

REVIEW

p63 and p73 in human cancer: defining the network

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The *p53*-related genes *p63* and *p73* exhibit significant structural homology to *p53*; however, they do not function as classical tumor suppressors and are rarely mutated in human cancers. Both *p63* and *p73* exhibit tissue-specific roles in normal development and a complex contribution to tumorigenesis that is due to their expression as multiple protein isoforms. The predominant *p63/p73* isoforms expressed both in normal development and in many tumors lack the conserved transactivation (TA) domain; these isoforms instead exhibit a truncated N-terminus (Δ N) and function at least in part as transcriptional repressors. *p63* and *p73* isoforms are regulated through both transcriptional and post-translational mechanisms, and they in turn regulate diverse cellular functions including proliferation, survival and differentiation. The net effect of *p63/p73* expression in a given context depends on the ratio of TA/ Δ N isoforms expressed, on physical interaction between *p63* and *p73* isoforms, and on functional interactions with *p53* at the promoters of specific downstream target genes. These multifaceted interactions occur in diverse ways in tumor-specific contexts, demonstrating a functional ‘*p53* family network’ in human tumorigenesis. Understanding the regulation and mechanistic contributions of *p63* and *p73* in human cancers may ultimately provide new therapeutic opportunities for a variety of these diseases.

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Introduction

The *p53* tumor suppressor functions as a key nodal point that integrates upstream signals and directs the response to DNA damage, oncogenic stress and other cellular stress conditions (Vogelstein *et al.*, 2000; Vousden, 2000). The tumor-suppressive property of *p53* is most closely linked to its ability to transactivate a diverse variety of downstream target genes involved in the regulation of cell-cycle progression, apoptosis, DNA repair and other functions (Vogelstein *et al.*, 2000).

Most human tumors exhibit inactivation of *p53*, either through direct mutation or deletion of *p53* itself, or through disruption of regulatory pathways essential for *p53* function.

The identification of the two *p53*-related genes, *p63* and *p73*, initially provoked speculation that all three genes might play an analogous role in human tumors (Yang and McKeon, 2000; Melino *et al.*, 2003; Moll and Slade, 2004). In particular, the striking homology among the family members within both their DNA-binding domain (DBD) and oligomerization domain (OD) suggested that these genes might regulate transcription of a common subset of target genes, by binding to common promoters as either homo- or heterotetrameric complexes. Work in the ensuing years, however, has revealed a much more complex picture of the contribution of *p63* and *p73* to human cancer. In contrast to *p53*, *p63* and *p73* have essential roles in normal development, they are most commonly expressed as N-terminally truncated isoforms, and they are rarely mutated in human tumors. In addition, the expression and function of *p63* and *p73* are regulated through distinct mechanisms that are only beginning to be understood. Nevertheless, a substantial body of evidence supports a contribution of *p63* and *p73* in many human tumors through both *p53*-dependent and *p53*-independent pathways.

Gene structure of functional domains of the *p53* family transcription factors

Although *p63* and *p73* are the more recently identified *p53* family members, a *p63/p73*-like gene is considered to be the ancestral gene of the family (Yang *et al.*, 2002). The proteins encoded by these two genes are more structurally similar to each other than to *p53*; however, all three family members possess several conserved protein domains (Figure 1). These include an N-terminal transactivation (TA) domain, a central DBD, and an OD (Yang and McKeon, 2000). The highest degree of homology among the three members is observed within the DBD (> 60% amino-acid identity between *p53* and both *p63* and *p73*, and ~85% amino-acid identity between *p63* and *p73*), including conservation of all essential DNA contact residues (De Laurenzi and Melino, 2000). These structural similarities allow for both physical and functional interactions among all three family members that are relevant in human cancer.

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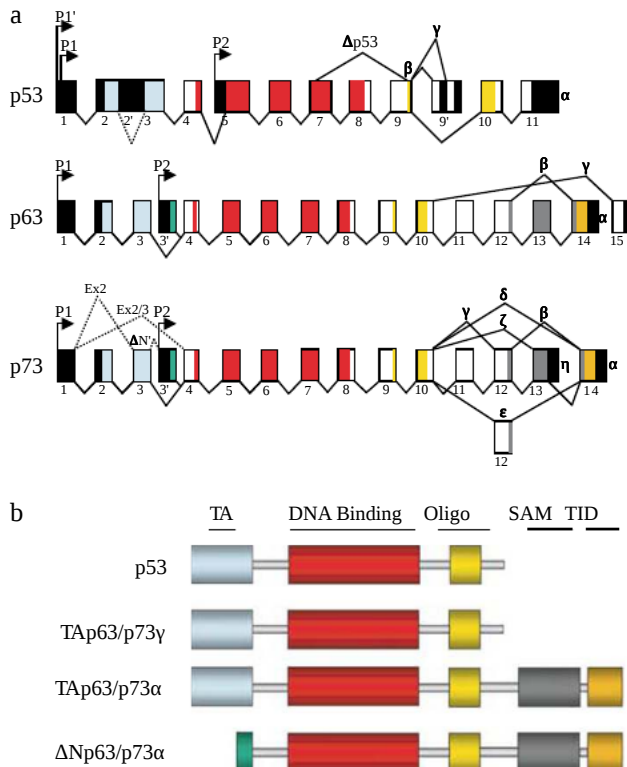


Figure 1 Structure and expression of p53 family members. (a) Structure of p53, p63 and p73 transcription units. Numbered boxes indicate exons, and black shading denotes untranslated sequences. The approximate regions encoding the transactivation (TA) domain (light blue), DN-specific region (green), DNA-binding domain (red), oligomerization domain (yellow), sterile alpha motif (SAM, grey), and transactivational inhibitory domain (TID, orange) are indicated. Distinct transcription start sites are indicated by arrows. N-terminal alternative splicing for p53 and p73 are indicated by dotted lines, and C-terminal splicing events for all p53 family members are indicated by solid lines and Greek letter designation. (b) Protein domains of p53 family members. All three family members share a homologous DNA-binding domain and oligomerization domain (oligo). The TA domain is shared by p53, TAp63, and TAp73 isoforms. TAp63g/TAp73g isoforms most closely resemble p53. N-terminally truncated DN isoforms possess unique N-terminal sequences. Alpha isoforms of p63 and p73 possess a C-terminal SAM domain followed by a transactivational inhibitory domain (TID). Other isoforms of p53, p63 and p73 are not shown.

Alternative promoter usage produces functionally distinct classes of p53, p63 and p73 isoforms

All three members of the *p53* gene family give rise to multiple protein products resulting from both alternative promoter usage and alternative mRNA splicing (Figure 1). Transcription of both *p63* and *p73* can occur from two distinct promoters: one upstream of exon 1 (P1) and another located within intron 3 (P2). Isoforms transcribed from P1 contain an N-terminal acidic TA domain (TAp63 and TAp73), which is highly homologous to the TA domain of full-length p53, whereas genes transcribed from P2 lack the N-terminal TA domain (DNp63 and DNp73) (Kaghad *et al.*, 1997; Yang *et al.*, 1998). In addition, 5⁰ exon splicing within the P1

transcripts of *p73* gives rise to additional mRNA isoforms whose protein products also lack the TA domain (DN⁰p73, Ex2Delp73 and Ex2/3Delp73) (Fillipovich *et al.*, 2001; Ishimoto *et al.*, 2002; Stiewe and Putzer, 2002). Recently, it has been reported that *p53*, which for many years was thought to encode a single protein product, also produces multiple isoforms through the use of two promoters and alternative mRNA splicing (Bourdon *et al.*, 2005). When over-expressed, TAp63 and TAp73 proteins are capable of transactivating distinct but overlapping subsets of known p53-regulated genes involved in cell-cycle arrest and apoptosis (Zhu *et al.*, 1998; Dohn *et al.*, 2001; Melino *et al.*, 2002). Both TAp63 and TAp73 also regulate independent sets of genes that are not transcriptional targets of p53 (Barbieri and Pietenpol, 2006; Harms *et al.*, 2004). In contrast, DNp63 and DNp73 proteins have been shown to function in part as dominant-negative inhibitors of the p53 family, leading to the hypothesis that these isoforms may exhibit proto-oncogenic function. Inhibition by DN isoforms occurs both through direct competition for DNA-binding sites and through formation hetero-oligomeric complexes with TAp63/TAp73, and less strongly with p53 (Yang *et al.*, 1998; Grob *et al.*, 2001; Stiewe *et al.*, 2002; Chan *et al.*, 2004). Recent studies by several groups have demonstrated that DNp63 is also capable of activating transcription through a cooperative effect of a DNp63-specific, N-terminal TA domain and a C-terminal proline-rich region (Ghioni *et al.*, 2002; Helton *et al.*, 2006). Although no analogous C-terminal domain has been identified in DNp73 isoforms, one study suggests that these isoforms may also contain an N-terminal TA domain (Liu *et al.*, 2004). Like TAp63, DNp63 activates a group of genes that includes but is not restricted to genes regulated by p53 (Dohn *et al.*, 2001).

C-terminal mRNA splicing generates additional structural and functional diversity

C-terminal splicing of both p63 and p73 transcripts generates a variety of TA and DN isoforms whose distinct functional contributions are only beginning to be understood (Figure 1). To date, at least seven C-terminal isotypes have been identified for p73; three have been identified for p63, and two for p53 (Moll and Slade, 2004; Bourdon *et al.*, 2005). The TAp63a and TAp73a isoforms are the largest proteins in each family. Internal alternative exon splicing generates the additional isoforms of p73, whereas both internal splicing and alternative 3⁰ exon usage generate p63 C-terminal isoforms. In addition, splicing-associated frameshifts yield unique C-terminal sequences for some p63 and p73 isoforms (Courtois *et al.*, 2004; Moll and Slade, 2004).

These distinct C-termini are thought to modulate the ability of the respective TA isoforms to transactivate gene expression. The TAp63g and TAp73g isoforms most closely resemble full-length p53. In overexpression studies, TAp63g has been shown to be as potent as p53

in inducing target gene expression and apoptosis, whereas the most potent transactivating p73 isoform appears to be TAp73b (Kaghad *et al.*, 1997; Yang *et al.*, 1998). Both p63a and p73a isoforms also contain a protein–protein interaction domain known as the sterile alpha motif (SAM) (Thanos and Bowie, 1999). The SAM is a globular domain composed of four α -helices and a small 3_{10} -helix. Although this motif is often found to mediate homodimerization within developmentally regulated proteins, in p53 family members the SAM domain is thought to be monomeric (Chi *et al.*, 1999b). An additional post-SAM region known as the transactivational inhibitory domain (TID) has been identified in p63a and p73a isoforms (Serber *et al.*, 2002). This region (~70 amino acids) has been proposed to inhibit the transcriptional activity of both TAp63a and TAp73a through inter- or intra-molecular association with the TA domain (Serber *et al.*, 2002). Indeed, both TAp63a and TAp73a isoforms have decreased potency in transactivation and apoptosis induction compared to other TA isoforms, and deletion of this region restores transactivation potency of both TAp73a and TAp63a (De Laurenzi *et al.*, 1998; Yang *et al.*, 1998; Serber *et al.*, 2002). The presence of this domain within DNp63a and DNp73a isoforms may allow trans-repression of associated TA isoforms, thereby explaining the potent inhibitory effect of DNp63a and DNp73a isoforms when bound to DNA as hetero-tetramers composed of both DNa and TA α isoforms (Serber *et al.*, 2002).

Tissue-specific roles for p63 and p73 in normal development

p63 is expressed in a highly restricted pattern during embryonic development. Its expression is first detectable within the primitive ectoderm, which gives rise to the epidermis as well as epithelial appendages including the mammary gland, prostate, teeth and sweat glands. p63 is also expressed in the apical ectodermal ridge, a specialized cluster of ectodermal cells required for inductive events during limb formation (Mills *et al.*, 1999; Yang *et al.*, 1999). Remarkably, p63 is essential for the development of most tissues in which it is expressed, as p63-null mice exhibit profound developmental abnormalities of the skin, limbs, mammary, prostate and other epithelial tissues (Mills *et al.*, 1999; Yang *et al.*, 1999). This ectodermal phenotype is recapitulated in humans who inherit a variety of heterozygous mutations in p63 that are thought to function as dominant-negative or potentially dominant gain-of-function alleles (van Bokhoven and Brunner, 2002).

Little overlap is observed in the embryonic expression patterns of p63 and p73, consistent with the distinct developmental phenotype associated with p73 nullizygosity. Expression of p73 is most prominent within discrete structures of the developing brain, and within the sympathetic superior cervical ganglia. p73-null animals demonstrate hippocampal dysgenesis,

hydrocephalus owing to probable hypersecretion from the choroid plexus, and chronic infection and inflammation likely owing to hypersecretion of mucous from the respiratory mucosa (Pozniak *et al.*, 2000; Yang *et al.*, 2000). These mice also exhibit abnormal social and reproductive behavior attributed to failed development of the vomeronasal organ that is essential for detection of pheromonal signaling (Yang *et al.*, 2000).

The contribution of individual p63 and p73 isoforms to their respective developmental phenotypes remains to be firmly established. Although mRNA for both TAp63 and TAp73 are detectable during embryogenesis, the predominant isoforms of both p63 and p73 expressed during development are the N-terminally truncated DN isoforms (Yang *et al.*, 1998, 2000; Pozniak *et al.*, 2000). As discussed below, these isoforms are also the predominant forms expressed in many human cancers, and they are therefore likely to contribute importantly to p63- and p73-dependent functions in tumorigenesis. Nevertheless, the fundamental mechanisms of endogenous DNp63 and DNp73 isoforms in development and tumorigenesis are poorly understood. Among the most central questions in this regard are (1) whether these isoforms function exclusively as repressors and to what degree they may have important roles as transcriptional activators; (2) whether their repressive function is directed toward their respective TA isoforms, toward another family member, or independently of the other family members; and (3) whether these isoforms perform analogous roles in normal development and tumorigenesis.

Expression and mutation of p63 and p73 in human cancer

DNp63a is commonly overexpressed in squamous epithelial malignancies

Both p63 and p73 were initially hypothesized to function as tumor suppressors based on their homology to p53. However, mutation of either of these genes in human cancer is quite rare ($\alpha 1\%$) (Hagiwara *et al.*, 1999; Sunahara *et al.*, 1999; Melino *et al.*, 2002). In fact, the p63 gene maps to chromosome 3q27–28, a region frequently amplified in squamous cell carcinomas (Bjorkqvist *et al.*, 1998; Hibi *et al.*, 2000; Massion *et al.*, 2003). Although some controversy exists as to whether p63 is the targeted gene driving amplification of this locus, several groups have reported increased wild-type p63 mRNA levels that correlate with an increase in p63 gene copy number in squamous cell carcinomas of the lung and head and neck (Table 1) (Hibi *et al.*, 2000; Tonon *et al.*, 2005). In other cases, overexpression of p63 appears to involve mechanisms independent of genomic amplification (Redon *et al.*, 2001). In any event, numerous studies have demonstrated p63 overexpression in up to 80% of primary head and neck squamous cell carcinomas (HNSCCs), and p63 overexpression is also commonly observed in other squamous epithelial cancers, including lung, nasopharyngeal, esophageal and cervical cancers (Wang *et al.*, 2001;

Table 1 Expression levels of p63 and p73 in cancer tissues (tumor vs normal)

Cancer type	TAp63	DNp63	TAp73	DNp73	Correlation with p53 ^b	References ^c
SCC ^d	rare	mm	mm	NC	p63 (variable)	A–D
Cervical	NC	mm	m	m	ND	E, F
Breast	mf	m ^e	m	m	p73 (variable)	G–I
Bladder ^e	NC	mm	m	ND	No (p63)	J, K
Neuroblastoma	ND	ND	m	m	ND	L, M
Glioma	ND	ND	mm	mm	ND	N, O
Ependymoma	ND	ND	mmf	mmf	ND	N
Colon	NC	Neg	m	m	p73	I, P
Gastric	mf	m ^e	mm	ND	No (p63 & p73)	Q
Ovary	ND	ND	m	mm	p73	R
Hepatocellular	Neg	Neg	m	m	No (p73)	S, T
Cholangiocarcinoma	mmf	mmf	m	ND	ND	T
CML	mm	Rare	mm ^e	mmf	ND	U, V
AML	ND	ND	mm	mm	ND	W
CLL	ND	ND	mm	mm	ND	X
Lymphoma ^f	mm	Neg	mm	mm	No (p73)	Y, Z

m, upregulation (T > N) in p50% of specimens; mm, upregulation in > 50% of specimens. Abbreviations: SCC, squamous-cell carcinoma; CML, chronic myeloid leukemia; AML, acute myeloid leukemia; CLL, chronic lymphoid leukemia; NC, no change in expression between tumor and normal tissues; ND, not determined; Neg, no expression detected in tumor and normal tissues. Refers to p73 isoforms that lack the TA domain (DNp73, DN⁰p73, Ex2Delp73, and Ex2/3Delp73).^bCorrelation between wild type p53 status and overexpression of the indicated p53 family member. Variable results between independent studies are noted. Select references are representative of the existing literature. References: A, Choi *et al.* (2002); B, Massion *et al.* (2003); C, Cui *et al.* (2005); D, Tokuchi *et al.* (1999); E, Wang *et al.* (2001); F, Liu *et al.* (2006); G, Ribeiro-Silva *et al.* (2005); H, Dominguez *et al.* (2001); I, Dominguez *et al.* (2006); J, Park *et al.* (2000); K, Chi *et al.* (1999a); L, Kovalev *et al.* (1998); M, Douc-Rasy *et al.* (2002); N, Kamiya and Nakazato (2002); O, Wager *et al.* (2006); P, Nylander *et al.* (2002); Q, Tannapfel *et al.* (2001); R, Concin *et al.* (2004); S, Muller *et al.* (2005); T, Ramalho *et al.* (2006); U, Yamaguchi *et al.* (2001); V, Peters *et al.* (1999); W, Rizzo *et al.* (2004); X, Leupin *et al.* (2004); Y, Zamo *et al.* (2005); Z, Cuadros *et al.* (2006).^dIncludes head and neck, lung, nasopharyngeal, and esophageal SCCs.^eLoss of p63 and/or p73 expression occurs in advanced stages and correlates with poor prognosis. Loss of p73 expression in a subset of specimens due to P1 promoter methylation.^fAnalyses did not discriminate between TA and DN isoforms.

Hu *et al.*, 2002; Weber *et al.*, 2002; Massion *et al.*, 2003; Sniezek *et al.*, 2004). Reports have varied as to the frequency of p63 expression in invasive breast carcinomas, with studies ranging from 0 to 30% (Wang *et al.*, 2002; Reis-Filho *et al.*, 2003; Koker and Kleer, 2004; Ribeiro-Silva *et al.*, 2005). It now seems clear, however, that p63 is expressed in at least a subset of breast tumors that are known to exhibit a basal epithelial phenotype (Perou *et al.*, 2000).

Although early studies of p63 expression used techniques that do not discriminate among different isoforms, several recent reports have used quantitative isoform-specific reverse transcription-polymerase chain reaction (RT-PCR) coupled with immunoblot analysis to demonstrate that DNp63a is the predominant p63 isoform expressed in squamous cell carcinomas (Table 1). Using such an approach, we recently found that TAp63 overexpression is rare in primary HNSCC tumors and tumor-derived cell lines, and that DNp63 mRNA expression was at least 100-fold more abundant than TAp63 mRNA expression in all cases (DeYoung *et al.*, 2006; Rocco *et al.*, 2006). These findings are consistent with the inability of many investigators to detect TAp63 protein isoforms by immunoblot analysis in either primary keratinocytes or HNSCC cells. One exception to the consistent overexpression of p63 observed in tumor cells is in bladder cancer. Whereas one study showed that the majority of invasive carcinomas of the bladder overexpress DNp63, others found that a subset of such cancers demonstrate loss of p63 expression (Park *et al.*, 2000; Urist *et al.*, 2002; Koga *et al.*, 2003). In the latter cases, loss of p63

expression was associated with progression to invasion and metastasis and correlated with a poor prognosis. On the other hand, overexpression of DNp63a in squamous cell carcinomas of both the lung and head/neck has been shown to be a favorable indicator of response to therapy and overall clinical outcome (Massion *et al.*, 2003; Zangen *et al.*, 2005). One possible model to reconcile these findings would be that DNp63a contributes to the early stages of tumorigenesis while maintaining epithelial cell fate (Green *et al.*, 2003; Troung *et al.*, 2006). In contrast, loss of p63 may mark tumors that have accumulated additional genetic events and have acquired mesenchymal properties, both of which are correlated with a refractory clinical behavior (Barbieri *et al.*, 2006).

Overexpression of multiple p73 isoforms is observed in diverse human cancers

Like p63, p73 was initially hypothesized to function as a classical tumor suppressor gene. This supposition was based both on its homology to p53 and its cytogenetic locus, 1p36.33, which is commonly deleted in a variety of cancers (Kaghad *et al.*, 1997). Subsequent studies have clearly demonstrated that p73 is not the target of deletion at this site. Furthermore, extensive mutational analysis has failed to demonstrate a significant frequency of p73 mutation in human tumors (0.10%) (Melino *et al.*, 2002; Moll and Slade, 2004). Studies of multiple tumor types have demonstrated that p73 is overexpressed, rather than mutated or deleted in human cancer. Overexpression of p73 mRNA and/or protein

relative to the respective normal tissues has been demonstrated in a large variety of tumor types, including neuroblastoma, glioma, breast, lung, colon, stomach, ovarian, bladder, liver, HNSCC, cholangiocellular carcinoma, ependymoma, chronic myelogenous leukemia and acute myelogenous leukemia (Table 1) (Moll and Slade, 2004). Many of these studies measured p73 mRNA using semiquantitative approaches and did not examine expression of multiple isoforms. Recent work, however, has provided more comprehensive expression analysis of p73 isoforms. These include TAp73 produced by the P1 promoter and DNp73 produced by the P2 promoter. Additional P1-transcribed N-terminal splice variants exist (DN⁰p73, Ex2-Delp73 and Ex2/3Delp73) and are all predicted to encode proteins lacking the TA domain (Stiewe *et al.*, 2002; Zaika *et al.*, 2002; Concin *et al.*, 2004). One recent study compared isoform-specific p73 expression levels in a large panel of ovarian tumors. DN⁰p73 and TAp73 mRNA were found to be co-upregulated in a substantial fraction of tumor samples compared to normal tissues (Concin *et al.*, 2004). Similarly, in primary rhabdomyosarcomas and tumor-derived cell lines, DNp73 and TAp73 protein isoforms are co-upregulated compared to normal muscle (Cam *et al.*, 2006). Consistent with an important function for truncated p73 isoforms, overexpression of the N-terminal splice variants, but not TAp73 mRNA, was shown to convey a poor prognosis in low-grade gliomas, and was associated with advanced stage in breast and colon carcinomas (Dominguez *et al.*, 2006; Wager *et al.*, 2006). Of note, methylation-induced silencing of the P1 (TAp73) promoter has been found in lymphoblastic leukemias and Burkitt's lymphoma (Corn *et al.*, 1999; Kawano *et al.*, 1999). Together with functional data discussed below, these findings imply that either DNp73/DNp63 overexpression or TAp73 promoter silencing may be required to inactivate a tumor-suppressive property of TAp73. In agreement with this view are our recent findings in squamous cell carcinomas. Although TAp73 isoforms were found to be dramatically overexpressed (18–30-fold) in HNSCC-derived cell lines and primary tumors compared to normal basal epithelia, DNp63a was also overexpressed in these tumors and was physically associated with TAp73, thereby inhibiting p73-dependent proapoptotic activity (DeYoung *et al.*, 2006; Rocco *et al.*, 2006).

Mechanisms of p63 and p73 of potential relevance to tumorigenesis

Cooperation and competition occur among p53 family isoforms

A complex picture emerges when trying to define the precise contribution of either p63 or p73 to tumor development. As demonstrated above, a major part of this complexity stems from the expression of both DN and TA isoforms of p63 and p73 in many human tumors. Studies described below support the view that TAp63/TAp73 isoforms, like p53, exhibit tumor-

suppressive properties, and that upregulation of DNp63/DNp73 isoforms is a common mechanism of their inactivation during tumorigenesis. Indeed, important physical and functional interactions among family members have now been demonstrated in tumor-specific contexts. These diverse interactions are mediated through two general mechanisms. First, cooperation and competition at the conserved p53 family binding sites within promoters of particular shared target genes are likely to regulate interactions among all three family members (Flores *et al.*, 2002; Stiewe *et al.*, 2002; Yang *et al.*, 2006). Second, direct physical interaction of isoforms is known to alter the function of the tetrameric complex required for DNA-binding and transcriptional regulation (Chan *et al.*, 2004). In ectopic expression studies, heteromeric complexes have been demonstrated between different isoforms of the same gene, between TAp63 and DNp73 isoforms, and between TAp73 and DNp63 isoforms (Chan *et al.*, 2004). In each case, the respective DN isoforms function as potent inhibitors of transactivation by the respective TA isoforms. Consistent with these findings, endogenous complexes have also been demonstrated between different p73 isoforms, and between DNp63 and TAp73 (DeYoung *et al.*, 2006; Rocco *et al.*, 2006). Wild-type p53 binds p63 and p73 with much lower affinity than p63 and p73 bind one another (Davison *et al.*, 1999). Despite the absence of a strong physical interaction, however, it seems highly plausible that in some tumor contexts both DNp63 and DNp73 serve to inhibit the function of p53 through promoter competition or other indirect mechanisms (Stiewe *et al.*, 2002).

Proliferation and differentiation are regulated by p63 and p73 in tumor cells

In normal basal epithelial cells, DNp63a promotes proliferation through regulation of shared p53 target genes such as p21^{Cip1}, and likely through other pathways as well (Patturajan *et al.*, 2002; Westfall *et al.*, 2003). Whether these effects depend entirely on the ability of p63 to functionally repress p53 is unclear, as studies have reached different conclusions using different strategies to ablate both p63 and p53 in human and mouse cells (Keyes *et al.*, 2005; DeYoung *et al.*, 2006; Troung *et al.*, 2006). Nevertheless, the ability of DNp63a to enhance proliferation and suppress cellular senescence during development suggests a possible contribution of p63 early in tumorigenesis (Keyes *et al.*, 2005). In addition to promoting proliferation, the expression of DNp63a is closely linked to the undifferentiated state in basal epithelial cells, and DNp63a expression is rapidly downregulated in normal cells during the course of differentiation (Parsa *et al.*, 1999; Green *et al.*, 2003). Although the mechanisms by which p63 may influence differentiation remain largely speculative, some evidence has been provided that TAp63 may directly control the expression of p53-independent genes required for keratinocyte differentiation, including loricrin and involucrin (De Laurenzi *et al.*, 2000). p63 isoforms could conceivably also regulate differentiation through

p53-independent effects on adhesive signaling, Notch activation, and regulation of Rb phosphorylation (Cam *et al.*, 2006; Carroll *et al.*, 2006; Nguyen *et al.*, 2006).

Despite their remarkably similar structures, p63 and p73 appear to regulate largely non-overlapping sets of cell-cycle regulatory genes. Although overexpression of TAp73 isoforms leads to induction of p63-regulated cell-cycle inhibitors, it is unclear whether most of these genes are direct targets of endogenous p73 (Harms *et al.*, 2004). However, the cyclin-dependent kinase inhibitor p57^{Kip2} is a well-established target gene of p73 (Blint *et al.*, 2002). Recent evidence has linked regulation of p57^{Kip2} to a differentiation effect mediated by DNp73. Thus DNp73, which is overexpressed in rhabdomyosarcoma cells, was shown to block both cell-cycle exit and differentiation of murine myoblasts (Cam *et al.*, 2006). These effects were shown to be owing to the ability of DNp73 to suppress p57^{Kip2} expression, resulting in pRb inactivation and a consequent block in myogenic differentiation (Cam *et al.*, 2006). Notably, both DNp73-dependent repression of p57^{Kip2} and DNp63a-mediated repression of p21^{Cip1} are at least in part owing to direct promoter binding rather than physical interaction with p53 or TAp63/73 isoforms. This example demonstrates that effects of DN isoforms in tumors are not mediated exclusively through a trans-repression effect on TA isoforms. As described below, however, repression through physical interaction with other family members appears to be an additional important mechanism by which DNp63 and DNp73 contribute to tumorigenesis.

Mouse models point to apoptosis regulation as a tumor-suppressive role for p63 and p73

Both p63 and p73 isoforms contribute to the regulation of cell survival and apoptosis in human tumors (Moll and Slade, 2004). Indeed, their ability to regulate apoptosis is clearly a major mechanism by which these genes contribute to human tumorigenesis (Rocco *et al.*, 2006). Initial studies in mice demonstrated the proapoptotic activity of endogenous p63 and p73. Germline deletion of *p63* or *p73* yielded mouse embryo fibroblasts (MEFs) that were less sensitive to DNA damage-induced apoptosis than wild-type cells when transfected by adenoviral E1A protein (Flores *et al.*, 2002). This phenotype was recapitulated in the embryonic mouse brain *in vivo*. Defective apoptosis observed in these mice is likely to reflect loss of the respective proapoptotic TA isoforms, which are the predominant isoforms induced in these cells following DNA damage. In agreement with this notion, reconstitution of TAp63 or TAp73, but not DNp63 or DNp73 isoforms into the respective null MEFs rescued apoptosis following doxorubicin treatment to some degree. Subsequent studies in mice with heterozygous deletion of *p63* or *p73* further supported the hypothesis that inactivation of these genes leads to a tumor-prone phenotype, potentially by disabling apoptosis (Flores *et al.*, 2005). Both *p63* and *p73* heterozygous mice developed spontaneous tumors characterized in most cases by loss of the

respective wild-type alleles (Flores *et al.*, 2005). Although these studies seemed to point to a clear role for these genes as tumor suppressors, their lack of mutation in human tumors fails to support this notion. In addition, mice harboring a distinct targeted *p63*-null allele did not develop tumors (Keyes *et al.*, 2006). In fact, these animals demonstrated a decreased incidence of tumors and accelerated features of aging. This phenotype was reminiscent of that induced following germline expression of a hypermorphic mutant p53 (Tyner *et al.*, 2002), and was seemingly the opposite of the phenotype expected following loss of a tumor suppressor. These disparate results might be attributable to differences in the p63 gene-targeting approach or to other factors (Mills, 2006).

Multiple mechanisms lead to tumor-specific inactivation of proapoptotic TAp73

Whether p63 and p73 promote or inhibit human tumorigenesis may depend on the predominant isoform(s) expressed in a given tissue. Most studies concur that TAp73 isoforms exhibit proapoptotic activity and potentially other suppressor properties in tumor cells. For example, several studies have demonstrated that TAp73 is specifically activated and is an important mediator of apoptosis following chemotherapy-induced DNA damage (Gong *et al.*, 1999; Yuan *et al.*, 1999; Irwin *et al.*, 2003). As discussed below, the ability of certain mutant p53 species to specifically inactivate TAp73 provides additional evidence for their anti-tumorigenic properties. Furthermore, p73 is silenced in a number of tumor types through methylation, as described above. Finally, overexpression of DNp63 and DNp73 isoforms appears to be an important and common mechanism for inhibiting the proapoptotic activity of TAp73 in human tumors. Indeed, DNp73 isoforms have been demonstrated to suppress apoptosis induced by expression of either E1A or c-Myc in primary fibroblasts (Petrenko *et al.*, 2003). This effect seems at least in part to be owing to transdominant inhibition of p53, and potentially TAp73 and TAp63. Similarly, the DNp63a isoform functions as a survival factor in certain tumors including squamous cell carcinomas, at least in part through its ability to suppress TAp73, which is highly upregulated in these same tumors (Rocco *et al.*, 2006).

In addition to expression of DNp63/p73 isoforms, another important mechanism of TAp73 inhibition in tumor cells is through expression of particular p53 mutant proteins. In contrast to the weak binding of wild-type p53, significant binding has been reported between p63/p73 and certain p53 mutants harboring mutations within the DBD (Di Como *et al.*, 1999; Gaiddon *et al.*, 2001). Rather than binding through the OD, however, interaction with these mutant p53 proteins and p63/p73 occurs through the p53 DBD and the OD of p63/p73 (Gaiddon *et al.*, 2001). Furthermore, this interaction is regulated by a common Arg/Pro polymorphism at codon 72 of p53. Cancer-associated mutants of p53 that harbor the 72R

polymorphism interact more strongly and are therefore more effective inhibitors than those expressing 72P (Marin *et al.*, 2000). This interaction has been shown to inhibit the function of p63/p73 in part through down-regulation of their protein expression. The presence of such mutant p53 forms has been shown to inhibit the ability of p73 to mediate apoptosis during the DNA damage response, thereby promoting chemotherapy resistance (Bergamaschi *et al.*, 2003). In a mouse model, germline knock-in of the p53R175H DBD mutation enhanced cellular transformation through an inhibitory effect on p63 and p73 (Lang *et al.*, 2004). In human head and neck cancers, p53 mutations in the context of 72R have been correlated with an inferior clinical outcome (Bergamaschi *et al.*, 2003). In addition to providing a new twist on the mechanisms of mutant p53, these data provide further support for the contention that inhibiting certain functions of p63 and p73 may be important to promote both tumorigenesis and resistance to therapy. Conceivably, these observations might also explain at least in part why p53 is so commonly targeted for mutation rather than degradation in tumors. Finally, these findings suggest that mutant p53 could in some cases be an attractive therapeutic target, because eliminating its inhibitory function might activate a tumor-suppressive function of p63 and/or p73.

A p53/p63/p73 functional network contributes to squamous carcinogenesis

These numerous and diverse potential functional interactions among the three p53 family members are manifest in distinct, tumor-specific contexts. One example that illustrates this principle is HNSCC (Figure 2). As previously noted, these tumors commonly overexpress DNp63a relative to normal basal epithelial cells. Initially it was speculated that this p63 isoform might inhibit p53 function, thereby abrogating the requirement for p53 mutation in these tumors. Although an initial study supported this possibility (Hibi *et al.*,

2000), subsequent reports have not demonstrated a consistent correlation between p63 overexpression and wild-type p53 status in these tumors (Hibi *et al.*, 2000; Choi *et al.*, 2002; Sniezek *et al.*, 2004). Instead, recent studies by our group and others have suggested that DNp63a functions as an essential repressor of TAp73, rather than p53 in these tumors. Knockdown of DNp63a by RNA interference (RNAi) induces cell death that is p53-independent but is instead mediated by TAp73. In HNSCC cells, DNp63a binds TAp73, thereby blocking its ability to transactivate proapoptotic bcl-2 family members and to induce cell death (Rocco *et al.*, 2006). Consistent with this model, tumor-derived cell lines that lacked DNp63a expression instead exhibited high-level bcl-2 expression, which was sufficient to block TAp73-dependent apoptosis in these cells. Notably, the DNp63a-dependent survival pathway appears tumor-specific, as TAp73 is not highly expressed in primary basal epithelia (Carroll *et al.*, 2006). The absence of significant TAp73 expression in normal primary cells may explain why p63 inhibition in these cells triggers senescence rather than the high levels of cell death observed in tumor cells (DeYoung *et al.*, 2006). In an ironic twist, the requirement for DNp63a to suppress TAp73-dependent apoptosis in HNSCC cells may in fact explain why a correlation has been observed in some studies between p53 mutation and absence of DNp63a overexpression in these tumors. As mentioned above, it is predicted that certain p53 mutant proteins that also contain the 72R polymorphism are able to functionally inhibit TAp73. Therefore, tumors that express these particular mutant p53 proteins may not require DNp63a upregulation to inhibit TAp73 (Figure 2). As a result, low DNp63a expression might be predicted in tumors that express this subset of p53 mutant proteins. Although confirmation of such an association awaits further studies, collectively these data demonstrate the existence of a functional p53 family network relevant to human cancer.

Upstream regulation of p63 and p73 transcription

Oncogenic stress induces TAp73 expression

As illustrated by the above examples, regulation of p63 and p73 expression in different tumor and tissue types dictates to a large degree how these genes contribute to human cancer. Both p63 and p73 exhibit transcriptional regulation through distinct, largely non-overlapping upstream pathways. Although most studies have focused their attention on the P1 promoters of p63 and p73 that drive expression of the respective TA isoforms, recent work has begun to explore the internal promoters found within intron 3 (P2) that regulate transcription of DNp63 and DNp73. Thus far, it appears that the P1 and P2 promoters of both genes possess distinct regulatory elements. In the case of p73, endogenous TAp73a and TAp73b are known to be induced by oncogenic stress through activation of E2F-1 and potentially c-Myc, as well as expression of the viral oncoprotein E1A (Melino

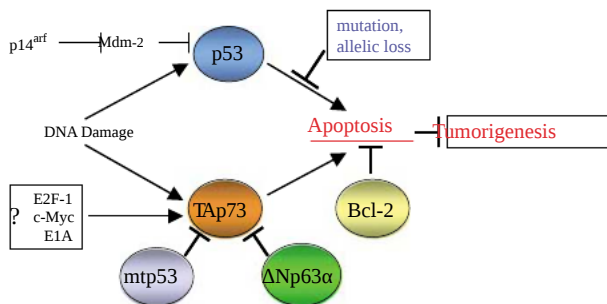


Figure 2 Pathways involving the p53 family functional network in squamous cell carcinoma. DNA damage and oncogenic stress (through p14^{arf}) trigger p53 activation, leading to selective pressure for its mutation or loss to avoid apoptosis. Similarly, DNA damage and potentially oncogenic stress induce TAp73 expression and activation. TAp73 activity can be suppressed through overexpression of DNp63a or certain missense p53 mutants (mtp53). Alternatively, apoptosis can be averted in DNp63a-negative tumors through overexpression of bcl-2, which inhibits the proapoptotic function of TAp73 target genes.

et al., 2002). E2F-1 regulates TAp73 transcription directly by binding to E2F sites within the P1 promoter (Irwin *et al.*, 2000; Seelan *et al.*, 2002). The view that TAp73 is an important endogenous E2F-1 target gene is supported by recent work on the mechanism by which E1A increases TAp73 levels. E1A expression in tumor cells induces both TAp73 mRNA and protein, and this induction is dependent on both the Rb-binding domain within E1A and the E2F-1-binding site within the p73 P1 promoter (Flinterman *et al.*, 2005). Furthermore, E1A-induced activation of p73 is sufficient to cause apoptosis in p53-mutant tumor cells, in keeping with the notion that activation of p73 in this setting is functionally relevant (Flinterman *et al.*, 2005). Additional evidence suggests that E2F-1-dependent transcription of TAp73 may be important to the DNA damage response in p53-mutant cells. The checkpoint kinases Chk1 and Chk2 can regulate TAp73 transcription following genotoxic insults via stabilization and consequent activation of E2F-1 (Urist *et al.*, 2004). The role of the E2F-1-TAp73 pathway in normal cells is more controversial, as different experimental approaches have led to different conclusions as to whether induction of p73 is required *in vivo* for E2F-1-dependent apoptosis in lymphocytes (Wan and DeGregori, 2003; Senoo *et al.*, 2004). Another area of controversy is the role of c-myc in the regulation of TAp73 expression and activity. Studies have demonstrated the ability of c-myc to increase TAp73 protein levels, as well as the possibility of both negative and positive effects on p73-dependent transcription through physical interaction between c-myc and TAp73 (Zaika *et al.*, 2001; Uramoto *et al.*, 2002; Watanabe *et al.*, 2002). Finally, several studies have pointed to an important role for DNA methylation in the regulation of TAp73 expression. One intriguing example is methylation within the TAp73 first intron that affects sites for the ZEB transcriptional repressor (Fontemaggi *et al.*, 2001). Lack of ZEB binding as a result of methylation of its binding site appears to be a mechanism for tissue-specific regulation of TAp73 during cellular differentiation. In contrast to TAp73, few direct mechanisms that regulate transcription of TAp63 have been defined. It does seem clear, however, that TAp63 is not induced by prominent regulators of TAp73 such as E2F-1 (Waltermann *et al.*, 2003).

Expression of p63 and p73 is regulated through novel feedback loops

Several potential autoregulatory feedback loops have been proposed for the regulation of p53 family members. The P2 promoter of p73 has been shown to be positively regulated by p53 and TAp73, leading to the induction of DNp73 (Grob *et al.*, 2001; Nakagawa *et al.*, 2002). These findings imply a potential negative feedback loop that may restrict p53 and TAp73-dependent transcription. Both positive and negative regulation of DNp63 mRNA and protein have been shown by different groups to be mediated by both p53 and DNp63 itself (Harmes *et al.*, 2003; Waltermann *et al.*,

2003; Antonini *et al.*, 2006; Romano *et al.*, 2006). DNp63 may also be positively regulated by TAp63g in a manner that is independent of p53, suggesting yet another possible feedback mechanism (Li *et al.*, 2006). Additional feedback mechanisms with potential relevance to human cancer have been proposed and involve distinct p63 target genes. For example, DNp63a expression is promoted by epidermal growth factor receptor (EGFR) signaling through activation of the phosphatidylinositol 3-kinase (PI3K) pathway in both normal keratinocytes and SCC cells (Barbieri *et al.*, 2003; Matheny *et al.*, 2003). In turn, EGFR itself is a transcriptional target of p63 (Nishi *et al.*, 2001; Carroll *et al.*, 2006), implying positive feedback regulation through p63. Similarly, Notch signaling, which is important in many human tumors and which limits proliferation and promotes differentiation in keratinocytes, has been shown to inhibit DNp63a transcription. DNp63a, however, appears to function as a direct repressor of some Notch-induced genes, suggesting equilibrium between Notch and p63 activity in keratinocytes and potentially some cancers (Nguyen *et al.*, 2006). Detailed functional interrogation of these pathways in tumor cells will be important to define which of these interactions may be relevant in a cancer-specific context.

Regulation of p63 and p73 activity

Ubiquitin-like modifications regulate both p63 and p73
In addition to regulation through altered transcription, multiple post-translational mechanisms are being uncovered that regulate the expression and function of particular p63 and p73 isoforms. These mechanisms are likely to have important implications for future therapeutic targeting of p63 and p73 in human cancer. One emerging theme in p63/p73 regulation involves ubiquitin and ubiquitin-like modifications (Watson and Irwin, 2006). MDM2 is an E3 ubiquitin ligase that functions as an essential negative regulator of p53 through ubiquitination and subsequent proteasome degradation (Momand *et al.*, 2000). Notably, all three essential residues of p53 that contact MDM2 (F19, W23 and L26) are conserved in both TAp63 and TAp73 (Kussie *et al.*, 1996; Kaghad *et al.*, 1997; Yang *et al.*, 1998). Although it has been shown that MDM2 can associate with TAp73, MDM2 apparently does not induce ubiquitination or degradation even though it does inhibit p73 transcriptional activity (Balint *et al.*, 1999; Zeng *et al.*, 1999). A recent study suggests that MDM2-dependent inhibition of TAp73 may be required for cellular transformation. A short isoform of p21 ras, p19 ras, was found to suppress ras-induced transformation by abrogating the p73-MDM2 interaction, leading to p73 activation (Jeong *et al.*, 2006). Whether MDM2 associates significantly with p63 or plays a role in regulating p63 stability and activity remains inconclusive (Little and Jochemsen, 2001; Calabro *et al.*, 2002).

Additional E3 ubiquitin ligases have been found to interact with p73 and p63. NEDL2, a NEDD4-related E3 ubiquitin ligase has been shown to bind to a C-terminal proline-rich (PY) motif found in p73a and b isoforms (Miyazaki *et al.*, 2003). NEDL2-dependent ubiquitination of p73 promotes its stabilization and increased TAp73 transcriptional activity by an unknown mechanism. In contrast, another NEDD4-related E3 ligase named Itch has been shown to interact with the PY motif of endogenous p63a and p73a (both TA and DN isoforms), thereby promoting their proteasome-dependent degradation (Rossi *et al.*, 2005, 2006a, b). Itch does not interact with p53, which lacks a PY motif. Consistent with these findings, primary keratinocytes derived from Itch knockout mice have increased levels of DNp63a (Rossi *et al.*, 2006a). The p73a and p63a isoforms can also be regulated by conjugation with the small ubiquitin-like modifier SUMO-1. Sumoylation was shown to modestly inhibit the transcriptional activity of p73 and p63 (Minty *et al.*, 2000; Ghioni *et al.*, 2005). However, the relatively small fraction of total cellular p63 and p73 found to be sumoylated may not be sufficient to significantly inhibit their overall transactivational functions (Blandino and Dobbstein, 2004). Another unresolved issue regarding these findings is that neither the E3 ubiquitin nor SUMO ligases have been shown to clearly distinguish between TA and DN isoforms of p63 and p73.

Kinase-dependent pathways contribute to both positive and negative regulation of p63 and p73

Multiple phosphorylation events are likely to be important for regulation of p63 and p73 in both normal and tumor cells. TAp73, an important mediator of the DNA damage response in tumor cells, is phosphorylated at Tyr-99 by the c-Abl kinase in response to a subset of DNA damaging agents, potentiating p73-dependent apoptosis (Agami *et al.*, 1999; Gong *et al.*, 1999; Yuan *et al.*, 1999). Phosphorylation of p73 promotes its association with the prolyl isomerase Pin1, which in turn enhances acetylation of p73 by p300 (Mantovani *et al.*, 2004). Both p73 acetylation and its association with Pin1 have been shown to stabilize p73 following chemotherapeutic exposure. Another DNA damage-induced pathway for p73 regulation involves association of TAp73a with the checkpoint kinase Chk1 (Gonzalez *et al.*, 2003). This association results in Ser-47 phosphorylation of TAp73a and increased proapoptotic activity. Kinase-dependent signaling also contributes to negative regulation of TAp73 activity. Kinase pathways that appear to be involved in restraining p73 proapoptotic activity include the PI3K/AKT pathway, the PKA pathway and the CDK pathway (Basu *et al.*, 2003; Gaiddon *et al.*, 2003; Hanamoto *et al.*, 2005). One such example is phosphorylation-dependent regulation of the Yes-associated protein, YAP, a potent co-activator of p73-dependent transcription (Strano *et al.*, 2001). AKT-dependent inhibition of TAp73a involves phosphorylation of YAP, which promotes association of YAP with 14-3-3 and subsequent nuclear export

(Basu *et al.*, 2003). Data suggest that YAP might be particularly important in promoting the proapoptotic function of TAp73 following DNA damage (Strano *et al.*, 2005).

The precise contribution of phosphorylation to the regulation of DNp63 and DNp73 isoforms remains largely unknown. Increased phosphorylation of DNp63a at Ser-66/68 and Ser-361 was observed in response to ultraviolet (UV) radiation and chemotherapeutic exposure (Westfall *et al.*, 2005). This phosphorylation correlated with downregulation of DNp63a in epithelial cells following these stimuli. A similar effect was demonstrated following treatment with the chemotherapy agent cisplatin. DNp63a was phosphorylated in response to cisplatin treatment, which promoted its association with stratifin (also known as 14-3-3s) (Fomenkov *et al.*, 2004). This interaction was shown to mediate nuclear export of DNp63a into the cytoplasm where RACK1 (receptor for activated protein C kinase 1) targets DNp63a for proteasomal degradation. RACK1 itself does not contain any motifs characteristic of E3 ubiquitin ligases, but it remains conceivable that RACK1 facilitates the degradation of DNp63a by recruiting an unidentified E3 ubiquitin ligase. Of note, DNp73 is also known to undergo rapid downregulation following treatment with DNA damaging agents (Maisse *et al.*, 2004). Although it is unknown whether this degradation is phosphorylation-dependent, it was shown to be independent of the Itch ubiquitin ligase, which is itself downregulated following DNA damage (Rossi *et al.*, 2005). Despite many unanswered questions, a consistent picture emerges whereby certain forms of DNA damage induce an apoptotic response mediated at least in part through degradation of anti-apoptotic DN isoforms and stabilization of proapoptotic TA isoforms.

Oncogenesis versus tumor suppression mediated by p63 and p73

Collectively, the data summarized above point to important contributions of both p63 and p73 to human tumorigenesis. The complexity in defining their specific contribution results to a large degree from tissue- and tumor-specific differences in isoform expression. As noted above, defective apoptosis observed in p63- and p73-null mouse fibroblasts is likely to reflect loss of the respective proapoptotic TA isoforms (Flores *et al.*, 2002). Similarly, the tumor-prone phenotype of the respective heterozygous mice may be linked mechanistically to loss of these particular isoforms. Tumors arising in p63- and p73-heterozygous mice are known to exhibit loss of the respective wild-type alleles, presumably reflecting a selective pressure to inactivate the TA isoforms (Flores *et al.*, 2005). Nevertheless, human cancers rarely utilize mutation or deletion of p63 and p73 as mechanisms for inactivation of these genes. In a subset of tumors, inhibition is achieved by methylation-induced promoter silencing. In others, overexpression of

either DNp63 or DNp73 isoforms likely contributes to functional suppression of TAp63, TAp73, and probably p53, thereby promoting tumorigenesis.

Inhibition of apoptosis mediated by TAp63/TAp73 isoforms is likely to explain one contribution of DNp63 and DNp73 to human cancer. However, it still remains to be determined whether apoptosis is the sole function of TAp63 and TAp73 that is essential for their proposed tumor-suppressive property. In addition, it remains to be established to what degree DNp63 and DNp73 isoforms function exclusively as trans-suppressors of TA isoforms, or, perhaps more likely, whether they regulate additional TA-independent pathways. As noted, TAp73 isoforms are well-established mediators of apoptosis in both normal and tumor cells. TAp63 isoforms are not as prominent in this regard, although recent data support their role as context-specific proapoptotic factors (Jacobs *et al.*, 2005; Suh *et al.*, 2006). Nevertheless, several additional p63- and p73-dependent pathways relevant to human cancer have been defined. Evidence exists for contributions of p63 and p73 target genes to proliferation, differentiation, cellular adhesion, growth factor signaling, angiogenesis and other pathways (Senoo *et al.*, 2002; Barbieri *et al.*, 2005; Cam *et al.*, 2006; Carroll *et al.*, 2006; Nguyen *et al.*, 2006; Troung *et al.*, 2006). These functions may be particularly relevant for p63, which seems to exhibit a multifaceted developmental role that is less tightly linked to suppression of apoptosis than that of p73. More sophisticated *in vivo* models, coupled with isoform-specific knockout and RNAi knockdown approaches will be required to clarify which among these pathways are most relevant for human tumorigenesis.

Future therapeutic targeting of p63 and p73 in human cancer

Ultimately, it is hoped that understanding how p63 and p73 contribute to tumorigenesis may lead to new therapeutic approaches for the relevant cancers. In the near term, expression of particular p63 and/or p73 isoforms may prove to be useful clinical markers of sensitivity to specific chemotherapeutic agents. For example, recent data have suggested that expression of p63 in SCCs is correlated with the therapeutic response to cisplatin (Zangen *et al.*, 2005). This observation may be linked to the ability of cisplatin to specifically activate TAp73, which is co-overexpressed with DNp63a in SCC tumors but not normal epithelial cells (DeYoung *et al.*, 2006). DNp63a normally suppresses the potent proapoptotic activity of TAp73 in tumor cells, but cisplatin treatment induces profound downregulation of DNp63a (Figure 3) (Fomenkov *et al.*, 2004). At the same time, TAp73 undergoes a variety of post-translational modifications that are required for its activation following cisplatin treatment (Oberst *et al.*, 2005). Thus, downregulation of DNp63a and activation of TAp73 mediate cisplatin sensitivity in these tumors. We recently showed that ablation of TAp73 isoforms in SCC cells induced

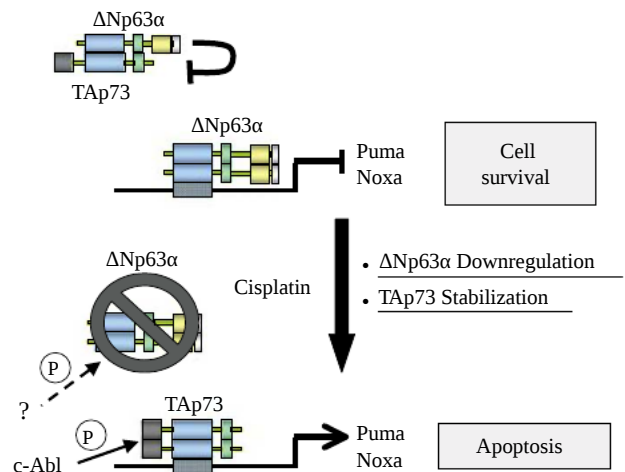


Figure 3 p63/p73 pathway mediates cisplatin sensitivity in squamous carcinoma cells. In proliferating tumor cells, DNp63a inhibits the proapoptotic transcriptional activity of TAp73 through both direct physical interaction and through direct binding to the promoters of TAp73 target genes. Cisplatin treatment induces DNp63a downregulation and TAp73 stabilization, thereby activating the TAp73-dependent apoptotic program. Phosphorylation of TAp73 by c-Abl and potentially other kinases is important for its activation following DNA damage. Phosphorylation may also contribute to downregulation of DNp63a in this context. Note that proteins are shown schematically as dimers but in fact are thought to bind DNA as tetramers.

marked cisplatin resistance, supporting a TAp73-dependent pathway for sensitivity in these cells (Rocco *et al.*, 2006). Given that they are direct mediators of chemotherapy-induced apoptosis, expression of these particular p63 and p73 isoforms could predict a favorable therapeutic response in a variety of tumors.

Much remains to be learned about the mechanisms that mediate the complex interplay between different p63 and p73 isoforms under conditions such as genotoxic stress. Beyond providing a potential means to predict chemosensitivity, understanding these mechanisms may provide new and more specific ways to target these proteins themselves for cancer therapy. Although promising p53-directed therapies have been slow to emerge, it is conceivable that p63 and p73 might be more amenable to therapeutic targeting. In support of this concept, recent data from several groups have demonstrated that established tumor cells remain dependent in some fashion on p63/p73 expression (Barbieri *et al.*, 2006; Cam *et al.*, 2006; Rocco *et al.*, 2006). Thus, ablation of DNp73, which is overexpressed in rhabdomyosarcoma cells, can lead to growth arrest and differentiation (Cam *et al.*, 2006). Similarly knockdown of DNp63, overexpressed in SCCs, induces apoptosis (Rocco *et al.*, 2006).

Of particular interest for future targeting of p63 and p73 are the variety of post-translational modifications that regulate the stability and activity of particular isoforms. Thus, inhibiting ubiquitin or SUMO ligases that target TAp63/TAp73 isoforms could stabilize these proteins and thereby promote a selective therapeutic response in tumors that overexpress these isoforms.

Unfortunately, the apparent lack of TA/DN isoform specificity in the modifications identified to date may limit the usefulness of this approach. Alternatively, targeting specific kinases may be a more attractive possibility, given the ability of several kinase pathways to inhibit the function of p73. Theoretically, targeting the appropriate kinase in the correct tumor-specific context could have profound effects through p63- or p73-dependent pathways. Such therapeutic effects hold some promise of sparing normal tissues, given the large number of examples of tumor-specific expression of particular p63 and p73 isoforms. Undoubtedly, a more

detailed understanding of the diverse contributions of p63 and p73 to human cancer could ultimately yield a variety of more effective therapeutic strategies for refractory malignancies.

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