The Mdm2 ubiquitin ligase enhances transcriptional activity of human papillomavirus E2

Citation for published version:

Digital Object Identifier (DOI):
10.1128/JVI.01551-08

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published in:
Journal of Virology

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
The Mdm2 Ubiquitin Ligase Enhances Transcriptional Activity of Human Papillomavirus E2

Noor Gammoh, Daniela Gardiol,† Paola Massimi, and Lawrence Banks*

International Centre for Genetic Engineering and Biotechnology, Padriciano 99, I-34012 Trieste, Italy

Received 23 July 2008/Accepted 4 November 2008

The regulation of human papillomavirus (HPV) gene expression by the E2 protein is a critical feature of the viral life cycle. Previous studies have shown an important role in transcription for the ubiquitin-proteasome pathway, but its role in HPV gene expression has not been addressed. We now show that HPV E2 requires an active proteasome for its optimal transcriptional activator function. This involves an interaction with the Mdm2 ubiquitin ligase, which together with E2 acts synergistically to activate the HPV type 16 promoter. We also show that HPV E2 recruits Mdm2 onto HPV promoter sequences, providing an explanation for this cooperative activity.

Viruses are intracellular parasites that rely upon their host cells for the completion of their productive life cycles. Therefore, viruses need to use cellular machinery to support their life cycles. The replication of the double-stranded DNA genomes of human papillomaviruses (HPVs) is directly regulated by the viral helicase, E1, and the transcriptional regulator, E2 (19). The E2 protein is a multifunctional, DNA binding protein, consisting of a transactivation domain in the N-terminal half of the protein, a middle nonconserved hinge region, and a C-terminal domain that mediates DNA binding and protein dimerization. Four E2 binding sites are present in the long control regions (LCRs) of HPV genomes (30): two sites flank the viral origin of replication, a third site lies directly upstream of the early promoter which controls expression of viral early genes (24, 27), and a fourth site lies at the 5' end of the LCR. The binding of E2 to the LCR facilitates the binding of the E1 helicase to the viral origin of replication for the initiation of DNA replication and the binding of transcription factors, such as the TATA-binding protein and Sp1, that are required for viral gene expression (29). In addition, a number of direct interactions of E2 with cellular proteins such as Brg-1 (18), TopBP1 (5), and Brm (11) further contribute to the regulation of viral gene expression.

The role of the ubiquitin-proteasome machinery in transcriptional regulation is now well recognized (20), although how it functions most likely varies depending upon the precise promoter complex. It may involve a form of licensing where ubiquitination links the activities of specific transcription factors to their own destruction (26). Alternatively, ubiquitin-modified transcription factors may recruit protein-remodeling factors to the promoter and enhance corepressor/coactivator exchange (7, 21). Specific examples of recruitment and enhancement include the regulation of gene expression by c-myc and steroid hormone receptors (1, 23) as well as the activation of the hTERT promoter by HPV E6, which is dependent on the interaction between E6 and the E6AP ubiquitin ligase (15).

In the case of the HPV promoter and, more specifically, of the function of E2, the involvement of the proteasome in transcriptional regulation has not been documented. In order to investigate this, we first analyzed the effects of proteasome inhibition upon E2 transcriptional activity (8). To do this, U2OS cells were transfected with an E2-responsive luciferase reporter construct (p6xE2BS-Luc/E2-Luc reporter plasmid, kindly provided by Ian Morgan) together with an untagged HPV type 16 (HPV-16) E2 expression plasmid (22). After 24 h, the cells were treated in the presence of 50 μM of the proteasome inhibitor CBZ (Sigma) or dimethyl sulfoxide, as a control, for a further 5 h. Then, the cells were lysed, and their luciferase activity was determined using the Dual-Luciferase assay kit (Promega). The results obtained are shown in Fig. 1a, left panel, and demonstrate a clear inhibition of E2 transcriptional activity following proteasome inhibition. To investigate the specificity of proteasome inhibition on E2 transcriptional activity, we also included a glucocorticoid receptor (GR)-responsive plasmid, MMTV-Luc (kindly provided by Olivier Kassel [10]), which was shown previously to be unaffected by proteasome inhibition (14). Figure 1a, right panel, shows that CBZ did not suppress dexamethasone (Dex)-induced GR transactivation. In the case of other transactivators, such as p53 and E2F, proteasome inhibition did affect their transcriptional activity (data not shown), which is in agreement with previously published data (13, 31).

Treatment with proteasome inhibitors is known to provide a block to the entire proteasome machinery, but this result led us to speculate whether or not a known ubiquitin ligase might be involved in E2 transcriptional activity. We analyzed the effects of a number of ubiquitin ligases that had previously been linked to HPV function on E2 transcriptional activity. Therefore, plasmids expressing E6/AP (kindly provided by Martin Scheffner), Mdm2 (kindly provided by Claudio Schneider), β-TrCP (16), Smurf, and Cbl were cotransfected with E2 and E2-Luc expression constructs, and luciferase assays were performed after 24 h. The results obtained are shown in Fig. 1b, where it can be seen that Mdm2 induces a dramatic increase in the transcriptional activity of E2. In contrast, none of the other

* Corresponding author. Mailing address: Tumour Virology Lab, ICGEB, Padriciano 99, 34012 Trieste, Italy. Phone: 39 040 3757328. Fax: 39 040 226555. E-mail: banks@icgeb.org.
† Present address: IBR/CONICET, Facultad de Bioquímica, Sui-pacha 531 (2000), Rosario, Argentina.
‡ Published ahead of print on 12 November 2008.
ubiquitin ligases had any significant effect on the ability of E2 to activate transcription, highlighting the specificity of the Mdm2 activity with respect to E2. These results suggest that the Mdm2 ubiquitin ligase activity might mediate this effect.

The C-terminal end of Mdm2 contains a RING domain conferring E3 ligase activity which mediates its ability to target several proteins for degradation, including p53 (2), pRb (28), and the androgen receptor (9). In addition, the middle region of Mdm2 also contains nuclear export and nuclear localization sequences and was shown to increase the transcriptional activity of a number of factors such as the p53 homolog p63 (3) and estrogen receptor α (25). To further investigate the role of Mdm2 in the transcriptional activity of E2, we repeated the luciferase assay using a point mutant of Mdm2 that no longer has ubiquitin ligase enzymatic activity (Mdm2C462A; kindly provided by Claudio Schneider) and including proteasome inhibition as an additional control. Figure 2a shows again that Mdm2 exerts a potent stimulatory effect upon E2 transcriptional activity and that this is abolished following treatment with CBZ. Most importantly, the Mdm2C462A mutant is also defective in its ability to stimulate E2 transcriptional activity, demonstrating that Mdm2 ubiquitin ligase activity is required for its ability to upregulate the E2 transcriptional activator function.

To exclude a possible indirect role for p53 in these assays, we repeated the experiment with SAOS-2 cells (p53−/− pRb−/−) and H1299 cells (p53−/−). Figure 2b shows that Mdm2 cooperates with the transcriptional activation function of E2 in both cell lines, demonstrating that this is independent of Mdm2’s ability to degrade either p53 or pRb. Furthermore, expression of Mdm2 in increasing amounts in H1299 cells resulted in a progressive increase in the transcriptional activity of E2 (Fig. 2b, right), demonstrating that Mdm2 cooperates with E2’s transcriptional transactivation function in a dose-dependent manner. We also tested whether inhibiting the activity of endogenous Mdm2 would affect the transcriptional activity of E2. To do this, SAOS-2 cells transfected with E2 and E2-Luc plasmids were treated with two different Mdm2 inhibitors, Nutlin-3 and Mdm2 E3 ligase inhibitor, which were used previously to inhibit Mdm2 functions that are independent of p53 degradation (4). The results obtained are shown in Fig. 2c, where it can be seen that inhibiting endogenous Mdm2 activity by either inhibitor results in a decrease in E2’s transcriptional activity. Finally, we also wished to determine whether or not
Mdm2 can affect the levels of E2 protein expression. To do this, U2OS cells were transfected with the E2 expression plasmid together with Mdm2 and a β-galactosidase (β-Gal) marker for transfection efficiency, and 24 h later, the levels of E2 expression were ascertained by Western blot analysis using polyclonal anti-E2 antibodies (17). The results in Fig. 2d show that the levels of E2 remain largely unchanged with respect to the β-Gal loading control in the presence of Mdm2. This demonstrates that the increased transcriptional activation exhibited by E2 in the presence of Mdm2 is not the result of increased levels of E2 expression. Taken together, these results demonstrate that E2 requires the functional proteasome machinery for optimal transcriptional activity and that this appears to involve the Mdm2 ubiquitin ligase.

Since we had seen that Mdm2 affects E2 transcriptional activity without affecting its protein expression levels, we then sought to examine whether Mdm2 and E2 can interact. Using an in vitro binding assay, bacterially expressed glutathione S-transferase (GST) fusion proteins (6) were incubated with in vitro translated and radiolabeled Mdm2 (as described in reference 8). Figure 3a shows that Mdm2 can bind to GST-16E2, albeit less strongly than it binds to GST-p53; no binding is seen with GST alone. To identify the region of E2 that mediates its interaction with Mdm2, we used a number of GST-tagged E2 fragments, including the N- and C-terminal domains and truncation fragments of the C-terminal domain (Fig. 3b, right). These were previously described in reference 6. Figure 3b shows that E2 binds to Mdm2 mainly through its C-terminal half and, more specifically, through a region spanning amino acid residues 322 to 335.

In order to verify that E2 and Mdm2 can form a complex in vivo, we performed a coimmunoprecipitation assay with 293 cells that were transfected with either Mdm2 alone or Mdm2 plus GFP-tagged E2. At 24 h posttransfection, E2 was immunoprecipitated from cell extracts, using antibodies against green fluorescent protein (GFP) (polyclonal; Santa Cruz), for 3 to 4 h. After extensive washing, the immunoprecipitate was analyzed by Western blotting, using an anti-Mdm2 monoclonal antibody (kindly provided by Giannino Del Sal). Figure 3c shows that a complex between Mdm2 and E2 can be detected.
in cells expressing Mdm2 and E2 but not in cells expressing Mdm2 alone, demonstrating that E2 and Mdm2 can form a complex in vivo.

Since the recruitment of ubiquitin ligases to promoters is one means by which the proteasome can be linked directly to transcriptional activation, we examined whether E2 could similarly recruit Mdm2 to the HPV promoter by using a chromatin immunoprecipitation assay (Upstate Biotechnology). 293 cells were transfected with the E2-Luc construct together with GFP-E2 and FLAG-Mdm2 expression constructs (kindly provided by Ian Morgan and Giannino Del Sal, respectively). At 24 h posttransfection, cells were cross-linked with 1% formaldehyde for 10 min at 37°C, lysed, and sonicated to generate 200- to 1,000-bp DNA fragments. Cell lysates were then incubated with the indicated antibodies, and immunoprecipitated complexes were analyzed by PCR to detect protein interaction with DNA. Initially, we verified that GFP-E2 and FLAG-Mdm2 could form a complex in vivo by using anti-FLAG antibodies (M2; Sigma) to immunoprecipitate Mdm2, followed by Western blot analysis using anti-E2 antibodies (17). The results in Fig. 4a again confirm the binding of both proteins in vivo. In parallel, cell extracts were immunoprecipitated (IP) using polyclonal anti-GFP antibodies, followed by Western blot analysis using antibodies against Mdm2 or GFP. An asterisk indicates nonspecific bands. -ve, untransfected cells.

This study shows for the first time a role for a ubiquitin ligase, Mdm2, in the transcriptional activity of HPV-16 E2. This observation is supported by the abilities of Mdm2 and E2 to interact in vivo and in vitro. The effects of Mdm2 on E2 transcriptional activity are not due to alterations in the protein levels of E2 but most probably due to the ability of E2 to recruit Mdm2 to the HPV promoter. The exact molecular mechanisms by which Mdm2 influences the transcriptional activity of E2 are still to be identified. Mdm2 may increase the ubiquitination of E2, it might modulate the recruitment of cellular factors that may facilitate E2 transcriptional activity, or it may direct the degradation of some of the transcriptional machinery, thereby allowing increased transcriptional licensing and processivity. At present we cannot completely differentiate between these different possibilities; however, a role in transcriptional licensing seems to be most likely. Clearly, an active proteasome is required, which
targets the p53 transcription cofactor JMY for degradation. EMBO Rep. 8:84–90.

