Tumor and Stem Cell Biology

Deficiencies in the Fanconi Anemia DNA Damage Response Pathway Increase Sensitivity to HPV-Associated Head and Neck Cancer

Jung Wook Park1, Henry C. Pitot1, Katerina Strati1, Nicole Spardy3, Stefan Duensing3, Markus Grompe2, and Paul F. Lambert1

Abstract

Patients with the rare genetic disease, Fanconi anemia (FA), are highly susceptible to squamous cell carcinomas arising at multiple anatomic sites including the head and neck region. Human papillomaviruses (HPVs), particularly HPV16, are associated with ~20% of head and neck squamous cell carcinomas (HNSCCs) in the general population. Some but not other investigators have reported that HNSCCs in FA patients are much more frequently positive for HPV. In addition, studies have demonstrated an interaction between the HPV16 E7 oncoprotein and the FA pathway, a DNA damage response pathway deficient in FA patients. On the basis of these studies, it was hypothesized that the FA pathway contributes to repair of DNA damage induced by HPV16 E7, providing one explanation for why FA patients are predisposed to HPV-associated HNSCCs. To determine the importance of the FA pathway in modulating the oncogenic abilities of E7, we crossed K14E7 transgenic (K14E7) and fancD2 knockout mice (FancD2−/−) to establish K14E7/FancD2−/− and K14E7/FancD2+/+ mice and monitored their susceptibility to HNSCC when treated with a chemical carcinogen. K14E7/FancD2−/− mice had a significantly higher incidence of HNSCC compared with K14E7/FancD2+/+ mice. This difference correlated with an increased proliferative index and the increase in expression of biomarkers that are used to assess levels of DNA damage. These animal studies support the hypotheses that FA patients have increased susceptibility to HPV-associated cancer and that the FA DNA damage response pathway normally attenuates the oncogenic potential of HPV16 E7. Cancer Res; 70(23); 9959–68. ©2010 AACR.

Introduction

Fanconi anemia (FA) is a heterogeneous, recessive, genetic disease characterized by congenital abnormalities, progressive bone marrow failure, and a predisposition to leukemia and solid tumors, particularly squamous cell carcinomas (SCCs) including head and neck SCCs (HNSCCs), at remarkably young ages. The frequency of HNSCCs in FA patients is highly elevated compared with that of the general population (1–4). So far, hematopoietic stem cell transplantation (HSCT) is the only way to treat bone marrow failure, which is the main cause of death in FA patients. Even after HSCT, FA patients suffer from a high incidence of HNSCCs (5–7) most likely due to defects in DNA damage repair, and consequent increases in genomic instability, in epithelial cells of the head and neck region.

Fanconi anemia is caused by biallelic mutations in 1 of at least 13 different genes (FA genes). FA proteins (Fanc proteins; Fanc A, B, C, D1, D2, E, F, G, I, J, L, M, and N) encoded by these genes act together to protect genomic integrity, though the mechanism by which they do this remains poorly understood. The FA pathway is known to be activated by DNA interstrand cross-links (ICLs) induced by chemicals and/or found at the sites of stalled DNA replication forks (8). Eight of the FA gene products interact in a holo-complex that localizes to the sites of damage or stalled replication forks. This, in turn, leads to the monoubiquitination of another FA gene product, FancD2 (9), DNA damage induced by ultraviolet infrared radiation and chemical compounds can also activate the FA pathway through phosphorylation of FancD2 protein by the ATM kinase; however, sensitivity of the FA pathway to these forms of damage is less than that to ICLs (10–12).

High-risk human papillomaviruses (HPVs) are etiologic agents in approximately 20% of HNSCCs in the general population, primarily amongst tumors of the oropharynx. HPV type 16 (HPV16) is present in more than 90% of the HPV-positive HNSCCs (13, 14). HPV16 encodes 3 oncoproteins, E5, E6, and E7. A mouse model for HPV-associated HNSCC has been developed...
in which HPV16 transgenic mice, when treated with a chemical carcinogen that induces DNA adducts akin to those caused by tobacco-associated carcinogens synergizes with HPV16 oncogenes to induce HNSCC. The cancers that arise in these mice share many histopathologic properties with HPV-positive HNSCC in humans. The site at which tumors arise is less restrictive than in humans, presumably reflective of the pattern of HPV transgene expression throughout the mouse oral/upper gastrointestinal epithelia. Between E6 and E7, HPV16 E7 has greater potential to cause head and neck cancer in animal models (15), with E6 contributing to increased incidence in combination with E7 (16). The contribution of HPV16 E5 to HNSCC in this mouse model has not been fully evaluated but appears to be much less than that of E7 (Strati and Lambert, unpublished data).

In FA patients from North America, a high percentage (84%) of HNSCC arising at various sites in the head and neck region (i.e., not restricted to the oropharynx) were found to be positive for high-risk HPV DNA. Consistent with a role of HPV in these cancers, mutations in p53, a tumor suppressor that is inactivated by HPV16 E6, were not found in HNSCCs from these patients. However, in patients from European countries, HNSCCs were negative for HPV DNA and more than 50% of these tumors had p53 mutations (17, 18). Given these conflicting clinical data, it remains unclear whether HPVs play a major role in HNSCCs arising in FA patients.

Several studies point to a contribution of FA deficiency in HPV-associated disease at the molecular level. In tissue culture, expression of the HPV16 oncogene was shown to stimulate transcription of fancD2 (19) and activate the FA pathway (20). In another study making the use of organotypic cultures of human keratinocytes to recapitulate the HPV life cycle, HPV16-transgenic mice (22). Briefly, mice were treated with 4-nitroquinoline-1-oxide (4-NQO; 10 mg/mL) in their drinking water for 8 weeks and then held off treatment for an additional 16 weeks. At the end point or when mice became moribund, they were sacrificed, tumors in the tongue and the esophagus were scored, and tissues were collected for histopathologic analyses.

### Materials and Methods

#### Mice

K14E7 transgenic mice (25), on the FVB genetic background, were crossed with fancD2 gene knockout (fancD2–/–) mice (23), on the 129 genetic background, to generate F1 mice, K14E7/ FancD2–/– and NTG/FancD2–/– (FVB/129 mixed background). All experimental mice (NTG/FancD2–/+; NTG/FancD2–/–, K14E7/FancD2–/+; and K14E7/FancD2–/– mice) were males generated by intercrossing F1 mice. All mice were genotyped by PCR. Mice were injected intraperitoneally with 0.3 mL of bromodeoxyuridine (BrdUrd; 12.5 mg/mL) 1 hour before being sacrificed to measure cell proliferation. Tongues and esophagi were harvested and processed as described previously (22).

Mice were housed in the Association for Assessment of Laboratory Animal Care–approved McArdle Laboratory Animal Care Unit. All procedures were carried out in accordance with an animal protocol approved by the University of Wisconsin Institutional Animal Care and Use Committee.

#### 4-Nitroquinoline-1-oxide–induced head and neck carcinogenesis study and histologic analysis

The treatment and guidelines for histologic analysis of tumors were described previously (22). Briefly, mice were treated with 4-nitroquinoline-1-oxide (4-NQO; 10 μg/mL) in their drinking water for 8 weeks and then held off treatment for an additional 16 weeks. At the end point or when mice became moribund, they were sacrificed, tumors in the tongue and the esophagus were scored, and tissues were collected for histopathologic analyses.

#### Immunofluorescence

Immunofluorescence was performed as described previously (26, 27). Antibodies used included anti-p16 (1:50 in 5% nonfat milk/5% horse serum; M156, Santa Cruz Biotech), anti-Mcm7 (1:200 in 5% horse serum; Neomarkers), anti-53BP1-positive foci cells or in cells knocked down in its expression whereas restoration of fancA expression attenuated this effect (21). These studies indicate that there is an interplay between HPV and the FA pathway. The implications of this interplay on HPV-associated carcinogenesis remain unclear.

Given these findings, we performed experiments with mice to ask whether deficiency in the FA pathway leads to an increase in HPV16 E7–mediated HNSSC. We crossed K14E7 transgenic mice, which display heightened susceptibility to head and neck cancer (15, 22), to fancD2 gene knockout mice (23) and the incidence of head and neck cancers in HPV transgenic and nontransgenic mice was scored in fancD2-deficient and fancD2-deficient backgrounds. We found a significantly increased incidence of head and neck tumors in K14E7/ FancD2–/– mice compared with that in K14E7/FancD2–/+ mice. No tumors arose in nontransgenic mice regardless of fancD2 status. Increased tumor incidence in the FA-deficient, E7 transgenic mice correlated with increases in cell proliferation and DNA damage foci. In addition, we found that 2 biomarkers, p16 and MCM7 (22, 24), used in distinguishing between HPV-positive and HPV-negative HNSSC arising in humans are upregulated in the tumors arising in E7 transgenic mice regardless of FA-status. Our findings support the hypotheses that FA patients have greater susceptibility to HPV-associated HNSSC and that the oncogenic properties of E7 are attenuated by a functional FA pathway. On the basis of these conclusions, HPV-specific prophylactic vaccines could be useful in reducing SCC burden in FA patients.

#### Quantifying BrdUrd-positive nuclei and γH2AX- and 53BP1-positive foci cells

At least 3 mice of each genotype, NTG/FancD2–/+; NTG/ FancD2–/–, K14E7/FancD2–/+; and K14E7/FancD2–/– mice, were selected and ~8 to 10 frames (×400) of cells within the suprabasal (CK14 negative) and basal (CK14 positive) layers of tongue and esophagus epithelia were quantified for each mouse.

#### Statistical analysis

The MSTAT software program4 was used for determining statistical significance. Two-sided Fisher’s exact test was used

4http://www.mcardle.wisc.edu/mstat/
to determine the significance of differences in tumor incidence between each group of mice (Table 1). To determine the significance for BrdUrd, γH2AX foci, and 53BP1-positive foci cells between each group of mice, a 1-sided Wilcoxon rank-sum test was used (Figs. 2 and 3).

Results

funcD2 deficiency sensitizes mice to HPV-associated tumorigenesis

To test the hypothesis that FA deficiency leads to increased susceptibility to head and neck cancers caused by HPV, we made use of a mouse model for HPV-associated head and neck cancer (15, 22) in which HPV transgenic mice develop head and neck cancers when exposed to a chemical carcinogen, 4-NQO. This chemical carcinogen is absorbed by the epithelia lining the oral cavity and esophagus where a metabolite of 4-NQO causes DNA mutations. Prolonged treatment (16 weeks) with 4-NQO at a high dose (×10 that used in our own studies) is sufficient to efficiently induce head and neck cancers in nontransgenic mice (28). At the 10-fold lower dose used in our studies, 4-NQO synergizes with HPV16 oncogenes to induce head and neck cancers with few if any cancers arising in nontransgenic mice (22). In the current study, we treated mice at the dose used in our past studies but for a shorter duration (8 weeks treatment compared with 16 weeks). This shorter treatment regimen was chosen because it confers a shorter duration (8 weeks treatment compared with 16 weeks).

As stated earlier, of the HPV16 oncogenes, E7 contributes greatest to head and neck cancer in mice (15). Because of this, and the fact that tissue culture studies indicated that the FA pathway promotes repair of E7-induced damage (21), we crossed K14E7 mice to fancD2-null mice (23) to generate 4 different genotypes: NTG/FancD2+/−, NTG/FancD2−/−, K14E7/FancD2+/−, and K14E7/FancD2−/−. Male mice were treated with 4-NQO for 8 weeks and then held for an additional 16 weeks before being sacrificed. Visible tumors on the tongues and esophagi of mice were counted, and tissues were collected for histopathologic analyses. No tumors were detected in either the NTG/FancD2+/− or NTG/FancD2−/− mice, indicating that FA deficiency alone was not sufficient to induce head and neck cancer under this carcinogen treatment regimen (Table 1). Only 4 of 20 K14E7/FancD2+/− mice (20%) had overt tumors (Table 1), consistent with prior observations that tumors arise in only a small fraction of E7 mice treated for only 8 weeks with 4-NQO (Jabbar et al., manuscript in preparation). However, a much higher fraction (11 of 21; 52%) of K14E7/FancD2−/− mice developed overt tumors (Table 1). This incidence of tumors in the K14E7/FancD2−/− mice was significantly higher than in the K14E7/FancD2+/− mice (P = 0.05; 2-sided Fisher’s exact test). These data indicate that FA deficiency increases the susceptibility of mice to E7-induced head and neck tumors.

The majority of overt tumors arising in K14E7/FancD2−/− mice are carcinomas

Tissues from mice with overt tumors were harvested, fixed, sectioned, and subjected to detailed histopathologic analysis. Specifically, every tenth 5-μm section of the tongue and esophagus was stained with hematoxylin and eosin (H&E) and analyzed histopathologically to determine the worst stage of neoplastic disease in each animal (Table 2). As described previously (22), a progressive disease was observed in the E7

Table 1. Comparison of 4-NQO induced over tumor incidences in animal tissues (tongue and esophagus)

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Group size, n</th>
<th>Animal tissues with overt tumor, n (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Tongue and esophagus</td>
<td>Tongue</td>
</tr>
<tr>
<td>NTG/FancD2+/−</td>
<td>24</td>
<td>0 (0)</td>
</tr>
<tr>
<td>NTG/FancD2−/−</td>
<td>26</td>
<td>0 (0)</td>
</tr>
<tr>
<td>K14E7/FancD2+/−</td>
<td>20</td>
<td>4 (20)</td>
</tr>
<tr>
<td>K14E7/FancD2−/−</td>
<td>21</td>
<td>11 (52)</td>
</tr>
</tbody>
</table>

NOTE: The difference in tumor incidence between K14E7/FancD2+/− and K14E7/FancD2−/− groups was statistically significant (P = 0.05). Also, the differences in the tumor incidence between K14E7/FancD2+/− and NTG/FancD2+/− (P = 0.04), and NTG/FancD2−/− groups (P = 0.03) are statistical significant. All statistical comparisons were performed using a 2-sided Fisher’s exact test.

Table 2. Histopathologic analysis of sample with overt lesions

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Grade of overt lesions, n (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Papilloma</td>
</tr>
<tr>
<td></td>
<td>Grade I</td>
</tr>
<tr>
<td>K14E7/FancD2+/−</td>
<td>3 (75)</td>
</tr>
<tr>
<td>K14E7/FancD2−/−</td>
<td>3 (27)</td>
</tr>
</tbody>
</table>
transgenic mice in this study (see Supplementary Fig. S1), ranging from normal epithelium to benign papillomas to invasive cancer (i.e., carcinomas). Carcinomas were subdi-
vided into grades I, II, and III, based on the degree of
differentiation (keratinization) within the cancer. While 1 of
the tumors arising in the K14E7/FancD2\(^{+/+}\) mice was a
carcinoma, 8 of 11 tumors arising in the K14E7/FancD2\(^{-/-}\) mice were carcinomas (Table 2). These histopathologic find-
ings demonstrate that FA deficiency increases the severity of
neoplastic head and neck disease in E7 transgenic mice.

Expression of 2 biomarkers in carcinomas arising
in K14E7/FancD2\(^{+/+}\) and K14E7/FancD2\(^{-/-}\) mice

Two biomarkers, p16 and MCM7, have proven useful in
distinguishing HPV-positive from HPV-negative HNSCCs both
in mice (22) and in humans (26, 30–32). HPV16 E7 is thought
to play a dominant role in the induction of MCM7 and p16 in
both head and neck (22) and cervical (26) cancers. To deter-
mine whether these proteins were also upregulated by E7 in
head and neck cancers arising on a FA-deficient background,
sections from cancers arising in K14E7/FancD2\(^{+/+}\) and K14E7/
FancD2\(^{-/-}\) mice were subjected to p16- and MCM7-specific
immunofluorescence. Both proteins were highly expressed in
cancers arising in E7 transgenic mice regardless of fancD2
status (Fig. 1). Furthermore, the expression patterns of MCM7
and p16 in normal epithelium of the tongue and esophagus
were similar to those of HPV-positive and HPV-negative
cancers, respectively (Supplementary Fig. S2). Consistent with these findings, we previously
observed MCM7 and p16 staining exclusively in HPV-positive
head and neck tumors in our mouse model (22). These
findings, when taken together, suggest that these biomarkers
will retain their usefulness in identifying HPV-positive disease
in the FA patients with HNSCCs.

Deficiency in fancD2 induces DNA synthesis in the basal
epithelial compartment but not in the suprabasal
epithelial compartment, and this activity is
independent of E7

A prior study showed that FA deficiency could lead to
hyperplasia in the context of organotypic raft cultures of

Figure 1. Examination of 2 biomarkers, p16 and MCM7, in carcinomas arising on the tongue and esophagus in K14E7/FancD2\(^{+/+}\) and K14E7/FancD2\(^{-/-}\) mice treated with 4-NQO, a carcinogen. Shown are representative images from sections stained with anti-p16 (green) and anti-MCM7 (red) antibodies and counterstained with 4',6-diamidino-2-phenylindole (DAPI; blue). Magnified images of areas highlighted in the dashed boxes are shown to the right. Scale bar, 50 \(\mu\)m.
HPV oncoprotein-immortalized human keratinocytes (21). This raised the possibility to us that increases in cell proliferation could contribute to the increase in head and neck cancers in the fancD2-deficient, E7 transgenic mice. We, therefore, monitored cell proliferation in the epithelia lining the tongue and esophagus of the different mouse genotypes used in this study. For this experiment, groups of mice (n = 3) of each genotype were injected intraperitoneally with BrdUrd 1 hour before being sacrificed, and BrdUrd-specific immunofluorescence was performed to detect its incorporation into newly synthesized DNA (Fig. 2A). The frequency of BrdUrd-positive cells was then quantified in each tissue (Fig. 2B). On the fancD2-sufficient background, E7 caused significant increases in the frequency of BrdUrd-positive cells in both the basal and suprabasal compartments of the tongue and esophagus epithelia (K14E7/FancD2+/+ vs. NTG/FancD2+/+ mice; P < 0.05), consistent with prior observations (15). In the absence of E7, deficiency in fancD2 alone caused a significant increase in the proliferative index in the basal but not in the suprabasal compartment of the epithelia in both the tongue and the esophagus (NTG/FancD2−/− vs. NTG/FancD2+/+ mice; P < 0.05 for basal only). In the presence of E7, deficiency in fancD2 also caused a significant increase in the proliferative index in the basal but not in the suprabasal compartment of the epithelia in both the tongue and the esophagus (K14E7/FancD2−/− vs. K14E7/FancD2+/+ mice; P < 0.05 for basal only). In addition, we scored cells progressing through G2/M by using immunofluorescence of histone 3 phosphorylated at serine-10 (H3S10), which is a well-known marker for mitosis (33). We found that fancD2 deficiency or expression of HPV16 E7 oncogene led to increased numbers of H3S10-positive cells (Supplementary Fig. S3). This correlated with the increase in DNA synthesis in these same mouse strains (Fig. 2). fancD2 deficiency, however, led to only subtle increases in the percentage of cells progressing through G2/M.
of H3S10-positive cells in the E7 transgenic tissue (Supplementary Fig. S3). This correlates with the observation that the induction of DNA synthesis of E7 is only slightly enhanced on a fancD2-deficient background (Fig. 2). Taken together, these findings indicate that both HPV16 E7 oncoprotein and fancD2 deficiency act independently and additively induce cell-cycle progression specifically in the basal epithelia of the animal tissues.

DNA damage positive foci cells accumulate in head and neck epithelia in E7-expressing mice: influence of FA pathway

A number of observations support the hypothesis that HPV16 E7 induces genomic instability. Expression of E7 in cells leads to an accumulation of DNA breaks on the basis of the use of the comet assay, which scores for the presence of single- and/or double-strand DNA breaks (DSBs), as well as DNA ICLs damage (34, 35). Expression of E7 in cells also causes an accumulation of chromosomal abnormalities as evidenced by losses or gains of specific alleles (34, 36) or gross changes scored by karyotypic analyses for chromatid breaks, chromatid fusions, or polyploidy (36). That E7 causes an accumulation of damaged DNA is further supported by the observation that in the nuclei of cells expressing E7, there is an increased frequency of DNA damage foci (34), as detected by using antibodies specific to histone 2AX phosphorylated at serine-139 (γH2AX), which is a marker for activated DNA damage responses triggered by the presence of damaged DNA in the nuclei of cells (37, 38).

All of these studies were conducted in tissue culture. We wanted to determine whether E7 is capable of inducing DNA damage in the context of our mouse model for head and neck cancer and, if so, learn whether this property of E7 is affected by the status of the FA pathway. Specifically, we wanted to test the hypothesis that the FA pathway suppresses the capacity of E7 to induce DNA damage. It is not possible to directly quantify DNA damage in situ in the context of tissue samples; therefore, we monitored for the presence of DNA damage indirectly by quantifying the abundance of cells with DNA damage foci. γH2AX-specific immunofluorescence was performed on sections of the tongue and esophagus from E7 transgenic and nontransgenic mice on the fancD2-sufficient and fancD2-deficient backgrounds (Fig. 3A). E7 led to a large and statistically significant increase in cells with γH2AX-positive nuclear foci in both the basal and suprabasal compartments of the epithelia lining the tongue and the esophagus (Fig. 3B), consistent with prior findings in tissue culture (34). This E7-dependent induction in the number of cells with γH2AX-positive foci was further increased on the fancD2-deficient background (Fig. 3B). This latter increase was statistically significant in the basal and suprabasal compartments of the esophagus and the suprabasal compartment of the tongue and marginally significant in the basal compartment of the tongue (Fig. 3B). The fact that there was greater frequency of cells with DNA damage foci in FA-deficient, E7 transgenic epithelia than in FA-sufficient, E7 transgenic epithelia is consistent with the hypothesis that the FA pathway suppresses the capacity of E7 to induce DNA damage. Similar results were observed in the epidermis lining the K14E7 mouse torso, another stratified epithelia in which E7 is expressed. In this tissue, we again observed E7-dependent induction of γH2AX-positive nuclear foci in both the basal and suprabasal compartments, and this induction was further heightened on the fancD2-deficient background (Supplementary Fig. S4).

A recent study carried out in tissue culture also supports the hypothesis that the FA pathway promotes repair of E7-induced damage (21). Specifically, in HPV18 E6/E7-immortalized, fancA-deficient keratinocytes grown in organotypic cultures to produce stratified epithelium, there was observed an increased frequency of cells with high numbers of 53BP1-positive nuclear foci compared with a derivative cell line that had been complemented for fancA. 53BP1, like γH2AX, is a marker for DNA damage foci and provides an indirect measure of the level of DNA damage in a cell (39). We repeated our own analysis of mouse tissues by using 53BP1 as an alternative marker for DNA damage foci (Fig. 3C). As observed with γH2AX-specific immunofluorescence (Fig. 3B), E7 caused a large and statistically significant induction in the frequency of cells with 53BP1-positive nuclear foci in both the basal and suprabasal compartments of the tongue and esophagus epithelia (Fig. 3D). In fancD2-deficient tissue, E7 caused a further increase in the frequency of cells with 53BP1-positive nuclear foci in both the basal and suprabasal compartments of the tongue and esophagus. This further increase was again statistically significant in both the compartments of the esophagus and the suprabasal compartment of the tongue and marginally significant in the basal compartment of the tongue (Fig. 3D). Thus, using 2 different markers for DNA damage...
damage foci, we find evidence in support of the hypothesis that the FA pathway suppresses E7-dependent induction of DNA damage.

In the absence of E7, we found no evidence for fancD2 deficiency leading to an increase in the frequency of cells with γH2AX-positive nuclear foci, but there was a modest yet significant increase in the frequency of cells with 53BP1-positive nuclear foci specifically in the suprabasal compartment of the tongue and esophagus epithelia (Fig. 3D). It is unclear what this modest increase reflects, as in nontransgenic mice, the compartment of the epithelia is postmitotic; therefore, it is not likely to reflect DNA damage arising from normal DNA replicative processes.

Discussion

FA pathway suppresses HPV-associated carcinogenesis in the tongue and the esophagus

A link between HPV16 and SCCs from FA patients is of interest to both the clinical and basic research fields. In prior studies of FA patients, geographic and technical differences between study groups make establishing such a link unclear (17, 18). Some researchers, however, have demonstrated clear correlations between the oncogenic activity of HPV16 and deficiency in the FA pathway in vitro (20, 21). Our in vivo findings that HPV16-associated cancer incidence is significantly induced in the tongue and the esophagus when the FA pathway is compromised by the lack of fancD2 gene (Tables 1 and 2) supports the conclusions of prior in vitro studies. Our findings might explain why HPV16 E7 activates the FA pathway in human cells (20). Such an activation could counteract the oncogenic activities of E7. Our results are also consistent with the observation in vitro that rescue of the FA pathway inhibits HPV16-associated hyperplasia (21). On the basis of the cumulative studies, we hypothesize that the FA pathway suppresses the oncogenic activities of HPV16 E7. Moreover, these data provide further argument for the value of early vaccination of FA patients against HPV16 E7 transgenic mice to develop cancer correlated with an overall heightened rate of basal cell proliferation.

FancD2 controls cell proliferation in basal epithelial cells

We observed fancD2 deficiency increased the frequency of cells supporting DNA replication in the basal epithelium, even in the absence of HPV16 E7 expression (Fig. 2). This supports the hypothesis that increases in cell proliferation contribute to epithelial cancers in FA patients. This finding also correlates with prior findings that posttranslational modification of FancD2 protein by the ATM and ATR pathways plays a role in the S-phase checkpoint in cells in vitro (10, 12, 40). In the absence of exposure to exogenous DNA-damaging agents, ubiquitinated FancD2 protein is observed in the S phase of cells (10, 12, 41). Furthermore, lymphoblastoid cell lines deficient in the FA pathway lack the ability to delay S-phase progression in response to DNA damage from DNA cross-linking agents (42, 43). In the latter cell type, a corresponding induction of programmed cell death is thought to contribute ultimately to bone marrow failure in FA patients (44).

Deregulation of cell proliferation by HPV16 E7 is induced by deficiency in the FA pathway

Unscheduled entry into S phase and the deregulation of cyclin expression in epithelium are the well-known properties of HPV16 E7 (45). fancD2 gene knockdown increases the proliferation in organic raft culture system by using keratinocytes immortalized by HPV16 and HPV18 oncogenes in vitro (21). Our finding that deficiency in the FA pathway increases cell proliferation in epithelium in vivo induced by E7 expression (Fig. 2) is consistent with the previous observation. We did not observe an effect of fancD2 deficiency on proliferation within the suprabasal compartment of epithelia in the presence of E7 expression. This would suggest that the ability of E7 to deregulate the cell in the suprabasal compartment is not modulated by the FA pathway. However, deficiency in the FA pathway did result in increased proliferation in the basal compartment of epithelium expressing the E7 oncoprotein (Fig. 2B). But because FA deficiency, in the absence of E7 expression, can induce basal cell proliferation (see above), it remains unclear whether the increase in basal cell proliferation in fancD2-null, E7 transgenic epithelia reflects an ability of the FA pathway to partially suppress E7-induced proliferation or an ability of FA deficiency to act independently to cause cell proliferation. Regardless, the predisposition of FA-deficient, E7 transgenic mice to develop cancer correlated with an overall heightened rate of basal cell proliferation.

FA pathway modulates DNA damage induced by HPV16 E7

Whether the FA pathway acts directly to suppress DNA damage induced by HPV16 E7 is an important question in light of the fact that E7 is more oncogenic on an FA-deficient background in mice. E7 activates FA pathway as shown by the accumulation of monoubiquitinated FancD2 protein in vitro (20). E7 induces DNA damage, as detected by the comet assay (34), and DNA damage response, as measured by the induction of γH2AX-positive nuclear foci in vitro (34). Our findings that E7-dependent DNA damage responses were increased on the FA-deficient background in vivo, as evidenced by the increase in numbers of cells with γH2AX- and 53BP1-positive nuclear foci (Fig. 3), is consistent with recent in vitro results showing that fancA gene complementation significantly reduced the number of 53BP1 foci per nucleus in fancA gene-deficient keratinocytes immortalized by HPV18 (21). Together, these results support the hypothesis that the FA pathway suppresses E7-induced DNA damage and raise the interesting corollary that this property of the FA pathway contributes to its ability to suppress HPV-induced neoplasia.

One of the possible forms of DNA damage induced by E7 is DSBs, given that γH2AX- and 53BP1-positive nuclear foci are commonly considered to be readouts for DSBs and DNA damage responses to infrared radiation (46, 47). γH2AX/53BP1 double-positive nuclear foci were observed in the epithelium expressing HPV16 E7 (data not shown). In addition, anaphase bridges, which represent chromosomal fusion caused by DSBs, have been observed in cells expressing E7 (35). These data are consistent with the hypothesis that E7 induces DSBs and that E7-induced DSBs accumulate to a
greater extent on an FA-deficient background. Further studies are needed to clearly define the nature of the DNA damage arising in the context of our mouse model for HPV-associated HNSCC.

**HPV and HNSCCs in FA patients**

Taken together, our studies and that of others in the field point to a model in which cell proliferation and DNA damage induced by the dominant HPV oncogene, E7, arise to a greater extent in an FA-deficient cellular context. Consistent with this model, recent data indicate a role of the FancD2 protein in preventing chromosome instability and aneuploidy (48). Accumulated, unrepaired DNA damage is likely to lead to increased genomic instability. This instability of the human genome may, in turn, contribute to increases in the incidence of SCCs in HPV-positive FA patients. In addition, the increased epithelial proliferation seen in FA-deficient cells/tissues may increase the infectivity of HPVs, thereby increasing the chance for persistent infections arising in FA patients (21). Together, these properties conferred by FA deficiency are likely to contribute to increased susceptibility of FA patients to HPV-associated cancers.

**Disclosure of Potential Conflicts of Interest**

No potential conflict of interest were disclosed.

**Acknowledgment**

We thank Dr. Doug Lowy (NCL, Bethesda, MD) for first proposing to us to make use of our mouse models to investigate the relationship between HPV oncogenesis and the FA pathway.

**Grant Support**

This research was supported by grants from the NIH (DE017315) to P.F. Lambert and (CA112596-) to S. Duensing.

Received 04/09/2010; revised 09/08/2010; accepted 09/12/2010; published OnlineFirst 10/08/2010.

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www.aacajournals.org

Cancer Res; 70(23) December 1, 2010

9967

Published OnlineFirst October 8, 2010; DOI: 10.1158/0008-5472.CAN-10-1291

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Deficiencies in the Fanconi Anemia DNA Damage Response Pathway Increase Sensitivity to HPV-Associated Head and Neck Cancer


Cancer Res 2010;70:9959-9968. Published OnlineFirst October 8, 2010.