53-mediated transactivation of pro-apoptotic p53 target genes, including Bax, PUMA, and Fas/CD95 (Samuels-Lev et al., 2001; Wilson et al., 2013). In addition, given the fact that ASPP2 localizes at cellular junctions in a PAR3-dependent manner (Sottocornola et al., 2010), it is tempting to speculate that the MAGI-1-induced junctional recruitment of PAR3 could play some role in the pro-apoptotic activity of ASPP2. It is also interesting to note that the inactivation of p53 by E1B did not affect the ability of ASPP2 to induce apoptosis (Kobayashi et al., 2005), suggesting that ASPP2 can induce apoptosis
Figure 32. A. Cartoon summarizing the regulation of TJ integrity and apoptosis by MAGI-1. A possible role for the nuclear pools of the protein in inhibiting RhoA activity is also depicted. Double arrows refers to the interdependent regulation of TJ proteins. B. Infection with high risk HPV and expression of E6 leads to the proteasome-mediated degradation of membrane-bound and nuclear pools of MAGI-1, resulting in the destabilization of junctional complexes and loss of junctional integrity. This might also potentially lead to the loss of MAGI-1-mediated NET1 regulation with downstream effects on RhoA activity.
in a p53-independent manner. In addition, recent studies showed that loss of occludin mediated the resistance of squamous cell carcinoma cells to apoptotic stimuli (Rachow et al., 2013), suggesting that the maintenance of TJ integrity can play important roles in the regulation of apoptosis.

**Part II:**

**Regulation of HPV-18 E6 expression by hScrib**

From the data presented in this thesis and elsewhere (Thomas et al., 2001; Nguyen et al., 2003a; Thomas et al., 2005; Simonson et al., 2005; Shai et al., 2007; Kranjec and Banks, 2011) it is clear that the targeting of PDZ domain-containing proteins by E6 plays an important role in the pathogenesis of cervical cancer. In addition, E6 oncoproteins can select specific PDZ proteins to target for proteasome-mediated degradation and recent studies indicated that different subcellular pools of PDZ proteins are subjected to differential regulation by E6 (Narayan et al., 2009; Krishna Subbaiah et al., 2012). Increasing evidence also suggests that certain PDZ domain-containing proteins or specific subcellular pools can cooperate with E6 in the maintenance of the transformed phenotype (Krishna Subbaiah et al., 2012). In our study we identified an unexpected role for hScrib in the context of the HPV-related pathology through the regulation of HPV-18 E6 protein translation. Previous studies already suggested that the maintenance of high-risk HPV episomes in human keratinocytes is dependent upon the ability of E6 to interact with its PDZ domain-containing substrates (Lee and Laimins, 2004; Nicolaides et al., 2011; Delury et al., 2013). In addition, the interaction of HPV-16 E6 with multiple host encoded PDZ domain-containing proteins was shown to regulate its levels of expression, suggesting that this effect is mediated by the engagement of the E6 PBM with multiple PDZ proteins rather than involving a specific PDZ domain-containing substrate of E6. However, all of these assays involved overexpression settings, and an analysis of the potential regulation of E6 by PDZ domain-containing proteins at an endogenous level was still missing. By ablating a pool of PDZ domain-containing proteins in HeLa cells we found that only loss of hScrib expression reduced endogenous levels of HPV-18 E6 expression (Figure 26). This suggests that in the context of endogenously expressed protein only hScrib appears to modulate E6 levels of expression.
Before discussing the hScrib data in more detail, it is worth considering the results obtained in Figure 26 with the ablation of the other PDZ domain-containing proteins. Upon silencing of hScrib, hDlg, TIP2, PSD95 and PTPN3, we observed a general increase in E6AP expression levels. In the case of hScrib, the upregulation of E6AP expression could be related to the reduction of E6 expression, since previous studies showed that E6 can promote the proteasome-mediated degradation of E6AP (Kao et al., 2000). However, the fact that the loss of the other PDZ proteins elevated E6AP levels, without affecting the expression of E6, could suggest a more direct involvement of these proteins in the regulation of E6AP levels. Similarly, p53 levels were shown to be increased upon the ablation of all of the PDZ proteins included in our analysis. So far, previous studies identified only TIP1 as a putative PDZ protein able to modulate p53 protein levels (Han et al., 2012). Nevertheless, our data strongly suggest that the expression of additional PDZ proteins could modulate the pattern of p53 expression in HPV-positive cells, at least in part, in a E6-independent manner. Whether this is a general stress response triggered by the loss of these PDZ proteins, or a more specific effect remains to be determined. Furthermore, we also observed that there is a significant interplay between the different PDZ domain-containing proteins in HPV-positive cells. This is particularly evident in the case of hScrib, whose levels of expression were dramatically increased upon ablation of hDlg in HeLa cells. Although previous studies failed to observe a change in the levels of hScrib expression upon loss of hDlg (Ivanov et al., 2010), our data suggest that compensatory effects between different PDZ domain-containing proteins might exist in HeLa cells.

Further analysis of the mechanisms through which hScrib exerts these effects on E6 expression appears to rule out an effect on E6 protein turnover, since its half-life was unchanged upon ablation of hScrib (Figure 28). Furthermore, in our fractionation experiments we failed to detect any variation in the pattern of subcellular localization of HPV-18 E6 upon loss of hScrib (Figure 27), suggesting that the pattern of E6 expression was not affected by loss of hScrib. This assay did however highlight a number of points about E6. First we confirmed that HPV-18 E6 displays a differential pattern of subcellular localizations, with the bulk of it being expressed at membrane bound sites (Grossman et al., 1989). In addition, previous studies had shown that HPV-18 E6
promotes the nuclear export of p53 in order to drive its degradation primarily through the cytosolic proteasome pathway, although E6 can drive the nuclear degradation of p53 albeit with lower efficiencies (Freedman and Levine, 1998; Stewart et al., 2005). We found that p53 localizes in nuclear as well as membrane fractions in siLuciferase transfected HeLa cells, and the reduction of the levels of E6 expression induced by the loss of hScrib expression led to an increase in p53 protein levels in both nuclear and in extra-nuclear fractions of HeLa cells, confirming that HPV-18 E6 can degrade different pools of p53. However, this does not appear to fit with the E6-mediated relocation of p53. We also observed that HeLa cells express high levels of nuclear hScrib and E-cadherin. Previous studies have defined that the tumor-suppressive functions of hScrib are highly dependent upon its membrane localization, and consistent with this the displacement of hScrib from the membrane to the cytoplasm has been described to interfere with hScrib pro-apoptotic activity (Liu et al., 2010; Zhan et al., 2008) and with its ability to regulate the Hippo pathway (Cordenonsi et al., 2011). In HeLa cells we detected hScrib predominantly in the nucleus and in the membrane, with lower levels of expression present in the cytoplasm. Importantly, so far no nuclear localization for hScrib has been described, and it is interesting to speculate that E6 might play a role in the nuclear accumulation of hScrib, although the possible function of nuclear pools of hScrib remains to be determined. On the other hand, the aberrant cleavage of E-cadherin and the nuclear localization of its cytoplasmic domain have been correlated with the loss of the epithelial phenotype and acquisition of tumorigenic properties in epithelial cells (Ferber et al., 2008; Chetty et al., 2008; Salahshor et al., 2008). However, recent studies detected high levels of full length E-cadherin expression in the nucleus of a proportion of metastatic colorectal cancer cells, indicating that the mislocalization of full length E-cadherin is potentially an important event during invasive cancer progression (Salahshor et al., 2008). The nuclear expression of E-cadherin in HeLa cells might then be consistent with their high tumorigenic potential. The HPV oncoproteins are known to downregulate the E-cadherin expression by inducing hyper-methylation of its promoter (Laurson et al., 2010; D'Costa et al., 2012), however these data suggest that part of the residual E-cadherin expressed in HeLa cells might be aberrantly localized in the nucleus, possibly contributing to their tumorigenic potential.

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Previous studies have shown that the pattern of endogenous HPV-18 E6 expression in HeLa cells can be modulated by some of its cellular binding partners, including E6AP and 14-3-3 proteins (Tomaić et al., 2009; Boon and Banks, 2013), with loss of E6AP associated with a strong reduction of E6 half-life (Tomaić et al., 2009). Ablation of hScrib in HeLa cells did not significantly affect E6 turnover or the transcription of its mRNA (Figure 28), but dramatically perturbed the recovery of HPV-18 E6 protein levels upon release from the inhibition of protein translation (Figure 29); this is consistent with the involvement of hScrib in the regulation of E6 translation, previously shown to be cap-dependent (Tan et al., 1994; Stacey et al., 2000). It is also interesting to note that although E6 and E7 are transcribed from the same mRNA, they appear to be translated through different mechanisms; with E7 translation displaying a reduced cap-dependency and being potentially translated through an IRES-dependent mechanism (Stacey et al., 1995; Stacey et al., 2000).

Intriguingly, we found that upon loss of hScrib the half-life of p53 (Figure 28a) was also significantly increased in HeLa cells, consistent with reduced levels of E6 expression, whereas its translation efficiency was largely unaffected (Figure 29a). However, p53 has been reported to be translated through both cap-dependent and cap-independent mechanisms due to the presence of a internal ribosome entry site (IRES) in its 5'-UTR (Ray et al., 2006). Therefore, this suggests that the pattern of p53 expression upon loss of hScrib is linked to the reduced expression of HPV-18 E6 but is independent from the hScrib-regulation of protein translation.

As an attempt to define the molecular mechanism by which loss of hScrib could affect protein translation we analysed the effects on the phosphatidylinositol-3 kinase (PI3K)/mammalian target of rapamycin complex 1 (mTORC1) pathway. This pathway is known to integrate the availability of nutrients present in the environment surrounding the cells to with the activation of anabolic pathways, and the stimulation of protein translation is the best understood mechanism through which the PI3K/mTORC1 pathway promotes cell growth and proliferation (Fingar and Blenis, 2004). Since the functionality of both pathways is required for the effective activation of protein translation, it is important to note that our study highlighted that E6 and hScrib might act synergistically to activate protein translation through the regulation of separate components of
PI3K and mTORC1 pathways. Our data suggest that silencing of E6 in HeLa cells leads to a reduction in the levels of PDK1 expression (Figure 31a). PDK1 is a direct downstream effector of PI3K, and one of the better understood functions associated with its activity is the phosphorylation of Akt in its activation loop (or T-loop) at threonine 308 (T308). Previous studies suggested that, upon activation of the PI3K pathway, the kinetics of Akt activation involve its mTORC2-mediated phosphorylation at S473, which in turn facilitates the subsequent T308 phosphorylation by PDK1 (Scheid et al., 2002; Sarbassov et al., 2005). Although alternative mechanisms of Akt activation have also been proposed (Toker and Newton, 2000), it is clear that the phosphorylation of Akt at both sites is a crucial requirement for its full activation (Alessi et al., 1996; Scheid et al., 2002).

Previous studies suggested that the expression of HPV-16 E6 was sufficient to maintain high levels of active Akt (Spangle and Monger, 2010; Spangle and Münger, 2013), and this indicates that the E6-mediated upregulation of PDK1 expression might be in part responsible for driving high levels of Akt activity. It is also interesting to note that some of the biological activities associated with Akt function can be specifically linked to one of the activating phosphorylation events. For instance, while the S473 phosphorylation is required for Akt to regulate cell survival pathways, the PDK1-mediated T308 phosphorylation of Akt was suggested to be most critical for the activation of components of the mTORC1 pathway involved in protein translation (Jacinto et al., 2006). Thus, our data suggest that the regulation of PDK1 levels by E6 might represent a prime mechanism through which E6 stimulates the PI3K/mTORC1 pathway and protein translation.

In addition, the expression of HPV-16 E7 has also been shown to drive the activation of Akt in organotypic raft cultures, and this activity was linked to the ability of E7 to inactivate pRB (Menges et al., 2006). Moreover the E7-mediated activation of Akt was shown to induce cell migration in human keratinocytes by driving the Akt-mediated cytoplasmic mislocalization of p27 (Charette and McCance, 2007). This indicates that HPV oncoproteins coordinately induce a stimulatory effect on Akt, suggesting that they regulate a wide variety of biological processes through the modulation of PI3K pathway.
Previous studies had indicated that hScrib is a negative regulator of PI3K signaling. hScrib was shown to facilitate downregulation of Akt by promoting the membrane recruitment of the Ser/Thr protein phosphatase PHLPP1 (Li et al., 2011). Although we failed to detect an upregulation of phosphorylated Akt upon loss of hScrib in HeLa cells (Figure 30b), we believe that decreased levels of phosphorylated Akt might be a reflection of decreased levels of PDK1 expression driven by the reduced levels of HPV-18 E6 in cells transfected with siRNA against hScrib. We hypothesize that hScrib might have a more direct effect on the pattern of total and phosphorylated p70 and p85 S6 kinase expression (Figure 31). The function of the p70 isoform of S6 kinase has been shown to be strongly implicated in the induction of cap-dependent protein translation and cell cycle progression, and its mTORC1-mediated phosphorylation at threonine 389 (T389) has been shown to be critical for these activities (Lane et al., 1993; Jefferies et al., 1997; Zhou et al., 2011). Similarly, p85 S6 kinase can be phosphorylated by mTORC1 at the same position, however the biological consequences of the activation of p85 are less clear, although this isoform has also been linked to the induction of cell cycle progression (Reinhard et al., 1994). The fact that hScrib seems to regulate the total levels of both isoforms of the S6 kinase might argue that hScrib directly regulates the levels of S6 kinase expression, rather than its activation downstream of activated mTORC1.

Taken together these data provide an unexpected function for hScrib in HPV-positive cells, and suggest that the maintenance of a critical level of hScrib expression in HPV-positive cell monolayers could, in part, contributes to the pro-oncogenic activity of E6 and E7 through the positive regulation of p70 and p85 S6 kinase, and this is also likely to contribute indirectly to hScrib-mediated regulation of translation, including that of HPV-18 E6.

It is also interesting to note that the treatment of HeLa cells with the proteasome inhibitor MG-132 produced a dramatic increase in the levels of phosphorylated p85, but not of p70, S6 kinase expression (Figure 31b). This suggests that the two isoforms of the S6 kinase are regulated through different mechanisms, and that the mTORC1-mediated phosphorylation of p85 enhances its proteasome-mediated degradation. In addition, upon ablation of hScrib, the proteasome inhibition
appears to rescue, at least in part, the levels of phosphorylated p85 S6 kinase expression, indicating that loss of hScrib might contribute to the proteolytic degradation of phosphorylated p85. Recent studies defined that p85 S6 kinase positively regulates apoptosis under oxidative stress, promoting the inhibition of mdm2 and accumulation of p53 (Jia et al., 2013). Although this activity of p85 was shown to occur in a mTORC1-independent manner, the enhanced proteasome-mediated degradation of phosphorylated p85 might interfere with this activity.

The different modalities of regulation displayed by the two isoforms of S6 kinase could be reflected by their different pattern of subcellular distribution. Previous studies suggested that the presence of a nuclear localization signal in the extended N-terminus of p85 induces its nuclear accumulation (Reinhard et al., 1994). However, their localizations appear to be dynamic, since p70 has been shown to translocate in the nucleus upon phosphorylation by mTORC1 in the G1 phase of the cell cycle and cytoplasmic pools of p85 have also been identified (Rosner and Hengstschläger, 2011). So far, it is not clear in which subcellular compartment the degradation of p85 occurs, in addition, the mechanism involved in its nucleo-cytoplasmic shuttling is not known. An interesting possibility is that hScrib might regulate the stability of phosphorylated p85 also through the control of its subcellular localization. Thus, the expression of hScrib might contribute to the correct localization of p85 and p70 S6 kinase isoforms, and its loss would therefore potentially lead to the mislocalization of S6 kinase to cellular compartments where the kinase is normally degraded. Although the levels of p70 S6 kinase are not rescued upon proteasome inhibition, previous studies suggested that p70 is degraded through a caspase-dependent mechanism (Dhar et al., 2009). Therefore these data suggest the intriguing possibility that the two isoforms of S6 kinase are regulated by different proteolytic pathways and that hScrib might play a role in modulating their levels of expression. However, whether hScrib might protect p70 S6 kinase from caspase cleavage needs still to be determined. A summary of the potential regulation of PI3K/mTORC1 pathway by E6, E7 and hScrib is shown in Figure 33.

Taken together, these studies define a new function for hScrib in affecting protein translation, most likely through the modulation of S6 kinase activity. These studies also highlight the role of E6 in
fine-tuning the levels of expression and function of its target proteins, such that optimal conditions for viral replication are attained. However, the stimulation of growth-promoting pathways ultimately predispose cells to the acquisition of tumorigenic capacities during malignant progression.
Figure 33. Regulation of the PI3K/mTORC1 pathway and protein translation by HPV oncoproteins and hScrib. Insulin or growth factor stimulation leads to the activation of the PI3K/mTORC1 pathway (see text). Both E6 and E7 have been shown to converge on the activation of this pathway through the regulation of Akt, and E6 may also stimulate Akt through the maintenance of high levels of PDK1 expression. E6 could also indirectly activate mTORC1 signaling, and protein translation, through the modulation of hScrib expression patterns leading to the upregulation of p70 and p85 S6 kinase isoforms. The ability of hScrib to regulate levels of p70 S6 kinase expression may then directly contribute to the expression of E6 through the regulation of its cap-dependent translation. The pattern of p85 S6 kinase appears to differ from that of the p70 isoform, and the mTORC-1 mediated phosphorylation may enhance its proteasome-mediated degradation. Apparently, the expression of hScrib and/or its modulation by E6 may counteract the degradation of p85. (PIP2, Phosphatidylinositol (3,4)-bisphosphate; PIP3, Phosphatidylinositol (3,4,5)-trisphosphate).
Materials and Methods

Plasmids

pCDNA-3 FLAG-tagged MAGI-1 has been described previously (Glaunsinger et al., 2000). The K499E MAGI-1 mutant was generated using the GeneArt Site-Directed Mutagenesis System (Invitrogen) according to the manufacturer’s instruction, using the following primers:

forward primer 5’ TCCTGCAGATCGAAAGCCTCGATGGTCCT;

reverse primer 5’ ACGAGGCTTTTCGATCTGCAGGAACTCATCAGGCTC.

Untagged HPV-18 E6 and HPV-16 E6 pCDNA-3 expression plasmids have been described previously (Gardiol et al., 1999; Pirn et al., 1994), as have the GST-fusion proteins HPV-18 E6 and HPV-16 E6 (Pirn et al., 2000). The GST-fusion protein HPV-58 E6 was generated by subcloning PCR amplified HPV-58 E6 from the respective pcDNA construct, into compatible BamH I and EcoR I restriction sites of pGEX2T using the following primers:

forward primer 5’ ATGGATCCATGTTCCAGGACGCAGAG;

reverse primer 5’ CGGAATT CTT AC ACTT GT GTTT GT CT GC.

pCMV MYC-tagged Net1 was described previously (Garcia-Mata et al., 2007) and HA-tagged β-catenin was kindly given by Prof. Claudio Brancolini.

Cell culture and transfection

HEK 293 (human embryonic kidney), U2OS (human osteosarcoma), HeLa (HPV-18-positive), CaSKi (HPV-16-positive), SiHa (HPV-16-positive), HaCaT (human immortalized keratinocytes) and H1299 (non-small cell lung carcinoma) cells were maintained in Dulbecco’s modified Eagles Medium (DMEM) supplemented with 10% fetal bovine serum, penicillin-streptomycin (100 U/ml) and glutamine (300 µg/ml). For all siRNA (Dharmacon) delivery the cells were seeded on 6 cm dishes at a confluence of 1.2 x 10⁵ and transfected using Lipofectamine 2000 (Invitrogen) with siRNA against luciferase, HPV-16 E6/E7 (5’UUAAUGACAGCUACAGAG), 18 E6/E7
(5’CAUUUACCAGCCCGACGAG), 18 E6 (5’CUCUGUGUAUGGAGACACA), E6AP or siRNA against the different PDZ-proteins (relevant Dharnacon Smart Pools). For siRNA transfection followed by immunofluorescent analysis, HeLa cells were seeded at a confluence of 1.2 x 10^5 on glass coverslips.

DNA transfection in HEK 293 cells was performed using the standard calcium phosphate precipitation protocol as described previously (Matlashewski et al., 1987c). For DNA transfection in U2OS cells followed by immunofluorescent analysis, cells were seeded on glass coverslips at a confluence of 1.5 x 10^5 and transfected using the calcium phosphate precipitate protocol followed by glycerol shock. Briefly, 5 hours after the addition of the DNA precipitate, cells were treated with 15% glycerol in PBS for 1 minute. Cells were then washed for three times with 1X PBS and left to grow for additional 24 hours. For DNA transfection in HeLa, cells were seeded on 6 cm dishes at a confluence of 1.5 x 10^5 and transfected using Fugene HD (Promega). For DNA transfection followed by immunofluorescent analysis HeLa and HaCaT cells were seeded at the same confluence on glass coverslips.

**Inhibitors**

The proteasome inhibitor Z-leu-leu-leu-al (CBZ; Sigma) was dissolved in DMSO and used at 50 µM for the indicated time.

**Antibodies**

The following antibodies were used: mouse monoclonal anti-HA antibody 12CA5 (Roche), mouse monoclonal anti-ZO1 (ZO1-1A12) (Invitrogen), rabbit polyclonal anti-PAR3 (Millipore), mouse monoclonal anti-human pRB (BD Pharmingen). Mouse monoclonal anti-PSD95 (6G6-1C9) and mouse monoclonal anti-p84 (5E10) were from Abcam. The following antibodies were purchased from SIGMA: rabbit polyclonal anti-MAGI-1 (M5691), rabbit polyclonal anti-PTPN-3 (T6453) mouse monoclonal anti-α-tubulin (T6199), mouse monoclonal M2 anti-FLAG antibody (F3165) and rabbit polyclonal anti-FLAG (F7425). The following antibodies were purchased from Santa Cruz Biotechnology: mouse monoclonal anti-p53 (DO-1), mouse monoclonal anti-α-actinin (H-2),
mouse monoclonal anti-Dlg (2D11), goat polyclonal anti-Scribble (C-20), goat polyclonal anti-TIP2 (N-19), rabbit polyclonal anti-FAP-1 (H-300), rabbit polyclonal anti-E-cadherin (H-108), mouse monoclonal anti-Myc (9E10) and mouse monoclonal anti-vimentin (V-9). The following antibodies were from Cell Signaling Technology: rabbit polyclonal anti-Akt (9272), rabbit polyclonal anti-phosphorylated Akt (T308) (9275), rabbit polyclonal anti-phosphorylated Akt (S473) (9271), rabbit polyclonal anti-PDK1 (3062), rabbit monoclonal anti-phosphorylated PDK1 (S241) (C49H2), rabbit monoclonal anti-p70 S6 kinase (49D7), mouse monoclonal anti-phosphorylated p70 S6 kinase (T389) (1A5). The mouse monoclonal antibody anti HPV-18 E6 (N-terminus #399) was generated and generously provided by the Arbor Vita Corporation.

**Western blotting and immunoprecipitation**

For western blot sample preparation, cells were lysed in 2x SDS sample buffer (100mM Tris HCl pH 6.8; 200mM DTT, 4% SDS, 20% glycerol, 0.2% bromphenol blue) and the whole cell extracts were separated by SDS-PAGE and blotted on 0.22 nitrocellulose membranes (Schleicher and Schuell). The membranes were blocked at 37°C for 1 hour in 10% milk/PBS, except for those probed with anti-MAGI-1, anti-PTPN-3, and anti-PSD95 which were blocked in 5% milk/PBS; all membranes probed with the antibodies from Cell Signaling Technology were incubated in 5% milk/TBS 0.1% TWEEN 20; the membranes probed with the anti-HPV-18 E6 antibody were incubated in 2% BSA/5% milk in 1xTBS 0.1% TWEEN 20. The membranes were incubated with the appropriate primary antibodies diluted in 10% milk/PBS 0.5% TWEEN 20; except for the anti-MAGI-1, anti-PTPN-3 and anti-PSD95 antibodies which were diluted in 5% milk/PBS 0.05% TWEEN 20; all the antibodies from Cell Signaling Technology were diluted in 5% BSA/1xTBS 0.1% TWEEN except for the anti-phosphorylated p70 S6 kinase that was incubated in 5% milk/1xTBS 0.1% TWEEN 20. The HPV-18 E6 antibody was incubated in 1% BSA/2.5% milk in 1xTBS 0.1% TWEEN 20. The incubation times were 2 hours at room temperature for all antibodies, except for the anti-PTPN-3, anti-FAP1, anti-E-cadherin, anti-PSD95, all the Cell Signaling Technology antibodies and the anti-HPV-18 E6 antibody, which were incubated
overnight at 4°C. After several washes the membranes were incubated with the appropriate HRP-conjugated secondary antibody (DAKO) for 1 hour at room temperature. After extensive washing the blots were developed with ECL or ECL plus reagent (GE Healthcare) according to the manufacturer’s instructions. Protein band intensities were quantitated where possible using the OptiQuant quantification program.

For co-immunoprecipitation experiments cells were scraped in ice cold PBS and extracted in lysis buffer (1% Triton X-100, 50mM Tris [pH 7.5], 300mM NaCl, 1mM EGTA, 1mM EDTA) supplemented with protease inhibitors (Set1, Calbiochem). The extracts were then passed through a 26G needle multiple times and then cleared by centrifugation. Extracts from cells expressing FLAG-tagged MAGI-1 constructs, were incubated with anti-FLAG beads (SIGMA) for 2 to 3 h on a rotating wheel at 4°C. For the immunoprecipitation of MYC-tagged NET1, cell extracts were incubated with the MYC antibody or the control antibody for approximately 3 hours on a rotating wheel at 4°C. Protein-A-Sepharose beads (GE Healthcare) were then added for an additional 60 minutes at 4°C. The beads were then extensively washed, and the immunoprecipitated proteins were analysed by western blotting.

*Fusion protein purification and in vitro binding assays*

GST-tagged fusion proteins were expressed and purified as described previously (Thomas *et al.*, 1996). Briefly, 40 ml of an overnight culture of *E.Coli* strain DH5-α previously transformed with the appropriate expression plasmids were inoculated into Luria Broth containing ampicillin (75μg/ml) and grown at 37°C up to an OD of 0.6 at 395 nm. Recombinant protein expression was induced for 3 hrs with 1mM isopropyl-β-D-thiogalactopyranoside (IPTG, Sigma). The cells were harvested by centrifugation, disrupted by sonication in lysis buffer (1% Triton X-100 /1xPBS) and the lysates were cleared of cell debris by centrifugation. The GST-fusion proteins were then incubated for 1 hour with glutathione-conjugated agarose beads at 4°C. The purity of all fusion proteins was determined by SDS-PAGE and Coomassie Brilliant Blue R (Sigma) staining.
For *in vitro* binding and degradation assays, proteins were transcribed and translated *in vitro* in rabbit reticulocyte lysate using the Promega TNT system according to the manufacturer's instructions. The HPV-18 and HPV-16 E6 proteins were radiolabelled with $[^{35}S]$-cysteine while MAGI-1 proteins were radiolabelled with $[^{35}S]$-methionine.

Equal amounts of *in vitro*-translated proteins were added to GST fusion proteins bound to glutathione resin and incubated for 1 hour at 4°C. After extensive washing with PBS containing 0.5% NP-40, the bound proteins were analysed by SDS-PAGE and autoradiography.

For GST pull-down assays using cell extracts, FLAG-tagged wild type and K499E mutant MAGI-1 were transfected into HEK 293 cells. 24h after transfection cells were scraped in ice-cold PBS and extracted in lysis buffer (1% Triton X-100, 50mM Tris [pH 7.5], 300mM NaCl, 1mM EGTA, 1mM EDTA) supplemented with protease inhibitors (Set1, Calbiochem). The extracts were then passed through a 26G needle multiple times and cleared by centrifugation. Extracts from cells expressing FLAG-tagged MAGI-1 constructs, were incubated with the indicated GST-fusion proteins for 1-2 hours on a rotating wheel at 4°C. The beads were then extensively washed, and the immunoprecipitated proteins were analysed by western blotting.

*In vivo degradation assays*

HEK 293 cells were transfected with 1µg of either wild type or K499E MAGI-1 constructs along with 0.3 µg of LacZ. pCDNA3 18 E6 plasmid was also included at increasing concentrations: 2, 5, 10µg. 24 hours post-transfection, the cells were harvested and analyzed by western blotting.

*In vitro degradation assays*

Degradation assays were performed as previously described (Thomas *et al.*, 2001). Briefly, radiolabelled proteins were mixed and incubated for the indicated times at 30°C. Volumes were adjusted using water-primed lysate. The residual MAGI-1 proteins were analyzed by SDS-PAGE and autoradiography.
**Subcellular fractionation assays**

HeLa cells were seeded on 6 cm dishes and transfected with the relevant siRNAs. After 72h, cells were removed from the dishes by trypsinization and differential extraction of HeLa cells was performed to obtain cytoplasmic, membrane, nuclear and cytoskeletal fractions using the ProteoExtract Fractionation Kit (Calbiochem) according to the manufacturer's instructions. The differential protein expression plus fraction-specific markers, was analysed by SDS-PAGE western blotting.

**Immunofluorescence microscopy and EdU staining**

Cells were fixed with 3.7% paraformaldehyde in PBS for 20 minutes and permeabilized with 0.1% Triton X-100 in PBS for 5 minutes. Slides were incubated with primary antibodies for 2 hours at 37°C, extensively washed in PBS and incubated for 30 minutes at 37°C with secondary anti-rabbit or anti-mouse antibody conjugated to fluorescein or rhodamine (Molecular Probes). Samples were washed several times with water and mounted with Vectashield mounting medium (Vector Laboratories) on glass slides. Slides were analysed with either a Leica DMLB fluorescence microscope with a Leica photo camera (A01M871016), or a Zeiss LSM 510 confocal microscope with two lasers giving excitation lines at 480 and 510 nm. The data were collected with a 60x objective oil-immersion lens.

For EdU staining, cells were seeded on glass coverslips and transfected with FLAG-tagged wild type or K499E mutant MAGI-1 constructs. 24 hours after transfection EdU was added to the culture medium at a final concentration of 20μM for 2 hours. After labeling, cells were fixed with 3.7% paraformaldehyde in PBS for 20 minutes and permeabilized with 0.1% Triton X-100 in PBS for 5 minutes. Primary antibodies were incubated for 2 hours at 37°C, extensively washed in PBS and incubated for 30 minutes at 37°C with secondary anti-rabbit or anti-mouse antibody conjugated to fluorescein or rhodamine (Molecular Probes). After several washes in PBS, incorporated EdU was detected by incubating coverslips with the reaction mix solution (5mM (+)Na-L-Ascorbate (Sigma), 1mM copper sulphate, 0,05mM 6-Carboxyfluorescein-TEG azide) for 30 minutes at room temperature. Samples were washed several times with water and mounted with Vectashield.
mounting medium (Vector Laboratories) on glass slides. Slides were analysed with Zeiss LSM 510 confocal microscope with two lasers giving excitation lines at 480 and 510 nm. The data were collected with a 60x objective oil-immersion lens.

**TUNEL assays**

Cells were seeded on glass coverslips and transfected with FLAG-tagged wild type or K499E mutant MAGI-1 constructs. 24 hours after transfection, were fixed with 3.7% paraformaldehyde in PBS for 20 minutes and permeabilized with 1xPBS 0.1% sodium citrate, 0.1% Triton X-100 for 5 minutes. The coverslips were incubated with the rabbit polyclonal FLAG antibody for 2 hours at 37°C, followed by incubation with the rhodamine-conjugated anti-rabbit antibody (Molecular Probes) for 30 minutes at 37°C. After several washes in PBS, apoptotic cells were detected using the fluorescein-conjugated *in situ* cell death detection kit (Roche) according to the manufacturer's instructions. Samples were washed several times with water and mounted with Vectashield mounting medium (Vector Laboratories) on glass slides. Slides were analysed with a Zeiss LSM 510 confocal microscope with two lasers giving excitation lines at 480 and 510 nm. The data were collected with a 60x objective oil-immersion lens.

**Half-life experiments**

72h post transfection, cells were treated for different time points as indicated with cycloheximide (50μg/ml in DMSO) to block protein synthesis. DMSO treated cells were used as the control. Total cellular extracts were then analyzed by Western blot and the intensity of the bands was measured using Optiquant program. The standard deviation was calculated from three independent assays.

**Determination of HPV-18 E6 and p53 translation efficiency**

HeLa cells were seeded on 6cm dishes at a confluence of 1.2 x 10⁵ and transfected using Lipofectamine 2000 (Invitrogen) with siRNA against Luciferase or hScrib (Dharmacon). 72h after transfection cells were treated with cycloheximide (50μg/ml in DMSO) for additional 6 hours. Cells treated with DMSO alone were used as control for the expression of HPV-18 E6 and p53. In
order to monitor the recovery of E6 and p53 protein translation cycloheximide was removed and, after several washes in PBS, cells were left to grow for different time points in fresh DMEM supplemented with 10% fetal bovine serum, penicillin-streptomycin (100 U/ml) and glutamine (300 μg/ml). Total cellular extracts were prepared by harvesting cell in 2X SDS sample buffer, and then analyzed by Western blotting.
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