

E2F transcription factors and digestive system malignancies: How much do we know?

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Abstract

E2F family of transcription factors regulates various cellular functions related to cell cycle and apoptosis. Its individual members have traditionally been classified into activators and repressors, based on *in vitro* studies. However their contribution in human cancer is more complicated and difficult to predict. We review current knowledge on the expression of E2Fs in digestive system malignancies and its clinical implications for patient prognosis and treatment. E2F1, the most extensively studied member and the only one with prognostic value, exhibits a tumor-suppressing activity in esophageal, gastric and colorectal adenocarcinoma, and in hepatocellular carcinoma (HCC), whereas in pancreatic ductal adenocarcinoma and esophageal squamous cell carcinoma may function as a tumor-promoter. In the latter malignancies, E2F1 immunohis-

tochemical expression has been correlated with higher tumor grade and worse patient survival, whereas in esophageal, gastric and colorectal adenocarcinomas is a marker of increased patient survival. E2F2 has only been studied in colorectal cancer, where its role is not considered significant. E2F4's role in colorectal, gastric and hepatic carcinogenesis is tumor-promoting. E2F8 is strongly upregulated in human HCC, thus possibly contributing to hepatocarcinogenesis. Adenoviral transfer of E2F as gene therapy to sensitize pancreatic cancer cells for chemotherapeutic agents has been used in experimental studies. Other therapeutic strategies are yet to be developed, but it appears that targeted approaches using E2F-agonists or antagonists should take into account the tissue-dependent function of each E2F member. Further understanding of E2Fs' contribution in cellular functions *in vivo* would help clarify their role in carcinogenesis.

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Key words: E2F; Colorectal cancer; Gastric cancer; Esophageal cancer; Pancreatic cancer; Hepatocellular carcinoma; Digestive system malignancies

Core tip: The E2F family of transcription factors has been in the focus of cancer research because its members regulate significant cellular functions related to cell cycle and apoptosis. E2Fs may act either as tumor-promoters or as tumor-suppressors, depending on the tissue. This review highlights the role of E2Fs in digestive system malignancies and their possible implication in diagnosis, treatment and prognosis.

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INTRODUCTION

The E2F family of transcription factors is involved in a vast number of cellular functions related to cell cycle and apoptosis. The study of E2F began in the mid 1980s when it was identified as a transcription activator of the adenoviral *E2* gene promoter^[1,2]. The role of the prototype member, E2F1, in cancer was identified in the early 1990s through its ability to bind to and regulate the retinoblastoma protein pRb^[3-7] with several members to follow either through their homology to E2F1 or through their association with pRb-related proteins (pocket proteins)^[8-16].

Early *in vitro* studies rose expectations that, through the traditional classification of the E2F family members into activators and repressors, accurate predictions about their contribution in human carcinogenesis could be possible, with oncogenic behavior expected for the former and tumor-suppressing function for the latter group. Nevertheless, *in vivo* studies have sunk the initial enthusiasm as their role appears to be by far more complicated^[17].

E2F1 is the most thoroughly investigated member of the E2F family in human malignancies. Other members have also been studied but in lesser extent. In non-small cell lung carcinoma, increased E2F1 and E2F3 expression has been associated with worse patient prognosis^[18-21]. In breast cancer, enhanced E2F1 or E2F4 expression have been proposed as poor prognostic indicators, whereas increased E2F5 expression has been reported in certain histological subtypes^[22-26]. In ovarian cancer, E2F1-5, E2F7 and E2F8 expression is reportedly increased. In addition, increased E2F4 and E2F7 expression has been related to better overall or disease-free survival, respectively, whereas that of E2F8 was linked to worse overall survival^[27-30]. In prostate cancer, E2F2 and E2F3 expression increases, while E2F1 is absent^[25,31]. In urothelial carcinomas of the bladder, E2F3 expression is enhanced, while that of E2F1 depends on the presence of invasion^[25,32-37]. Increased E2F1 expression has also been observed in thyroid cancer, small cell lung carcinoma, glioblastoma and lymph node metastases from malignant melanoma^[38-42].

The aim of the current review is to summarize the collective knowledge on the role of various E2F family members in digestive system malignancies and to identify possible clinical implications for patients' diagnosis and prognosis and for future treatment strategy design.

E2F STRUCTURE AND REGULATION

To date, eight members of the mammalian E2F family have been recognized and characterized^[36,43], though the most recently identified, namely E2F7^[44,45] and E2F8^[46,47], bear little homology to their traditional counterparts (Figure 1). Two E2F3 proteins, E2F3a and E2F3b, have been identified, which are produced from the same gene through the use of alternate promoters^[48,49]. E2F7 also has two isoforms, E2F7a and E2F7b, which are produced through by alternative splicing of the primary transcript^[50].

The greatest homology among the different members

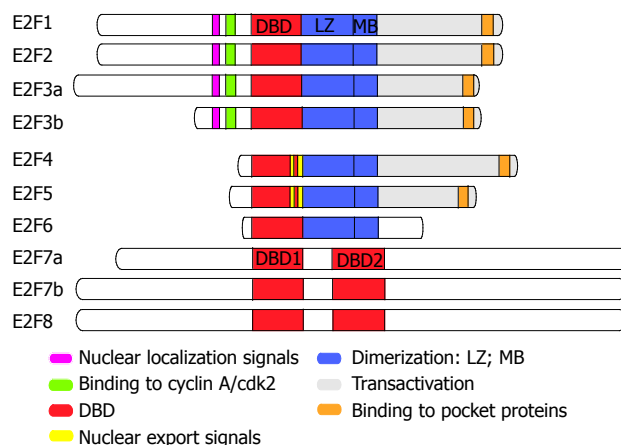


Figure 1 Mammalian E2F family of transcription factors. In the context of digestive system malignancies, E2F1 may exhibit a tumor-suppressing role in colorectal, gastric and esophageal adenocarcinoma, as well as in hepatocellular carcinoma. On the contrary, in pancreatic ductal adenocarcinoma and esophageal squamous carcinoma a tumor-promoting role has been shown. A tumor-promoting role is demonstrated for E2F4 in colorectal, gastric and liver carcinogenesis. E2F8 may contribute to hepatocarcinogenesis, as it has been shown to be strongly upregulated in human hepatocellular carcinoma. DBD: DNA binding domain; LZ: Leucine zipper; MB: Marked box.

of this family is observed in the DNA binding domain. The older members E2F1-6 possess N-terminal DNA binding domain, followed by leucine zipper and marked box domains that mediate heterodimerization. With the exception of *E2F6*, the established members of the family possess a C-terminal transactivation domain containing the pocket protein binding region^[36]. E2F1-3 have nuclear localization signals adjacent to their cyclin A-binding domain. This ensures their movement to the nucleus, thereby modulating E2F activity in a cell cycle-dependent manner^[51-53]. E2F1-6 require heterodimerization with one of the dimerization partner (DP) proteins, DP1, DP2 or DP3 in order to form functional transcription factors which can bind DNA with high affinity^[54-59]. E2F4 and E2F5 have bipartite nuclear export signals, which mediate their export to the cytoplasmic compartment and they rely on heterodimerization with one of DP proteins for their translocation to the cell nucleus^[60,61]. The proteins DP2 and DP3 are thought to be alternatively spliced products of a single gene. The role of DP subunits is not completely elucidated and it appears that the function of E2F-DP heterodimer is dictated by the E2F subunit^[56,57].

The transcriptional activity of E2F1-5 is regulated through their binding with the pRb protein or the related pocket proteins p107 and p130^[62-64]. E2F1-3 bind to pRb when the latter is found in its hypophosphorylated form^[13], E2F4 can bind to any of the pocket proteins, whereas E2F5 associates predominantly with p130^[65,66]. Generally, when a pocket protein is hypophosphorylated can associate and block the transcriptional activity of E2F-DP heterodimers by masking the transcription activation domain of E2Fs, rendering them inactive (passive repression)^[43]. Furthermore, the pocket protein/E2F-DP complex is guided to E2F binding sites where it can

recruit histone deacetylases that suppress transcription by remodelling the nucleosome (active repression)^[67-70]. E2F6-8 are presumed to repress E2F-responsive genes independently of pocket proteins^[10,11,50,71].

ROLE AND FUNCTION OF E2F TRANSCRIPTION FACTORS

E2F family members have been traditionally classified as activators and repressors. E2F1-3a are often referred to as activators because they transcriptionally activate certain target genes, for example cyclin E. This E2F subclass is expressed in a cell cycle-regulated manner exhibiting highest levels in the late G1 and S phase. In other words, they induce the entrance of quiescent cells in the S phase of cell cycle and overcome arrest mediated by the p16^{INK4a} cyclin-dependent kinase inhibitor^[43,72]. E2F3b-5 comprise the repressor subclass because their main function seems to be the repression of transcription of some E2F target genes when they associate with pocket proteins. This subgroup is expressed constitutively, but transcriptional repression by these factors takes place predominantly in cells which are in quiescence and early G1 phase^[43]. E2F6-8 are also considered as repressors but they do so, as previously stated, by a manner independent of pocket protein family members^[10,11,16,44-46,71]. The abovementioned classification, which is based on results of *in vitro* studies, is probably oversimplified and does not accurately reflect the dynamics of E2F-dependent transcriptional control^[17,43]. The study of E2Fs' role *in vivo* has been challenging because of three main obstacles impending complete understanding of their functions. Firstly, there is a high degree of functional redundancy among activators and repressors. Secondly, there is a functional antagonism between E2F-mediated activation and repression in the regulation of normal cell proliferation. Thirdly, the members of this family have the ability to regulate each others expression, forming complex feedback loops to ensure a balance between activators and repressors in each phase of the cell cycle^[17].

E2FS IN DIGESTIVE SYSTEM MALIGNANCIES

Esophageal cancer

Amplification of E2F1 is often found in esophageal squamous cell carcinomas and the survival of patients with such aberration is significantly lower than that of patients without it^[73]. Furthermore, positive E2F1 immunostaining correlates with histological grade and tumor stage with the overall survival being worse for patients with E2F1-positive tumors^[74,75]. E2F1 expression is also shown to be positively associated with cell proliferation but not apoptosis^[76]. Interestingly, the sequential transfer of the wild-type *p53* and *E2F1* genes into esophageal cancer cell lines induces tumor cell apoptosis *via* E2F1/ARF/MDM2/p53 pathway^[77]. It is possible that reduced

apoptosis *in vivo* can be explained by a model suggested in non-small cell lung carcinoma, whereby tumors with deregulated E2F1/pRb network cannot promote p53-dependent apoptosis under conditions of *p53* mutation or MDM2 overexpression^[19]. The situation is quite the opposite in esophageal adenocarcinomas arising in the background of Barrett esophagus. In such cases, E2F1 immunohistochemical expression exhibits a positive correlation with apoptosis and an inverse relationship with cell proliferation, implying that apoptosis is probably the tumor-suppressive mechanism activated by E2F1. The tumor-suppressing activity of E2F1 in adenocarcinomas of Barrett esophagus could be explained by the intestinal-type nature of the metaplastic mucosa and it may also be dictated by the embryological origin of the lower third of esophagus from the foregut^[78].

Gastric adenocarcinoma

E2F1 is found to be overexpressed in about 40% of gastric adenocarcinomas, whereas gene amplification of E2F1 rarely occurs^[79-81]. Experimental studies have provided evidence that adenovirus-mediated E2F1 overexpression in gastric carcinoma cells induces widespread apoptosis, probably through direct or indirect upregulation of phosphatase and tensin homolog (PTEN) expression, activation of caspase-3 and -9 and decrease in nuclear factor kappa-light-chain-enhancer of activated B cells expression *via* PI3K/PTEN/Akt signalling pathway, especially when combined with cyclin-dependent kinase inhibitors, such as roscovitine. This points to a tumor-suppressing role of E2F1 in this type of cancer^[82-86]. Interestingly, at least one study has demonstrated the opposite effect, *i.e.*, downregulation of E2F1 significantly inhibited the infiltration and proliferation abilities of human gastric cancer cells. This inconsistency was attributed to the difference in activation of E2F1 at different points of the cell cycle to keep a dynamic balance^[87]. E2F1 immunoreactivity was shown to independently predict favorable overall survival in gastric adenocarcinoma patients who received adjuvant chemoradiation therapy with 5-fluorouracil and leucovorin after gastrectomy and correlated with localized tumor, intestinal histological subtype and thymidylate synthase expression, supporting its role as a potential biological marker, predictive of clinical outcome in this particular setting^[88]. Similar to colorectal adenocarcinomas, microsatellite unstable gastric adenocarcinomas frequently exhibit mutation of the adenosine-guanine-cytosine (AGC) repeat of the *E2F4* gene, that probably represents an early event in this context, allowing for additional gene anomalies to accumulate during tumor progression^[89-94].

Colorectal adenocarcinoma

There are a number of studies that investigated the role of E2F family members, especially E2F1, in the context of colorectal cancer. E2F1 expression was indeed found increased in some early studies^[81,95]. Later on, increased E2F1 expression was found directly related to increased

apoptotic levels and inversely related to cell proliferation, particularly when serial or semiserial sections were analyzed^[25,96,97], suggesting a tumor-suppressing role. E2F1 expression is higher in lung metastasis of colon adenocarcinoma and also correlates closely with the expression of thymidylate synthase in both the primary tumor and metastases, indicating worse response to 5-fluorouracil due to resistance^[98,99].

On the other hand, E2F4 has been directly associated with cell proliferation in colorectal cancer, suggesting a tumor-promoting role^[97,100]. This finding is in agreement with experimental observations in cell line and animal models demonstrating increased nuclear expression of E2F4 in the replicating colon epithelium^[101-104]. Of interest, the immunohistochemical expression of E2F1 was inversely correlated with that of E2F4 when studied in serial histological sections, suggesting a possible mechanistic interlink between the two family members that has yet to be identified^[97]. An other interesting observation is that *E2F4* contains a stretch of 13 serine residues in its trans-activation domain encoded by a microsatellite trinucleotide AGC repeat within the *E2F4* gene. This repeat is often found mutated in various gastrointestinal tumors, including human colorectal cancer with microsatellite instability and it is believed to be one of the targets of DNA mismatch repair deficiency^[93,105-107].

E2F2 has only recently been investigated in colorectal adenocarcinoma. Its expression at the tissue level was found to be very low without any relationship to kinetic parameters, leading to the hypothesis that E2F2 expression does not contribute in colorectal carcinogenesis but rather reflects the functional redundancy between E2F members of the same subgroup^[97].

Hepatocellular carcinoma

In a recent study, nuclear immunohistochemical expression for E2F1 was positively related to tumor apoptotic index in a series of human hepatocellular carcinomas, supporting a pro-apoptotic role of E2F1 in this type of cancer^[108]. Interestingly, studies investigating HCC-cell lines or mouse models have provided evidence pointing towards a tumor-promoting role of E2F1 by demonstrating that its overexpression led to increased expression of upstream cell proliferation or anti-apoptotic genes^[109-112]. Other investigators have demonstrated that, in a transgenic mouse model, endogenous c-myc was upregulated in the early stages of hepatocarcinogenesis, whereas p53 was overexpressed in the tumors, suggesting that both E2F1-mediated proliferation and apoptosis are operative but at different stages of hepatocarcinogenesis^[113].

E2F3 and E2F4 are also shown to be upregulated in HCC^[114-116]. Of note, HCCs exhibiting microsatellite instability has shown deletions in AGC triplet repeats in the coding region of the *E2F4* gene in a similar manner as demonstrated for microsatellite unstable colorectal cancer^[93,105-107,117]. These results suggest that both microsatellite instability and mutations of *E2F4* commonly occur in HCC and may play an important role in hepatocarcinogenesis^[117].

Lastly, it has been demonstrated that E2F8 is strongly upregulated in human HCC and it could thus contribute to oncogenesis and progression in this type of cancer. Mechanistic analyses indicated that E2F8 could bind to regulatory elements of cyclin D1, regulating its transcription and promoting accumulation of S-phase cells^[118].

Pancreatic cancer

E2F1 may have a tumor-promoting role in pancreatic ductal adenocarcinoma. A direct correlation has been found between E2F1 immunohistochemical expression and cell proliferation index, as well as an inverse relationship between E2F1 immunopositivity and histological grade and disease-associated survival^[119]. Interestingly, stable overexpression of E2F1 and decreased pRb expression resulting in the liberation of E2F in pancreatic cancer cell lines may be responsible for the demonstrated increase in chemotherapy-induced apoptosis^[120]. Moreover, infection of pancreatic cancer cells lines by E2F1-expressing adenoviral vector has been shown to increase gemcitabine-induced apoptosis as well as etoposide- or roscovitine-induced apoptosis^[121,122].

ISSUES IN E2F BIOLOGY

Deregulated expression of E2F family of transcription factors is a common phenomenon in human cancer. Little is known though about the magnitude and the nature of their contribution. The prevailing view is that E2F activators and repressors operate in a coordinated manner to achieve proper cell cycle progression and/or apoptosis and that disturbance of this well orchestrated interaction can contribute to carcinogenesis. According to the traditional classification of the different E2F members into activators and repressors, it would be expected that clear predictions about their function in cancer could be made. Unfortunately, this is not the case and this classical approach stemming from *in vitro* studies is openly challenged in practice^[17,43]. To complicate things further, numerous E2F target genes have been identified reflecting the fact that E2Fs participate in cellular processes beyond the cell cycle^[123-127].

Regarding digestive system malignancies, E2F1 may exhibit a tumor-suppressing role in colorectal, gastric and esophageal adenocarcinoma, as well as in hepatocellular carcinoma, probably through pro-apoptotic activity^[25,78,82-86,96,97,108]. On the contrary, a tumor-promoting role has been attributed to E2F1 in the context of pancreatic ductal adenocarcinoma and esophageal squamous carcinoma^[73-76,119]. It is very interesting though that in experimental models involving adenoviral transfer of E2F1 in esophageal squamous and pancreatic cancer cell lines apoptosis was evoked^[77,121,122]. The possible role, correlations and prognostic significance of E2F1 expression in digestive system malignancies is summarized in Table 1.

E2F4, a classical “repressor”, seems to play a tumor-promoting role in colorectal, gastric and liver carcinogenesis^[90,92,93,97,117]. It is also well documented that AGC

Table 1 Possible role, correlations and prognostic significance of increased E2F1 expression in digestive system malignancies

Tumor	Role	Clinicopathological relationships	Prognostic significance	Ref.
Esophageal				
Squamous cell carcinoma	Tumor-promoting	↑ tumor stage, ↑ histological grade, ↓ overall survival	Yes	[74,75]
Adenocarcinoma	Tumor-suppressing	↑ survival	Yes	[78]
Gastric adenocarcinoma	Tumor-suppressing	Localized disease, intestinal histological type, ↑ overall survival	Yes	[88]
Colorectal adenocarcinoma	Tumor-suppressing	↑ survival	Yes	[25,96]
Hepatocellular carcinoma	Tumor-suppressing		No	[108]
Pancreatic ductal adenocarcinoma	Tumor-promoting	↑ histological grade, ↓ disease-free survival	Yes	[119]

↑: Increased; ↓: Decreased.

repeats in the *E2F4* gene are commonly found mutated in various gastrointestinal malignant neoplasms exhibiting microsatellite instability and they are thought to represent one of the targets of DNA mismatch repair deficiency^[89-94,105-107,117]. Of note, in colorectal cancer, an inverse relationship between the immunohistochemical expression of E2F1 and E2F4 has been demonstrated when examined in serial histological sections^[97]. It would be interesting to investigate if such a relationship can be confirmed in other gastrointestinal cancers as well and, if so, whether there is a common “switch” connecting mechanistically these two opposing transcription factors.

CONCLUSIONS AND PERSPECTIVES

E2F family of transcription factors serves key roles in cell cycle progression, apoptosis, cell differentiation and stress responses. Following their traditional classification into activators and repressors, it has been tempting to assign to them oncogenic or tumor-suppressing functions, thus predicting their role in carcinogenesis. A number of investigators have focused into showing a prognostic value of E2F expression in different kind of digestive tract malignancies^[25,74-76,78,88,96,119]. Others have gone a step further and, based on their experimental work, suggest therapeutic strategies involving adenoviral transfer of *E2F* in a gene therapy context to sensitize cancer cells for conventional chemotherapeutic agents^[82,121,122].

However, clinical and experimental studies in mice openly challenge this traditional view, which does not appear to reflect the complexity of E2F function in tumorigenesis. It appears, though, that this function is exerted in a tissue-dependent manner. It is appealing to consider the development of treatment strategies involving E2F-antagonists, that would suppress cell proliferation, and E2F-agonists, that would promote apoptosis^[128]. Nevertheless, targeted therapeutic approaches against E2F family members should take into account the tissue-dependent function of each member.

It is quite obvious that, although our knowledge on this intriguing family of transcription factors is seemingly increasing, little is known about their function *in vivo*. The introduction and use of modern molecular techniques and experimental models have identified numerous targets for these factors, helping us unravel the mystery of

their contribution in normal tissues. This can be the necessary step in order to clarify to which extent they exert pivotal roles in cancer development^[17].

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