

# Topics: Pancreatic cancer — New horizons in diagnosis and treatment

# Molecular prognostic markers in pancreatic cancer

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Abstract Pancreatic cancer has a very poor prognosis and is a common cause of cancer death in the Western world. Certain genetic alterations may be important in the prognosis of pancreatic cancer. Activation mutations in the K-ras oncogene occur in around 90% of pancreatic cancers, and the overexpression of growth factors epidermal growth factor (EGF), transforming growth factor (TGF)a, TGFßs 1-3, acidic fibroblast growth factor (aFGF), basic FGF (bFGF), and growth factor receptors c-erbB-2 and -3 and TGFRßs 1-3 is common. High mutation levels of cell cycle control genes such as p53, p16, p21, SMAD4, and cyclin D1 are found, and there is abnormal expression of apoptotic genes, such as *bcl-2*, *bcl-XL*, and *bax*. The expression of several of these growth factors and their receptors has been found to be associated with poorly differentiated tumors of an advanced stage and decreased survival. However, the inactivation and loss of expression of p16, p53, and p21, and the expression of several apoptotic genes, such as bax and bcl-2, have not been found to be of any prognostic significance. The expression of wild type p53, however, may predict responsiveness to chemotherapy. TGF<sup>β1</sup> expression has been shown to be associated with longer survival in patients with pancreatic cancer. Two studies (including our own) have found *bcl-XL* expression to be significantly associated with poor survival. These and newer molecular markers may prove to be important in the choice of future therapies for pancreatic cancer.

Key words Pancreatic cancer · Molecular marker · Prognosis

## Introduction

Pancreatic cancer is a common cause of cancer-related death in the Western world, with an overall 5-year sur-

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vival of 0.4%.<sup>1</sup> This aggressive tumor presents at a late stage, and potentially curative surgical resection is possible in only about 10%-15% of patients.<sup>2,3</sup> Moreover, currently available radiotherapy and chemotherapy regimens have not shown improved survival in advanced disease; their role in adjuvant therapy is currently being assessed.<sup>4,5</sup> Prognostic markers may identify subgroups of patients who may benefit better from aggressive therapy given in an attempt to improve survival. Clinical parameters that are significant in predicting patient outcome are tumor grade, stage, resection margin status, and tumor size; patients with negative resection margins and stage I-II disease demonstrate superior survival rates.<sup>6-9</sup> Current staging systems in use include the International Union Against Cancer (UICC) TNM classification in the West<sup>10</sup> and the Japan Pancreas Society (JPS) system in Japan,<sup>11</sup> but unfortunately, they are not exactly comparable. This causes difficulties, because of "staging system" migration, when survival data are compared.

The absence of disseminated tumor cells both in the peritoneal cavity and in the bone marrow was found to be associated with significantly longer 5-year survival rates.<sup>12</sup> The serum concentrations of tumor markers such as CA 242, CA 19.9, and MUC 1 may have some prognostic significance in advanced disease, but not in patients with small tumors.13-15 In pancreatic cancer there is overexpression of growth factors and growth factor receptors, including epidermal growth factor (EGF), transforming growth factor (TGF) $\alpha$ , EGF receptor (EGFR), amphiregulin, c-erbBs 2-4, acidic fibroblast growth factor (aFGF), basic (b)FGF, FGFR, TGFβs1-3, and TGFβRs. Inactivation of the tumor suppressor genes (TS) p53, p16, and SMAD4,16 and activation of dominant oncogenes K-ras and cyclin D1 all play a significant role in tumorigenesis. The possible use of these molecular markers for prognosis in pancreatic cancer has been the subject of extensive work in our laboratory and others.

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### Growth factors and their receptors

Although pancreatic carcinoma demonstrates abnormal expression of numerous growth factors and their receptors, which may contribute to pancreatic tumor cell growth, some of these changes also occur in chronic pancreatitis. The pattern and level of expression of these receptor-ligand systems accounts for the different disease processes, but it is noteworthy that there is at least a sixfold increased incidence of pancreatic cancer in patients with chronic pancreatitis.

# *Epidermal growth factor receptor (EGFR) family and its ligands*

This family of type 1 growth factor receptors comprises four transmembrane tyrosine kinases: the epidermal growth factor receptor (EGFR) and c-erbBs-2, 3, and  $4.^{17}$  They share significant sequence homology with one another and are all frequently overexpressed in human pancreatic cancer. EGFR is activated by a family of peptide ligands that includes EGF, TGF $\alpha$ , heparin– binding EGF–like growth factor, betacellulin, and amphiregulin.<sup>18</sup>

EGF is a polypeptide of 53 amino acids that stimulates proliferation and differentiation of a wide variety of cell types through the EGFR.<sup>19</sup> The EGFR is encoded by the c-erbB-1 protooncogene and is a transmembrane growth factor receptor with tyrosine kinase activity. In the normal pancreas, EGFR is expressed only in the islets of Langerhans. The EGFR gene, however, is overexpressed in 95% of ductal adenocarcinomas and human pancreatic cell lines, because of an increase in gene transcription.20 EGFR binds EGF and TGF $\alpha$  with high affinity, and both of these ligands are overexpressed in pancreatic cancer.<sup>21</sup> The overexpression of EGFR has been shown to increase the production of EGF and TGFa, promoting autocrine and paracrine loops that promote cell proliferation.<sup>21</sup> TGFa is expressed at low levels in the ductal epithelium of the normal human pancreas, but it is overexpressed at high levels in 95% of ductal adenocarcinomas.<sup>20</sup> While EGF is not detectable in the normal pancreas, it is found in 12% of pancreatic cancers.<sup>20</sup> Several studies have shown that high levels of EGFR, EGF, and/or TGFa were correlated with reduced patient survival.22,23 Shorter postoperative survival was also demonstrated with the overexpression of amphiregulin and EGFR.<sup>24</sup>

The *c-erbB-2* gene encodes a 185-kDa transmembrane glycoprotein with tyrosine kinase activity,<sup>25</sup> and acts as a receptor for a class of ligands that includes the heregulins, gp30, and NEU-differentiation factor (NDF), but the full contribution of *c-erbB-2* to growth stimulation in pancreatic cancer remains unknown. *c-erbB-2* is overexpressed in bladder, breast, esophageal,

and gastric cancer, where it appears to have a role in lymph node metastases.<sup>26,27</sup> In invasive ductal adenocarcinomas of the pancreas and ampullary tumors, *c-erbB-*2 is overexpressed in 20%, and this is usually caused by *c-erbB-2* gene amplification.<sup>28</sup> One study showed a survival advantage for those patients with tumors that did not overexpress *c-erbB-2*,<sup>29</sup> and another study correlated survival with serum levels of *c-erbB-2*.<sup>30</sup> But other studies, including our own, with larger patient numbers did not reveal any prognostic significance for *c-erbB-2* expression.<sup>31</sup>

The *c-erbB-3* gene encodes a Mr 180000 transmembrane polypeptide that shares close structural homology with the EGF receptor and *c-erbB-2*, but it has no known natural ligands. In the normal pancreas, *c-erbB-3* is seen only in the islets of Langerhans, but has been detected in up to 90% of pancreatic and ampullary cancers.<sup>32,33</sup> Freiss et al.<sup>34</sup> found that *c-erbB-3* overexpression correlated with decreased patient survival. In our own series,<sup>31</sup> we found overexpression in 54% of tumors but found no correlation with survival.

*c-erbB-4* is a 180-kDa transmembrane tyrosine kinase whose extracellular domain is similar to that of *c-erbB-3*. The cytoplasmic kinase domain exhibits a high degree of homology with *EGFR* and *c-erbB-2*.<sup>35</sup> The heregulins and betacellulin can all activate *c-erbB-4*.<sup>36,37</sup> *c-erbB-4* is predominantly expressed in normal skeletal muscle, heart, pituitary gland, brain, and cerebellum, as well as being expressed in breast cancer cell lines. A recent study looked in detail at *c-erbB-4* expression in pancreatic cancer, using quantitative reverse transcriptionpolymerase chain reaction (RT-PCR) and immunohistochemistry. Survival analysis did not show any significant difference between patients with *c-erbB-4*positive tumors and those with negative tumors.<sup>38</sup>

#### $TGF\beta s$ and $TGF\beta$ receptors

Transforming growth factor-βs are a family of cytokines that actively influence cell division, cell death, and cellular differentiation. They bind to specific cell surface receptors that are able to downregulate transcription factors, decrease phosphorylation of target proteins, and inactivate cell-cycle regulatory enzymes. The end targets may be the G1 cyclins and cyclin-dependent kinases. The presence of mutant p53 has been correlated with the loss of TGF<sub>β</sub>-1 responsiveness in malignant epithelial cell lines. TGF<sub>β</sub>-1 may also induce the universal cyclin inhibitor p21 by a p53-independent pathway.<sup>39,40</sup> The three isoforms TGFβ-1–3 have been shown to be overexpressed in pancreatic cancer. Survival data from 60 patients with pancreatic cancer showed significantly decreased survival time with the overexpression of these isoforms.<sup>41,42</sup> In a more recent study, however, TGF $\beta$ -1 which was expressed in 31% of cancers, was significantly associated with increased survival.43 These contradictory findings deserve further investigation. The TGF $\beta$  receptors 1–3 are all found in normal pancreas, but in cancer there is overexpression of TGFβ-2 receptor only.44

#### Fibroblast growth factors

Fibroblast growth factors (FGFs) belong to a large group of closely homologous polypeptide growth factors which includes the two main members, acidic FGF (aFGF) and basic FGF (bFGF). These growth factors are highly abundant in the basement membrane and extracellular matrix of a variety of tissues. FGFs influence cell differentiation, tissue homeostasis, tissue regeneration and repair, cell migration, and angiogenesis. Binding to specific transmembrane receptors (which have intracellular tyrosine kinase activity) is dependent on the presence of heparin sulfate proteoglycans (on the cell surface or in the extracellular matrix) for which they have a high affinity. Both aFGF and bFGF are overexpressed in pancreatic cancer tissue at the mRNA and protein levels.45,46 The expression of bFGF and FGF receptor (R), but not aFGF, is associated with poor prognosis<sup>45,47</sup> (Table 1<sup>22,23,29,31,34,38,41,43,45,47-49</sup>).

### **Tumor suppressor genes**

Most tumor suppressor genes have pivotal roles in cell cycle control and apoptosis. Loss of function can be associated with uncontrolled cell growth and

						Surviv	/al	
Study	Year	No. of patients	Factor	Method	Expression	Median (months)	5-Year (%)	Р
Yamanaka et al. <sup>22</sup>	1993	87	EGF	IHC	+			
Uegaki et al. <sup>23</sup>	1997	86	EGF	IHC	+	21 25		<0.05 NS
			EGFR		+	23	—	
Dong et al.48	1998	57	EGF + R	IHC	+	25 10	_	NS
Gansauge et al.49	1998	82	EGF + R	IHC	+	17	_	< 0.002
Lei et al. <sup>29</sup>	1995	21	c-erbB-2	IHC	+	7		NS
Friess et al. <sup>34</sup>	1995	58	c-erbB-3	IHC	+	19 9	_	< 0.01
Kawesha et al. <sup>31</sup>	1997	142	c-erbB-2	IHC	+	13 8	_	< 0.04
Ruweshu et ul.	1777	112	c-erbB-3	IHC	+	9 9	_	>0.7
	1000	75			—	8	—	>0.7
Graber et al. <sup>38</sup>	1999	75	c-erbB-4	IHC	+		_	NS
Yamanaka et al.45	1993	78	aFGF	IHC	+	11 13	_	NS
			bFGF		+	9 16		< 0.001
Ohta et al.47	1995	32	bFGF	IHC	+	8 9	_	NS
			FGFR		+	6	_	< 0.01
Friess et al.41	1993	60	TGFβ-1	IHC	+	9 12		< 0.05
			TGFβ-2		+	7	—	
			TGFβ-3		+	13 7	_	< 0.001
Coppola et al.43	1998	42	TGFβ-1	IHC	+	12 13	$\overline{23}$	< 0.01
11			- 1.	-		5	4	< 0.05

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EGF, Epidermal growth factor; EGFR, epidermal growth factor receptor; IHC, immunohistochemistry; aFGF, acidic fibroblast growth factor; bFGF, basic fibroblast growth factor; FGFR, fibroblast growth factor receptor; TGFβ, transforming growth factor beta

proliferation, decreased apoptosis, and malignant transformation.

## p53

The p53 gene encodes a 53-kDa nuclear phosphoprotein consisting of 393 amino acids. Under normal conditions, the p53 protein is found in the cell nucleus. p53 controls the entry of cells into the growth cycle at the G1/S boundary and has a critical role in initiating the repair of damaged DNA before it is replicated.50 The inability to effect DNA repair with accuracy may result in p53-dependent apoptosis. The p53 gene is mutated in over 50% of human cancers.<sup>51,52</sup> In pancreatic cancer it is inactivated in approximately 65% of cases by a missense point mutation; loss of the remaining normal allele commonly occurs in pancreatic cancer cell lines, although this occurs less frequently in primary tumors.53 In contrast to ductal adenocarcinomas, only 33% of intraductal papillary adenocarcinomas, and no mucinous and adenosquamous pancreatic carcinomas, exhibit positive nuclear staining for p53.54,55 The majority of p53 mutations are found in exons 5–8, which contain the most highly conserved regions. Point mutations result in the production of mutant p53 proteins, which are more stable than the wild-type protein and accumulate within the nucleus. p53 gene mutations probably occur relatively early in the process of pancreatic carcinogenesis.55 Lundin et al.56 found that p53 mutations did not correlate with tumor stage, histology, age, sex, or survival. Our study, in which 35% of cancers were positive by immunostaining, demonstrated no correlation with patient survival<sup>31</sup> (Table 2).

When cells are exposed to either radiation or cytotoxic agents, the levels of wild-type p53 protein rise 5 to 60-fold (because of increased stability of the protein, rather than increased protein synthesis). It follows that tumors with functioning p53 may carry a better prognosis than those expressing the mutant protein, when exposed to radiation or DNA-damaging agents. Two studies investigated 58 patients, of whom 28 had surgery alone and the other 30 had adjuvant chemotherapy. Patients with p53 positive tumours (shown by immunostaining) who had chemotherapy had significantly better survival times than those who did not.<sup>57</sup> Patients with combined p53 positive and p21 negative tumors had significantly poorer survival and those in this group who had chemotherapy had a nonsignificant trend for improved survival.<sup>58</sup>

#### p16

The p16 tumor suppressor gene encodes a 16-kDa protein<sup>59</sup> that plays a key role in controlling the G1 checkpoint (or the restriction point, R) of the cell cycle (Fig. 1). The retinoblastoma gene product (pRb) is an active transcriptional repressor when bound to transcription factors such as the E2F family. Inactivation of pRb by phosphorylation (mediated by the complex formed by CDK4,6 and cyclin D) causes release of E2F and subsequent transcription of genes important for DNA synthesis.<sup>60</sup> The p16 protein prevents the association of CDK4 and 6 with cyclin D and the subsequent phosphorylation of pRb. This growth suppression by p16 requires functional retinoblastoma protein.61 Loss of p16 expression occurs in up to 85% of pancreatic cancer cell lines and xenografts,<sup>62</sup> caused by homozygous or heterozygous deletion, and hypermethylation.63 A study of 32 patients with pancreatic cancer found a significant correlation between p16 negativity and poor prognosis.<sup>64</sup> In our study of 142 patients, however, the p16 negativity rate on immunohistochemical staining was 80%, but there was no correlation with survival.<sup>31</sup>

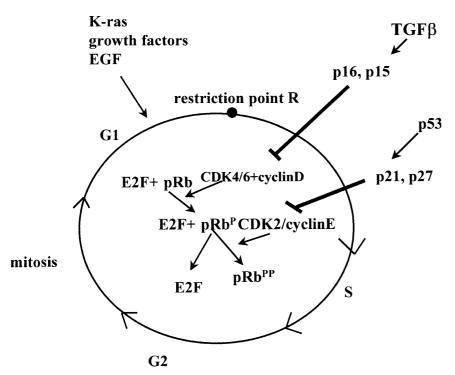
# p21<sup>WAFI</sup>

 $p21^{WAFI}$ , a cyclin-dependent kinase inhibitor, is a downstream target and effector of p53. The 21-kDa product of the *WAF1* gene forms part of a quaternary complex, along with cyclin/CDKs and the proliferating cell nuclear antigen (PCNA) in normal cells, but not in transformed cells, and is a universal inhibitor of CDK activity.<sup>65</sup> One consequence of p21 binding to and inhibiting CDKs is to prevent CDK-dependent phos-

 Table 2. Tumor suppressor genes in pancreatic cancer

Study	Year	No. of patients	Gene	Method	Expression	Median survival (months)	Р
Lundin et al.56	1996	133	p53	IHC	+	9	
						12	NS
Kawesha et al. <sup>31</sup>	1997	142	p53	IHC	+	10	
			1		_	8	>0.2
			p16	IHC	+	10	
			1			11	>0.2
			p21	IHC	+	11	
			-		_	8	>0.6

IHC, Immunohistochemistry



**Fig. 1.** The cell cycle. The retinoblastoma gene product, pRb, is central to G1 checkpoint control.<sup>60</sup> EGF, Epidermal growth factor;  $TGF\beta$ , transforming growth factor  $\beta$ 

phorylation and subsequent inactivation of the Rb protein, which is essential for cell cycle progression at both the G1 and G2 checkpoints. The negative regulatory action of *p21<sup>WAF1</sup>* on the cell cycle permits sufficient time for repair to extensive DNA damage to be completed. Functional p21 is essential for p53-mediated G1 arrest due to WAF1 inhibition of both CDK activity and PCNA-dependent DNA replication.65 Thus, p21 overexpression causes growth suppression, consistent with its role as an inhibitor of CDKs and as a tumor suppressor gene. Induced expression of  $p21^{WAF1}$  by p53directly, or by p53-independent mechanisms, results in as much as a 20- to 100-fold increase, depending on the cell type and mode of induction. Kinetic analyses of p53-dependent induction indicate that  $p21^{WAFI}$  expression begins to rise coincident with the accumulation of p53 in response to DNA damage. Failure to show this rise is associated with failure of G1 arrest and with inappropriate onset of apoptosis.<sup>66</sup> Nevertheless, all studies our own, included, have not shown any prognostic value in p21 expression, as demonstrated with immunohistochemistry.<sup>30,43,67,68</sup>

#### Oncogenes

#### K-ras

The *ras* family of protooncogenes, which includes H*ras*, N-*ras*, and K-*ras*, encodes proteins with GTP-ase activity, which, thereby, function as molecular switches in signal transduction. The K-ras gene encodes for a 2.0-kb transcript that is highly conserved across species and is translated into the p21-ras protein. Growth and differentiation signals from activated cell membrane receptors are transduced by K-ras to activate protein kinases, including cyclin kinases. Point mutations in codons 12, 13, and 61 of K-ras result in the expression of altered protein products that are capable of transforming cells into a malignant phenotype. The K-ras gene is mutated in 75% to 90% of pancreatic cancers.<sup>69,70</sup> The mutations present in pancreatic cancer are almost exclusively at codon 12, and only a minority of tumours demonstrate a mutation at codon 13. The spectrum of mutations in pancreatic cancer includes the aspartic acid mutation (GAT), valine (GTT), arginine (CGT), and cysteine (TGT).<sup>71</sup> The presence or the type of K-ras mutations in pancreatic tumors has not been shown to be associated with patient survival<sup>72,73</sup> (Table 3).

#### Cyclin D1

Cyclin D1 is a cell cycle regulator that may act as an oncoprotein. It forms part of the enzyme complexes that are active in G1 phase of the cell cycle and which inactivate pRb by phosphorylation. These enzyme complexes (CDKs) contain two components, a regulatory subunit — the cyclin — and a catalytic subunit — the cyclin-dependent kinase (cdk).<sup>74</sup> The CDKs can be activated by cdk binding cyclin and by phosphorylation of a conserved threonine by CDK-activating kinase (CAK).

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Study	Year	No. of patients	Gene	Method	Expression	Median survival (months)	Р
Hruban et al. <sup>72</sup>	1993	82	K-ras	RFLP	+	14	
					_	10	> 0.5
Kawesha et al.31	1997	142	K-ras	SSCP	+		
					_		NS
			Cyclin-D	IHC	+	9	
			2			8	>0.4
Gansauge et al.49	1998	82	Cyclin-D	IHC	+	10	
0			2			18	< 0.01

Table 3. Oncogenes in pancreatic cancer, and correlation to patient survival

RFLP, Restriction fragment length polymorphism; SSCP, single-strand conformational polymorphism; IHC, immunohistochemistry; NS, not significant

Inactivation of the active cdk-cyclin complex can occur by binding to CDK inhibitory subunits (CKIs).75 There are two classes of CKIs: the INK4 kinase inhibitors, p15, p16, p18, and p19, which specifically regulate complexes of cyclin D1, D2, and D3 with CDK4 and 6; and a second group, p21, p27, and p57, which inhibit all G1 cyclin/cdk complexes. The primary regulator of CDK activity is the cyclin subunit, whose levels oscillate during the cell cycle. The G1 cyclin complexes consist of Dtype cyclins (D1, D2, and D3) complexed with either cdk4 or 6, cyclin E complexed with cdk2, and cyclin A complexed with cdk2. The appearance of D-type cyclins is tightly linked to growth factor exposure, and their downstream cell cycle effects are caused by the inactivation of pRb by phosphorylation. Cyclin D1 has been implicated in the pathogenesis of a number of cancers, including esophageal, lung, head and neck, bladder, and pancreatic, as well as sarcomas. Overexpression of cyclin D1 leads to constitutive phosphorylation of pRb and, thus, deregulated (and increased) E2F activity. Also, activation mutations of the cdk4 have been identified in certain tumors, such as melanoma.76,77 Thus, both cyclin D1 and cdk4 can act as oncoproteins by inactivating pRb. A study of 82 pancreatic cancers demonstrated overexpression (by immunostaining) of cyclin D1 in 65% of tumors, and this was associated with shorter survival for these patients, but not independently of tumor stage and grade.49 In our series of 142 pancreatic cancers, we found no prognostic significance associated with the expression of cyclin D1.31

#### **Apoptotic factors**

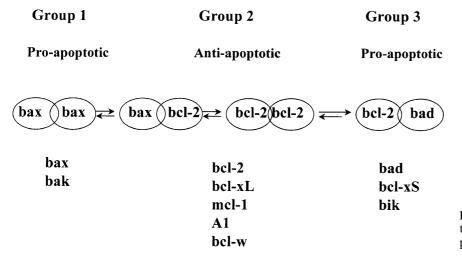
Apoptosis or programmed cell death is a central regulator of homeostasis in normal tissue. Damaged cells are eliminated without an immune response, and apoptosis balances cell proliferation under normal physiological conditions. There are numerous apoptotic pathways. The *bcl-2* family of apoptotic genes includes *bcl-2*, *bcl-x*, *bax*, and *bak*, plus others, and the majority have four conserved domains (Fig. 278). The first two domains are important for homo- and heterodimerization, and the fourth is important for normal function. bcl-2 is an antiapoptotic factor and sometimes is referred to as a cooperating oncogene. By itself it is unable to transform cells, but, when activated in the presence of other oncogenes, bcl-2 is vital to malignant transformation. *Bcl-x* is a *bcl-2*-related gene and exists as two subforms; *bcl-xL* is the longer form and functions as an apoptotic inhibitor;<sup>79</sup> bcl-xS is the shorter form and functions as an apoptosis promoter. bax is a promoter of apoptosis and is has been shown that the ratio between bax and bcl-2 can be important in determining cell survival. An excess of bax homodimers promotes cell death, whereas an excess of bcl-2 homodimers will inhibit apoptosis.80 Several recent studies have looked at these factors in pancreatic cancer (Table 4). In a study of 60 patients, tumor expression of bax immunostaining was associated with significantly longer survival compared with that in patients who had negatively staining tumors,<sup>81</sup> but this was not confirmed in our own study.82 bcl-2 also has no prognostic significance,<sup>81</sup> but several studies have shown that the expression of *bcl-xL* is significantly associated with poor survival.<sup>82-84</sup> This is suprising, because *bcl-xL* inhibits apoptosis, and this would suggest reduced antiapoptosis by heterodimerization.

#### **Tumor angiogenesis**

Angiogenesis is essential for tumor growth and metastasis. Angiogenic factors include aFGF and bFGF, which stimulate the locomotion and proliferation of endothelial cells, and TGF $\alpha$ , which has an effect on endothelial cell proliferation. These and other angiogenic factors (Table 5)<sup>85–88</sup> can be produced by the tumor, as well as by endothelial and stromal cells.

#### Angiogenin

Angiogenin (ANG) is a Mr 14100 polypeptide that is an inducer of vascularization. ANG may interact with en-



**Fig. 2.** Members of the *bcl-2* family and their role in apoptosis (after reference 78, personal communication)

 Table 4. Prognostic value of the bcl-2 family in pancreatic cancer

Study	Year	No. of patients	Factor	Method	Expression	Median survival (months)	Р
Friess et al. <sup>81</sup>	1998	60	bax	IHC	+	12	
					_	5	< 0.04
			bcl-2		+	_	
					_	_	NS
Friess et al.82	1998	74	bcl- $xL$	In situ	+	5	
					_	12	< 0.05
Evans et al.83	1998	24	bax	IHC	+	12	
					_	9	NS
			bcl- $xL$		+	6	
					—	20	< 0.002

IHC, Immunochemistry; in situ, in situ hybridization

#### Table 5. Angiogenic and stromal factors in pancreatic cancer

Study						Surv	ival	
	Year	No. of patients	Factor	Method	Expression	Median (months)	1 Year (%)	Р
Shimoyama et al.85	1996	37	ANG	In situ	+	10	33	
2						13	75	< 0.05
Fujimoto et al.86	1998	50	VEGF	IHC	+	12		
5					_	12		>0.04
			PD-ECGF		+	8		
					_	13		< 0.04
Cantero et al.87	1997	30	uPA + uPAR	IHC	+	9		
					_	18		< 0.006
Kuniyasu et al.88	1999	22	MMP2/9	In situ	High	18		
-			Ecad		Low			< 0.0002

ANG, Angiogenin; VEGF, vascular endothelial growth factor; PD-ECGF, platelet-derived endothelial cell growth factor; uPA, urokinase plasminogen activator; uPAR, urokinase plasminogen activator receptor; MMP, matrix metalloproteinase; Ecad, E-cadherin; IHC, immunohistochemistry; in situ, in situ hybridization

dothelial cells via a cell surface receptor and extracellular matrix (ECM) molecules such as proteoglycans.<sup>89</sup> ANG has been shown to bind to actin on the endothelial cell surface, and this complex may lead to the activation of several protease cascades. In patients with pancreatic cancer, high levels of mRNA expression and high levels of serum ANG were significantly associated with poorer survival.<sup>85</sup> Vascular endothelial growth factor (VEGF) and platelet-derived endothelial cell growth factor (PD-ECGF)

VEGF is a very potent and selective endothelial cell mitogen that has been shown to be associated with tumor progression and metastases in a variety of gastrointestinal malignancies. VEGF is a 38 to 46-kDa dimeric N-glycoprotein that is chemotactic, as well as mitogenic, for endothelial cells in vitro, induces angiogenesis in vivo, and increases the permeability of the vascular endothelium. In humans, four different isoforms have been identified (VEGF<sub>121</sub>, VEGF<sub>165</sub>, VEGF<sub>189</sub>, and VEGF<sub>206</sub>). In pancreatic cancer, the predominant species are VEGF<sub>121</sub> and VEGF<sub>165</sub>.<sup>86</sup>

PG-ECGF is a 55-kDa polypeptide that exists in vivo as a homodimer. PD-ECGF stimulates the chemotaxis of endothelial cells and, therefore, indirectly induces angiogenesis.<sup>88,90</sup> VEGF and PD-ECGF are frequently coexpressed in human cancers. Intratumoral microvessel density (MVD) is a potent prognostic marker in several tumor types, including breast cancer. Two studies in pancreatic cancer (a relatively hypovascular tumor) did not show prognostic value for MVD; the expression of PD-ECGF, however, was associated with a significantly reduced survival.<sup>86,91</sup> These two studies also showed no prognostic value for VEGF-expressing tumours, but a third study found significantly shorter survival for those patients with VEGF-positive tumors.<sup>92</sup>

#### Stromal factors and adhesion molecules

# Urokinase plasminogen activator (uPA) and its receptor (uPAR)

Plasminogen is an inactive proenzyme that can be converted to plasmin urinary or tissue plasminogen activator (uPA and tPA). uPA appears to play a pivotal role in pericellular proteolysis during cell migration and tissue remodelling. This enzyme is released initially from cells as an inactive proenzyme (pro-uPA) that can be cleaved by serine, cysteine, and other types of proteases.93 Pro-uPA and uPA bind to a specific cell surface receptor; following ligand binding, the uPA receptor increases the enzymatic activity of uPA itself. Plasminogen is converted to plasmin by uPA, leading to the degradation of fibrin, type IV collagen, fibronectin, and laminin. Plasmin also activates latent collagenases, such as procollagenase (matrix metalloproteinase 1 [MMP1]) and prostromelysin (MMP3).94,95 The activation of several growth factors, such as hepatocyte growth factor, TGFβ, and bFGF, is mediated by uPA, uPAR, and plasmin. The resultant cellular activation and extracellular matrix proteolysis enhance the ability of pancreatic cancer cells to invade and metastasize. As in other tumors, there is concomitant overexpression of uPA and uPAR in pancreatic cancer.<sup>87</sup> Coexpression of uPA and uPAR in pancreatic cancer was associated with significantly worse survival times compared with survival times in those patients with no tumor expression of either uPA or uPAR, or neither of these molecules.<sup>87</sup>

#### E-cadherin and matrix-metalloproteinases (MMPs)

E-cadherin is a transmembrane glycoprotein that is responsible for homotypic binding and morphogenesis of epithelial tissues; it is localized to the epithelial junction complex.<sup>96</sup> In cancer, decreased or absent expression of E-cadherin is associated with a decrease in cellular and tissue differentiation and higher metastatic potential. Transfection of E-cadherin has been shown to inhibit the motility and invasiveness of cancer cells.

The MMPs are a family of zinc-containing proteolytic enzymes that break down extracellular matrix proteins. One of the first steps of cancer invasion is the breakdown of the basement membrane, which is composed of predominantly type IV collagen. The level of MMP enzyme activity has been shown to correspond to tumor grade, regional lymph node metastases, and distant metastases. MMP-2 (gelatinase A) and MMP-9 (gelatinase B) are type IV collagenases and are overexpressed in pancreatic cancer.97-99 The expression of these MMPs has been shown to directly correlate with invasion and metastasis in pancreatic cancer. A recent study assessed the expression of E-cadherin and MMP-2 and MMP-9, using in-situ hybridization, in pancreatic cancer.<sup>88</sup> The expression of E-cadherin in pancreatic cancer was inversely correlated with tumor progression and the development of metastases. Patients with cancers that had an expression ratio of MMP: E-cad of less than 3 had a significantly better prognosis than those with a ratio of more than 3.

#### Conclusion

Increasing numbers of cellular and genetic markers are under investigation in pancreatic cancer. Certain growth factors and their receptors, tumor suppressor genes, angiogenic factors, and apoptotic genes have significant correlations with survival and/or treatment responsiveness in pancreatic cancer. Although the exact role of these markers in patient management remains to be established, their investigation places pancreatic tumor biology and tumor responsiveness to present and future therapies on a fundamental and mechanistic foundation. There should be cautious optimism for newer successful approaches for pancreatic cancer treatment over the next few years.

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