



# Insulin-like growth factor axis targeting in cancer and tumour angiogenesis – the missing link

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## ABSTRACT

Numerous molecular players in the process of tumour angiogenesis have been shown to offer potential for therapeutic targeting. Initially denoted to be involved in malignant transformation and tumour progression, the insulin-like growth factor (IGF) signalling axis has been subject to therapeutic interference, albeit with limited clinical success. More recently, IGFs and their receptors have received attention for their contribution to tumour angiogenesis, which offers novel therapeutic opportunities. Here we review the contribution of this signalling axis to tumour angiogenesis, the mechanisms of resistance to therapy and the interplay with other pro-angiogenic pathways, to offer insight in the renewed interest in the application of IGF axis targeting agents in anti-cancer combination therapies.

*Key words:* angiogenesis, IGF, insulin, IGF1R, cancer, resistance, therapy.

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## I. INTRODUCTION

Since the initial report of specific angiogenesis inhibitors in the early 1990s (Griffioen & Molema, 2000; Kerbel & Folkman, 2002), several angiostatic therapeutics have

made their entrance into the clinic (Carmeliet & Jain, 2011; Jain, 2014). While nearly all of these drugs target the vascular endothelial growth factor (VEGF)/VEGF-receptor axis, there is a great need for alternative and more specific strategies. Previous studies have identified new molecular

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targets (St Croix *et al.*, 2000; van Beijnum & Griffioen, 2005; van Beijnum *et al.*, 2006; Otsubo *et al.*, 2014). Among these are members of the insulin and insulin-like growth factor (IGF) signalling axis. The relevance of the IGF axis to cancer initiation and progression stems from the observation that mouse embryonic fibroblasts (MEFs) lacking the IGF1 receptor (IGF1R) could not be transformed, in contrast to wild-type MEFs (Sell *et al.*, 1993). Subsequently, numerous *in vitro* and *in vivo* studies demonstrated that blocking the IGF signalling axis could inhibit tumour growth and angiogenesis. However, to date clinical trials have largely failed to meet the high expectations set by preclinical mouse studies (Reidy *et al.*, 2010; Schmitz *et al.*, 2012). This can, in part, be explained by the intricate complexity of the interacting ligands, receptors and mediators of this system. Nevertheless, the relatively underappreciated importance of the IGF signalling axis in tumour angiogenesis could provide new angles for future application of (combination) therapies.

In this review, we discuss the role of insulin, IGFs and their receptors in tumour angiogenesis and the opportunities to target this signalling pathway in cancer treatment, with a focus on overcoming resistance to therapy.

## II. BLOOD BROTHERS

The IGF signalling axis comprises three ligands, insulin, IGF1 and IGF2, and three receptors, insulin receptor (IR), IGF1 receptor (IGF1R) and IGF2R. Next to this, circulating IGF binding proteins (IGFBPs) have been identified that are able to modify bioavailability of IGFs.

Both IGF1R and IR are dimeric receptor tyrosine kinases, each monomer consisting of an  $\alpha$  and a  $\beta$  chain generated through proteolytic cleavage of a single protein precursor (Fig. 1). The  $\beta$  chain has a transmembrane domain and fosters phosphorylation whereas the  $\alpha$  chain is fully extracellular and is responsible for ligand binding (Frattali & Pessin, 1993). IR and IGF1R are highly homologous, but have subtle differences in specific regions (reviewed by Siddle, 2012). IR transcripts can be alternatively spliced to form either IR-B, the full-length sequence, or IR-A, the isoform which lacks 12 amino acids in the C-terminus of the extracellular  $\alpha$  chain, and which is most similar to IGF1R. The general view is currently that IR and IGF1R mediate both metabolic and mitogenic effects, exerted by predominant signalling of phosphatidylinositol 3-kinase/AKT serine threonine kinase (PI3K/AKT) or RAS proto-oncogene/mitogen-activated protein kinase (Ras/MAPK) pathways [reviewed by Bach (2015); Belfiore *et al.* (2009); Bowers *et al.* (2015); Gao *et al.* (2012); Pollak (2012)]. The type of ligand binding to IGF1R or IR and their major intracellular receptor substrates, insulin receptor substrate (IRS)-1 and -2 and Src homology domain containing (SHC), influence the direction of signalling and ultimately the cellular response (Siddle, 2012). Notably, cellular context, i.e. relative expression of receptors and downstream cellular mediators, appears to be the major

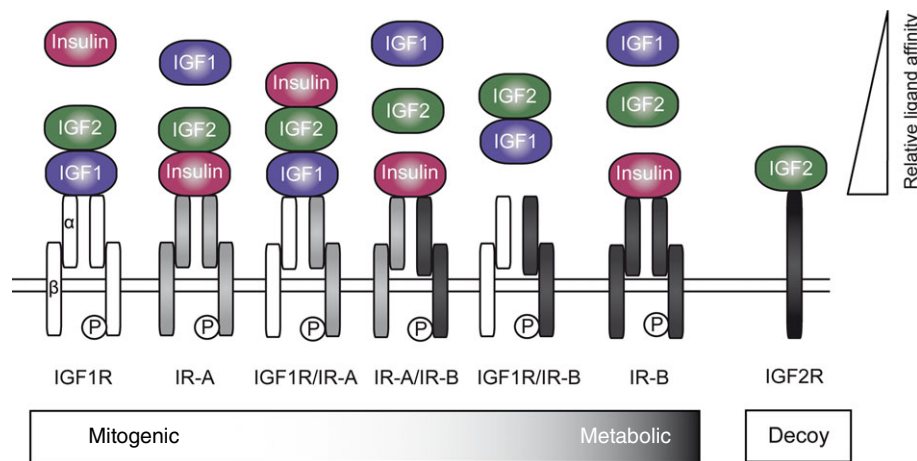
determinant in defining the response to insulin and IGFs (Siddle, 2012).

By lining the inside of blood vessels, endothelial cells (ECs) are continuously exposed to circulating insulin and IGFs. As such, the IGF signalling axis in endothelium has received scientific attention, although predominantly in the context of normal physiology or diabetic complications (Bach, 2015). It is now becoming clear that its role in tumour angiogenesis is of considerable importance.

### (1) Insulin-like growth factor 1 (IGF1) receptor and angiogenesis

Insulin-like growth factor 1 receptor (IGF1R) has a predominant affinity for IGF1 (Fig. 1), although IGF2 and insulin are also able to activate IGF1R. IGF1 expression is mainly regulated by growth hormone and originates predominantly in the liver, but can also be induced in an autocrine or paracrine fashion in target tissues, including malignancies (Bowers *et al.*, 2015). Increased IGF-IGF1R signalling is frequently observed in cancer, and in malignant transformation. Concordantly, mutations in IGF1R in cancer are rarely reported (Gao *et al.*, 2012). Tumour cells can also produce IGF1 making it available for endocrine, paracrine and autocrine interactions in the tumour microenvironment. IGFs predominantly act on ECs to promote angiogenesis through stimulation of VEGF, hypoxia-inducible factor 1 $\alpha$  (HIF1 $\alpha$ ) and endothelial nitric oxide (NO) synthase (eNOS) expression (Bach, 2015).

Although ECs themselves express negligible levels of IGF1, IGF1R is expressed by both large and small vessels (Delafontaine, Song & Li, 2004). Human umbilical vein ECs (HUVECs) express several-fold more IGF1R than IR, although this ratio may change over time in culture (Nitert *et al.*, 2005). Direct effects of IGF1 on ECs have been shown, however, not all studies controlled for the relative contributions of IR and IGF1R in the response to IGF1. Nevertheless, IGF1-IGF1R signalling is involved in EC migration and tube formation, vasorelaxation as a consequence of NO production and mediation of inflammatory responses. However, effects differed in ECs derived from various vascular beds (Nakao-Hayashi *et al.*, 1992; Shigematsu *et al.*, 1999; Che *et al.*, 2002; Bid *et al.*, 2013; Bach, 2015). *In vivo*, high levels of IGF1 were found to be associated with the development of diabetic retinopathy, a condition characterized by neovascularization in the eye (Merimee, Zapf & Froesch, 1983). These pro-angiogenic properties of IGF1 were later confirmed in both corneal and retinal neovascularization (Grant, Caballero & Millard, 1993). Of note, overexpression of IRS-1 has also been reported in corneal neovascularization (Cursiefen *et al.*, 2014). In a tumour setting, IGF1 was shown to stimulate VEGF expression from tumour cells in both HIF1 $\alpha$ -dependent and -independent mechanisms, contributing to sustained angiogenesis (Slomiany & Rosenzweig, 2006; Kurmasheva *et al.*, 2009; Li *et al.*, 2011). In addition, IGF1R activation may protect against apoptosis of ECs (Pan *et al.*, 2014).



**Fig. 1.** Receptors and ligands of the insulin-like growth factor (IGF) signalling axis. IGF1 receptor (IGF1R), insulin receptor A (IR-A) and IR-B consist of an extracellular ligand-binding  $\alpha$ -subunit and a catalytic transmembrane  $\beta$ -subunit derived from a single protein precursor, and are present in the membrane as dimers. Homo- and heterodimeric as well as hybrid receptor combinations are possible and driven by the relative expression of each protein. Depending on their composition, downstream signalling is predominantly mitogenic (IGF1R and IR-A) or metabolic (IR-B). IGF2R is a single-pass transmembrane monomer without tyrosine kinase activity which acts predominantly as a decoy receptor for circulating IGF2. The relative affinity of the different receptor combinations for the ligands IGF1, IGF2 and insulin is depicted in distance from the receptor. Adapted from Belfiore *et al.* (2009) and Chao & D'Amore (2008).

*In vivo* experiments demonstrated that a vascular-specific knockout of IGF1R reduced hypoxia-mediated retinal neovascularization in mice, albeit to a lesser extent than knockout of IR (Kondo *et al.*, 2003). In another study, knockdown of IRS-1 downstream of IGF1R, using an antisense oligonucleotide, inhibited corneal neovascularization in a rat model (Andrieu-Soler *et al.*, 2005). Furthermore, haploinsufficient IGF1R<sup>+/-</sup> mice exhibited altered vascular function (Abbas *et al.*, 2011), and IGF1R activation was shown to be critical during embryonic vascularization of the lungs (Han *et al.*, 2003). In cancer, IGF1–IGF1R signalling has been associated with increased tumour angiogenesis, and this is likely also mediated by indirect effects on the vasculature, e.g. through VEGF induction.

In addition to sprouting of ECs from pre-existing vessels, tumour angiogenesis is also facilitated by the incorporation of circulating endothelial progenitor cells (EPCs), usually derived from bone-marrow (Asahara *et al.*, 1999). Both IGF1 and insulin have been implicated in promoting EPC function and homing to sites of neovascularization (Sukhanov *et al.*, 2007; Thum *et al.*, 2007; Humpert *et al.*, 2008). In cancer, hypoxia-induced expression of stromal derived factor 1 (SDF1) and VEGF contribute to the mobilization of bone-marrow-derived progenitor cells that may incorporate in nascent vessels (Asahara *et al.*, 1999; van Beijnum *et al.*, 2015; Huijbers *et al.*, 2016). As such, this process contributes to tumour angiogenesis and progression, as well as therapy resistance (van Beijnum *et al.*, 2015; Huijbers *et al.*, 2016). Insulin and insulin analogues stimulated the outgrowth of EPCs *in vitro*, in a dose-dependent manner (Humpert *et al.*, 2008). Interestingly, inhibiting IR had no significant effect on this process, while blockade of IGF1R completely abrogated

insulin-stimulated EPC outgrowth (Humpert *et al.*, 2008). *In vivo* perfusion of mice with IGF1 resulted in increased EPC numbers in the blood (Sukhanov *et al.*, 2007). This was accompanied by an increase in eNOS activity, which is essential for IGF1-mediated EPC mobilization (Sukhanov *et al.*, 2007; Thum *et al.*, 2007). A definitive role for IGF1R in EPC mobilization and function was demonstrated by Thum *et al.* (2007). Growth hormone treatment of elderly individuals increased circulating IGF1 levels as well as EPC numbers. These EPCs express IGF1R and blockade of this receptor counteracted the effects of IGF1 on EPC migration, colony formation and incorporation in vessels (Thum *et al.*, 2007). Thus, by stimulating not only vascular growth but also the incorporation of progenitor cells into growing blood vessels, IGF–IGF1R signalling can contribute to sustaining tumour angiogenesis.

## (2) Insulin-like growth factor 2 (IGF2) receptor and angiogenesis

In contrast to IGF1R and IR, the IGF2R or mannose-6-phosphate receptor, is a single-pass transmembrane glycoprotein without tyrosine kinase activity. It shows affinity for IGF2, as well as for other mannose-6-phosphate-containing ligands but lacks affinity for IGF1 and insulin. It is generally seen as a regulatory receptor for IGF2 (Korner *et al.*, 1995; Livingstone, 2013) (Fig. 1) as circulating levels of IGF2 exceed that of IGF1 during human postnatal life (Bach, 2015). IGF2 binding to IGF2R has been suggested to lead to G(i) protein signalling to mediate cellular effects (Okamoto *et al.*, 1990), but this is still under debate (Korner *et al.*, 1995). As such, the role of IGF2R in tumour progression has been considered as

passive, modulating IGF2 availability for signalling through IR and IGF1R.

An initial role for IGF2R in angiogenesis was demonstrated by the discovery of the angiogenic factor proliferin, a member of the prolactin–growth hormone family (Jackson *et al.*, 1994; Volpert *et al.*, 1996), which was demonstrated to bind to IGF2R (Lee & Nathans, 1988). Placental angiogenesis is stimulated by proliferin, as was EC migration *in vitro* (Jackson *et al.*, 1994; Volpert *et al.*, 1996). Furthermore, a mutant form of IGF2 capable of only binding to IGF2R stimulates EC migration and chemotaxis (Volpert *et al.*, 1996; Groskopf *et al.*, 1997), which was suggested to be controlled by G(i) protein-mediated induction of the MAPK pathway (Groskopf *et al.*, 1997).

Direct angiogenic effects of IGF2 were demonstrated in the developing chick chorioallantoic membrane. Here, IGF2 dose-dependently stimulated capillary formation (Bae *et al.*, 1998). In addition, IGF2 increased EC migration, tube formation and invasion (Lee *et al.*, 2000). However, a direct involvement of IGF2R was not addressed in these studies, and the observed effects may have been mediated by IR and/or IGF1R. Direct involvement of IGF2/IGF2R signalling in angiogenesis was provided by Herr *et al.* (2003) who demonstrated that antibodies against IGF2R circumvented the induction of EC sprouting by IGF2. Pertussis toxin, an inhibitor of G-protein activation, abolished IGF2-induced sprout outgrowth, again suggesting involvement of G(i) signalling.

Not only insulin and IGF1, but also the IGF2–IGF2R pathway has been implicated in the process of EPC recruitment. EPCs express high levels of IGF2R, and IGF2 induced intracellular Ca<sup>2+</sup> localization, chemotaxis, adhesion and invasion of EPCs. Effects were inhibited by mannose-6-phosphate, competing with IGF2 for IGF2R and neutralizing antibodies to IGF2R (Maeng *et al.*, 2009). A G(i) protein antagonist blocked these effects, again suggesting that IGF2R may be a functional signalling receptor (Maeng *et al.*, 2009). IGF2 is highly upregulated in hypoxic tissues (Kim *et al.*, 1998), and hypoxia has been appreciated as a driving mechanism of EPC recruitment (Takahashi *et al.*, 1999). *In vivo*, IGF2 combined with bone-marrow-derived EPCs resulted in maximal vascularization in a Matrigel plug assay. More importantly, physiological relevance and IGF2R importance were shown in a hind-limb ischemia model where EPC homing was inhibited by neutralizing IGF2R function (Maeng *et al.*, 2009).

IGF2 is frequently overexpressed in cancers due to loss of imprinting (Cui *et al.*, 2003). This, in combination with mutations in IGF2R resulting in reduced affinity for IGF2, leads to increased circulating and local IGF2 that can promote cellular growth through IR and IGF1R, and is associated with increased cancer risk and poor prognosis (reviewed by Livingstone, 2013). Interestingly, polymorphisms in IGF2R have been associated with increased malignant potential in different ways. By affecting transcript stability and translation of IGF2R, genetic variants of IGF2R coincided with increased secretion of

procathepsin D and contributed to transforming growth factor  $\beta$  (TGF $\beta$ ) activation (Zavras *et al.*, 2003; Kotsinas *et al.*, 2008). Both cathepsin D and TGF $\beta$  are known for their stimulating effects on tumour angiogenesis (Hu *et al.*, 2008; van Meeteren, Goumans & ten Dijke, 2011). Taken together, the involvement of IGF2R in tumour angiogenesis is not uncontroversial, but its potential contribution should not be neglected.

### (3) Insulin receptor and angiogenesis

The pro-angiogenic effects of insulin have long been recognized in relation to its wound-healing properties, a process dependent on angiogenesis (Gurd, 1937). Later, the stimulatory effects of insulin on ECs were demonstrated (Nakao-Hayashi *et al.*, 1992). The intricate role of insulin in diabetic conditions further sheds light on its involvement in angiogenesis as insulin treatment in diabetic patients may lead to an initial worsening of diabetic retinopathy, reflective of excessive angiogenesis (Roysarkar *et al.*, 1993). Indeed, vascular endothelial specific knockout of IR resulted in a 57% decrease in hypoxia-induced retinal neovascularization (Kondo *et al.*, 2003). Subcutaneous insulin injection induced angiogenesis in mouse skin. Here, vessels were longer and more branched, and a higher presence of pericytes [ $\alpha$  smooth muscle actin ( $\alpha$ SMA) staining] was observed, suggesting vessel maturation (Liu, Petreaca & Martins-Green, 2009). In addition, insulin treatment of microvascular ECs led to increased migration and tube formation (Liu *et al.*, 2009; Rensing *et al.*, 2010). By contrast, others reported that microvascular ECs are relatively resistant to insulin *in vitro* due to a higher expression of IGF1R than IR (Nitert *et al.*, 2005; Johansson, Chisalita & Arnqvist, 2008). IR signalling affects angiogenesis through the PI3K/AKT pathway (Liu *et al.*, 2009) which induces the release of NO through phosphorylation of eNOS (Zeng & Quon, 1996; Michell *et al.*, 1999). NO is a critical factor in angiogenesis and plays a key role in EC survival, proliferation and migration (Cooke, 2003) and provides a positive feedback loop *via* the induction of VEGF expression (Dulak *et al.*, 2000).

The two isoforms of insulin receptor, IR-A and IR-B, can form homodimers as well as heterodimers (IR-A/B), and can form hybrid receptors with IGF1R, resulting in different affinities for IGF1, IGF2 and insulin (Fig. 1). Insulin receptor isoform expression is regulated developmentally, as well as in a tissue-specific manner (Seino & Bell, 1989; Mosthaf *et al.*, 1990). IR-B is highly expressed in liver and is considered to be the major metabolic receptor for insulin (Mosthaf *et al.*, 1990). By contrast, IR-A is regarded as the oncofetal form, with high expression during fetal development and cancer (Frasca *et al.*, 1999). Although the receptors differ in only 12 amino acids at the C-terminus of the  $\alpha$  chain, their ligand binding and signalling properties are quite divergent. IR-A signalling primarily induces class I PI3K activation with mitogenic effects whereas IR-B signalling through class II PI3K ultimately results in glycogen synthesis (Leibiger *et al.*, 2001). Whether or not caused by a higher sequence similarity to IGF1R (Denley *et al.*, 2003), IR-A has a higher

affinity for IGFs, and a slightly higher affinity for insulin, as compared to IR-B (Frasca *et al.*, 1999). In addition, IR-B has prolonged autophosphorylation activity over IR-A and different internalization kinetics (Vogt *et al.*, 1991; Kellerer *et al.*, 1992). The exact mechanisms driving the alternative splicing have not been fully elucidated, though hormonal and metabolic factors may be involved as it was shown that insulin and high glucose levels can upregulate IR-B (Denley *et al.*, 2003).

We and others have demonstrated that tumour ECs overexpress IR relative to non-activated normal tissue ECs (van Beijnum *et al.*, 2006, 2015; Rensing *et al.*, 2010; P. Nowak-Sliwinska, J. R. van Beijnum, E. J. Huijbers, T. J. Wong & A. W. Griffioen, in preparation), most notably the IR-A isoform. Moreover, many cancer types overexpress this variant (Denley *et al.*, 2003; Belfiore *et al.*, 2009; Andres *et al.*, 2013). Tumour growth and angiogenesis were suppressed in xenograft tumours lacking IR, possibly mediated by reduced VEGF signalling (Zhang *et al.*, 2010). Overexpression of IR-A increased proliferation, colony formation, migration, invasion, and resistance to apoptosis in prostate cancer cells (Heidegger *et al.*, 2014), whereas overexpression of IR-B reduced proliferation and accelerated differentiation in colon cancer cells (Andres *et al.*, 2013). IR-A has a higher affinity for IGF2 than for IGF1 (Belfiore *et al.*, 2009), and overexpression of IR-A as well as its ligand IGF2 in tumours accelerates tumour growth and angiogenesis through autocrine and paracrine stimulatory loops (Denley *et al.*, 2003).

#### (4) Hybrid receptors and angiogenesis

Due to the high homology between the different receptors and their dimeric nature, hybrid receptors can be formed consisting of monomers of IR-A or IR-B and IGF1R (Fig. 1). The relative abundance of the individual monomers dictates the distribution of the hybrid receptors as a function of the molar fractions of each individual receptor (Baillyes *et al.*, 1997; Belfiore *et al.*, 2009), and as such will determine the eventual tissue response. In addition, other factors affect the precise signalling that is initiated upon receptor–ligand interactions (reviewed by Siddle, 2011, 2012). Among these factors are (i) differences in interactions of IGF1R and IR with different intracellular adaptors and scaffolds, (ii) post-translational modifications, (iii) their internalization kinetics, and (iv) expression of receptor substrates in a particular cell or lipid raft domain.

Hybrid receptors display differential affinity for IGFs and insulin (Fig. 1). Hybrid receptors consisting of IGF1R and IR-A have high affinity for IGF1 and IGF2 and markedly reduced affinity for insulin as compared to IR-A. Hybrids between IR-B and IGF1R lose their affinity for insulin, and have lower IGF affinities than IGF1R/IR-A hybrids (Pandini *et al.*, 2002). Hybrid IR-A/IR-B essentially function as IR-A (Janssen & Varewijck, 2014). IR-A-containing receptors function predominantly as mitogenic receptors whereas IR-B-containing receptors are thought to act mainly as metabolic mediators (Belfiore *et al.*, 2009).

ECs generally express more IGF1R than IR and hybrid IGF1R/IR have been found in HUVECs, however, incorporation of IR-A *versus* IR-B was not addressed (Chisalita & Arnqvist, 2004; Nitert *et al.*, 2005). IGF1 but not insulin was able to activate IGF1R/IR hybrids at low concentrations (Li *et al.*, 2005; Nitert *et al.*, 2005), suggesting that increased hybrid receptor expression reduces insulin sensitivity and enhances IGF responsiveness. Moreover, high IGF1R expression over IR drives the assembly of hybrid receptors and reduces the availability of IR homoreceptors, further contributing to a shift from insulin towards IGF reactivity with concomitant growth-promoting effects. Reduced insulin sensitivity can lead to hyperinsulinemia which has been associated with increased cancer progression through its actions on the pro-proliferative IR-A receptor. In addition, high insulin levels may in turn stimulate growth hormone receptor and IGF1 expression in the liver, positively feeding IGF signalling (Janssen & Varewijck, 2014).

The precise contribution of the hybrid receptors to cellular physiology is difficult to establish due to a lack of specific reagents. Antibodies distinguishing between IR-A and IR-B are not available, and most (therapeutic) monoclonal antibodies generated against IGF1R show no cross-reactivity with IR (Janssen & Varewijck, 2014). Although antibodies with reactivity towards both hybrid receptors and IGF1R or hybrid receptors and IR have been documented (Belfiore *et al.*, 2009), so far no selective targeting of hybrid receptors has been demonstrated. As such, the use of R-cells, mouse 3T3-like fibroblasts without IGF1R (Pandini *et al.*, 2002), in which human IR and/or IGF1R were introduced, have been instrumental in studying hybrid receptor characteristics. Nevertheless, this system precludes drawing firm conclusions on distribution and function *in vivo*.

#### (5) Insulin-like growth factor binding proteins (IGFBPs) and angiogenesis

IGFBPs regulate IGF bioavailability and stability through binding of IGFs in the circulation with high affinity, thereby modulating (either inhibiting or stimulating) IGF signalling. Furthermore, upon binding of IGFBPs, IGFs are protected from degradation which prolongs their half-life. Proteolytic cleavage of IGFBPs, e.g. through matrix metalloproteinases (MMPs), releases IGFs (Rajaram, Baylink & Mohan, 1997), although partial cleavage may retain IGF1 binding (Andress *et al.*, 1993; Lalou, Lassarre & Binoux, 1996; Firth & Baxter, 2002). In addition, native IGFBPs can also have independent cellular actions (Rajah *et al.*, 1995; Firth & Baxter, 2002; Wheatcroft & Kearney, 2009). Thus far, six IGFBPs have been identified (IGFBP1–6). IGFBP1, and -3 have been ascribed dual roles in tumour angiogenesis, which might be the result of divergent actions of direct cellular effects of these proteins *versus* IGF binding properties. High IGFBP1 levels have been associated with reduced cancer and cardiovascular disease risks, implying a vascular protective effect (Janssen *et al.*, 1998; Spoerri *et al.*, 1998). On the other hand, IGFBP1 is induced by hypoxia and was shown to induce EC migration (Kahn *et al.*, 2011).

Most circulating IGF is bound by IGFBP3, as such limiting IGF bioavailability. Through its heparin-binding domain, IGFBP3 can bind ECs independently of IGF binding (Janssen *et al.*, 1998; Hwa, Oh & Rosenfeld, 1999). IGFBP3 inhibited the proliferative effects of VEGF on ECs and reduced prostate cancer growth through inhibition of angiogenesis (Franklin, Ferry & Cohen, 2003; Liu *et al.*, 2007). By contrast, activation of sphingosine-1-phosphate by IGFBP3 in HUVECs protected the cells from serum starvation-induced apoptosis and enhanced cell migration (Takuwa *et al.*, 2010). Furthermore, IGFBP3 was shown to stimulate MMP2 and MMP9 activation and concomitantly tube formation of ECs (Granata *et al.*, 2007). Another pro-angiogenic effect of IGFBP3 is that it can directly stimulate EPCs or haematopoietic stem cells to develop into ECs and subsequently enhance cell migration and tube formation (Chang *et al.*, 2007).

IGFBP2 is recognized for its pro-angiogenic properties. Interestingly, one of its mechanisms involves nuclear translocation and VEGF expression-promoting activities (Azar *et al.*, 2011). In addition, IGFBP2 was shown to bind and activate  $\alpha V\beta 3$  integrin on ECs and tumour cells, leading to the expression of VEGF *via* the PI3K pathway (Das *et al.*, 2012). Furthermore, IGFBP2 promoted EC–EPC interactions and cellular motility through binding with its tripeptide Arg-Gly-Asp (RGD) domain to  $\alpha 5\beta 1$  integrin (Wang *et al.*, 2006; Feng *et al.*, 2015). However, in these studies the relative contributions of autocrine/paracrine *versus* intracellular functions of IGFBP2 were not clearly addressed. Interestingly, exogenously administered protease-resistant IGFBP2 inhibited cancer cell proliferation and angiogenesis *in vitro* and *in vivo* (Soh *et al.*, 2014).

The anti-angiogenic properties of IGFBP4 have been attributed to the C-terminal domain of the protein which shows anti-cathepsin B activity, and thus inhibits an important angiogenic lysosomal protease (Premzl, Turk & Kos, 2006; Das *et al.*, 2012; Moreno *et al.*, 2013). Furthermore, IGFBP4 reduced tube formation in human brain endothelial cells (HBECS), which was thought to be caused by the inhibition of VEGF-induced effects (Moreno *et al.*, 2006). IGFBP5 was also demonstrated to be an anti-angiogenic factor. IGFBP5 inhibits the activation of AKT and eNOS by VEGF, and thereby impairs proliferation, migration and tube formation in ECs (Rho *et al.*, 2008). The various inhibitory actions of IGFBP6 on tumour growth were initially mainly attributed to the inhibition of IGF2 (Bach, 2005). Later it was shown that IGFBP6 inhibited VEGF-induced angiogenesis both *in vitro* and *in vivo*, however, the exact mechanism behind this inhibitory function is unclear (Zhang *et al.*, 2012).

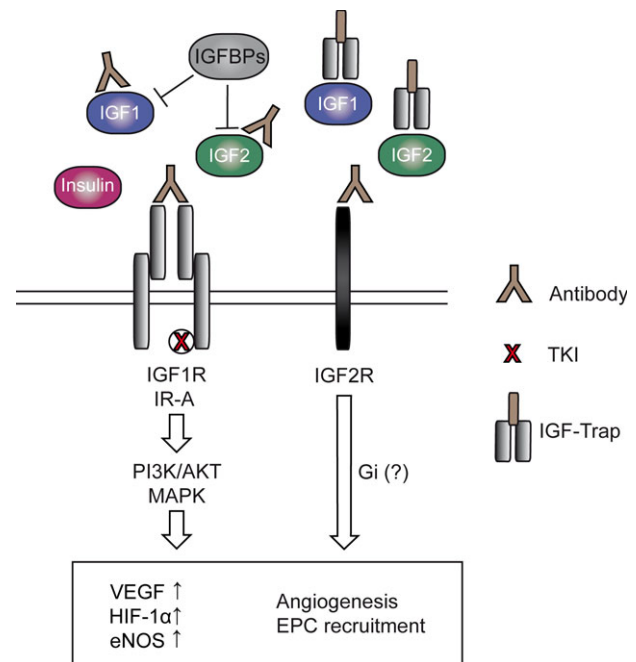
Although a series of IGFBP-related proteins, structurally related to the IGFBPs, have been identified and termed IGFBP7 and higher (Hwa *et al.*, 1999), their binding properties and contribution to the IGF system are not established. It is however, relevant in light of this review to point out that IGFBP7 specifically binds insulin, resulting in functional IR inhibition (Yamanaka *et al.*, 1997; Ruan

*et al.*, 2016). Interestingly, this protein has been associated with angiogenesis and has also been named ‘angiomodulin’. However, its exact role remains to be elucidated since stimulatory, as well as inhibitory effects have been described, that may possibly be concentration dependent (van Beijnum *et al.*, 2006; Tamura *et al.*, 2009; Zhu *et al.*, 2014; Zhao *et al.*, 2016).

### III. THERAPEUTICS, RESISTANCE AND ANGIOGENESIS

#### (1) Targeting the insulin-like growth factor (IGF) axis

The dominant involvement of the IGF signalling pathway in cancer and tumour angiogenesis has led to the development of different therapeutics aimed at inhibiting its actions (Fig. 2; Table 1). An initial major concern however, was to circumvent the induction of hyperglycemia, insulin resistance



**Fig. 2.** Insulin-like growth factor (IGF) signalling axis therapeutics and anti-angiogenic actions. To inhibit signalling along the IGF axis, different strategies have been developed: (i) antibodies targeting the IGF1 receptor (IGF1R) and its ligands IGF1 and IGF2, (ii) receptor tyrosine kinase inhibitors (TKIs) and (iii) recombinant soluble IGF1R (sIGF1R) fused to an antibody heavy chain Fc region (IGF-Trap). Downstream signalling of the receptors induces angiogenesis and endothelial progenitor cell (EPC) recruitment, in part through induction of vascular endothelial growth factor (VEGF) signalling. eNOS, endothelial nitric oxide (NO) synthase; Gi, inhibitory G protein second messenger; HIF-1 $\alpha$ , hypoxia-inducible factor 1 $\alpha$ ; IGFBP, IGF binding protein; IR-A, insulin receptor A; MAPK, mitogen-activated protein kinase; PI3K/AKT, phosphatidylinositol 3-kinase/AKT serine threonine kinase; VEGF, vascular endothelial growth factor.

Table 1. Drugs targeting the insulin-like growth factor (IGF) axis

Name	Target	Alternative name	Type
Medi-573	IGF1/2		Ab
BI 836845	IGF1/2		Ab
Figitumumab	IGF1R	CP-751,871	Ab
Dalotuzumab	IGF1R	MK-0646; h7C10	Ab
Cixutumumab	IGF1R	IMC-A12	Ab
Ganitumab	IGF1R	AMG-479	Ab
R1507	IGF1R	RO4858696	Ab
Robatumumab	IGF1R	SCH 717454	Ab
AVE-1642	IGF1R		Ab
BIIB022	IGF1R		Ab
XL-228	IGF1R		TKI
Linsitinib	IGF1R/IR	OSI-906	TKI
KW-2450	IGF1R/IR		TKI
AXL1717	IGF1R/IR	Picropodophyllin (PPP)	TKI
BMS-754807	IGF1R/IR		TKI

IGF-axis-targeting agents in clinical trials ([www.clinicaltrials.gov](http://www.clinicaltrials.gov)). Modified from Bowers *et al.* (2015); Brahmkhatri, Prasanna & Atreya (2015); Iams & Lovly (2015) and King *et al.* (2014).

Ab, antibody; IGF1R, IGF1 receptor; IR, insulin receptor; TKI, tyrosine kinase inhibitor.

and hyperinsulinemia from inhibiting the IR (Gualberto & Pollak, 2009; Pollak, 2012; King *et al.*, 2014). Different IGF-axis targeted therapeutics have been developed over time [reviewed by Bowers *et al.* (2015); Gao *et al.* (2012)], which potentially give rise to different glucose homeostasis related toxicities. Tyrosine kinase inhibitors (TKIs) have been developed that target the receptors, however, these may induce hyperglycemia *via* the direct inhibition of IR (Gualberto & Pollak, 2009; King *et al.*, 2014). Anti-IGF1R antibodies generally do not cross-react with IR, but may interact with the hybrid receptors. They impair glucose tolerance through induction of circulating growth hormone, IGF1 and IGF1R in response to blockade of pituitary IGF1R (King *et al.*, 2014). Scavengers neutralizing IGF1 and IGF2 such as antibodies (Haluska *et al.*, 2014), IGF-Trap (a soluble part of the IGF1R fused to the Fc portion of an IgG and capable of scavenging both IGF1 and IGF2 but not insulin; Wang *et al.*, 2015) and protease-resistant IGF1R (Rosenzweig & Atreya, 2010), have generally less effect on glucose homeostasis (Gualberto & Pollak, 2009; King *et al.*, 2014).

Anti-receptor antibodies, ligand scavengers and small-molecule TKIs have all shown promising results in preclinical studies, but none of the agents lived up to this promise in clinical trials [reviewed by Gao *et al.* (2012); King *et al.* (2014)]. The intrinsic complexity of the pathway may have enabled escape signalling to take place; additionally poor study design and patient selection may have contributed. Sensitivity to anti-IGF1R therapy, e.g. by measuring IGF levels or screening for activating mutations downstream of the receptor was not taken into account (Pollak, 2012; Janssen & Vwarewijnck, 2014; Bowers *et al.*, 2015). Nevertheless, while not yet successful as a monotherapy [except for in sarcoma-type tumours (Baserga, 2013)], targeting IGF1 signalling as part of a carefully designed combination therapy may still hold promise.

Below we discuss several resistance and escape mechanisms that may contribute to inadequate therapeutic success of interference with the IGF1 signalling axis, with a focus on implications for angiogenesis inhibition.

## (2) Resistance mechanisms within the family

Different explanations for failure of IGF-axis targeted therapies have been postulated, which can be roughly divided into intrinsic resistance and adaptive/evasive resistance. First, IGF-independent growth, when tumours primarily rely on other growth factors, may pose an intrinsic resistance mechanism. Second, subcellular IGF1R localization may also contribute to intrinsic resistance to anti-IGF signalling therapeutics. For example, aberrant IGF1R glycosylation, impairing insertion into the plasma membrane (Kim *et al.*, 2012), and nuclear localization of IGF1R (Asmane *et al.*, 2012) prevent antibody–receptor interactions and were associated with reduced responsiveness. Although one might expect that this would decrease responsiveness to IGFs and thus impair the malignant potential of tumours, this was not reported. Apparently, not only the relative balance of, but also the dependence on, the different receptors in the IGF(R) axis will determine responsiveness to IGFs. Third, constitutively activated PI3K/AKT or Ras/MAPK pathways that function downstream of the IGF and IR receptors, will sustain signalling even in the presence of receptor inhibitors. In addition, redundancy in downstream signalling cascades, shared with other receptor tyrosine kinases (RTKs), may limit inhibitory action of IGF axis therapeutics (King *et al.*, 2014).

Cells expressing a low ratio of IGF1R:IR are more likely to show intrinsic resistance to IGF1R therapeutics (Buck *et al.*, 2010; Ulanet *et al.*, 2010; Garofalo *et al.*, 2011). Due to the high specificity of the targeted agents, the more prevalent hybrid IR/IGF1R receptors will not be inhibited, and signalling can proceed (Fig. 3). Very recently it was

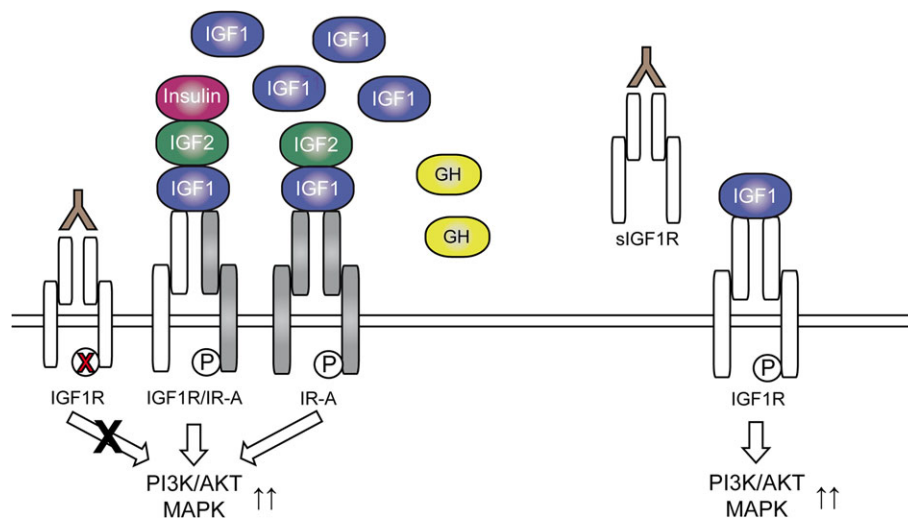
reported that total IR expression correlates with resistance against the anti-IGF1R agent cixutumumab (Forest *et al.*, 2015). Moreover, the relative expression of IR-A versus IR-B will determine to what extent continued IR signalling contributes to either mitogenic signalling (preferred by IR-A) or metabolic signalling (preferred by IR-B) (Sacco *et al.*, 2009; Garofalo *et al.*, 2011, 2012; Giudice *et al.*, 2011). Since enhanced IR-A signalling is recognized to mediate growth-promoting effects during IGF1R blockade, co-targeting of IR-A and IGF1R is advocated (Salisbury & Macaulay, 2003; Buck *et al.*, 2010). OSI-906 is a TKI which inhibits both IR and IGF1R, and indeed proved more effective in inhibiting tumour growth than an anti-IGF1R antibody (Buck *et al.*, 2010). However, a recent phase 3 study in adrenocortical carcinoma did not report significant clinical benefit of OSI-906 (Fassnacht *et al.*, 2015).

Recently, circulating IGF1R has been reported in cancer patients (Xu *et al.*, 2014). Although its relevance and exact nature remain to be determined, it is hypothesized that this might contribute to resistance against IGF1R therapeutics. Circulating receptors can interfere with cellular interaction of anti-IGF1R antibodies. In addition, it was suggested that displacement of soluble receptor-bound IGFs by the antibodies increases bioavailability of IGFs and potential for cellular interactions (Janssen & Varewijck, 2014) (Fig. 3). However, solid experimental evidence for these mechanisms is lacking. Next to intrinsic unresponsiveness to blockade of the IGF signalling axis, adaptive/evasive resistance mechanisms have been elucidated that diminish efficacy. Upon antibody blockade of IGF1R, its cell surface expression is suppressed due to internalization, and the balance shifts to increased dominance of IR-A signalling, leading to

therapy resistance (Buck *et al.*, 2010; Ulanet *et al.*, 2010; Garofalo *et al.*, 2011, 2012). In addition, IGF1R expression may be downregulated as a consequence of conventional anticancer therapy, e.g. by tamoxifen (Janssen & Varewijck, 2014), rendering anti-IGF1(R) therapeutics less effective. Furthermore, impaired signalling of IGF1R results in a compensatory feedback mechanism culminating in increased IGF1 production due to enhanced growth hormone secretion (Wan *et al.*, 2007; Moody *et al.*, 2014) (Fig. 3).

As an alternative strategy, antibody-mediated blockade of IGF1 and IGF2 has been explored, as this may circumvent resistance to receptor blockade. This antibody inhibited primary tumour growth in mice, albeit not metastatic colonization (Haluska *et al.*, 2014). Also, the IGF-Trap (Wang *et al.*, 2015) is currently under investigation. However, such scavengers can only block free, bioactive IGFs, after being released from their binding partners, the IGF-BPs. Moreover, a reduction in circulating IGF1 results in activation of growth hormone secretion and subsequent IGF1 production by the liver (Belfiore *et al.*, 2009) which will result in restored tumour growth and therapy resistance. Selective blockade of IGF2 is not expected to have such feedback effects. Moreover, given the dominant expression of high IGF2-affinity hybrid receptor containing the IR-A isoform in cancer and tumour endothelium, in combination with the high circulating IGF2 levels in humans, IGF2 inhibition might promise a more effective strategy over IGF1 inhibition alone. Indeed, neutralization of IGF2 restored sensitivity to anti-IGF1R antibody *in vitro* (Forest *et al.*, 2015).

Taken together, the intricate interplay and diversity of responses of the different homo- and heterodimeric receptors precludes the specific therapeutic targeting of a



**Fig. 3.** Resistance to insulin-like growth factor (IGF) signalling axis inhibition. Antibody blockade or tyrosine kinase inhibitor (TKI)-mediated inhibition of IGF1 receptor (IGF1R) will downregulate IGF1R expression and result in predominant expression of insulin receptor A (IR-A) homodimers or IR-A/IGF1R hybrids that show enhanced responsiveness to insulin and IGFs and will promote mitogenic and pro-angiogenic signalling. In addition, pituitary IGF1R blockade will increase circulating growth hormone (GH) and IGF1. Alternatively, antibody blockade of soluble IGF1R (sIGF1R) will displace bound IGFs, making them available for cellular receptor interactions, and simultaneously reduce the availability of anti-IGF1R antibody for cellular receptor binding. MAPK, mitogen-activated protein kinase; PI3K/AKT, phosphatidylinositol 3-kinase/AKT serine threonine kinase.

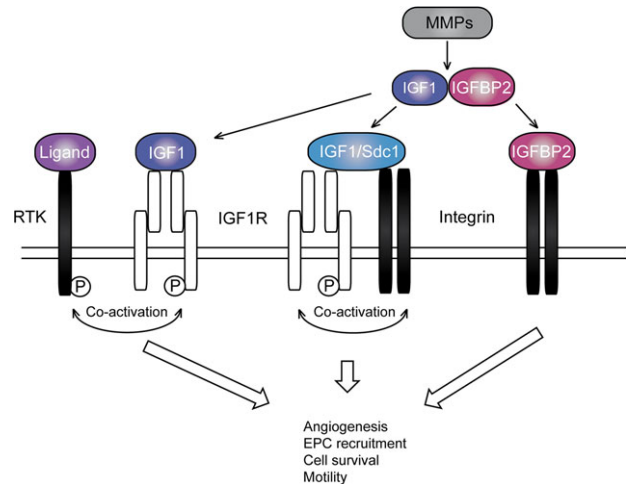
single player in this system to control tumour growth and angiogenesis.

### (3) Resistance mechanisms outside the family

Close relationships between IGF1R and IRs resulting in intrinsic or evasive resistance may not be the only explanation for reduced effectiveness of anti-IGF(1R) therapy. Extensive crosstalk also exists between IGF1R and growth hormone receptor (GHR), oestrogen receptor (ER), androgen receptor (AR), MET proto-oncogene receptor tyrosine kinase (c-MET), epidermal growth factor receptor (EGFR) and erb-b2 receptor tyrosine kinase HER2 signalling pathways (Janssen & Vreuwijk, 2014). Thus, other oncogenic signalling pathways can take over in the presence of IGF-axis blockade. In addition, interplay with important angiogenic signalling cascades has been described that can further amplify IGF signalling. Combining therapeutics directed against multiple activated cellular pathways therefore seems like an obvious choice.

Not only are the receptors of the IGF signalling axis capable of dimerizing with each other, interactions of IGF1R and IGF1 with other cell surface receptors have been described. In light of the pro-angiogenic actions of the IGF signalling axis, the interplay of IGF1R with integrins is highly relevant (Drake, Cheresch & Little, 1995; Clemmons & Maile, 2005; Beauvais & Rapraeger, 2010; Rapraeger, 2013; Rapraeger *et al.*, 2013) and provides additional therapeutic angles.  $\alpha V\beta 3$  integrin, involved in cell migration, is virtually absent in quiescent endothelium, but highly upregulated in angiogenic ECs (Drake *et al.*, 1995). It has been shown that syndecan-1 (Sdc1), a heparan sulfate proteoglycan, clusters and activates IGF1R and  $\alpha V\beta 3$  integrin (Beauvais & Rapraeger, 2010) (Fig. 4). Synstatin, a dominant-negative inhibitory peptide sequence of Sdc1, is capable of blocking the capture of  $\alpha V\beta 3$  integrin and IGF1R and thereby inhibits the activation of IGF1R (Rapraeger, 2013). In addition to IGF1R, IGF1 itself can directly bind  $\alpha V\beta 3$  and  $\alpha 6\beta 4$  integrins, thereby inducing ternary complex formation of IGF1R, IGF1 and integrins (Saegusa *et al.*, 2009; Fujita *et al.*, 2012; Fujita, Takada & Takada, 2013). Thus, escape signalling involving direct activation of integrins by IGF1 may be induced by blocking IGF1R. Indeed, this mechanism was found to be responsible for induced resistance against IGF1R antibodies in head and neck squamous cell carcinoma (HNSCC) and non-small cell lung cancer (NSCLC) (Shin *et al.*, 2013). Taken together, co-targeting of integrins may potentiate the effects of anti-IGF1R therapeutics or prevent the induction of therapy resistance.

As discussed above, induction of VEGF expression is a recognized mechanism by which signalling along the IGF/IGFR axis contributes to angiogenesis. Different accessory proteins and membrane receptors have linked IGF1 signalling to angiogenesis *via* VEGF. One of these is CD147, or basigin, a glycoprotein commonly overexpressed in tumour cells and involved in promoting tumour progression (Millimaggi *et al.*, 2007). Tumour cell-derived vesicles containing CD147 promoted an angiogenic



**Fig. 4.** Interplay between insulin-like growth factors (receptors) [IGF(R)s] and angiogenic signalling. IGF1R and other receptor tyrosine kinases (RTKs) can assemble and co-activate each other leading to enhanced pro-angiogenic signalling. IGF1 and syndecan-1 (Sdc1) can both cluster IGF1R and integrins, resulting in co-activation of both membrane proteins, resulting in an amplified pro-angiogenic response. Integrins can also be directly stimulated by IGF binding protein 2 (IGFBP2). Matrix metalloproteinases (MMPs) can disrupt the interaction between IGFs and IGFBP2, enhancing the bioavailability of both proteins further sustaining angiogenic actions. EPC, endothelial progenitor cell.

phenotype in endothelial cells *in vitro* (Millimaggi *et al.*, 2007). Others subsequently demonstrated that hypoxia-induced expression of IGF1, VEGF and CD147 contributed to a positive feedback mechanism with reciprocal induction of expression, and inhibition of CD147 subsequently reduced IGF1-driven angiogenesis (Chen *et al.*, 2012). Another mechanism of VEGF induction *via* the IGF/IGFR axis is mediated by mucin-1 (Muc1), a known epithelial tumour marker. In breast cancer cell lines, Muc1 induces IGF1R phosphorylation and subsequent VEGFR expression (Woo *et al.*, 2012). These data further exemplify the independent actions of IGF/IR ligands that may contribute to tumour progression and angiogenesis, even in the presence of agents that block IGF/IR signalling, and further stresses the notion that sole inhibition of this pathway is likely not sufficient for cancer management.

Very recently, it was shown that IGF1R as well as IR-A can interact with discoidin domain receptors (DDR) (Morcavallo *et al.*, 2011; Malaguarnera *et al.*, 2015). DDRs are receptor tyrosine kinases with collagens as their ligand. As such, they are involved in matrix adhesion and migration (Borza & Pozzi, 2014; Leitinger, 2014), and are frequently overexpressed in cancer (Valiathan *et al.*, 2012). DDRs are essential for vascular development (Morcavallo *et al.*, 2011), and knockdown of DDR1 ligand collagen 4A5 inhibited EC proliferation and tube formation (Xiao *et al.*, 2015). Interaction between IGF1R and DDR1 was induced upon IGF1 stimulation, and promoted cell proliferation and migration (Malaguarnera *et al.*, 2015), whereas IR-A

Table 2. Ongoing clinical trials of combinations of insulin-like growth factor (IGF) axis and vascular endothelial growth factor (VEGF) axis targeting

Trial	Drug	Type	Drug	Type	Condition	Phase
NCT00729833	Figitumumab	Ab	Sunitinib	TKI	Advanced solid tumours	1
NCT01008566	Cixutumumab	Ab	Sorafenib	TKI	Advanced liver cancer	1
NCT01263782	Cixutumumab	Ab	Bevacizumab	Ab	Non-small cell lung cancer	2
NCT00906373	Cixutumumab	Ab	Sorafenib	TKI	Advanced liver cancer	2
NCT00955305	Cixutumumab	Ab	Bevacizumab	Ab	Recurrent non-small cell lung cancer	2
NCT00974896	Ganitumab	Ab	Sorafenib	TKI	Advanced solid tumours	1
NCT00811993	R1507	Ab	Bevacizumab	Ab	Advanced solid tumours	1
NCT00811993	R1507	Ab	Sorafenib	TKI	Advanced solid tumours	1
NCT01498952	MEDI-573	Ab	Sorafenib	TKI	Metastatic/unresectable hepatocellular carcinoma	1
NCT00791544	AVE-1642	Ab	Sorafenib	TKI	Advanced or metastatic liver carcinoma	1/2
NCT00956436	BIIB022	Ab	Sorafenib	TKI	Hepatocellular carcinoma	1
NCT01334710	Linsitinib	TKI	Sorafenib	TKI	Advanced hepatocellular carcinoma	2

Ab, antibody; TKI, tyrosine kinase inhibitor.

stimulation by IGF2 induced DDR1 and DDR2 activation (Morcavallo *et al.*, 2011). Together, these studies provide an alternative route for growth- and angiogenesis-promoting effects not targeted by inhibitors of IGF1R.

#### (4) Anti-angiogenic therapy and IGF axis inhibition – brotherly love?

Since IGFs and IGFs appear to be rather promiscuous proteins in promoting tumour progression and angiogenesis through interactions with and activation of other cellular receptors and effectors, induction of evasive resistance to targeted therapeutics is not surprising. Although these mechanisms apply to tumour cells and tumour ECs alike, the direct exposure of ECs to IGFs and insulin in the blood in combination with the overexpression of IR-A in tumour ECs underscore the impact of such resistance for both anti-tumour and anti-angiogenic effects. Moreover, global pathway analysis of gene expression signatures of IGF1R inhibitor-resistant cell lines in comparison to sensitive cell lines revealed an enrichment for genes involved in VEGF signalling, axon guidance, hypoxia response and angiogenesis, suggesting that upon blocking IGF1R alternative mechanisms are activated that favour tumour vasculature growth and expansion (Garofalo *et al.*, 2011, 2012).

Combining anti-angiogenic therapeutics and IGF axis inhibitors has proven beneficial, albeit predominantly in pre-clinical models. Tumours expressing a dominant-negative isoform of IGF1R were more sensitive to VEGF blockade by bevacizumab (Avastin) and displayed reduced tumour growth and angiogenesis (Li *et al.*, 2011). Analogously, combined blocking of VEGF and IGF1R with bevacizumab and cixutumumab (IMC-A12) was more effective in inhibiting ovarian cancer growth than either antibody alone (Shao *et al.*, 2012). Interestingly, in this study, it was shown that blockade of IGF1R did overcome resistance to VEGF blockade (Shao *et al.*, 2012). At the time of writing, clinical trials combining anti-angiogenic agents and IGF(R) targeting are ongoing, but no results have been published so far (Table 2). For a recent overview of published clinical trials involving IGF1R pathway inhibition, see Iams & Lovly (2015).

Novel therapeutic moieties appearing on the horizon may also offer improved therapeutic efficacy over single treatments. For instance, a bispecific antibody fusion molecule targeting both IGF1R and VEGF crosslinks both targets and ensures internalization and degradation, and is a potent inhibitor of tumour growth in different xenograft models when compared to individual anti-IGF1R and anti-VEGF therapeutics. Moreover, this so-called bi-AbCap inhibited tumour growth and angiogenesis more effectively than combining anti-IGF1R and anti-VEGF antibodies (Shen *et al.*, 2015). In another study, adnectins, engineered target-binding protein therapeutics (Lipovsek, 2011), designed to inhibit VEGFR2 and IGF1R, demonstrated a potentiating effect on inhibiting tumour growth and angiogenesis in a Ewing sarcoma model (Ackermann *et al.*, 2012).

Although the combination therapies show more potent tumour growth inhibition, many of the published studies do not demonstrate superiority of the combination over the single therapies. Additional insight into the synergistic actions of IGFs with other growth factors on tumour angiogenesis and hence their therapeutic targetability could be of value for improving combined targeting. Furthermore, evidence-based therapeutic design, or stochastic modelling-based combination definition (Weiss *et al.*, 2015*a,b*; Nowak-Sliwinska *et al.*, 2016) is a powerful method to identify drugs that act synergistically with IGF(R) targeting agents. We expect that biomarker analysis, giving insight into the relative expression of the players in this signalling axis, will also aid in designing more effective combinations of inhibitors. Moreover, combining IGF/IGFR/IR therapeutics with other agents targeted at the tumour and endothelium will undoubtedly improve therapeutic outcome.

#### IV. CONCLUSIONS

- (1) The IGF signalling pathway is not only a driver of malignant transformation but also intricately involved in sustaining tumour angiogenesis.

(2) The initial excitement surrounding IGF-axis-interfering drugs for targeting tumour growth has largely subsided due to disappointing clinical results. The extensively documented resistance to IGF-axis-targeted therapeutics can be mainly attributed to the intricate complexity of the pathway. Most notably, crosstalk with angiogenesis-stimulating factors, with pivotal roles for integrins and VEGF, allows for escape of therapeutic repression.

(3) Several strategies have been proposed for overcoming resistance including novel dual-targeting therapeutic moieties. Such inventions might drive the development of other novel agents co-targeting IGFR/IR and its interaction partners essential for tumour growth and angiogenesis such as  $\alpha V\beta 3$  integrin. In addition, there is also opportunity for more effective interference in the IGF signalling axis itself.

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