

The Role of the IGF System in Cancer Growth and Metastasis: Overview and Recent Insights

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IGF-I receptor (IGF-IR) signaling and functions are mediated through the activities of a complex molecular network of positive (e.g., type I IGF) and negative (e.g., the type II IGF receptor, IGF-IIR) effectors. Under normal physiological conditions, the balance between the expression and activities of these molecules is tightly controlled. Changes in this delicate balance (e.g., overexpression of one effector) may trigger a cascade of molecular events that can ultimately lead to malignancy. In recent years, evidence has been mounting that the IGF axis may be involved in human cancer progression and can be targeted for therapeutic intervention. Here we review old and more recent evidence on the role the IGF system in malignancy and highlight experimental and clinical studies that provide novel insights into the complex mechanisms that contribute to its oncogenic potential. Controversies arising from conflicting evidence on the relevance of IGF-IR and its ligands to human cancer are discussed. Our review highlights the importance of viewing the IGF axis as a complex multifactorial system and shows that changes in the expression levels of any one component of the axis, in a given malignancy, should be interpreted with caution and viewed in a wider context that takes into account the expression levels, state of activation, accessibility, and functionality of other interacting components. Because IGF targeting for anticancer therapy is rapidly becoming a clinical reality, an understanding of this complexity is timely because it is likely to have an impact on the design, mode of action, and clinical outcomes of newly developed drugs. (Endocrine Reviews 28: 20–47, 2007)

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Abbreviations: AP-1, Adaptor protein; CDK, cyclin-dependent kinase; DMBA, dimethylbenz[α]anthracene; ECM, extracellular matrix; EGF, epidermal growth factor; EGFR, EGF receptor; ER, estrogen receptor; HIF-1 α , hypoxia-inducible factor 1 α ; IGFBP, IGF binding protein; IGF-IR, IGF-I receptor; IGF-IIR, IGF-II receptor; IR, insulin receptor; IRS, IR substrate; JAK, Janus kinase; JNK, c-Jun N-terminal kinase; LOI, loss of imprinting; MDM2, mouse double minute 2; MDR, multiple drug resistance; MEF, mouse embryo fibroblast; MMP, matrix metalloproteinase; PC, proprotein convertase; PI-3K, phosphatidylinositol 3-kinase; PIN, prostate intraepithelial neoplasia; PSA, prostate-specific antigen; PTEN, phosphatase and tensin homologous on chromosome 10; PTP-1B, protein tyrosine phosphatase 1B; RACK1, receptor for activated C kinases; sCLU, secretory clusterin; SH, Src homology; SHP-2, tyrosine phosphatase Src-homology 2-containing phosphotyrosine phosphatase-2; SHPS-1, Src homology 2 domain containing protein tyrosine phosphatase substrate-1; STAT, signal transducers and activators of transcription; TRAMP, transgenic adenocarcinoma of mouse prostate; uPA, urokinase plasminogen activator; uPAR, uPA receptor; VEGF, vascular endothelial growth factor; WT, Wilms' tumor.

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I. Introduction

CELL CYCLE PROGRESSION and cellular proliferation are regulated by a complex network of intrinsic factors and external stimuli. The very early events that rescue cells from cell cycle arrest are mediated through signals transmitted by a group of peptides, collectively known as growth factors. These molecules can be classified into two subgroups, namely the “competence” factors, such as the platelet-derived growth factor that enable cells to enter into the G₁ phase, and the “progression” factors, such as the IGFs that are required for progression from G₁ into the S phase and, ultimately, cell division (1, 2).

Overexpression of growth factors and/or their receptors is a common event in malignancy and provides the underlying mechanisms for one of the hallmarks of cancer, namely uncontrolled proliferation (3). Growth autonomy can occur when both growth factors and their receptors are overexpressed in the same cell, or when cells express constitutively activated receptors and lose their ligand dependency for growth. Overexpression of growth factor receptors in the absence of up-regulated ligand expression may, on the other hand, heighten tumor cell sensitivity and response to the appropriate ligand(s) and, thereby, regulate their growth in different microenvironments (4, 5).

II. The IGF System

The IGF system consists of two ligands, IGF-I and IGF-II; three cell-membrane receptors, IGF-I receptor (IGF-IR), insulin receptor (IR), and IGF-II receptor (IGF-IIR); and six high-affinity IGF binding proteins, IGFBP-1 through -6.

IGF-IR is a type 2 tyrosine kinase receptor that shares a 60% homology at the amino acid sequence level with the IR. The human IGF-IR cDNA contains an open reading frame of 4101 nucleotides that encode a protein of 1367 amino acids. The IGF-IR is synthesized as a single chain pre-propeptide with a 30-amino acid signal peptide that is cleaved after translation. The propeptide is then glycosylated, dimerized, and transported to the Golgi where it is processed at a furin cleavage site to yield α - and β -subunits (6). These subunits, through disulfide bonds, form a tetramer (β - α - α - β) that is transported to the plasma membrane (7). It has been shown that N-linked glycosylation of IGF-IR is required for its translocation to the cell surface (8, 9) and that this, in turn, may be rate-limited by the availability of dolichyl phosphate in the endoplasmic reticulum (8). For example, in MDA231 breast cancer cells, low cell-surface IGF-IR expression levels were linked to a low rate of *de novo* dolichyl phosphate synthesis and could be increased when additional dolichyl phosphate was provided to the cells (10). It has also been shown that the depletion of mevalonic acid in melanoma SK-MEL-2 cells reduced dolichyl phosphate biosynthesis and that this, in turn, reduced N-linked glycosylation and

IGF-IR cell surface expression levels, causing growth arrest (9).

The mature cell membrane-bound IGF-IR consists of two 130- to 135-kDa α -chains and two 90- to 95-kDa β -chains, with several α - α and α - β disulfide bridges (11). The α -subunits, which are entirely extracellular, form the ligand-binding domain (12) that binds one ligand molecule. IGF-I and IGF-II share a 62% homology in amino acid sequence, and there is a 40% homology between the IGFs and proinsulin (13). Several lines of evidence suggest that the binding sites for IGF-I and IGF-II on the receptor may be distinct (14, 15). Recent receptor binding affinity assays, using a recombinant, high-affinity form of the IGF-IR, and studies based on the surface plasmon resonance technology revealed a difference of 4-fold in the affinities of IGF-I (4.45 nM) and IGF-II (17.8 nM) for the recombinant human IGF-IR, and this agreed closely with cell-based assays (16). However, ligand binding affinities may vary with cell type and specific experimental conditions. For instance, in cultured adult bovine chromaffin cells, IGF-IR bound IGF-I and IGF-II with identical affinities (K_d ~ 1 nM) (17). It is of interest that, in human fetus and adult sera, IGF-II concentrations are 5- and 3.5-fold higher, respectively, than IGF-I levels (18). Interestingly, IGF-II can also bind to the insulin receptor subtype A (IR-A), with an affinity similar to that of insulin. IR-A is more mitogenic than subtype B (19, 20), the latter having a more metabolic function. IR-A is expressed in certain tumors, such as mammary cancers, and the IGF-II/IR-A interaction may play a role in cancer growth (for a more detailed discussion, see *Section X.F*). In addition, hybrid heterodimeric receptors consisting of insulin and IGF-I receptor subunits may form and could play a role in receptor signaling in normal and abnormal tissues. In a striking example, one study that examined eight human breast cancer cell lines and 39 human breast cancer specimens found that the hybrid receptor content exceeded the IGF-IR content in over 75% of the specimens. In the human breast cancer cell line MDA-MB157, these hybrid receptors were autophosphorylated in response to IGF-I, and this response exceeded IGF-IR autophosphorylation and led to increased proliferation, suggesting that the hybrid receptors were the major mediators of IGF signaling in these cells (21).

IGF-IR signaling is transmitted by an intracellular domain consisting of a binding site for phosphorylated substrates at tyrosine residue 950; a tyrosine kinase domain that contains an ATP-binding site at lysine 1003 and three critical tyrosines at positions 1131, 1135 and 1136; and a C-terminal domain containing several tyrosines and serines, such as tyrosines 1250, 1251, and 1316 and serines 1280–1283 that are phosphorylated and play a role in IGF-IR signaling. The contributions that these C-terminal domain amino acids make to IGF-IR function in normal and malignant cells are not fully understood and are the subject of active investigation in several laboratories, including our own (22–24). IGF-II and, with a much lower affinity, IGF-I can also bind to a second receptor, namely, IGF-IIR, which is identical to the cation-independent mannose-6-phosphate receptor and serves as a scavenger receptor (25).

The physiological activities of the IGFs are modulated by their association with the IGFBPs. These comprise a struc-

turally related superfamily of secreted proteins consisting of BP1–6 that bind the IGFs with different affinities (*e.g.*, IGFBP-6 binds IGF-II with a 20- to 100-fold higher affinity than IGF-I) and several related proteins that bind ligand with lower affinities (26, 27). The IGFbps regulate the biological accessibility and activity of the IGFs in several ways, which can be summarized as follows. They transport IGFs from the circulation to peripheral tissues (*e.g.*, IGFBP-1, -2, and -4), maintain a reservoir of IGFs in the circulation (a function principally of IGFBP-3), potentiate or inhibit IGF action, and mediate IGF-independent biological effects (for review, see Ref. 28).

III. Signal Transduction by the IGF-IR

Upon ligand binding, the intrinsic tyrosine kinase of the IGF-IR is activated, and this results in autophosphorylation of tyrosines on the intracellular portion of the β -subunit, including tyrosine residues in the juxtamembrane and C-terminal domains. Once phosphorylated, tyrosine 950 in the juxtamembrane domain can serve as a docking site for several receptor substrates, including the insulin receptor substrates (IRS) 1–4 and Shc (for reviews, see Refs. 29 and 30). These substrates can initiate phosphorylation cascades that serve to transmit the IGF-IR signal. Phosphorylated IRS-1 can activate the p85 regulatory subunit of phosphatidylinositol 3-kinase (PI-3K), leading to activation of several downstream substrates, including the p70 S6 kinase and protein kinase B (Akt) (31). Akt phosphorylation, in turn, enhances protein synthesis through mTOR activation and triggers the anti-apoptotic effects of IGF-IR through phosphorylation and inactivation of Bad (32). IRS-1 has also been implicated in signaling by other receptor systems, including those from other growth factors (33), cytokines (34), and integrins (35), and may therefore be involved in crosstalk between different signaling systems. In parallel to PI-3K-driven signaling, recruitment of Grb2/SOS by phosphorylated IRS-1 or Shc leads to recruitment of Ras and activation of the Raf-1/MEK/ERK pathway and downstream nuclear factors, resulting in the induction of cellular proliferation (36, 37) (summarized in Fig. 1).

In some cell types, the IGF-IR can also directly phosphorylate the Janus kinases (JAK)-1 and -2 that are involved in cytokine-mediated signaling, and JAK proteins may, in turn, phosphorylate IRS-1 (38). Phosphorylation of JAK proteins can lead to phosphorylation/activation of signal transducers and activators of transcription (STAT) proteins. STAT-3 (39) and STAT-3 activation, in particular, may be essential for the transforming activity of IGF-IR (40). Other effectors downstream of IGF-IR activation include Src (41), the pp125 focal adhesion kinase that is directly phosphorylated by IGF-IR (42), and the proto-oncogenes c-Crk II and CrkL (43, 44) that can link IGF-IR to integrin-mediated signaling and the cytoskeleton through p130 Cas and paxillin, thereby regulating cell shape and motility (42, 45). Because intracellular calcium levels increase in response to IGF-I, phospholipase C- γ is also thought to be indirectly involved through its products inositol 1,4,5-triphosphate and 1,2 diacylglycerol (24). This was also demonstrated by the fact that IGF could not rescue Plcg1

null (Plcg1^{-/-}) mouse embryonic fibroblasts (MEFs) from anoikis-induced apoptosis, but the response could be restored by reexpression of phospholipase C- γ in these cells (46). The relative importance of these pathways and the effectors engaged in signal transduction by IGF-IR are probably cell context-dependent and remain to be fully elucidated.

IV. IGF-IR and the Cell Cycle

The IGF-IR can regulate cell-cycle progression through control of several cycle checkpoints. It can facilitate G₀-G₁ transition through activation of p70 S6K, leading to phosphorylation of the S6 ribosomal protein and an increased ribosomal pool necessary for entry into the cycle (47). It can promote G₁-S transition by increasing cyclin D1 and CDK4 gene expression, leading to retinoblastoma protein phosphorylation, release of the transcription factor E2F, and synthesis of cyclin E (48, 49). The IGF-IR-induced increase in cyclin D1 synthesis can be mediated through several alternative mechanisms. It may be transcriptionally regulated through the ERK pathway (50), or it may be mediated through increased mRNA stability in a PI-3K/Akt-dependent manner (51). PI-3K/Akt signaling can also increase cyclin D1 levels through enhanced mTOR-mediated protein translation and inhibition of glycogen synthase kinase-3-mediated cyclin D1 phosphorylation (51–53). In addition, IGF-IR can also down-regulate the transcription of the cyclin-dependent kinase (CDK) inhibitor (CDKI) p27^{KIP1} or alter its processing and nuclear localization (54) through a PI-3K/Akt and phosphatase and tensin homologous on chromosome 10 (PTEN)-dependent mechanism (see diagram in Fig. 2). The IGF-IR may also exert a regulatory role at the G₂-M transition, possibly by increasing cyclins A and B and cdc2 synthesis (55). Taken together, the data suggest that the IGF-IR/IGF axis can positively regulate cell-cycle progression at several phases, but its major direct effect is probably exerted at the G₁-S interface, and this is mediated through the PI-3K/Akt and/or ERK pathways.

V. Post-Ligand Binding Receptor Processing and the Regulation of IGF-IR Activity

A. Role of phosphatases

IGF-I stimulates the phosphorylation of the membrane scaffolding protein Src homology 2 domain-containing protein tyrosine phosphatase substrate-1 (SHPS-1). Phosphorylated SHPS-1 subsequently recruits the Src homology 2 domain tyrosine phosphatase (SHP-2) to the phosphorylated IGF-IR (56). SHP-2 can have both positive and negative effects on IGF-IR signaling. The dephosphorylation of IGF-IR by SHP-2 attenuates PI-3K-mediated IGF-IR signaling, as has also been shown for the IR (57). In contrast, data suggest that MAPK signaling may actually be enhanced by SHPS-1 phosphorylation and SHP-2 recruitment (58) through Shc/Grb2 (59).

One of the molecules that can associate with SHP-2, Src, and the p85 subunit of PI-3K is the receptor for activated C

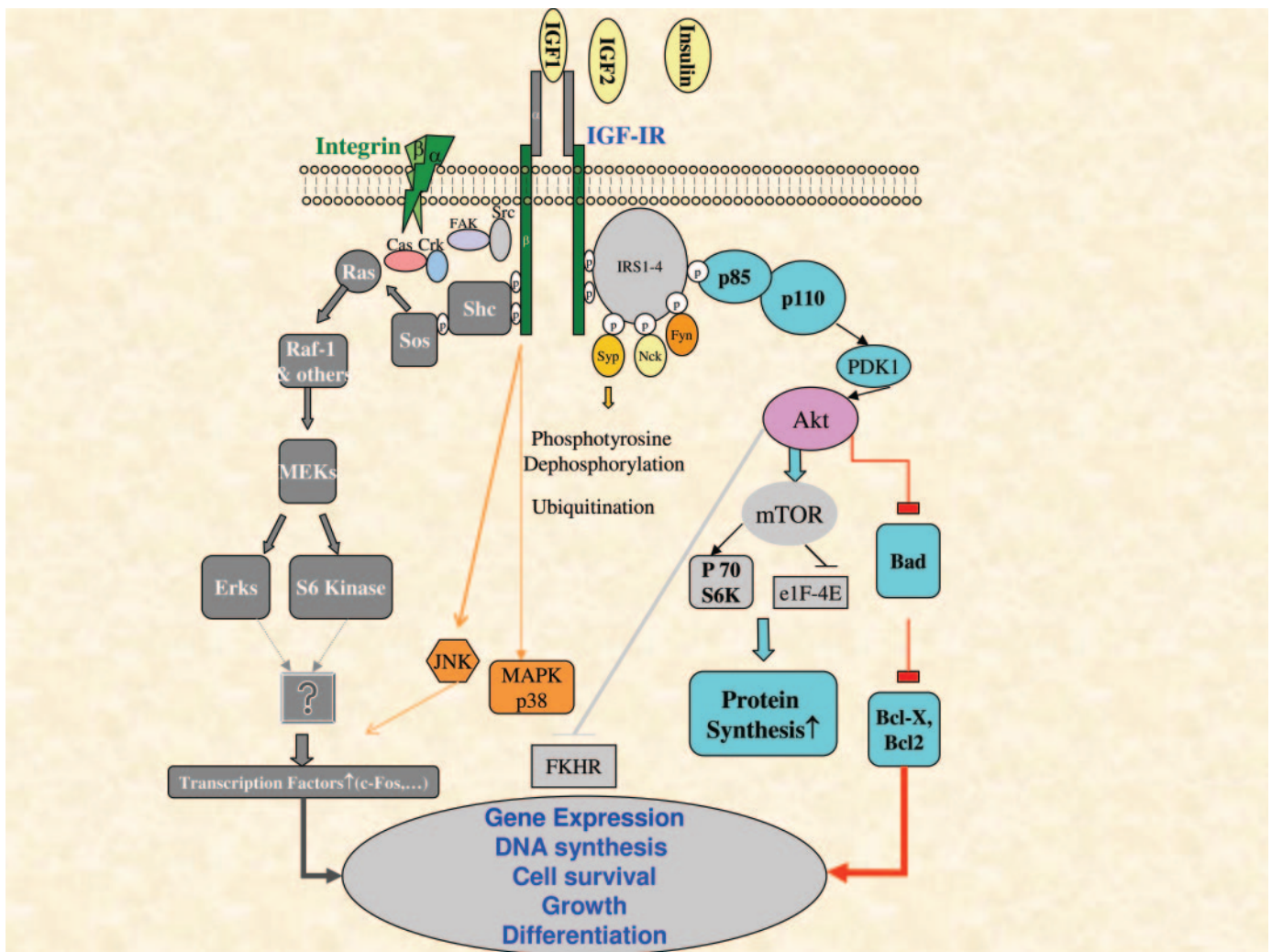


FIG. 1. Signal transduction pathways of the ligand-activated IGF-IR. A schematic representation of the major signaling pathways that can be activated by the autophosphorylated IGF-IR. The cell context, ligand concentrations, and crosstalk with other signaling systems affect the type and strength of the signal and the biological outcome.

kinases (RACK1), a homolog of the β -subunit of heterotrimeric G proteins. Recently, it has been shown that RACK1 also interacts with IGF-IR (60, 61) in a tyrosine kinase activity and receptor autophosphorylation-independent manner and that this requires an intact serine 1248 in the C terminus of the receptor. Interestingly, overexpression of RACK1 has a negative effect on the activation of the PI-3K pathway, but a positive effect on the activation of the MAPK and c-Jun N-terminal kinase (JNK) pathways (61), as was also shown for IGF-IR-associated SHP-2.

Protein tyrosine phosphatase 1B (PTP-1B), a 50-kDa non-transmembrane tyrosine phosphatase, is localized predominantly in the endoplasmic reticulum with its phosphatase domain oriented toward the cytoplasm (62). PTP-1B can dephosphorylate both IGF-IR (63) and IRS-1 (64), and, indeed, in MEFs derived from PTP-1B-deficient mice, IGF-I-induced IGF-IR autophosphorylation and kinase activity were higher than in controls (63). IGF-IR may, in turn, inhibit PTP-1B activity, perhaps through a negative feedback loop. Such a mechanism has been described for the IR. The IR can inac-

tivate PTP-1B by inducing a burst of intracellular hydrogen peroxide. The IR may also suppress serine phosphorylation and thereby inactivate PTP-1B (65).

B. Role of $\alpha\beta 3$

The integrin $\alpha\beta 3$ plays an important role in IGF-IR signaling and its biological functions (66). Maile *et al.* (67) showed that $\alpha\beta 3$ signaling changes the subcellular localization of SHP-2 in a way that decreases its access to phosphorylated IGF-IR, thereby prolonging IGF-IR signaling. Ling *et al.* (68) identified $\beta 3$ as the subunit that recruits SHP-2 and prevents its association with IGF-IR. In smooth muscle cells, echistatin, a disintegrin that blocks $\alpha\beta 3$ ligand binding, reduced receptor phosphorylation, cellular migration, and DNA synthesis in response to IGF-I (67). In some cells, IGF-I can induce a potent JNK response (69). JNK, in turn, can mediate serine phosphorylation of IRS-1 and thereby attenuate IGF-IR signaling (70).

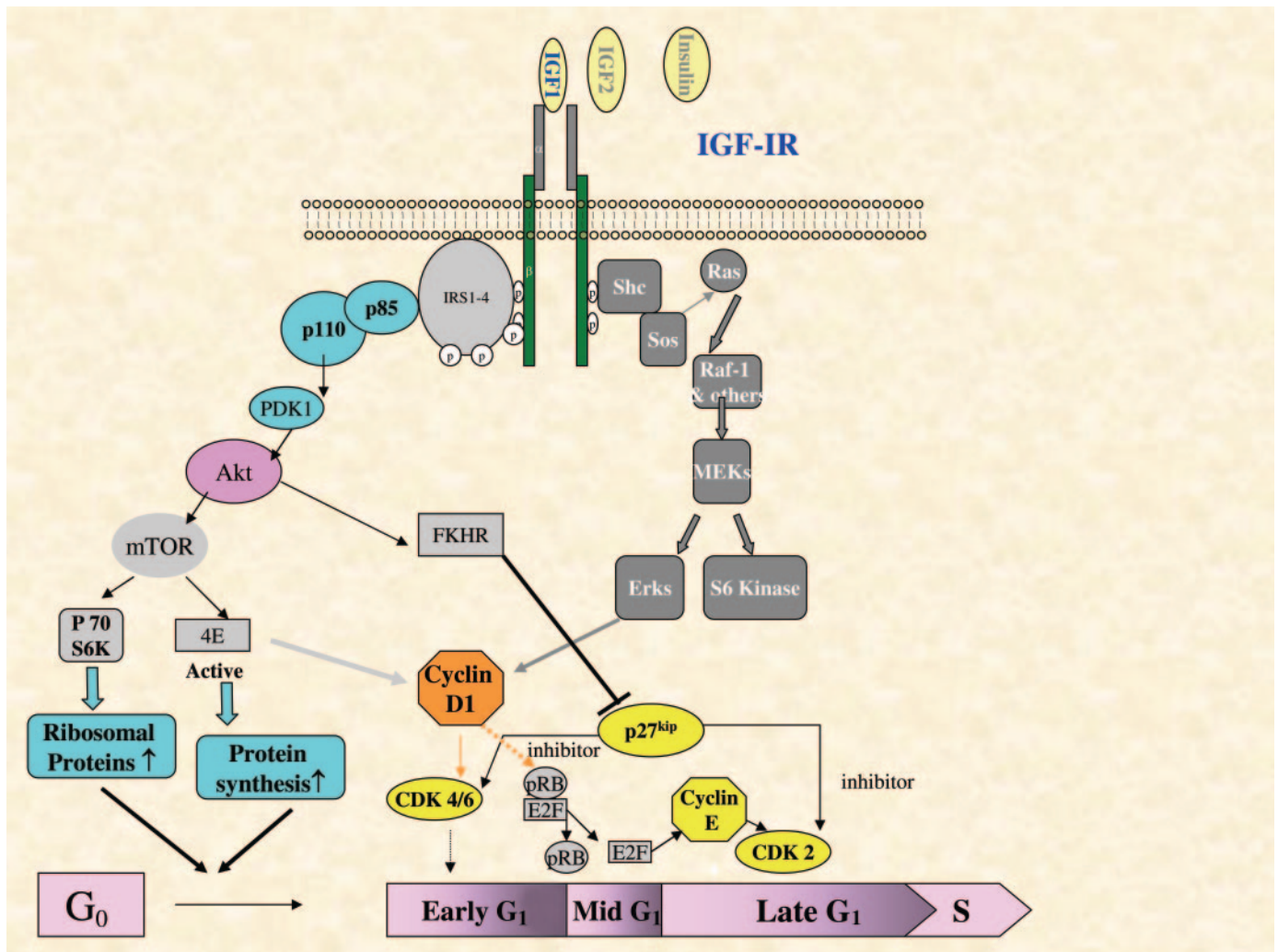


FIG. 2. The role of the IGF-IR in cell-cycle progression. The IGF-IR can affect cell-cycle progression through control of several cycle checkpoints, but its major direct regulatory effect is probably exerted at the G_1 -S interface, via the PI-3K/Akt and/or ERK pathways.

C. Intracellular processing of the IGF-IR/IGF complex

The signaling of receptor tyrosine kinases is tightly linked to, and regulated by, receptor endocytosis and trafficking. Emerging evidence suggests that IGF-IR internalization and signaling are regulated by mechanisms both akin to, and distinct from, those of other receptor kinases. For example, similar to other tyrosine kinase receptors such as the epidermal growth factor (EGF) receptor (EGFR), the mitogenic responses of IGF-IR were shown to be regulated by adaptor protein-2 (AP-2)-dependent endocytosis (71, 72), and two potential “linkers” of IGF-IR to α -adaptin of the AP-2 complex, EHD1 and SNAP29, have recently been identified (71). In addition, ligand-induced IGF-IR recruitment into lipid raft caveolae has also been documented (73–75).

Once in the endosomal compartment, ligand dissociation and proteolysis can also exert a regulatory role on signaling (76, 77). Although the proteolytic enzymes that degrade internalized IGF-I or IGF-II have not been fully characterized, recent work by the Brodt group (77) implicated an E-64-sensitive cysteine proteinase in this process, and this was confirmed in a recent report that documented limited pro-

teolytic cleavage of IGF-I at its C-terminal D domain by cathepsin B (78). In addition, recent studies by the Brodt group (79) suggest that, in intact tumor cells, cathepsin L also participates in this process.

D. Receptor ubiquitination

The ubiquitin system also plays a role in the processing of internalized IGF-IR. Recent studies with cultured cells have implicated two E3 ligases, namely, Nedd4 and mouse double minute 2 (MDM2), in IGF-IR ubiquitination and processing. Nedd4 binds IGF-IR through the adaptor protein Grb10. Studies in MEFs overexpressing Nedd4 and IGF-IR have shown that the Grb10/Nedd4/IGF-IR complex drives ligand-dependent ubiquitination of the internalized IGF-IR. In these cells, ubiquitination was shown to occur at the plasma membrane, probably before the formation of endocytic vesicles (80). Interestingly, mice with a disruption in the maternal Grb10 allele had embryo and placental overgrowth and were 30% overweight compared with wild-type controls, identifying Grb10 as a potent growth inhibitor (81).

Another member of the E3 ligase family involved in IGF-IR degradation is the MDM2 proto-oncoprotein, a RING finger ubiquitin ligase that is transcriptionally regulated by IGF-I (82). The MDM2 protein binds to the IGF-IR β -subunit through the adaptor β -arrestin (83), thereby recruiting ubiquitin to the IGF-IR and initiating its degradation (84).

E. Role of IGFBP-3

IGF-I up-regulates IGFBP-3 at the transcriptional and/or posttranscriptional levels (85). The cell context determines the final effect of IGFBP-3 on the cell and whether it acts as an inhibitor or potentiator of IGF functions. For instance, in both normal and transformed mammary epithelial cells, IGFBP-3 potentiates the mitogenic effects of IGF-I (86). However, in other cancer cells such as the human breast carcinoma cell line MCF-7, IGFBP-3 activates a phosphotyrosine phosphatase that dephosphorylates IGF-IR, thereby disrupting signaling. This inhibitory effect is independent of IGF-I binding (87). In several non-small cell lung cancer cell lines, IGFBP-3 has been shown to act as a potent inhibitor of IGF-IR signaling by interfering with both the PI-3K/Akt and MAPK signaling pathways, causing growth arrest and inducing apoptosis (88).

VI. The Evidence for the Involvement of IGF in Human Malignancy

The IGF-IR and its ligands play a critical role during embryogenesis and development in human and animal species. During postnatal development and longitudinal growth, many GH functions are mediated via IGF-I. During puberty, elevated sex steroid levels (particularly estrogens) stimulate GH production, leading to activation of the GH/IGF-I axis (89). Although serum IGF-I levels decline progressively after puberty, significant levels of circulating IGF-II are detectable throughout adult life. IGF-IR mRNA levels also decline after puberty, but remain high in some tissues such as the brain and kidney. However, increased expression of IGF-I, IGF-II, IGF-IR, or combinations thereof have been documented in various malignancies including glioblastomas, neuroblastomas, meningiomas (90), medulloblastomas (91), carcinomas of the breast (reviewed in Refs. 92 and 93), malignancies of the gastrointestinal tract, such as colorectal and pancreatic carcinomas, and ovarian cancer. Summarized in Table 1 are different studies that examined IGF-I and IGF-II levels in clinical specimens obtained from different tumor types. These data show that whereas a correlation between IGF-I/IGF-II expression levels and tumor progression could be consistently documented in some malignancies (*e.g.*, colorectal, hepatocellular, and pancreatic carcinomas), no consistent correlation was seen in others (*e.g.*, breast cancer). Moreover, in some cases, conflicting results were obtained in different studies that analyzed the same types of cancers (*e.g.*, gliomas). These discrepancies may have been due to differences in the methods used for the analyses or to other variables such as tissue preservation methods and sample size (see Table 1 and references therein). Taken as a whole, however, these studies suggest that the IGFs can play a paracrine and/or autocrine role in promoting tumor growth *in situ*

during tumor progression but that these roles may vary depending on the tissue of origin. These studies also highlight the fact that studies based on direct analysis of tissue specimens should be interpreted with caution.

Evidence from recent epidemiological studies is also consistent with the conclusion that IGFs play a role in tumor development. These studies have shown that high concentrations of serum IGFs (when the highest quartile is compared with the lowest, within the normal range) and/or lower levels of IGFBPs are associated with increased risk for several cancers, including premenopausal breast carcinoma (94–96), prostate carcinoma (97, 98), lung cancer (99), colorectal carcinoma (100–102), endometrial cancer (103), and bladder cancer (104), supporting a possible paracrine role for IGFs in tumor development. A very recent report identified the loss of imprinting (LOI) of the IGF-II gene, frequently observed in the colonic mucosa of colorectal carcinoma patients, as an individual risk factor for developing colorectal carcinoma. Using a DNA-based blood test, the same genetic alteration was also found in peripheral lymphocytes of the patients (105). In addition, an increased incidence of precancerous colonic adenoma (large or tubulovillous/villous) (106) and cervical squamous intraepithelial lesions (107) has been linked to higher levels of circulating IGF-I, suggesting that the IGF system may play a role in the early stages of transformation and carcinogenesis.

Although *in vitro* studies and animal models provide compelling evidence in support of the functional importance of the IGF-IR in cancer cell growth (see *Section VIII*), the clinical and prognostic significance of IGF-IR expression levels to human malignancies remains unclear. This is particularly true for breast cancer where conflicting data exist. For example, when IGF-IR expression was recently evaluated in 210 formalin-fixed, paraffin-embedded primary breast cancers using immunohistochemistry, IGF-IR overexpression was observed in 43.8% of the tumors, but it had no correlation with prognosis, tumor size, nodal status, histological grade, hormone receptor status, or human EGF2 status (108). In contrast, however, other studies using breast cancer specimens identified IGF-IR as a potential prognostic factor in this disease. For example, in a study of 35 cases of benign breast disease, 43% of the lesions were IGF-IR-positive, suggesting that the increase in IGF-IR could be a marker of progression (109). A study of a larger cohort that included 126 breast cancer samples revealed that 39% were IGF-IR-positive, a significant correlation between IGF-IR expression and estrogen receptor (ER) status was noted, and the expression of IGF-IR did correlate with disease-free survival (110). This study suggested that patients with ER-negative but IGF-IR-positive tumors have a worse prognosis than patients with ER- and IGF-IR-negative tumors. Another study of 150 cases of primary breast carcinoma revealed that 47% of the tumors had increased levels of IGF-IR, and this was correlated with lower nuclear grade, positive ER and/or progesterone status (111).

In prostate cancer, the evidence for the involvement of IGF-IR in disease progression is also controversial. For example, when expression of IGF-I, IGF-II, and their receptors was examined in 23 paired benign and neoplastic prostate specimens, no correlation was found between their expres-

TABLE 1. IGF-I and IGF-II expression levels in human cancer specimens

Tumor type	Method of detection	Summary of the findings	Ref.
Glioma	Slot blot and Northern blot analysis	IGF-I mRNA was increased 1.1- to 4.0-fold in glioma and anaplastic astrocytoma specimens as compared to normal brain tissue.	309
Glioma	Immunohistochemistry	IGF-II expression was increased 5- to 50- fold in 4 of 4 gliomas.	310
Astrocytoma	<i>In situ</i> hybridization and immunohistochemistry	IGF-I immunoreactivity was found in 6 of 9 gliomas. IGF-I and IGF-II were expressed in 10 of 10 human astrocytoma specimens.	311
Meningioma	Immunohistochemistry	IGF-II was expressed in 3 meningiomas.	312
Astrocytoma	Northern blot	IGF-I immunoreactivity in 39 astrocytomas showed positive correlation with histopathological grade. No expression of IGF-II was found in 5 astrocytomas and 2 glioblastomas.	313
Glioblastoma	Northern blot	No expression of IGF-II was found in 9 of 9 gliomas.	314
Glioma	Northern blot	IGF-II mRNA was found in 4 of 4 meningiomas.	315
Meningioma	Northern blot	IGF-II was expressed in 2 of 2 meningiomas.	310
Meningioma	Northern blot	IGF-II and IGFBP-2 expression was found in all meningiomas. High IGF-II/IGFBP-2 ratio was associated with poor prognosis and death.	90
Meningioma	cDNA microarray	IGF-II expression was increased in meningiomas.	316
Medulloblastoma	<i>In situ</i> hybridization	IGF-I was significantly increased in 14 of 14 tumor specimens whereas IGF-II showed variable but significant expression in 9 of 14 samples. No relationship could be established between clinical parameters and IGF-II mRNA expression levels.	317
Colon cancer	Northern blot	IGF-I mRNA was elevated 3- to 5-fold in 4 of 20 colon cancer specimens.	318
Colon cancer	Northern blot	IGF-II mRNA was increased 10- to 50-fold in 8 of 20 colon cancer specimens.	319
Colon cancer	Immunohistochemistry	IGF-II mRNA was increased 2- to 800-fold in 7 of 21 colon cancer specimens.	320
Colon cancer	Immunohistochemistry	IGF-II mRNA was detected in 68 of 92 colon cancer specimens. A positive correlation was found between IGF-II expression and tumor grade.	321
Colon cancer	RNase protection assay	IGF-II mRNA was detected in 68 of 92 colon cancer specimens. IGF-II protein levels were increased 2-fold.	322
Colon cancer	Oligonucleotide arrays and real time PCR	IGF-II expression was significantly increased in 139 primary tumors as compared to normal mucosae. However, they were significantly lower in liver metastases than in colorectal tumors or normal mucosae.	323
Gastric cancer	<i>In situ</i> hybridization	IGF-I mRNA expression was detected in 3 of 3 surgical specimens of gastric cancer.	324
Gastrinomas	RT-PCR	IGF-I expression was increased over 254-fold in 89% of the samples. Increased IGF-I levels correlated with increased tumor growth, aggressiveness, and liver metastasis.	325
Pancreatic cancer	<i>In situ</i> hybridization	IGF-I and IGF-II levels were increased 32-fold in 12 of 12 pancreatic cancer specimens.	326
Hepatoma	Northern blot	Low IGF-I expression was found in 7 of 7 hepatoma specimens.	327
Liver cancer	Northern blot	IGF-II expression was found in 4 of 7 specimens.	328
Hepatocellular carcinoma	<i>In situ</i> hybridization and immunohistochemistry	IGF-II mRNA was increased 40- to 100-fold in 9 of 40 liver cancer surgical specimens.	329
Hepatocellular carcinoma	Immunohistochemistry	IGF-II mRNA was increased in hepatocellular carcinoma specimens.	330
Hepatocellular carcinoma	DNA microarray	IGF-II expression was detected in 9 of 15 hepatitis B-positive patients and 10 of 39 hepatitis B-negative patients.	331
Lung cancer	RIA	Increased IGF-II expression was correlated with advanced tumor stage and poor prognosis.	332
Lung cancer	RIA	IGF-I concentration in cancerous tissue extracts was increased 3-fold as compared to normal lung tissue.	333
Tyroid cancer	RIA	IGF-I concentrations in cancerous thyroid extracts, was increased as compared to normal thyroid tissue.	334
Breast cancer	<i>In situ</i> hybridization	IGF-I mRNA was detected in 12 of 20 breast cancer surgical specimens but was limited to the stromal element.	332
Breast cancer	<i>In situ</i> hybridization	IGF-I and IGF-II mRNA were detected only in stromal cells and were not detected in either the normal or malignant epithelial cells. In 1 of 10 specimens IGF-II expression was detected in malignant epithelial cells.	333
Breast cancer	<i>In situ</i> hybridization	IGF-II mRNA was detected in 7 of 11 breast cancer surgical specimens but was limited to the stromal element.	334

TABLE 1. *Continued*

Tumor type	Method of detection	Summary of the findings	Ref.
Breast cancer	Real time PCR	IGF-I mRNA level was lower in the cancerous tissue than non-neoplastic breast tissue in 31 specimens.	286
Ovarian cancer	RNase protection assay	IGF-I mRNA was detected in 7 of 7 ovarian cancer surgical specimens.	335
Ovarian cancer	Real time PCR	IGF-II expression increased 300-fold in ovarian cancer as compared to normal tissue. High IGF-II gene expression was associated with high grade and advanced disease stage and was an independent predictor of poor survival in patients with epithelial ovarian cancer.	125
Endometrial cancer	Immunohistochemistry	IGF-I immunoreactivity was increased 7- to 20-fold and IGFBP-1 was decreased 3-fold in endometrial specimens.	336
Prostate cancer	<i>In situ</i> hybridization	IGF-II expression was increased by 30% in prostate adenocarcinoma as compared to benign epithelial cells.	113
Prostate cancer	Immunohistochemistry	IGF-I and IGF-II expressions were higher in high-grade as compared to low-grade tumor areas in 56 prostate cancer specimens.	337
Seminoma	Microarray and real time PCR	IGF-I expression did not differ significantly between normal testicular tissue and seminoma. IGF-II was down-regulated and did not seem to be involved in growth regulation of seminomas.	338
Osteosarcoma	PCR	IGF-I and IGF-II expression was detected in all surgical osteosarcoma specimens.	339
Gallbladder cancer	Immunohistochemistry	IGF-I and IGF-II immunoreactivity was detected in 55 of 57 primary tumors and in 17 of 18 metastases. No association was found with tumor stage, grade, or prognosis.	121
Renal cell carcinoma	Tissue microarray	IGF-I was detected in 110 of 134 clear cell, 8 of 22 chromophobes, and 3 of 20 renal cell carcinomas. All tumors lacked IGF-II. Expression of IGF-I was not related to tumor stage, grade, or prognosis.	340

sion and tumor grade, stage, perineural invasion, or extra-prostatic involvement (112). In another study that analyzed benign epithelium, high-grade prostate intraepithelial neoplasia (PIN), and adenocarcinomas, it was found that IGF-IR mRNA was decreased by 42% in PIN and by 35% in cancer cells compared with benign tissue, suggesting that IGF-IR expression levels were inversely correlated with progression (113). However, these findings were challenged based on another study that demonstrated a significant up-regulation of IGF-IR mRNA and protein expression in primary prostate cancers and bone metastases, compared with benign prostatic epithelium (114).

A role for the IGF system in cancer metastasis has recently been documented in several human cancers. For example, Barozzi *et al.* (115) recently studied a panel of markers, including TGF- α , EGFR, matrix metalloproteinase (MMP)-2, IGF-II, vascular endothelial growth factor (VEGF), and microvessel density in human colorectal cancer specimens as potential predictors of colorectal carcinoma metastasis, and they found that only the overexpression of TGF- α , MMP-2, and IGF-II was predictive of liver metastasis. This is consistent with another study by Hakam *et al.* (116) that showed a stepwise increase in the expression of IGF-IR during progression from colonic adenomas toward primary colorectal adenocarcinomas and metastases. Although moderate to strong cytoplasmic immunostaining was observed in over 90% of the adenocarcinomas and metastases, only a faint cytoplasmic stain was seen in the majority of adenomas. Strong IGF-IR positivity correlated with the stage of the disease (116). Although these data suggest that IGF-IR expression increases during the progression of this disease, it is important to note that a recent study based on tissue

microarray analysis, performed on 86 colorectal carcinoma metastases, revealed that IGF-IR and p53 expression levels were not significantly associated with long-term survival (117). Xie *et al.* (118) compared IGF-IR expression in human synovial sarcomas with different levels of lung metastases and found that overexpression of IGF-IR was significantly linked to gain of a metastatic phenotype in this malignancy. All-Ericsson *et al.* (119) found a significant correlation between high IGF-IR expression levels and the risk of liver metastasis and death in uveal melanoma patients. Similar findings were reported in studies of gastric cancer where it was found that IGF-IR overexpression in the primary tumor correlated with increased lymph node metastasis (120). Moreover, an analysis of gallbladder carcinomas revealed IGF-IR expression in 52 of 55 primary tumors and in all 17 corresponding metastases (121).

The link between IGF and metastasis may be the basis for the identification of IGF and IGF-IR as predictors of poor outcome in some other types of cancer. For example, a Kaplan-Meier analysis suggested that patients with IGF-IR-positive renal clear cell carcinoma (CC-RCC) had a significantly decreased cancer-related survival rate relative to those with IGF-IR-negative CC-RCC (122, 123). For adrenocortical tumors, a high risk of postsurgical recurrence is generally predicted in cases with regional invasion or distant metastases. Results of a recent prospective study involving 114 patients identified IGF-II overexpression as a reliable prognostic marker in this disease, suggesting that it can be used to identify patients with a high risk of recurrence (124). In a multivariate analysis with 109 epithelial ovarian cancer patients, the relative IGF-II expression level was found to be an

independent predictor of poor survival that was associated with high-grade, advanced-stage disease (125).

More recent findings have shown that IGF-I/IGFBP ratios may actually be better predictors of disease progression than either one of these factors independently. For example, in 51 patients that underwent radical cystectomy for bladder cancer, plasma IGF-I and IGFBP-3 levels, when measured separately, were not significantly different from those in healthy subjects. However, lower preoperative plasma levels of IGFBP-3 in these patients, when adjusted for serum IGF-I levels, were found to be associated with a higher incidence of lymph node metastases and a poorer clinical outcome (126). Similarly, among a group of markers analyzed, including serum prostate-specific antigen (PSA), IGF-I/PSA ratios, and TNM staging, IGFBP-3/PSA ratios were identified as the only significant variable for relapse-free survival and an independent predictor of survival in advanced prostate cancer (127).

When viewed collectively, these studies show that the significance of IGF and IGF-IR expression levels *per se* as indicators of tumor stage or predictors of disease outcome defies simple generalization and may be highly tumor-type specific. However, as discussed extensively below, the relevance of the IGF axis to cancer progression cannot be fully appreciated by analysis of the expression levels of the IGF-IR and its ligands alone because activation of the signaling pathway may occur through alternate mechanisms that bypass the requirement for receptor and/or ligand up-regulation.

VII. Role of the IGF Axis in Metastasis: Insight into Molecular Mechanisms

Cancer metastasis is a multistep process driven by complex molecular interactions between the disseminating cancer cell and its changing microenvironment. Among the rate-limiting steps regulating this process are tumor-induced neovascularization (angiogenesis and lymphangiogenesis), extracellular matrix (ECM) degradation, cell movement through tissue barriers, including entry into and exit from blood vessels, and survival/proliferation within new, otherwise hostile, organ microenvironments (128). As summarized in *Section VII*, the IGF axis can play a regulatory role at each of these intersections, thereby propelling the process forward.

A. Role of the IGF axis in angiogenesis and lymphangiogenesis

One of the major rate-limiting factors in tumor growth is the availability of nutrients and oxygen. Expanding tumors can overcome the lack of a nutrient supply and hypoxic conditions by inducing a process of neovascularization, *i.e.*, angiogenesis. Newly formed vessels also provide the tumor with access to the circulation that is essential for hematogenous metastasis.

Although hypoxia is a major trigger for tumor-dependent angiogenesis, the IGFs and insulin may actually play an early role in this process, preceding and/or augmenting the hypoxic stimulus. In cultured cells, IGF-I and IGF-II can induce

the expression of hypoxia-inducible factor 1 α (HIF-1 α) (129), and this can lead to the formation of the HIF-1 α /arylhydrocarbon receptor nuclear translocator complex. This complex is involved in transcriptional regulation of hypoxia response element-containing genes such as VEGF (130), a major tumor-derived angiogenic factor. In contrast to hypoxia, which can induce HIF-1 α expression by inhibiting its ubiquitination and degradation, IGF-I can induce HIF-1 α protein synthesis directly, via the MAPK and PI-3K pathways (131). In turn, HIF-1 α is required for IGF-II, IGFBP-2, and IGFBP-3 synthesis (129).

The IGF system is involved in angiogenesis through several other mechanisms. IGF-I and IGF-II can induce angiogenesis by stimulating the migration and morphological differentiation of endothelial cells (132, 133). IGF-I is transported via a paracellular route across the vascular endothelial cell lining and binds to the subendothelial ECM, where it may play a role in endothelial cell survival and stability (134). The direct effect of IGF on vascular endothelial cells, and thereby angiogenesis, has recently been confirmed using mice with a vascular endothelial insulin receptor knockout (VENIRKO) or a vascular endothelial IGF receptor knockout (VENIFARKO). The significant reduction in oxygen-induced retinal neovascularization in these mice, relative to controls, implicated both insulin and IGF-I signaling in retinal neovascularization and the regulation of the vascular mediators VEGF, endothelial nitric oxide synthase, and endothelin-1 (135).

Moreover, IGF synthesis is regulated by hypoxic conditions. For example, in newborn rats, hypoxia increased IGF-I mRNA synthesis in the heart and increased both IGF-I and IGF-IR mRNA in the lungs (136). The induction of IGF-II by hypoxia has been documented in the human hepatocellular carcinoma HepG2 cell line (137). The contribution of hypoxia to the up-regulation of IGF-II has been linked to its dual effect on the transcription factor Egr-1 and the Wilms' tumor (WT) 1 suppressor gene. Hypoxia induces the expression and activity of Egr-1, which in turn activates the IGF-II promoter. On the other hand, the expression of WT1, a repressor of IGF-II expression, is reduced under hypoxic conditions (138). In NIH 3T3 cells transfected with the luciferase reporter gene under the control of the IGF-IR promoter, hypoxia, acidic pH, and low-glucose conditions that are typically found in the microenvironment of solid tumors were found to activate the IGF-IR promoter and induce IGF-IR synthesis (139). Thus, the crosstalk between hypoxia and the IGF system, two inducers of angiogenesis, appears to be reciprocal.

The IGF system can cooperate with other tyrosine kinase receptors such as the EGFR in the induction of angiogenesis. This was recently demonstrated in NIH-3T3 cells expressing a truncated, constitutively active form of the EGFR. Under normoxic conditions, VEGF expression in these cells was comparable to control cells expressing an intact receptor, but it increased by up to 6-fold under hypoxic conditions. In the presence of IGF, however, VEGF expression in cells expressing the mutant EGFR was high under normoxic or hypoxic conditions, suggesting that hypoxia (0.1% O₂) did not have an additive effect on VEGF production in the presence of IGF-I (140).

In addition to neovascularization, tumor cells can also

induce the formation of new lymphatic vessels, a process known as lymphangiogenesis. The major angiogenic factors mediating this process are VEGF-C (141) and VEGF-D (142). These factors bind to the VEGFR-3, also known as *fms*-like tyrosine kinase 4 (Flt-4) (see review in Ref. 143). In several human cancers, increased expression of VEGF-C in the primary tumors was shown to correlate with regional lymph node metastasis. VEGF-C may recruit preexisting lymphatic vessels that may then become directly involved in tumor cell chemotaxis, intralymphatic intravasation, and distal dissemination (144). Recent studies by the Brodt group (145) identified the IGF-IR as a positive regulator of VEGF-C production and lymphatic metastasis. The PI-3K signaling pathway was implicated in this induction. A more recent study in an experimental animal model confirmed the role of the IGFs in lymphatic metastasis and showed that, in addition to the induction of VEGF-C, lymphangiogenesis may also be driven by a direct activation of the IGF-IR on lymphatic endothelial cells, resulting in increased motility and proliferation (146).

B. The role of the IGF axis in tumor invasion

1. *Regulation of MMP expression and activity.* The Zn^{2+} -dependent MMPs play a major role in ECM remodeling and tissue homeostasis under normal physiological conditions. They have been identified as the major molecular mediators of ECM degradation and tumor invasion in malignant progression and metastasis (see review in Ref. 147). In particular, the type IV collagenases MMP-2 and MMP-9 and the membrane type 1 MMP (MMP-14) have been implicated in ECM degradation and cellular invasion that are associated with both tumor-dependent angiogenesis and tumor invasion. The IGF system plays a role in the regulation of several of the MMPs and can, thereby, promote tumor invasion. Several groups, including our own, identified IGF-IR as a promoter of MMP-2 synthesis and tumor invasion, as measured *in vitro* in Matrigel (148–151). Down- or up-modulation of IGF-IR expression altered MMP-2 expression levels, invasion, and metastasis in a Lewis lung carcinoma model of liver metastasis (150). Using IGF-IR mutants with tyrosine-alanine substitutions in the kinase and C-terminal domains, it was found that signals from both regions of the receptor were required for MMP-2 induction and tumor invasion (152). Subsequently, it was shown that the IGF-IR can exert a dual regulatory effect on MMP-2 production, up-regulating it when the PI-3K signaling pathway is optimally activated, but reducing it under conditions that preferentially activate the MAPK pathway. This may partially explain an apparent dichotomy in the role of IGF in MMP-2 regulation, because both positive and negative regulatory effects have been reported (148).

The MMPs are generally produced as inactive proenzymes and require activation through proteolytic processing (147). MMP-14 is a major proteolytic activator of pro-MMP-2, and has recently been identified as another member of the MMP family that is subject to regulation by the IGF-IR, via PI-3K/Akt/mTOR signaling (153). Thus, the IGF system can optimize ECM degradation and invasion by coordinately promoting MMP-2 production and its activation.

IGF-I has also been implicated in the regulation of a second collagenase, namely MMP-9. Mira *et al.* (154) have shown that in the breast carcinoma MCF-7 cell line, IGF-I significantly increased cell surface-associated MMP-9 activity and enhanced cell migration through vitronectin. However, in this model, the increased production of MMP-9 did not appear to correlate with the invasive phenotype of MCF-7 cells.

It should be noted that, whereas positive regulation of metalloproteinases by IGF-I has been well documented in tumorigenic cells, this may not be the case for normal cells or tumor cells with a nonaggressive phenotype. For instance, in mesangial kidney cells obtained from nonobese, diabetic mice, IGF-I decreased MMP-2 expression and activity, and this was thought to contribute to reduced turnover of ECM and the development of glomerulosclerosis, shortly after the onset of diabetes (155). In mouse skeletal myoblasts, IGF-I did not induce MMP-2 expression or activity (156). Yoon and Hurta (149) reported that IGF-I could induce MMP-2 production in metastatic H-ras transformed C3 cells, but not in the parental 10T1/2 cells or H-ras transformed cells that form benign tumors *in vivo*. A lack of a direct regulatory link has also been reported for the poorly metastatic MDA-MB-231 human breast cancer cells that express IGF-IR as well as MMP-2 and MMP-9 (157). Taken together, the studies suggest that tumor progression through the accumulation of genetic alterations, a hallmark of cancer, may enable an IGF-mediated regulation of MMP-2 (possibly through the release of a negative regulation of PI-3K signaling), and that the crosstalk between the two systems is reciprocal. Indeed, in cells where IGF-IR regulates MMP expression, MMPs in turn, can increase IGF bioavailability by degrading IGFBP-3 (158) and IGFBP-5 (159). This regulatory loop was recently demonstrated in the DU-145 androgen-independent human prostate adenocarcinoma cell line. When these cells were transfected with an MMP-9 antisense DNA, cell proliferation was markedly reduced, and this reduction could be reversed by the addition of IGF-I. The reduction in cell proliferation in this system was linked to reduced IGFBP-3 proteolysis and decreased IGF-IR-mediated signaling (160). In agreement with these observations is the finding that tissue inhibitor of metalloproteinases-1, an inhibitor of MMP-mediated proteolysis, blocks IGFBP-3 proteolysis and can reduce IGF-IR signaling (161).

Finally, several recent studies have implicated the matrix metalloproteinase MMP-7, an enzyme frequently up-regulated during malignant progression (162), in proteolytic processing of all six IGFBPs, identifying it as an enhancer of IGF-IR phosphorylation and signaling (162–164).

2. *Regulation of the uPAR/uPA system.* The urokinase plasminogen activator (uPA) receptor (uPAR)/uPA system also plays a major role in ECM proteolysis and tumor invasion. Secreted uPA binds to its cell membrane-associated receptor and converts serum plasminogen to plasmin, a broad-spectrum serum protease that can degrade basement membrane proteins. In addition, tumor and endothelial cell-derived uPA can also promote angiogenesis. IGF-IR was shown to regulate uPA expression in breast cancer cells (157) and both uPA and uPAR in pancreatic cancer cells (165). In the latter study, it was shown that the IGF-I-dependent migration and

invasion of human pancreatic carcinoma L3.6 pl cells were uPA/uPAR-driven, because they could be blocked by antibodies directed to either uPA or uPAR. The role of IGF-IR in uPA regulation was also demonstrated when murine mammary carcinoma EMT6 cells were transfected with an antisense IGF-IR construct, which led to a reduction in uPA expression (166).

IGF can up-regulate uPA transcription directly through the AP-1 and Ets sites in the uPA promoter in a MAPK- and PI-3K-dependent manner (167). Alternatively, as was recently shown in a rhabdomyosarcoma cell line, IGF-I and -II can increase binding of single-chain uPA to cell-surface uPAR, possibly through the posttranscriptional modification of the uPAR by a mechanism yet to be defined (168).

C. Role of IGF in tumor survival and growth in secondary sites

Metastasis to secondary organs is not an efficient process (169). The majority of tumor cells invading a secondary site either die or cannot proliferate in the foreign microenvironment. The ability of tumor cells to colonize secondary sites is determined by a combination of tumor and host-dependent factors. Site selectivity of metastasis is thought to reflect a complementarity between tumor cell properties and unique favorable growth conditions in the target organ. Work by Brodt *et al.*, using variants of the Lewis lung carcinoma, identified IGF-I as the major factor promoting the growth of highly metastatic tumor cells in the mouse liver. Site-directed mutagenesis showed that tyrosines in the kinase and C-terminal domains of the IGF-IR were involved in promoting liver metastasis in this model (152). Moreover,

highly metastatic H-59 cells engineered to express a soluble IGF-IR molecule (IGF-IR⁹³³), consisting of the entire extracellular domain of the receptor, had a significantly diminished potential to form liver metastases (Fig. 3), directly implicating paracrine, hepatic IGF-I in liver metastasis in this model (170).

A validation of these findings in an animal model of colon adenocarcinoma was recently provided by the LeRoith group (171). In this study, murine colon 38 adenocarcinoma tissue fragments were orthotopically implanted onto the cecum of mice with a liver-specific IGF-I deficiency (LID mice), in which serum IGF-I levels were reduced to 25% of control levels. Mice were then divided into two groups; one group was injected with IGF-I twice daily for 6 wk, and the other received saline injections. IGF-I treatment significantly increased the growth of “primary” cecal tumors, as well as liver metastasis, compared with the saline-injected controls. VEGF expression and vessel abundance in the cecal tumors were shown to be dependent on serum IGF-I levels (171).

Several other lines of evidence support the conclusion that the IGF system plays a role in the regulation of metastases formation in the liver. For example, in hepatic resections of colorectal carcinoma patients, immunohistochemical analyses have shown that the invasive margins of liver metastases were highly positive for IGF-II and IGF-IR. Overexpression of IGF-II mRNA and protein was demonstrated in the normal liver adjacent to the tumor, suggesting that a paracrine interaction may exist between the tumor cells and the adjacent normal stroma (172).

As alluded to earlier, the IGF system regulates lymphangiogenesis. New lymphatic vessels recruited to the tu-

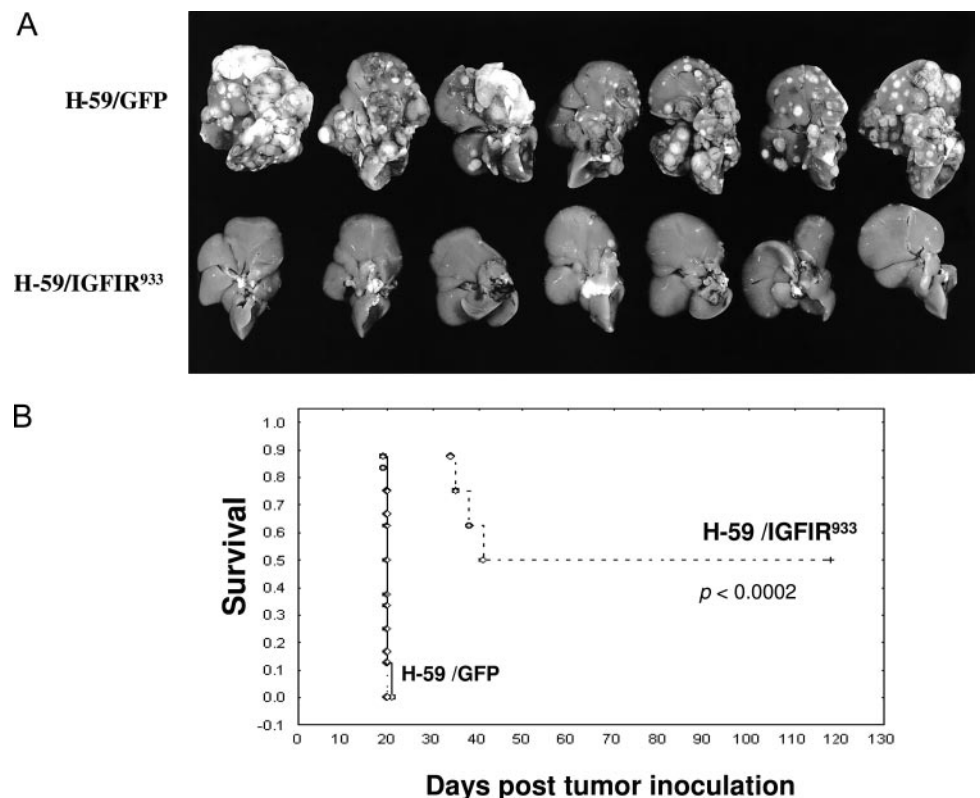


FIG. 3. The soluble IGF-IR⁹³³ blocks hepatic metastasis of carcinoma cells, resulting in increased animal survival. H-59 carcinoma cells were transduced with retroviral particles expressing (or not, H-59/GFP) sIGF-IR⁹³³, and 10⁵ cells were injected into syngeneic mice by the intrasplenic/portal route (A). Liver metastases were enumerated 14 d later. Animal survival (experiment shown in panel B) was monitored for up to 180 d. [Adapted from A. A. Samani *et al.*: *Cancer Res* 64:3380–3385, 2004 (170).]

mor serve as a route of tumor dissemination to the draining lymph nodes and the circulation. In a recent study, the Brodt group has shown that lymphatic stromal cell-derived IGF-I and EGF promote the growth of human and rat breast carcinoma cells, suggesting that IGF may also be involved in tumor cell survival and growth in this organ (173).

The IGF-IR and its ligands may also promote growth of metastatic cancer cells in the bone, the preferred site of metastases for different cancers, including prostate carcinoma (174). The IGFs are among the more abundant growth factors in bone tissue and are synthesized by various bone cells, including osteoblasts and bone endothelial cells (175, 176). Osteoblasts also produce multiple IGFBPs (177). A recent study has shown that medium conditioned by the PA-III prostate carcinoma cells could degrade IGFBPs produced by osteoblastic cells, and uPA was identified as the proteolytic enzyme involved (178). This proteolytic activity could potentially increase the bioavailability of IGFs at the site of the invading tumor, with a resulting increase in the growth of both metastatic carcinoma cells (paracrine effect) and osteoblasts (autocrine effect), eventually leading to the osteoblastic reaction characteristic of bone-metastatic prostate cancers (179). In another study, the injection of MDA-Pca-2b human prostate carcinoma cells into the bone of severe combined immunodeficient mice was recently shown to induce *de novo* bone formation within 2 wk of the injection. Coculture of primary mouse osteoblasts derived from the same mice with MDA Pca 2b cells induced DNA synthesis in prostate carcinoma cells, and this was coincidental with IGFBP-3 downregulation in these cells (180). It is highly relevant to note that preoperative plasma IGFBP-3 levels were found to be reduced in patients with prostate cancer metastases and were identified as an independent predictor of tumor progression after surgery, presumably because of an association with occult metastatic disease present at the time of radical prostatectomy (181). Findings relevant to the role of IGF in prostate carcinoma bone metastasis were recently obtained when it was shown that the growth of MDA Pca 2b tumors in human bone fragments that were preimplanted in severe combined immunodeficient mice was drastically reduced after injection of a rat antihuman IGF-I/IGF-II antibody (KM1468) (64).

VIII. Animal Models Confirm the Importance of the IGF System in Cancer Growth and Metastasis

Compelling evidence for the role of the IGF system in cancer initiation, progression, and metastasis has also been obtained from the study of animal models, particularly from genetically altered mice. For example, in the transgenic adenocarcinoma of mouse prostate (TRAMP) model, selective overexpression of the human IGF-I DNA in basal epithelial cells of the prostate resulted in overexpression of IGF-IR in these cells and the spontaneous and stepwise development of the early stages of prostate carcinoma (182). The forced overexpression of IGF-I in the epidermal cells of HK1.IGF-I transgenic mice hypersensitized these cells to tumor induction by promoters such as 12-*O*-tetradecanoylphorbol-13-acetate. Additionally, the exposure of the epidermis to tumor

promoters in these mice resulted in both a reduction in the latent period and a dramatic increase in the number of tumors per mouse, compared with nontransgenic controls (183). In epidermal cells derived from 12-*O*-tetradecanoylphorbol-13-acetate-treated HK1.IGF-I mice, both the IGF-IR and EGFR were constitutively activated. Recently, overexpression of human IGF-I with the bovine keratin 5 (BK5) promoter (BK5.IGF-I transgenic mice) was shown to induce persistent epidermal hyperplasia and lead to spontaneous skin tumor formation in a PI-3K/Akt dependent manner (184).

The tumor-promoting effect of transgenic IGF may be independent of its binding to the IGFBPs. This was demonstrated in mice that overexpress the transgene des-IGF-I, an IGF-I analog with low affinity for IGFBP that retains a high binding affinity for IGF-IR. In WAP-DES mice, there was a marked increase in the incidence of mammary adenocarcinomas, with 53% of the mice developing tumors by 23 months of age (compared with no tumors in the controls). Interestingly, when these mice were mated with mice transgenic for a mutant form of p53 (p53172R-H), the incidence of mammary tumors in the WAP-DES/p53 bitransgenic offspring was similar to that seen in WAP-DES mice, but 2- to 3-fold higher than that in p53172R-H females (185), suggesting that the IGF system can provide the “second hit” needed for malignant transformation after loss of tumor suppressor expression.

In another study by Carboni *et al.* (186), mice were engineered to express a novel human CD8 α -IGF-IR fusion protein under the control of the mouse mammary tumor virus promoter. The extracellular CD8 α portion of this protein could homodimerize through disulfide bond formation, constitutively activating the intracellular IGF-IR portion in a ligand-independent manner. These mice developed salivary and mammary adenocarcinomas as early as 6 wk after birth, with a palpable mammary mass at 8 wk of age. The salivary gland tumors were associated with scattered lymphatic vessels and invaded the adjacent striated muscle. The mammary adenomas and adenocarcinomas were multifocal and seen within adjacent lobules (186).

Supporting evidence for the role of IGF in the development of mammary and prostate carcinomas was obtained from a study using Noble rats implanted sc for 1 yr with testosterone and estradiol capsules. In these rats, a stepwise tumor progression from hyperplasia/dysplasia to carcinoma *in situ* and adenocarcinoma was observed. All 62 treated rats developed prostatic hyperplasia within 2 months, 51 rats showed dysplastic features, and 24 rats had microscopic tumors that fully developed into macroscopic adenocarcinomas within 7 months after treatment. Immunohistochemical analysis of the prostate glands confirmed that the exposure to increased hormone levels caused increased IGF-I production in prostate stromal cells and that this, in turn, caused increased prostatic epithelial cell proliferation in a paracrine manner. VEGF overexpression was detectable during the dysplastic and carcinomatous phases. Eventually, the malignant epithelial cells were able to produce IGF-I and promote their own growth in an autocrine manner (187). This paracrine/autocrine switch was coincidental with the progression to a malignant phenotype. Interestingly, similar to

findings in the TRAMP model (above), IGF-IR was weakly expressed in glandular epithelial cells of the normal prostate, but its expression was strongly increased in hyperplastic, dysplastic, and neoplastic epithelial tumor cells.

Increased, IGF-induced tumor incidence is not specific for glandular hormone-dependent malignancies. In an IGF-II transgenic model, transgene overexpression in the lung epithelium induced lung tumors with morphological characteristics of human pulmonary adenocarcinoma in 69% of mice older than 18 months. Analysis of tumor sections revealed that downstream mediators of IGF-IR signaling such as Erk1/2, were hyperphosphorylated in these cells. This model validated earlier clinical studies that identified increased levels of IGF-II as a risk factor for human pulmonary adenocarcinoma (188).

Compelling evidence for the potential role of the IGF system in malignant progression in the pancreas was recently obtained using transgenic RIP1-Tag2 mice that overexpress the SV40-T antigen under the control of an insulin promoter. These mice have focally up-regulated IGF-II expression in the pancreatic islet β -cells, causing the formation of hyperproliferative/dysplastic β -cell lesions. The role of IGF-II in this process was confirmed by crossing these mice to IGF-II^{-/-} null mice. The double transgenic RIP1-Tag2/IGF-II^{-/-} mice developed markedly smaller tumors than RIP1-Tag2 mice, and this was linked to a 5-fold increase in β -cell apoptosis (189). To assess whether the low IGF-IR levels expressed in the β -cells limited the progression of hyperplastic foci to malignant/invasive lesions in these mice, the RIP1-Tag2 mice were crossed with RIP7-IGF-IR mice that overexpress human IGF-IR under the control of the insulin promoter. The overexpression of both IGF-II and the IGF-IR in the offspring resulted in accelerated β -cell tumor formation, with the rapid development of lymph-node metastases (190). This study confirmed previous observations based on genetically altered tumor cell lines, and provided strong *in vivo* evidence that IGF-IR can drive the acquisition of an invasive/metastatic phenotype by tumor cells.

In human embryonic development, IGF-II expression is maternally imprinted under the control of the upstream, untranslated *H19* gene. Deletion of the *H19* gene results in a biallelic expression (LOI) of IGF-II. To test the effect of IGF-II overproduction on the development of colon tumors, Sakatani *et al.* (191) engineered a novel mouse model by crossing a male *Apc*^{+/^{Min} *Min* mouse carrying a mutation in the *Apc* gene with a female *H19*^{+/-} mouse. The *H19*^{+/+} progeny had a 2-fold increase in IGF-II expression levels and developed twice as many adenomas as control *H19*^{+/+} mice in both the small intestine and the colon. Interestingly, *H19*^{+/+} mice also had longer intestinal crypts, independently of *Apc* status. This increase did not result from increased cell proliferation or decreased apoptosis in the crypt and may have been due to a shift in the ratio of undifferentiated to differentiated epithelial cells in the mucosa, as suggested by the increased expression of stem cell markers such as *musashi1* in these crypts. These findings may be highly relevant to the human disease, because an analysis of routine colonoscopy biopsies recently revealed that 90–100% of patients with LOI in their colonic specimens also exhibited abundant expression of *musashi1* and altered colon epithelial maturation. Together,}

these observations suggest that loss of IGF-II imprinting triggers a dedifferentiation in colon mucosal cells, and this sets the stage for a tumor initiation process.

If overexpression or constitutive activation of positive effectors of the IGF system promotes cancer, it follows that down-regulation of these molecules should have the opposing effect, namely, inhibition of tumor growth. Indeed, down-regulation of IGF-I or overexpression of IGFBP-1 has been associated with reduced tumorigenicity in animal models. In *Lit/lit* mice that have a defect in GH production and, therefore, have a significant reduction in IGF-I expression in all tissues, a reduction in the growth of xenotransplanted human MCF-7 cells was observed (192). Likewise, *dw/dw* dwarf mice that are deficient in GH/IGF-I were shown to be resistant to dimethylbenz[α]anthracene (DMBA)-induced carcinogenesis. In transgenic mice that express a GH antagonist and have decreased circulating IGF-I levels, a reduced incidence of mammary tumors relative to controls was observed after exposure to the carcinogen DMBA (193). However, it should be pointed out that in these models, the involvement of other factors affected by reduced GH levels cannot be ruled out. In *LID* mice with a 75% decrease in circulating IGF-I levels (see above), there was a decrease in the incidence of mammary tumors induced with DMBA or the SV40-large T antigen transgene (194). Further evidence for the involvement of the IGF axis in carcinogenesis came from transgenic C57BL/6 mice overexpressing an inducible, human IGFBP-1 cDNA under the control of the mouse metallothionin promoter (195). In control mice, a single ip injection of diethylnitrosamine induced the formation of preneoplastic hepatic lesions that generally overexpressed both IGF-I and IGF-II. However, when IGFBP-1 gene expression was induced by adding ZnSO₄ to the drinking water, hepatocarcinogenesis was inhibited (196), suggesting that IGFBP-1 could effectively interfere with carcinogenesis, presumably by blocking IGF-I functions.

A reduction in serum IGF-I levels can also be achieved through a calorie-restricted diet. When IGF-I was infused into calorie-restricted, p53-deficient mice, the anticarcinogenic effect of calorie restriction was abolished (197). Similar results were obtained when GH or IGF-I was administered to calorie-restricted Fischer rats bearing mononuclear cell leukemia (198). The role of IGF-I in the obesity-linked cancer risk is, however, still unclear. It is thought that in obese individuals, hyperinsulinemia may lead to increased IGF-I and decreased IGFBP-1 levels, resulting in an overall increase in IGF bioavailability and in enhanced IGF-IR and/or IR-A activation. In a study conducted by Yakar *et al.* (199), it was recently found that obese animals have an increased incidence of transplanted tumors, and that this was linked to higher systemic levels of insulin and IGF-I. In the same study, it was also shown that, in the presence of sera from obese mice, anchorage-independent growth of tumor cells, as measured in semisolid agar, was significantly augmented relative to controls, suggesting that factors present in the sera of obese mice can promote several parameters of tumorigenicity (199). However, it should be emphasized that obesity can have multiple physiological effects on the mice and cause up-regulation of multiple serum proteins. The interpretation of these findings, particularly the elucidation of the role of

IGF-I in tumor promotion in these mice, will therefore require further analysis.

IX. The IGF System Confers Radioresistance and Multiple Drug Resistance

The IGF axis may affect the clinical course of malignant disease not only by promoting tumor progression and the acquisition of an aggressive phenotype, but also by providing escape mechanisms from conventional treatment regimens. For the majority of cancers, radio- and chemotherapy are still the treatments of choice. Often, however, tumors develop resistance to these treatments and eventually recur with a more aggressive phenotype. Recent studies suggest that the IGF-IR may play a role in protection from DNA-damaging agents such as chemotherapeutic drugs, UVB and ionizing radiation (200–205). This acquired drug resistance may involve IGF-IR-mediated cell rescue from apoptosis via the PI-3K pathway and/or protection from drug-induced cytostatic effects through activation of the MAPK pathway (201). In addition, the IGF system may play a role in conferring a multiple drug resistance (MDR) phenotype on the cancer cells through the induction of MDR-related genes such as *mdr-1*, *c-H-ras*, and *MnSOD* (206).

IGFs can also interfere with the normal function of p53, a suppressor gene that can trigger cell growth arrest and/or apoptosis in cells with radiation-induced DNA damage. In a recent study, Heron-Milhavet and LeRoith (82) have shown that, in IGF-IR-overexpressing NIH-3T3 cells that are exposed to 4-nitroquinoline-1-oxide-induced DNA damage, IGF-IR can up-regulate MDM2 mRNA synthesis through p38 MAPK activation, but cannot increase the MDM2-p19^{ARF} association. Free, unbound MDM2 translocates to the nucleus, where it can ubiquitinate p53, thereby targeting it to the cytoplasm for proteasomal degradation (82) and reducing its apoptotic effects (207).

Finally, a recent study suggests that IGF-IR may also provide radio-resistance through up-regulation of secretory clusterin (sCLU), a protein that plays a role in breast and colon cancer cell survival. A recent report by Criswell *et al.* (208) implicated IGF-I in the irradiation-induced up-regulation of sCLU in MCF-7 breast carcinoma cells. It was shown that after irradiation, MCF-7 cells overexpress IGF-I, and this results in the phosphorylation/activation of IGF-IR in an autocrine fashion, leading to MAPK signaling, transactivation of *egr-1*, and transcriptional activation of the sCLU gene. Irradiation-induced sCLU expression in these cells could be abrogated by adding IGFBP-3 or a tyrosine kinase inhibitor (AG1024) (208).

In view of the role of the IGF axis in conferring drug and radiation resistance onto malignant cells, receptor and ligand expression levels may provide useful criteria for the selection of a preferred treatment strategy. For example, for patients with locally advanced squamous cell carcinoma of the head and neck that were enrolled in a phase III, combined radiotherapy and chemotherapy trial, loss of heterozygosity for the IGF-IIR was associated with a 3-fold reduction in the 5-yr relapse-free survival and locoregional control in the group that was treated with radiotherapy alone. Interestingly, these

patients benefited most from concurrent chemotherapy (209).

X. Multiple Molecular Mechanisms Can Contribute to the Changes in IGF/IGF-IR Expression and/or Function That Underlie Malignant Progression

Under normal physiological conditions, the IGF system is tightly regulated. The evidence detailed above clearly demonstrates that changes in any of the components of this system may disrupt this equilibrium and consequently trigger and drive malignant progression.

Although IGF-IR and IGF overexpression was recognized early on as a major promoter of tumor progression, it has become clear in recent years that the IGF system can also be altered through diverse molecular mechanisms that do not directly affect receptor or ligand expression levels. These changes can occur via genetic and epigenetic changes in gene expression, perturbed protein synthesis, and posttranslational modifications of different proteins that affect IGF-IR receptor function. They may result in enhancement of pro-malignant effectors such as the IGF ligands, or they may inhibit the production and/or activities of proteins with tumor suppressor functions such as the IGF-IIR, leading to augmented cell growth and tumorigenesis. A review of these diverse mechanisms that alter the function of the IGF system is provided below. A summary can be found in Table 2.

A. Overexpression of IGF-II through loss of imprinting

In human adults, IGF-II is the predominant endocrine IGF ligand, with plasma levels 3- to 7-fold higher than IGF-I (210). In humans, the IGF-II gene is normally maternally imprinted (210). However, several reports on bi-allelic expression (LOI) of the IGF-II gene in different tumors suggest that the dysregulation of IGF-II imprinting may contribute to tumorigenesis. LOI has been reported in colorectal carcinomas (105), Wilms tumor (211), juvenile nasopharyngeal angiofibromas (212), and childhood acute lymphoblastic leukemia (213). In cells that express both parental IGF-II alleles, the

TABLE 2. Multiple molecular mechanisms can alter IGF/IGF-IR expression and/or function and contribute to malignant progression

Mechanism	Effect
LOI	IGF-II overexpression
Gene amplification	IGF-IR overexpression
Overexpression of PCs	Overexpression of multiple effectors
Overexpression of AP-2 transcription factors	Overexpression of multiple effectors
Altered glycosylation of the IGF-IR	Increased ligand binding affinity
Altered IGFBP synthesis or proteolysis	Increased bioavailability of ligands
Constitutive activation of downstream effectors of the IGF-IR	Ligand-independent signaling
Loss of tumor suppressor genes	Overexpression of multiple effectors
	Reduced degradation of IGF-IR
	Downregulation of IGFFBPs

increase in IGF-II production may be the major mechanism promoting cancer development. A recent report on a mouse model of IGF-II LOI and overexpression (described in detail above) supports the role of IGF-II as a tumor initiator in intestinal cancers (191).

B. IGF-IR gene amplification

Gene amplification is a common mechanism for overexpression of proto-oncogenes associated with cellular transformation and tumor progression. IGF-IR gene amplification has been reported in malignant melanoma (214), primary breast cancers (215), and in pancreatic adenocarcinoma where an amplification of band 15q26 was observed (216). However, as discussed in detail above, the frequency of IGF-IR overexpression in human malignancies and its functional relevance to tumor development are the subject of conflicting reports and controversy.

C. Overexpression of the IGFs and IGF-IR through deregulated expression of proprotein convertases

Overexpression of convertases of the proprotein family has been documented in several cancers (217). To date, seven dibasic, specific mammalian proprotein convertases (PCs) have been identified, including the ubiquitously expressed furin, PC1/PC3, PC2, PC4, PACE4, PC5/PC6, and PC7/LPC/PC8. These convertases mediate the processing of multiple polypeptide precursors. In addition to the ubiquitously expressed furin that has been implicated in the processing of multiple proteins of the IGF axis, including IR, IGF-IR, and IGFs (218, 219), several other convertases have been implicated in tissue-specific processing of polypeptide precursors. These include PC5A for IGF-IR (220); PC6A and LPC for IGF-I (218); PACE4, PC6A, PC6B, and LPC for IGF-II (221); and PACE4 for IR (222). In addition, PACE4 and PC6 are also involved in the processing of stromelysin-3 (MMP-11 or Str-3) and membrane type 1-MMP (223), respectively. Inhibition of furin by stable expression of the α 1-antitrypsin Portland (PDX) cDNA in two astrocytoma cell lines inhibited their tumorigenesis (224). In human colon carcinoma HT-29 cells treated in a similar manner, the ability of exogenous IGF-I to activate IGF-IR was suppressed, and this resulted in reduced angiogenesis and suppressed tumor growth following sc implantation (220). These studies demonstrate that enhanced expression of convertases may be an additional mechanism for increasing the activity of the IGF system. This effect can be direct, or it may involve enhanced MMP production that, in turn, can increase IGF bioavailability through IGFBP degradation.

D. Enhanced IGF and IGF-IR expression mediated through overexpression of the AP-2 transcription factors

The AP-2 transcription factors are required for normal growth and morphogenesis during mammalian development. Potential AP-2 binding sites have been identified in the promoters of both the IGF and IGF-IR genes (225, 226). Therefore, the overexpression of AP-2 factors may contribute to the enhanced production and activity of the IGF system. For instance, a significant association between increased expres-

sion of AP-2 γ , a factor frequently amplified in breast cancer cell lines and breast carcinoma (227), and the increased expression of IGF-IR was documented in breast carcinoma specimens (228), whereas in rhabdomyosarcoma cells, an increase in AP-2-dependent IGF-II mRNA expression relative to normal human adult skeletal muscle was reported (229).

E. Posttranslational modification of IGF-IR alters binding affinities

Malignant cells frequently display aberrant protein glycosylation that can result in altered protein function (230). Altered glycosylation of the IGF-IR has been reported in several tumor systems. For example, in glioma cell lines established from different human brain tumors of glial origin (astrocytoma grades III and IV), expression of a 130-kDa IGF-IR α -subunit that binds IGF-I and IGF-II with equal affinities has been reported (231), possibly providing a mechanism for increased utilization of IGF-II by these cells. A 105-kDa form of the β -subunit was identified in two murine neuroblastoma cell lines. Glycopeptidase F digestion confirmed that the increased molecular mass was due to altered N-linked complex-type glycosylation in the extracellular domain of this subunit (232). Interestingly, the same pattern has been reported for rat fetal skeletal muscle IGF-IR β . During fetal development and for 2 wk postnatally, a 105-kDa β -chain is predominant and it is subsequently replaced by the 95-kDa form. This fetal receptor, unlike the mature IGF-IR, can be autophosphorylated in the presence of low physiological concentrations of either insulin or IGF-I (233). The expression of this altered β -chain could therefore enable a response to low concentrations of IGF, providing them with a growth advantage.

F. Overexpression of the insulin receptor (IR)-A

The IR can be expressed in two isoforms (IR-A and IR-B) that differ by the presence or absence of 12 amino acids due to alternative splicing of exon 11. As alluded to earlier, IR-A, unlike IR-B, can bind IGF-II with the same affinity as insulin, and this can induce a mitogenic response (20) (reviewed in Ref. 234). Interestingly, Pandini *et al.* (235) recently demonstrated that the binding of IGF-II or insulin to this receptor in cultured cells, even within the same cell context, can have distinct outcomes and induce different gene expression profiles. In this model, cell cycle progression, DNA synthesis, and angiogenesis were preferentially induced by IGF-II. In another model, the differential effects of IGF-II and insulin were compared in leiomyosarcoma cells deficient in IGF-IR. Although IGF-I had no effect on these cells, IGF-II was more potent than insulin in activating the Shc/ERK pathway and stimulating cell migration, whereas insulin was more potent in activating the PI-3K/Akt pathway and rescuing cells from apoptosis (236).

Under normal physiological conditions, IR-A is expressed in fetal cells. However, increased expression of IR-A has been reported in human breast, colon, and lung tumor specimens (20) and on primary cultures and cell lines derived from

human tumors such as ovarian and thyroid carcinoma cells (234). Because IGF-II is the predominant circulating IGF in human adults, this added mechanism for response to IGF-II can clearly provide the cells with a growth advantage.

G. Reduced expression of IGF-BPs can promote cancer progression

In many cancer cell lines, IGF-BP-3 was shown to have an inhibitory effect on IGF functions. For example, in human MCF-7 breast cancer cells, IGF-BP-3 activates a phosphotyrosine phosphatase that dephosphorylates IGF-IR (87), attenuating its functions. IGF-BP-3 can induce apoptosis in an IGF-I-dependent and -independent manner. Reduced IGF-BP-3 levels can, therefore, affect cell growth in multiple ways, such as increasing IGF bioavailability, attenuating an inhibitory effect on the IGF system through down-regulation of phosphatase activity, and reducing IGF-independent growth inhibitory effects. Indeed, lower IGF-BP-3 levels were linked to increased risk and poor prognosis in many cancers (237, 238). Recently, hypermethylation of the IGF-BP-3 promoter has been identified as one of the mechanisms down-regulating IGF-BP-3 synthesis and resulting in potentiation of the IGF response in non-small cell lung cancer. In this malignancy, IGF-BP-3 promoter hypermethylation was found to be a frequent event, strongly associated with poor prognosis, and the only independent predictor of disease-free survival in stage I disease (239, 240).

Recently, a link was identified between IGF-BP-3 and cathepsin L, a cysteine proteinase that is frequently overexpressed and secreted in transformed and malignant cells and that has been implicated in tumor invasion and metastasis (77, 241). In MEF derived from cathepsin L-deficient mice, an accumulation of IGF-BP-3 in the conditioned medium was revealed, suggesting that increased IGF bioavailability may be one mechanism by which secreted cathepsin L may enhance the invasive/metastatic phenotype (242).

The mechanisms that control IGF-BP synthesis are complex, and the role of IGF in their synthesis appears to be variable and cell type-specific. For example, in primary chondrocytes, IGF-I was shown to increase IGF-BP-3 and IGF-BP-5 synthesis, and MAPK and PI-3K signaling were implicated (243). In contrast, in the SNU-484 human gastric carcinoma cell line, IGF-BP-3 synthesis was down-regulated in a PI-3K-dependent manner (244). Similarly, IGF can also have divergent effects on IGF-BP processing and was shown to inhibit (245) or promote (246) IGF-BP-5 proteolysis, apparently in a cell type-specific manner.

Insulin also affects IGF-BP synthesis. It is the principal regulator of hepatic IGF-BP-1 production (247), rapidly decreases plasma IGF-BP-1 levels in response to nutritional intake (248), and can down-regulate IGF-BP-3 levels (249). Because obesity is frequently associated with chronic hyperinsulinemia, this effect of insulin on IGF-BP synthesis may provide one possible mechanism underlying the link observed between obesity and increased risk for several cancers, such as breast and ovarian carcinomas (250).

H. Overexpression and/or constitutive activation of downstream effectors conveying the IGF signal increase IGF-mediated functions

The IRSs are a family of adaptor proteins that can link the IGF-IR to downstream signal transducers, regulating cellular growth. The four members of the IRS family, IRS-1 to -4, share a high degree of homology. IRS-1 is the most extensively studied of these proteins. This 165- to 195-kDa molecule does not contain Src homology (SH)2 or SH3 domains, but can bind to the IGF-IR β -subunit through a PTB (pTyr-binding) domain. It contains at least 20 potential tyrosine phosphorylation sites and can act as a multisite "docking" protein associating with multiple downstream signaling proteins, including the PI-3K, Syp, Fyn, Nck, and Grb-2, through their SH2 domains (30).

IRS-1 is constitutively activated in various solid tumors, including breast cancers, leiomyomas, Wilms tumor, rhabdomyosarcomas, liposarcomas, leiomyosarcomas, and adrenal cortical carcinomas (251). Overexpression of IRS-1 in MCF-7 breast carcinoma cells was shown to be inversely correlated with the requirement for estrogen (252). In some cancers, overexpression or constitutive activation of IRS-2 seems to be more important than that of IRS-1 for malignant progression. For example, abundant IRS-2 expression was found in ductal carcinoma of the pancreas (253, 254). When IRS phosphorylation status in bone-metastasizing human breast carcinoma MDA-231-BO cells was compared with parental, nonmetastatic MDA-MB-231 cells, IRS-2 (and not IRS-1) was found to be preferentially phosphorylated, in response to IGF-I (255). Recent studies, based on murine models of diethylnitrosamine and SV40 large T antigen-induced hepatocarcinogenesis, as well as on analyses of human hepatocellular carcinoma specimens and Hep3B hepatoma cell lines, identified the coordinated up-regulation of IGF-II, IRS-1, and IRS-2 as one of the common early events in hepatocellular carcinogenesis (256).

Constitutive phosphorylation/activation of ERK1/2 is another mechanism that may reduce tumor cell dependency on exogenous IGFs or on IGF-IR expression. For instance, primary melanoma cells do not produce IGF-I and depend on exogenous ligand for growth (through the MAPK pathway) and β -catenin stabilization (through the PI-3K pathway). However, metastatic melanoma cells become independent of IGF for these functions due to constitutive activation of the MAPK pathway (257).

I. Loss of tumor suppressor genes enhances IGF expression and/or function

Changes in IGF expression and function in cancerous cells may occur as a result of loss or altered expression of several suppressor genes known to regulate different proteins of the IGF axis. Some of these changes are listed below.

1. *p53*. The p53 protein is a nuclear transcription factor that is activated in response to genotoxic stress and hypoxia. Activation of p53 triggers cell cycle arrest and apoptosis through DNA-specific transcriptional activation, transcriptional repression, and protein-protein interactions. Wild-type p53 can exert a suppressive effect on the IGF axis by

up-regulating IGFBP-3 (258) and down-regulating the expression of IGF-IR (259), IR (260), IGF-II (261–263), and IRS-3 (264). However, in over 50% of all human cancers, p53 is mutated, and this can alter the IGF system by reducing IGF-FBP-3 synthesis while simultaneously increasing expression of positive effectors of the IGF system, such as IGF-IR. Mutated p53 can induce expression of the positive mediators of IGF signaling through the release of a repressive mechanism or through gain of function. For example, a mutation in codon 249 (p53mt249) that can be induced by aflatoxin B1 results in up-regulation of IGF-II synthesis through increased formation of transcriptional complexes that bind to the IGF-II promoter (261). This mechanism is thought to contribute to hepatocarcinogenesis. Indeed, transfection of p53-negative Hep3B hepatoma cells with p53mt249 increased IGF-IR and IGF-II expression (265). p53 mutants can also up-regulate IGF-IR by recruiting the ubiquitin ligase MDM2, thereby reducing IGF-IR ubiquitination and increasing intracellular IGF-IR levels (84). IGF-IR, in turn, can regulate MDM2 expression levels and thereby increase wild-type p53 ubiquitination (82).

2. *WT1*. The Wilms tumor suppressor gene *wt1* encodes a zinc-finger, DNA-binding protein that functions as a transcriptional repressor. WT1 binds to multiple sites on the IGF-IR and IGF-II promoters, inhibiting transcription. In Wilms tumors, however, mutations/deletions in WT1 result in overexpression of IGF-IR (266, 267) and IGF-II (268). An inverse correlation between functional WT1 levels and the expression of IGF-II and IGF-IR has also been documented in breast cancer (269).

3. *PTEN*. The tumor suppressor and lipid phosphatase PTEN dephosphorylates phosphatidylinositol 3,4,5-triphosphate, thereby blocking activation of Akt, a major transducer of the IGF-IR signal. In malignant cells, the *PTEN* gene is frequently mutated, leading to increased Akt activation. Recently, it was shown that IGF-II can both initiate and “turn off” Akt-mediated IGF-IR signaling in mammary gland epithelial cells. When the inguinal mammary glands were injected with IGF-II, it was observed that, in addition to Akt activation, PTEN expression was up-regulated. This, in turn, caused a reduction in Akt phosphorylation and an increase in the degradation of cyclin D1 (a substrate downstream of Akt) (188). Transfection of MEF with a luciferase-tagged PTEN promoter construct revealed that IGF-II up-regulates PTEN transcription via *egr-1* (188). Conversely, we and others have shown that PTEN can down-regulate IGF-IR, IGF-I, and IGF-II expression and functions and up-regulate IGFBP-3 expression in a wide range of human and mouse cancer cell lines including prostate, gastric, and lung carcinoma cell lines (153, 244, 270, 271). Thus, loss of PTEN function can enhance IGF signaling by several different mechanisms; it can increase IGF-IR-induced PI-3K signaling, increase the expression of IGF-IR and/or its ligands, and reduce the expression of IGFBP-3.

4. *The IGF-IIR*. The IGF-IIR binds IGF-II with a Kd of 0.5 nM and IGF-I and insulin with 10 times and 10⁵ times lower affinities, respectively (17). Although the IGF-IIR was initially thought to potentiate the growth-promoting effect of

IGF-II (272, 273), recent evidence identified the IGF-IIR as a negative regulator of IGF signaling. Compelling evidence for this role was obtained from mice with a double deficiency in the *IGF-IR* and *IGF-IIR* genes. Mice with an isolated *IGF-IR* deficiency invariably died within minutes of birth but could be rescued if they carried a second, null mutation in the *IGF-IIR* gene. It has been postulated that deletion of *IGF-IIR* may increase the bioavailability of IGF-II for the insulin receptor, thereby providing an alternative growth mechanism for the embryos (274).

Frequent mutations, loss of heterozygosity, and microsatellite instability that affect the *IGF-IIR* gene have been reported in several primary human tumors (275–278). Overexpression of a dominant-negative IGF-IIR that could not bind IGF-II in human prostate cancer LNCaP cells induced a higher and more rapid proliferation index compared with mock-transfected cells. Conversely, forced expression of IGF-IIR in PC-3 human prostate cancer cells resulted in decreased proliferation (279). Similarly, it was recently shown that overexpression of IGF-IIR in a mouse mammary tumor cell line had an antiproliferative effect on the cells, inhibiting the formation of mammary tumors *in vivo* (280). It should be noted that, in addition to its role in the binding and targeting IGF-II for lysosomal degradation, IGF-IIR could regulate cellular growth by several other mechanisms. It can activate TGF- β 1, a potent growth inhibitor for most cell types (281), and it can affect tumor susceptibility to the host immune system. In a recent study, the IGF-IIR was shown to play a key role in the intracellular transport of the cytotoxic T cell-derived granzyme B, an apoptosis-inducing serine proteinase (282). Taken together, these studies identify the IGF-IIR as a functional “tumor suppressor” (283), and its loss can therefore provide an alternative mechanism for enhancement of tumor cell growth.

XI. Controversies and Conflicting Evidence on the Role of IGF-IR in Malignancy

Although it has been generally recognized that the IGF axis promotes tumor progression, driving the process toward the acquisition of an aggressive phenotype, the evidence regarding the role of the IGF-IR itself and the clinical significance of increased IGF-IR expression levels have been the subject of some conflicting reports and controversy (as also discussed in *Section VI*). For example, studies with the TRAMP mice model of prostate carcinoma revealed an increase in the expression of prostate-specific IGF-I during prostate cancer progression, but the expression levels of IGF-IR and IGF-IIR were unaltered in primary prostate cancers and dramatically decreased in metastatic lesions (172). These findings were in fact in agreement with clinical data obtained by Tennant *et al.* (113) showing a 42% reduction in IGF-IR positivity (as assessed by immunohistochemistry), and a concomitant 30% increase in IGF-II expression in malignant, compared with benign epithelium. These findings are at variance with results of other clinical studies that showed an incremental increase in the expression of IGF-IR, IRS-1, IGF-I, and IGF-II during tumor progression from early PIN to metastatic lesions (114, 284). Interestingly, a similar

discrepancy can also be found in results from breast cancer studies. Although some studies identified an overexpression of IGF-IR and its ligands in human breast carcinomas, others reported that expression of IGF-IR and IRS-1 were inversely correlated with high proliferation rates in dedifferentiated breast cancers (285). More recently, Chong *et al.* (286) found no difference in IGF-IR expression levels when breast cancer and the adjacent non-neoplastic tissue were compared in 20 breast cancer specimens.

Other studies relevant in this context are those that identified IGF-IR as a negative regulator of cell motility. This, for example, was shown for MCF-7 cells where receptor overexpression was reported to stimulate cell aggregation (287), whereas reduced expression was shown to increase motility (288), suggesting that reduced IGF-IR expression may actually promote the metastatic properties of some tumor cells. These studies are, however, at variance with other observations using the same (289) or other (152, 290) tumor models, suggesting that variations in assay conditions and/or the particular cell context may determine the outcome of altered IGF-IR expression levels. It is important to note in this context that in all animal studies reported to date (without exception), where IGF-IR or its ligands were targeted directly, a loss of tumorigenicity and/or metastatic ability was observed.

The apparent discrepancies between results of laboratory and clinical studies may be due to the obvious differences between investigations based on cell and animal models and those dependent on analysis of human specimens. Whereas in the former, molecular effectors of the IGF axis can be forcibly overexpressed or depleted under experimental conditions where other variables (*e.g.*, genetic background, host immune parameters, exposure to environmental factors, other oncogenic triggers, *etc.*) are controlled, in the analysis of clinical specimens, multiple tumor-specific and host factors may alter the actual contribution of the IGF-IR and its ligand(s) to malignant progression, and their contribution may therefore remain unappreciated. Furthermore, the conflicting reports on the significance of altered IGF-IR expression to malignant progression may also be reconciled when the IGF signaling system is viewed as a whole, and the expression levels and state of activation of different signaling effectors are all taken into account. Namely, it should be recognized that a reduction in IGF-IR expression *per se* may not always reflect and/or translate into a decline in IGF signaling. Several observations support this conclusion. For example, Knowlden *et al.* (291) observed that in breast carcinoma cell lines, MCF-7 and T47D, comparable levels of IGF-IR phosphorylation could be seen in response to IGF-I, despite significantly higher receptor levels in the former. These findings suggest that the levels of phosphorylated (*i.e.*, activated) IGF-IR or downstream signaling effectors in tumor specimens may be a more reliable indicator of IGF function and its contribution to disease progression than the number of receptors *per se*. Indeed, Del Valle *et al.* (292) found that in 10 of 17 biopsies of human medulloblastoma, the levels of phosphorylated IGF-IR were significantly higher than in control cerebellar tissues. In addition, studies with an animal model of leiomyoma (the Eker rat) revealed that the progression of normal uterine cells to leiomyomas was accom-

panied by a reduction in IGF-IR expression levels with a concomitant 7.5-fold increase in IGF-I expression and a 5.7-fold increase in the levels of phosphorylated IRS-1 (293).

XII. Targeting the IGF System for Cancer Therapy

The central role that the IGF system plays in initiating and promoting tumor progression makes it an attractive target for cancer therapy. Various strategies have been used to target components of this system in established animal and human tumor cell lines (*in vitro* studies) and in animal models of cancer (*in vivo* studies), and some of these strategies may be advancing to clinical use (294). Among them are down-regulation of IGF-IR by antisense oligonucleotides (295), antisense RNA (296, 297), small interfering RNA (298), triple helix-forming oligodeoxynucleotides (299), single-chain antibody (300), fully humanized anti-IGF-IR monoclonal antibodies (301, 302), and specific kinase inhibitors (303–305). IGF-I was targeted by similar strategies including IGF-I peptide analogs (306), antisense oligonucleotides (299), and triple helix-expressing vectors (307). Overexpression of IGF-II (281) and IGFBP-3 (88) were used to decrease the bioavailability of IGF-II and IGF-I, respectively. The Brodt group (170) recently described a novel soluble IGF-IR molecule, namely IGF-IR⁹³³, that consists of the entire extracellular domain of the receptor. It was shown that IGF-IR⁹³³ can neutralize the effects of exogenous IGF-I and significantly diminish liver metastasis formation by highly invasive Lewis lung carcinoma H-59 cells, markedly increasing long-term animal survival (Ref. 170 and Fig. 3). Thus far, the evidence *in vitro* suggests that one of the humanized antireceptor antibodies is internalized and can down-regulate IGF-IR levels, resulting in a profound inhibition of receptor signaling (294), but no effect on the IR functions. The small molecule IGF-IR tyrosine kinase inhibitors also have a profound effect on IGF-IR activity and tumor cell growth *in vitro* and *in vivo* in a range of tumor models; however, their potential cross-reactivity with the IR system needs to be further evaluated (294).

The available data suggest that targeting of the IGF system *in vivo* may inhibit cancer progression and/or cause cancer regression directly by inducing apoptosis and cell growth arrest. In addition to these direct effects, it has been shown that inhibition of IGF action could increase the efficacy of other therapeutic modalities, such as radiotherapy (308).

XIII. Concluding Remarks

The evidence reviewed above shows that the role of the IGF system in the development and progression of malignant disease is complex and multifactorial. Although data based on cellular and animal models have demonstrated a causal link between receptor and/or ligand overexpression and malignancy, the evidence for a functional involvement of IGF-IR and its ligands in human malignancies is not as clear-cut. This may be the result of the obvious limitations that cell- and animal-based systems have as models for the human disease. It is also likely, however, that in addition to IGF-IR and ligand overexpression, more indirect mechanisms for

engaging the IGF system, some of which may actually bypass the requirement for receptor overexpression, are at play, and they can be equally effective in promoting human malignancy. This complexity and intertumoral variability are likely to hinder progress toward developing IGF-targeted therapeutics with global anticancer efficacy. Similar to the experience with other biology-based therapies, effective targeting of the IGF system may require a customized approach in which tumor profiling guides the selection of the appropriate drugs.

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