

TOPIC HIGHLIGHT

Harry HX Xia, PhD, MD, Series Editor

Reactivation of the insulin-like growth factor- II signaling pathway in human hepatocellular carcinoma

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Abstract

Constitutive activation of the insulin-like growth factor (IGF)-signaling axis is frequently observed in human hepatocellular carcinoma (HCC). Especially the overexpression of the fetal growth factor IGF- II, IGF- I receptor (IGF-IR), and cytoplasmic downstream effectors such as insulin-receptor substrates (IRS) contribute to proliferation, anti-apoptosis, and invasive behavior. This review focuses on the relevant alterations in this signaling pathway and independent *in vivo* models that support the central role IGF- II signaling during HCC development and progression. Since this pathway has become the center of interest as a target for potential anti-cancer therapy in many types of malignancies, various experimental strategies have been developed, including neutralizing antibodies and selective receptor kinase inhibitors, with respect to the specific and efficient reduction of oncogenic IGF- II /IGF-IR-signaling.

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INTRODUCTION

Human hepatocellular carcinoma (HCC) is considered the fifth most frequent malignancy worldwide and the third most common cause for cancer mortality with an increasing incidence in Asia and Africa, but also in industrial countries^[1]. In more than 80% of cases, a well-defined etiology such as viral infection with hepatitis B- and C-viruses (HBV and HCV), aflatoxin B1 intoxication, chronic alcohol abuse, or hereditary diseases is associated with its development (Figure 1); however, clinical diagnosis of HCC is difficult due to the lack of reliable serum markers. Moreover, the therapeutic options for HCC patients are sobering due to the high angiogenic capacity of the tumor.

Although the underlying molecular mechanisms responsible for the development and progression of HCC have not been completely delineated, it has become clear that aberrant activation of growth factor signaling pathways is a pivotal event in hepatocarcinogenesis. Besides the hepatocyte growth factor (HGF)/MET, Wnt/frizzled/ β -catenin, transforming growth factor α (TGF α)/EGF-R, and transforming growth factor β (TGF β)/T β R-signaling, dysregulation of the evolutionary highly conserved insulin-like growth factor (IGF) pathway is critically involved in proliferation and anti-apoptosis of HCC cells associated with uncontrolled tumor growth and chemoresistance^[2]. In fact, based on its central regulatory position in tumor cell homeostasis, this signaling axis is considered a promising therapeutic anti-cancer target in many human malignancies. This review focuses on the molecular changes of IGF-signaling detected in human HCC, animal model systems that underline the central role of IGF- II -signaling in hepatocarcinogenesis, as well as resulting therapeutic strategies for the treatment of human liver cancer.

COMPOSITION OF THE IGF-PATHWAY

The key molecules in this pathway are the ligands IGF- I and IGF- II, IGF-binding proteins (IGFBP1-6), membrane-associated receptors [IGF- I receptor (IGF-IR), mannose-6-phosphate receptor/IGF- II receptor (IGF- II R)], and insulin receptor substrates (IRS-1-6).

IGF- I and IGF- II are small, secreted molecules that are predominantly produced by the liver and which stimu-

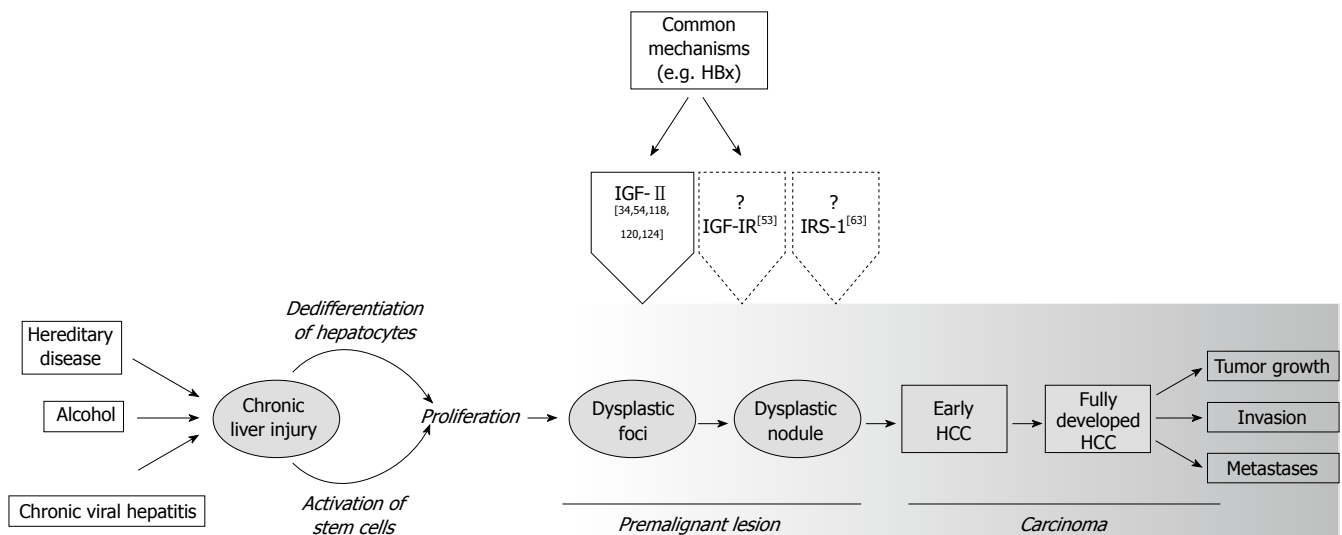


Figure 1 Schematic representation of human hepatocarcinogenesis. Human HCC usually develops on the background of a chronic liver disease (e.g. hepatitis, alcoholic liver disease, hemochromatosis). Dysplastic foci and dysplastic nodules are regarded as premalignant lesions preceding the development of HCC. In addition, “early” HCCs (< 2 cm, highly differentiated, non-invasive) are distinguished from fully developed HCCs (fast growing, invasive). However, human hepatocarcinogenesis represents a developmental continuum where a clear cut classification of a given lesion is often impossible. Increasing evidence suggests that aberrant IGF- II expression represents an early event in hepatocarcinogenesis; however, comparable data are currently not available for IGF-IR, and IRS. Nevertheless, reactivation of the IGF- II /IGF-IR signaling pathway seems to be a progression step in human liver cancer.

late different cell types in both an autocrine and paracrine manner. These factors display differing expression kinetics as the expression of IGF- II declines while the bioavailability of IGF- I increases shortly after birth. Besides the transcriptional regulation (e.g. genomic imprinting of the *igf- II* gene promoter), ligand bioavailability is further influenced by the presence of IGF-BPs in tissues and serum^[3]. Secreted IGF-BPs bind extracellular IGFs with affinities comparable to IGF-IR and therefore modulate ligand bioactivity. For instance, 70% of IGF- II is bound to IGFBP-3, which is the most abundant BP in serum^[4]; however, depending on the cellular context, both inhibitory as well as stimulatory effects of IGF-BPs on IGF-signaling have been described. All IGF-BPs are substrates for proteases and their bioavailability/bioactivity is regulated by limited proteolytic cleavage with an impact on IGF-dependent physiological processes^[5]. However, IGF-independent biological effects under pathophysiological conditions have also been described for several IGF-BPs^[6].

The signaling of IGF- I and IGF- II is mediated by IGF-IR, a heterotetrameric protein (two α - and β -chains), which consists of an extracellular ligand binding site and an intracellular tyrosine kinase domain. IGF-IR binds IGF- I with 15- to 20-fold higher affinity than IGF- II^[7]. Ligand binding and receptor tyrosine kinase (RTK)-dependent phosphorylation of intracellular substrates such as IRS and Src homology collagen (Shc) then lead to the activation of the phosphatidylinositol 3-kinase (PI3-kinase)/protein kinase B (PKB/AKT)-axis and the Ras/mitogen activated protein kinase (MAPK)-pathway^[8]. IRS proteins are a family of six (IRS-1 to IRS-6) related adaptors that integrate and coordinate signaling of the insulin receptor (IR) and also the IGF-IR. They are responsible for most of the biological activities of IGF-IR^[9].

In addition, IGF- II (but not IGF- I) efficiently binds and activates a distinct isoform of the insulin receptor lacking exon 11 (IR-A)^[10-12]. IR and IGF-IR are highly homologous RTKs (up to 84% in the tyrosine kinase domain and 100% at the ATP-binding site)^[13], but there are substantial functional differences between both molecules: while both receptors exert metabolic effects, IGF-IR is anti-apoptotic, mitogenic, and it facilitates a malignant phenotype^[14]. However, IR-A plays a central role not only in metabolic processes, but also in IGF- II-induced migration in cells lacking IGF-IR^[11]. These different biological effects are possibly based on ligand/receptor abundance, protein turnover or currently undiscovered peculiarities of the distinct signaling axes. In addition, recent findings show that structural features in the domain governing ligand specificity do distinguish IGF-IR from IR^[15].

In contrast, IGF- II R which is structurally unrelated to IGF-IR, does not exhibit cytoplasmic kinase activity^[16]. Although this receptor does not directly contribute to IGF-signaling, it regulates IGF- II turnover and bioavailability through receptor-mediated endocytosis and subsequent degradation^[17]. IGF- I and insulin cross-react very weakly with IGF- II R and therefore are not regulated by its (inhibitory) activity^[18].

IGF-SIGNALING IN HEPATOCARCINOGENESIS

Alterations in the IGF-signaling pathway have been described in several adult and pediatric human tumors such as Wilms tumors^[19], as well as colon^[20,21], lung^[22], breast^[23,24], and prostate cancer^[25]. The reactivation of IGF-

signaling in HCC predominantly occurs at the level of IGF-II expression, which is secreted by the tumor cells themselves, which is suggestive of autocrine mechanisms of stimulation^[26,27]. This growth factor is highly expressed in the fetal liver and early after birth, but its expression is strongly reduced in adulthood in humans, mice and rats^[28-30]. Several studies have shown elevated expression levels for IGF-II in preneoplastic lesions (Dysplastic Nodules) and very high levels in HCC (Table 1, Figure 1), which is mainly based on aberrant activation of the epigenetically regulated *igf-II* promoters P1-P4^[31]. Indeed, HCCs showing high level of expression of IGF-II exhibit reconstitution of the fetal type transcription pattern due to a loss of promotor-specific imprinting and hypomethylation^[26,32-35]. Furthermore, viral proteins have been reported to facilitate IGF-II overexpression in HBV- and HCV-associated HCCs. For example, the HBV-derived HBx protein and the HCV-derived core gene product induce IGF-II expression through interaction with transcription factors activity such as Sp1 and Egr1^[36,37]. In addition, the inactivation of tumor suppressor genes such as p53 by aflatoxin-induced mutations in codon 249 increases IGF-II expression through the formation of transcriptional complexes^[38].

Besides the direct transcriptional induction of IGF-II expression, additional mechanisms may contribute to elevated IGF-II bioavailability in HCC cells. Firstly, reduced levels of IGFBP-1, -2, -3, and -4 in HCCs were found to be associated with IGF overexpression^[39,40]. These IGFBP-based effects on IGF-concentration may be even more complex, since a reduced degradation of IGFBPs by matrix-metalloproteinases (MMPs) was regulated by tissue inhibitors of MMPs (TIMPs). The regulation of TIMP-1, which is repressed in many HCCs, is associated with changes in IGF-II abundance^[41,42]. Secondly, the downregulation or inactivation of IGF-II R theoretically leads to increased concentrations of IGF-II based on insufficient internalization and degradation. Here, the reduced expression of IGF-II R, the loss of heterozygosity (LOH) at the *igf-II* r gene locus, homozygous deletions, and missense mutations with an impact on ligand binding have been described with respect to HCCs^[43-49]. However, other studies did not detect any genetic alterations at the *igf-II* r locus, which may be due to methodological and population-based differences^[50-52]. Moreover, few studies described elevated IGF-II R levels in HCCs^[53,54]. Independent of the underlying molecular mechanism, IGF-II overexpression denominates a group of HCCs with fewer tumor infiltrating lymphocytes, a lower apoptosis rate^[55] and extrahepatic metastasis^[56]. Thus, serum IGF-II availability was proposed as a tumor marker discriminating HCC from cirrhosis^[57].

IGF-I - and IGF-II-mediated signaling may occur through IGF-IR and IR holoreceptor dimers as well as through IGF-IR/IR hemireceptor complexes^[58,59]. Particularly IGF-II has been shown to efficiently activate both IGF-IR and IR-A. However, our own results suggested that the presence of IR was not essential for IGF-II-mediated oncogenic properties in liver tumor cells, since efficient siRNA-dependent inhibition of IR (all isoforms) did not lead to changes in proliferation, apoptosis, or migration in HCC cells (unpublished data). Therefore, in HCC cells IGF-IR is the relevant receptor for protumorigenic IGF-II

Table 1 Expression of IGF-(II) signaling axis constituents in human HCC

Signaling constituent	Dysregulation (%)
IGF-II	9.2 ^[117]
	22.5 ^[26]
	25.6-60 ^[118]
	66.7 ^[54]
	40 ^[119]
	100 ^[120]
IGF-IR	50 ^[121]
	14 ^[55]
IRS-1	7-78 ^[117]
	40 ^[53]
IRS-2	46.7 ^[53]
	100 ^[122]
IRS-4	53.3 ^[53]
	86 ^[123]
	46.7 ^[53]

signaling. This finding is supported by the fact that IGF-IR is highly expressed in many human malignancies and that only IGF-IR-signaling is crucial for oncogenic transformation and tumor cell survival^[60]. Indeed, while IGF-IR levels were constitutively low in normal hepatocytes, IGF-IR was overexpressed in HCC and HCC cell lines (Table 1). Just as it was observed for elevated IGF-II expression, viral-based molecular mechanisms and mutational inactivation of tumor suppressor genes caused IGF-IR overexpression: HBV-derived HBx protein as well as p53 mutations in codon 249 induce IGF-IR^[61,62], suggesting that these protumorigenic events modulate several IGF-pathway constituents such as IGF-II and IGF-IR to reach maximal (oncogenic) signaling efficiency.

Lastly, IRS-1, -2, and -4 are overexpressed in most HCCs (Table 1). So far, most analyses are reported for IRS-1, showing that elevated IRS-1 levels mediate anti-apoptosis^[63], tumor cell growth^[64], and mitosis^[65]. Further, it has been found that the HCV-derived core protein reduced IRS-1 expression in HCC cell lines^[66]. To our knowledge, no molecular mechanisms responsible for the elevated IRS-1 expression (e.g. other viral proteins) have been described so far. Whether other IRS family members serve identical functions in HCC cells has not yet been analyzed.

In summary, several lines of evidence suggest a ‘multi-hit’ model for the oncogenic activation of IGF-II signaling in HCC. Firstly, the sum of protumorigenic events detected in HCCs (e.g. increased IGF-II, IGF-IR, and IRS bioavailability) indicates the potential for multiple hits in one single tumor. Secondly, viral proteins and the inactivation of tumor suppressor genes induce several IGF-II pathway constituents. Although increased bioavailability of IGF-II appears to be the dominant mechanism in human hepatocarcinogenesis, many hits in this pathway may be necessary to obtain full malignant competence.

ANIMAL MODELS

The pivotal oncogenic function of IGF-II-signaling

in hepatocarcinogenesis is supported by several animal models. Transgenic mice expressing IGF-II (20-30-fold increased levels in serum) develop hypoglycemia and many types of malignancies, which are most frequently HCC^[67]. In contrast, overexpression of IRS-1 is associated with increased DNA-synthesis, but liver tumor development was not detected^[68]. In knockout model systems the disruption of the *igf-IIr* gene leads to elevated IGF-II levels; but since these animals exhibit lethal organ abnormalities (e.g. organomegaly), no further studies concerning liver tumor development have been carried out^[69-71].

In addition to these IGF-pathway-specific transgenic and knockout animals, additional models, initially not intended for the examination of the IGF-axis, supported the functional relevance of especially dysregulated IGF-II in hepatocarcinogenesis. Both mice with liver-directed expression of SV40T-Ag or HBV presurface gene products (preS1 and preS2) developed HCCs, which is associated with a high level of IGF-II expression^[72]. Moreover, transgenic mice overexpressing the woodchuck hepatitis virus/c-MYC^[73], c-MYC^[74], and TGF α ^[75] developed HCCs accompanied by elevated IGF-II expression in the tumors. Equally, liver tumors in p53-null animals exhibited increased amounts of IGF-II as compared to normal littermates after delivery of polyoma virus middle T antigen (PyMT)^[76].

Cross-breeding experiments underlined the importance of IGF-II-signaling in hepatocarcinogenesis. Interbreeding of IGF-II knock-out mice with SV40T-Ag animals resulted in a reduced frequency (up to 15-fold) and size of liver tumors as compared to animals only expressing the oncogene^[77], suggesting an important role of IGF-II-signaling in tumor progression. This anti-tumorigenic effect for IGF-II-deficiency in tumor models was supported by similar results in animals expressing SV40T-Ag in Langerhans cells showing widely identical results^[30]. In a more indirect approach, TIMP1 overexpression reduced IGF-II-driven HCC development in SV40T-Ag transgenic animals based on reduced tumor cell proliferation and vascularization^[41,78,79]. However, it is also noteworthy that mice expressing the c-MYC oncogene and which are deficient for IGF-IR only showed a marginally reduced HCC incidence compared to animals expressing the oncogene alone^[74].

The functional connection between the viral infection of hepatocytes and IGF-II abundance was supported by studies utilizing the woodchuck model system. After woodchuck hepatitis virus (WHV) infection, a high level of IGF-II expression was detected in precancerous woodchuck liver and in up to 45% of HCCs, which correlates with repressed viral DNA replication and n-MYC expression in early precancerous lesions^[34,80]. Further studies revealed that IGF-II availability protected from n-MYC-induced apoptosis especially under serum-free conditions^[81]. Therefore, the selection for cells with high IGF-II levels may rescue a more unfavorable tumor phenotype and therefore promote tumor progression. Lastly, a reactivation of IGF-II expression in experimentally induced liver tumors using different chemical substances (3'-Me-DAB, 2-AAF, DENA) has been described in rats^[82-84].

These data clearly show that IGF-II overexpression and intactness of the IGF-II/IGF-IR pathway is also a common event in murine liver tumor development, independent of the underlying molecular mechanisms (e.g. oncogene activity, regeneration processes, chemically induced carcinogenesis)^[72].

THERAPY

IGF-II is highly expressed during prenatal development and early after birth but levels rapidly decline in adulthood^[28,29]. Since IGF-II signaling is frequently reactivated in human hepatocarcinogenesis, inhibition of this pathway unlikely affects normal liver function under physiological conditions and therefore represents a favorable therapeutic strategy. Several techniques have been developed to modulate the activity of IGF-(II) signaling in different tumor cell types^[85]. Many approaches, such as neoexpression of dominant-negative receptor mutants (dnIGF-IR) or transfection of IGF-IR-specific antisense oligodeoxynucleotides, attained convincing inhibitory effects on IGF/IGF-IR signaling *in vitro* and *in vivo*^[85]. However, neutralizing antibodies binding IGF-IR and IGF-IR-specific small inhibitory molecules are currently the most promising therapeutic and clinically relevant approaches^[60].

Neutralizing antibodies

Recently, numerous blocking antibodies recognizing different membrane-bound RTKs such as EGF-R/HER1 (Cetuximab/Erbitux) and HER2 (Trastuzumab/Herceptin) have been developed^[86]. Besides IGF-II-binding antibodies that physically inhibit ligand/receptor interaction^[87,88], many neutralizing antibodies specific for IGF-IR have been described such as alpha-IR3^[89], mAb391^[90], scFv-FC^[91], CP-751,871^[92], IMC-A12^[93], 7H2HM^[94], EM164^[95], h7C10^[96], 4G11^[97], 19D12^[98], R1507^[60], AMG479^[60], and 19D12^[60]. Reduced IGF/IGF-IR signaling is presumably based upon lysosome-dependent degradation of IGF-IR^[90,91]. Since proteasome inhibitors (e.g., Brefeldin) as well as protein synthesis inhibitors (e.g., cyclohexamide) did not affect antibody-dependent downregulation of the receptor^[90,91], it has been speculated that anti-IGF-IR antibodies hampered steady-state protein turnover based on endosomal accumulation of antibody/receptor complexes^[99]. Although the anti-tumor effects of these antibodies were tested for several different cell types in preclinical studies, no comprehensive analyses regarding the anti-tumorigenic impact on HCC cells have been published to date. However, it is noteworthy that for other tumor entities, clinical trials for antibodies targeting IGF-IR have been launched such as CP-751, 871 (Pfizer), IMC-A12 (ImClone Systems), R1507 (Roche), and AMG479 (Amgen)^[60].

Tyrosine kinase inhibitors

In addition to neutralizing antibodies, small molecule inhibitors targeting RTKs such as EGF-R/HER1 (Gefitinib/Iressa), BCR/ABL fusion product (Glivec/Imatinib), or cellular kinases (the multi-kinase inhibitor Sorafenib/Nexavar recognizing VEGF-R, PDGF-R, c-kit, Raf, and

RET) have been developed. Since IGF-IR and the IR are structurally related, highly specific IGF-IR inhibitors are necessary to prevent diabetogenic effects in patients. Published IGF-IR-selective RTK-inhibitors are tyrphostins (AG538^[100,101], AG1024^[102], AG1034^[102]), cyclolignans (picropodophyllin^[103,104]), 6-5 ring-fused compounds^[105], pyrrole derivatives (NVP-AEW541^[106,107], NVP-ADW742^[108,109]), PQIP^[110], BMS536924^[111], and BMS-554417^[112]. Anti-tumorigenic effects of some inhibitors on HCC cells have been demonstrated. The application of NVP-AEW541^[113] and picropodophyllin (Nussbaum *et al*, unpublished data) was shown to reduce tumor cell proliferation and increase apoptosis. Equally, IGF- II induced tumor cell motility was reduced by picropodophyllin (Nussbaum *et al*, unpublished data). In addition, the inhibition of IGF-IR-signaling by a combination of AG1024 and EGF-R-signaling by RTK-inhibitors or blocking antibodies synergistically reduced tumor growth^[114,115]. However, NVP-ADW742 affects the viability of hepatocytes in a concentration-dependent manner. This RTK-inhibitor potentiated bile acid-induced cell death in normal hepatocytes, suggesting liver toxicity in patients with aberrant bile flow^[116]. Because IGF-IR signaling is almost absent in normal hepatocytes, it is questionable whether these effects were IGF-dependent or independent. Thus, the effects of IGF-IR-specific inhibition on normal and diseased liver have to be analyzed carefully.

Although the anti-tumorigenic effects of IGF-IR-specific small molecules have been analyzed in numerous tumor cell types in preclinical setups^[60], to our knowledge, no clinical trials have been initiated to date.

CONCLUSION

Several components of the IGF-signaling axis, such as IGF- II, IGF-IR and IRS, are frequently dysregulated in human hepatocarcinogenesis. The oncogenic reactivation of IGF- II-signaling has been verified in several *in vivo* models and supports the therapeutic relevance of this pathway. However, aberrant growth factor bioactivity involved in tumor development cannot be understood in a mono-dimensional manner since an intense cross-talk between IGF-IR signaling and other oncogenic pathways have been described^[2]. Indeed, first functional studies revealed the necessity for multi-modal approaches for optimal anti-tumorigenic results and dose reduction. Therefore, it is questionable whether the highest specificity is the 'gold standard' for efficient treatment of malignancies, especially with respect to the development of (IGF-IR specific) RTK inhibitors. Thus, inhibitors targeting IGF-IR and other RTKs or combinations of different specific substances targeting distinct pathways might be attractive therapeutic approaches in the future.

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