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Review

Insulin-like growth factor I and its binding proteins in the cardiovascular system

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1. Introduction

Insulin-like growth factor I (IGF I) is a ubiquitous peptide that has a fundamental role in both prenatal and postnatal development (reviewed in [1,2]). It is the major mediator of growth hormone's effects on postnatal growth. IGF II and insulin are structurally-related hormones with 40%-50% amino acid sequence similarity. This review will focus primarily on IGF I and its actions and expression in the cardiovascular system.

IGF I is the product of the IGF I gene which has been mapped to chromosome 12 in humans [3] and to chromosome 10 in mice [4]. The mammalian gene consists of at least six exons [2,5-7]. Transcription of the mammalian gene results from at least two transcription start sites located on exon 1 and exon 2. Exons 1 and 2 encode mutually exclusive 5' untranslated regions and there are several in-frame translation initiation codons yielding signal peptides differing at their N-terminus. The mature peptide coding sequence is present in exons 3 and 4. Additional complexity results from the presence of distinct carboxyterminal E domains of the IGF I preprohormone (Ea and Eb variants). Exon 1- and Ea-containing transcripts are expressed ubiquitously whereas exon 2 and Eb transcripts are expressed more specifically in the liver. Northern blot hybridization of mammalian tissues reveals multiple IGF I transcripts varying from around 0.9 kb to 7.5 kb in length. IGF I expression is regulated both at the level of transcription, mRNA stability and post-translationally. For a more detailed discussion of the organization of the IGF I gene the reader is referred to recent reviews [2,7].

IGF I exerts all of its known physiological effects upon binding to the type 1 IGF receptor (reviewed in [8]). The related peptide IGF II binds to both the IGF I and IGF II receptors. The IGF II receptor is identical to the cation-independent mannose-6-phosphate (M-6-P) receptor [9]. It is felt, however, that the physiological effects of IGF II are mediated on binding to the IGF I receptor and that the M-6-P receptor functions essentially as a scavenging receptor mediating the degradation of IGF II. A possible exception, however, may be during early fetal development, i.e., in the pre-implantation embryo [10].

The human IGF I receptor (IGF IR) is the product of a single-copy gene located on chromosome 15 [11]. The IGF IR resembles the insulin receptor in primary and tertiary structure [12]. The mature receptor is a tetramer consisting of two extracellular α -chains and two intracellular β -chains. The putative IGF I binding-site is within the cysteine-rich domain in the extracellular α -subunit. The β -chain includes an intracellular tyrosine-kinase domain that is thought to be essential for most of the receptor's biological effects. For a detailed discussion of the molecular organization of the IGF IR gene the reader is referred to a recent review [8].

The IGF-binding proteins are proteins that are present in the circulation and in extracellular fluids and bind with high affinity to both IGF I and IGF II. Six IGF-binding proteins have been isolated (reviewed in [1]). The IGF-binding activity in rat and human serum consists predominantly of a 150 kDa complex consisting of IGFBP-3, an acid-labile subunit (ALS) and IGF I or IGF II. A smaller complex in serum (40-50 kDa) contains IGF I or II bound to IGFBP-1, IGFBP-2, or IGFBP-4. This smaller complex may also contain some IGFBP-3. IGFBP-5 and IGFBP-6 in rat and human serum are present in extremely low concentrations. It is felt that IGFBP-3 in serum is essentially saturated whereas IGFBP-1 and -2 are unsaturated [13]. The large 150 kDa ternary complex likely acts to increase the half-life of IGF I in the circulation, providing a stable serum source of bioactive peptide. This complex does not cross the endothelium [14], whereas data in the rat have demonstrated that smaller binding proteins, namely BP-1, BP-2 and BP-4, may traverse the endothelium [15,16]. It has thus been hypothesized that lower molecular weight binding proteins may increase translocation of IGF

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I into the vasculature and tissues and thus modulate IGF I action. It is of note that while the IGF-binding proteins consistently have extremely high affinity for their ligands, the N-terminally truncated des(1-3) IGF I [17] and a variety of IGF I analogs [18] have markedly reduced affinity for binding proteins but retain normal affinity for IGF receptors.

2. Expression of IGF I, the IGF I receptor and IGFbinding proteins in the cardiovascular system

2.1. In vivo studies

In situ hybridization analysis has demonstrated expression of IGF I in multiple tissues in the human fetus, as reported by Han et al. [19]. In this study, IGF I expression in the heart was localized predominantly to the epicardium and in coronary vessel walls. The presence of IGF I transcripts in conduit or resistance arteries was not reported in this study. Studies in neonatal rat have demonstrated that ventricular tissue contains both IGF I and IGF II receptors [20]. Additionally, in situ data indicate that neonatal rat cardiomyocytes express predominantly IGF II and low amounts of IGF I transcripts. In the adult rat IGF I mRNA is expressed at low levels in the left ventricle [21-23]. In situ hybridization data are lacking but immunostaining shows low level myocyte staining. IGF IR is likewise expressed at low levels in normal rat heart [22]. In conduit (elastic) arteries IGF I mRNA is expressed at low levels in the adventitia and in the media [24-26]. IGF I expression is significantly higher in resistance (muscular) arteries (P. Delafontaine, unpublished results). The IGF IR is expressed mainly in the media in normal rat aorta [27,28]. Limited data exist on expression of IGF-binding proteins in the cardiovascular system. However, in situ hybridization analysis has demonstrated that the hepatic portal venous and sinusoidal endothelium expresses abundant IGFBP-3 mRNA [29]. It is thus hypothesized that a majority of circulating BP-3 may originate from the endothelium. Recently IGFBP-3 and IGFBP-4 expression have been demonstrated in rat aorta [30].

2.2. In vitro studies

IGF I is synthesized by rat [31,32] and porcine [33–35] vascular smooth muscle cells (VSMC) in vitro. There are primarily three transcripts, sized 0.9-1.2 kb, 1.7 kb and 7.5 kb. Solution hybridization/RNase protection analysis has demonstrated that rat aortic tissue possesses only the class C 5' untranslated IGF I mRNA transcripts [36]. Radioligand binding studies have demonstrated that VSMC in vitro express significant levels of the high-affinity type 1 IGF receptor [37-41]. Binding-affinity for IGF I is between 0.1 and 5 nM (K_d). Binding studies and cross-linking studies have indicated that VSMC in vitro possess no detectable cell surface IGF-binding proteins [42]. However, both porcine and rat aortic smooth muscle cells secrete several binding proteins, specifically IGFBP-2, IGFBP-3 and IGFBP-4 [42-46]. In rat aortic smooth muscle cells, two glycosylated forms of IGFBP-4 have been demonstrated [42]. Macrovessel and microvessel endothelial cells also express high-affinity IGF IR [47–49]. There is also low level expression of IGF I in endothelial cells [31,50], although measurements of IGF I in conditioned medium from endothelial cells may reflect to a significant extent IGF I sequestered from serum [51]. Endothelial cells in culture secrete IGF-binding proteins [52,53]. Recently porcine endothelial cells have been shown to express mRNA for IGFBP-2, 3, 4, 5 and 6 [54]. Microvessel endothelial cells secrete predominantly IGFBP-2 and IGFBP-3, while large vessel endothelial cells secrete essentially IGFBP-3 and IGFBP-4 [54]. Recently IGFBP-3 and IGFBP-5 have been shown to associate with endothelial cell surfaces through C-terminal heparin-binding domains [55]. This allows competition for binding by heparin and heparan sulfate.

3. Regulation of IGF I, the IGF IR and IGF-binding proteins in cardiac and vascular cells in vitro

3.1. IGF I

As noted previously, IGF I is secreted by VSMC in vitro [31-35]. Stiles et al. have shown that in BALB/c3T3 fibroblasts IGF I functions as a "progression" factor to stimulate passage of cells through G₁ into S phase, in contradistinction to platelet-derived growth factor (PDGF) that induces "competency," i.e., entry of cells from G_0 into the G_1 phase of the cell cycle [56]. Clemmons et al. have demonstrated that anti-IGF I antiserum inhibited PDGF-induced growth of VSMC [33]. Additionally, anti-IGF I antiserum inhibited growth hormone-induced fibroblast DNA synthesis [57]. Increased IGF I immunoreactivity in conditioned medium from PDGF-treated cells has suggested that PDGF induces synthesis of IGF I [35]. Subsequent expression studies have reported conflicting results, potentially related to differences in cell types and conditions of quiescence. Thus PDGF and serum have been reported to both increase [32] or decrease [46,58] IGF I mRNA levels in VSMC. IGF I acts additively with PDGF and insulin in the induction of the c-myc protooncogene and cellular proliferation in bovine aortic VSMC [59]. Yamamoto et al. have shown that in primary rabbit VSMC, IGF I is required for cells to enter the S phase [60]. IGF I stimulates elastin [61] and fibronectin [62] gene expression in rat aortic VSMC. Recently it has been reported that angiotensin II transcriptionally regulates the IGF I gene in rat aortic VSMC and that angiotensin II-induced growth of smooth muscle cells is completely inhibited by anti-IGF I antiserum [63]. These findings support a central role for IGF I in mediating VSMC growth. Unlike angiotensin II, thrombin downregulates IGF I mRNA and protein levels in aortic smooth muscle cells [64], as has been described in fibroblasts [65,66]. It is of note that IGF I stimulates growth of myometrial smooth muscle cells [67] and of airway [68] and pulmonary artery smooth muscle cells [69].

IGF I stimulates neutral amino acid and glucose uptake and DNA synthesis in microvessel but not macrovessel bovine endothelial cells [47]. However, IGF I stimulates DNA synthesis in human corneal endothelial cells [70]. IGF I is a potent stimulator of myogenic differentiation [71-73], inducing expression of myogenin in L6 myoblasts [72]. Furthermore, IGF I stimulates hyperplasia and hypertrophy of skeletal myofibers [74]. A variety of recent reports have documented an important role for IGF I and the IGF IR in cardiac myocyte growth. Thus ventricular myocytes from rat ventricular tissue post myocardial infarction express higher levels of IGF I and IGF IR [75]. Ito et al. [76] have reported that IGF I induces hypertrophy of neonatal rat cardiomyocytes, with induction of expression of myosin light chain-2, troponin I, and skeletal α -actin. Kajstura et al. [77] have reported that IGF I stimulates DNA synthesis in neonatal rat cardiac myocytes and that antisense IGF IR oligonucleotides suppress cardiocyte replication. Adult rat cardiomyocytes in long-term culture upregulate their IGF IR, and respond to IGF I with enhanced myofibril development and downregulation of smooth muscle α -actin [78]. Furthermore, IGF I is a potent stimulator of adult cardiomyocyte protein synthesis [79].

3.2. IGF IR

The IGF IR is a membrane tyrosine-kinase consisting of two alpha chains and two beta chains linked through disulfide bonds (reviewed in [8]). The receptor binds IGF I and IGF II with high affinity and insulin with at least a hundred-fold lower affinity. Recently, the existence of insulin receptor-IGF IR hybrids has been demonstrated [80,81]. IGF IR signaling involves autophosphorylation and subsequent tyrosine phosphorylation of IRS-I and potentially other tyrosine-containing substrates. IRS-I serves as a docking-protein and can activate multiple signaling pathways including PI3-kinase, Syp, Nck, and the Ras-MAP kinase pathway. For a detailed discussion of IGF I/insulin signaling the reader is referred to recent reviews [8,82]. A variety of growth factors and specifically PDGF, fibroblast growth factor (FGF), angiotensin II and thrombin upregulate IGF IR on VSMC [37,83,84]. This upregulation of IGF IR may play a critical role in the growth response of smooth muscle cells. Thus antisense transcription of a rat IGF IR cDNA in VSMC markedly suppresses growth of these cells in response to 10% serum [85]. This anti-proliferative effect correlates with a reduction in receptor number of approximately 50%, without changes in binding-affinity. These findings suggest that the upregulatory effects of growth factors on IGF IR may be a important component of their ability to induce competency. This concept is supported by data from Pietrzkowski et al., indicating that in BALB/c3T3 cells overexpressing IGF I and IGF IR. IGF I mediated growth occurs independently of the EGF and PDGF receptors [86]. Furthermore, SV40 T antigen transformation of BALB/c3T3 cells markedly increases secretion of IGF I, and antisense targeting of the IGF IR inhibits the growth of these transformed cells [87]. These cells still require PDGF or 1% serum for growth; however, if the IGF IR is overexpressed in SV40 T antigen transformed cells, they will grow in serum-free medium. In mouse fibroblasts a functional IGF IR is required for the mitogenic effects of the EGF receptor [88]. These data again support the concept that IGF IR number per cell is important in cellular growth responses. Thus downregulation of IGF IR using antisense phosphorothioate oligonucleotides markedly inhibits the growth response of rat aortic VSMC to serum as well as to angiotensin II and thrombin [84,89]. A recent report has documented that a sense oligonucleotide targeting the AUG site of the rat IGF IR mRNA markedly upregulates IGF IR, leading to increased growth responses [89]. The mechanism for this effect is incompletely understood but may be related to the presence of a natural antisense transcript, a transcriptional or a translational repressor protein. It has been reported that PDGF and FGF-induced upregulation of IGF IR on VSMC is protein kinase C (PKC)-dependent, but that angiotensin II upregulation of IGF IR is PKC-independent [37]. Similarly, FGF-induced DNA synthesis has been reported to be PKC-dependent [37,90], whereas angiotensin II-induced growth responses in VSMC [37] and in cardiac fibroblasts [91] are PKC-independent. Molecular mechanisms whereby growth factors upregulate IGF IR are poorly understood. A recent report has demonstrated that the PDGF-responsive sequence of the IGF IR gene is located within ~ 100 bp proximal to the transcription start site [92].

As noted above, the ability of several growth factors to increase IGF IR density may be critical for their mitogenic effects. Thus upregulation of IGF IR could lead to stimulation of IGF IR mediated signaling events. This is consistent with cross-talk between growth factors and the IGF IR, and has been recently demonstrated in the case of thrombin stimulation of VSMC growth [84]. More direct mechanisms of cross-talk between the IGF IR and other growth factors may exist. Thus Yoshinouchi et al. [162] have suggested that FGF may transphosphorylate the IGF IR. Furthermore, angiotensin II and thrombin have been shown to increase phosphorylation of IRS-1 in VSMC (P. Delafontaine, unpublished results). Potential cross-talk between the IGF IR and other growth factors may have profound implications for understanding pathways whereby growth factors exert their effects in vivo. Thus the IGF IR could function as the final common mediator for the effects of multiple growth stimulatory peptides.

3.3. IGF-binding proteins

VSMC in culture synthesize IGFBP-2, IGFBP-3 and IGFBP-4 [42-46]. In rat aortic VSMC, FGF [42] and PDGF [46] have been reported to increase IGFBP-4 production. Porcine VSMC express BP-4 and BP-2 mRNA and secrete primarily BP-2. Cohick et al. have reported no effect of PDGF, FGF, transforming growth factor β (TGF β), and epidermal growth factor (EGF) on BP-2 and BP-4 mRNA levels in porcine VSMC [45]. The regulation of IGF-binding protein levels in smooth muscle cells is affected by various proteases. Thus porcine VSMC secrete IGFBP-2, IGFBP-4, and IGFBP-5 proteases [93,94]. In rat aortic VSMC, biosynthesis and IGF-dependent proteolysis of IGFBP-4 are increased with the confluent state [95]. Recently angiotensin II [96] and thrombin (P. Delafontaine, unpublished results) have been shown to markedly reduce IGFBP-4 levels in rat aortic VSMC conditioned medium. It is of note that thrombin also downregulates IGF-binding-protein production by rat skeletal muscle cells and mouse myocytes [97]. The physiological significance of these binding proteins secreted by VSMC remains to be

determined. IGFBP-1 has been shown to inhibit VSMC growth in serum-free medium [98], but to increase VSMC growth in the presence of low concentrations of plateletpoor plasma [99]. BP-1 binds via its RGD sequence to the $\alpha 5\beta 1$ integrin receptor, and this may be necessary for its growth-stimulatory effect [100]. This stimulatory effect has also been ascribed to the phosphorylated isoform of BP-1 [101]. Bovine BP-2 has likewise been shown to have bifunctional effects on VSMC growth with an inhibitory effect in serum-free medium and a stimulatory effect in platelet-poor plasma [102]. The effect of BP-3 on VSMC growth has not been determined but preincubation of fibroblasts with BP-3 potentiates the IGF I response [103], possibly because of prevention of IGF IR downregulation [104]. The cell-surface association of IGFBP-3 appears to be required for this potentiating effect. Conversely, coincubation of IGF I and BP-3 results in inhibition of the IGF I response [103]. It is of note that a direct growth inhibitory effect of IGFBP-3 has been suggested [105]. BP-4 does not adhere to cell-surfaces and inhibits IGF I growth effects on VSMC [45]. It is thus possible that angiotensin II and thrombin-induced downregulation of IGFBP-4 production serves to increase availability of free IGF I. In microvessel endothelial cells BP-2 may potentiate the effect of IGF I on glucose transport and α -aminoisobutyric acid uptake [106]. Stimulation of cAMP markedly increases BP-4 mRNA levels in a clonal endothelial cell line [107]. Recently serum deprivation or contact inhibition of porcine endothelial cells has been shown to be associated with markedly increased gene expression and secretion of IGFBP-3 [108]. Because IGFBP-3 may have marked antiproliferative effects [105], it is possible that BP-3 acts as a growth-arrest gene for endothelium.

4. Regulation of IGF I, the IGF IR and IGF-binding proteins in cardiovascular tissues in vivo

4.1. Hemodynamic forces, hypertension, ischemia

In vitro data have indicated that stretch increases autocrine secretion of IGF I from skeletal muscle cells [109], suggesting that alterations in physical forces may regulate IGF I expression in vivo. An increase in vascular load induced by ligation of the femoral artery in the rat produces increased IGF I immunoreactivity in endothelium and smooth muscle cells in the contralateral femoral artery [110]. In the heart, supravalvular aortic stenosis in the rat results in rapid increases in IGF I mRNA levels in the left ventricle [23]. These findings are consistent with hemodynamic regulation of IGF I. A variety of studies have documented increases in cardiac IGF I mRNA and protein levels in hypertensive rats. Models have included suprarenal aortic constriction; the uninephrectomized spontaneously hypertensive rat; the uninephrectomized, deoxycorticosterone-treated, saline-fed rat (DOCA salt); and the two-kidney, one clip, hypertensive rat [21,22]. Furthermore, volume-overload induced by creation of an aortocaval fistula in the rat is associated with marked induction of IGF I expression in the right ventricle [111]. In these models conclusive demonstration of the site of IGF I synthesis remains to be determined. However, immunohistochemical analysis has suggested increases in IGF I staining in the subendocardium. In these models of cardiac hypertrophy, expression of the IGF IR appears unchanged. It is of note, however, that in right ventricular biopsies from patients with hypertrophic cardiomyopathy, there is an increase in IGF IR binding sites [112]. Consistent with hemodynamic regulation of IGF I expression are data indicating that IGF I mRNA expression is increased in the rat bladder following urethral ligation [113]. In this model IGF IR mRNA levels are unchanged, but there is a significant induction in IGFBP-2 and IGFBP-4 mRNA [114]. Recently, infusions of IGF I in the rat following myocardial infarction have been shown to enhance ventricular hypertrophy and to have potentially beneficial effects on hemodynamic function [115].

IGF I-stimulated myocardial growth could result from the effects both of systemic IGF I that crosses the endothelium [15,16,51], and of locally synthesized peptide [21-23,111]. Local synthesis of IGF I potentially derives both from myocyte and non-myocyte cells, notably endothelium, VSMC, and fibroblasts. In view of their abundance in areas of myocardial scarring, one may speculate that fibroblasts serve as a significant source of IGF I in the postischemic remodeling myocardium. Clearly myocytes from infarcted hearts have higher levels of IGF I and IGF IR [75]. In addition, monocytes in ischemic hearts may produce IGF I [128]. Although adult cardiac myocytes are terminally differentiated, evidence exists suggesting that myocytes close to the infarct zone undergo DNA replication [75], consistent with the ability of IGF I to stimulate myocyte proliferation in vitro [77]. The specific role of IGF-binding proteins in modulating IGF I effects on the heart is largely unexplored but of great potential interest.

IGF I mRNA levels have been shown to be increased in hypertensive aortae from rats following abdominal aortic coarctation [24]. In situ hybridization analysis has shown that the induction of IGF I is localized to the smooth muscle cell layer. These data are consistent with a role for IGF I as an autocrine mediator of hypertrophic/hyperplastic responses in hypertension. However, in the DOCA/salt model of hypertension in the rat, it has been reported that there is no change in IGF I mRNA [116]. The increase in aortic expression of IGF I mRNA in the abdominal coarctation model of hypertension is accompanied by a progressive decrease in IGF IR expression [117]. This is consistent with ligand-induced downregulation of the receptor, a phenomenon previously demonstrated in cultured VSMC [37]. Recently IGFBP-4 mRNA levels have been shown to be markedly elevated in the hypertensive aorta following abdominal coarctation in the rat [30]. The induction of IGFBP-4 is limited to the hypertensive blood vessel, because IGFBP-4 mRNA levels in the normotensive abdominal aorta and in the liver are transiently decreased. These data suggest that increases in vascular load directly stimulate IGFBP-4 expression. The transient decrease in hepatic IGFBP-4 and IGFBP-3 expression in this model may be related to effects of circulating angiotensin II, consistent with in vitro data [96]. Because IGFBP-4 may function as a inhibitory binding protein [45], its induction in the hypertensive vasculature may serve a counterregulatory role to blunt growth responses.

Potential regulation of IGF I and its binding proteins in human hypertension is largely unexplored. However, one group has reported higher circulating IGF I levels in patients with essential hypertension and left ventricular hypertrophy [118–120]. Larger trials to address this issue are clearly warranted.

4.2. Injury

A variety of studies are consistent with an important role for the IGF I-IGF IR autocrine system in vascular injury. An initial report by Hansson et al. demonstrated that IGF I immunoreactivity was increased in endothelial cells and in the neointima following femoral artery injury in the rat [121]. Studies from Cercek et al. [36] and Khorsandi et al. [26] showed peak induction of IGF I mRNA at 7 days in the balloon-injured rat aorta, with a reciprocal decrease in IGF IR expression. The increase in IGF I expression following balloon injury in rat aorta is localized to the smooth muscle cell layer and to the neointima. Consistent with the major role of growth hormone in regulating IGF I expression in vivo, there is a marked decrease in the intimal hyperplasia that develops following aortic balloon-injury in the hypophysectomized rat [122,123]. Interestingly, intimal proliferation is a characteristic change that occurs after subarachnoid hemorrhage [161]. It has recently been shown that exposure of rat femoral artery to periarterial blood results in a marked increase in IGF I mRNA expression and IGF IR binding sites [124]. This provides further evidence for a role of the IGF I autocrine system in vascular growth responses. Bornfeldt et al. [125] have also reported increases in IGF I mRNA in balloon-injured rat aorta; however, in this study IGF IR mRNA levels were also increased. It is of note that in this study the infusion of IGF I increased DNA synthesis in injured aorta in the diabetic rat.

4.3. Angiogenesis and wound healing

IGF I stimulates migration and tube formation by vascular endothelial cells [126] and has been shown to promote rat aortic angiogenesis in vitro [127]. Following microembolisation in the porcine heart there is increased IGF I mRNA expression in infiltrating monocytes in areas of capillary sprouting, consistent with a role for IGF I in angiogenesis in vivo [128]. It is of note that macrophage IGF I synthesis is inhibited by interferon- γ [129]. Several studies have documented that IGF I (alone or complexed to binding proteins) accelerates wound healing in vivo [130–132].

4.4. Diabetes, hyperinsulinemia

The function of IGF I as a potential mediator of vascular growth responses in insulin-dependent diabetes and in hyperinsulinemic states is unclear. Murphy et al. have reported that insulin increases IGF I expression in rat aorta [25]. In the streptozotocin diabetic rat, IGF I mRNA levels are markedly decreased in the heart, skeletal muscle and aorta, and levels are restored by insulin infusion but not by IGF I infusion [133]. In the insulin-deficient diabetic rat,

DNA synthesis following balloon-injury of the aorta has been reported to be either decreased [125] or unchanged [134,135]. There are conflicting reports regarding the potential association between higher circulating IGF I levels and the incidence and progression of diabetic retinopathy [136-139]. It is of note that IGF I has been shown to significantly improve control of blood glucose in the insulin-resistant state; however, its use in humans has been associated with significant deleterious side-effects [140]. The recent demonstration that advanced glycosylation end-products (AGE) induce IGF I synthesis by human monocytes may have relevance to understanding mechanisms whereby hyperglycemia induces vascular proliferative changes [141]. Indeed, it is possible that AGE-induced IGF I synthesis by monocytes within the subendothelial space promotes VSMC growth. Furthermore, the effect of IGF I and of insulin to stimulate plasminogen activator inhibitor type 1 (PAI-1) synthesis [142] may be relevant to understanding mechanisms of accelerated atherosclerosis in diabetes.

4.5. IGF I and vasodilation

IGF I has been shown to induce renal arteriolar (glomerular) dilation with increases in renal plasma flow and glomerular filtration rate [143,144]. This effect is likely mediated by induction of nitric oxide (NO) production. Indeed IGF I stimulates release of NO from cultured endothelial cells [160]. A beneficial effect of IGF I in animal models of acute renal failure has been demonstrated [145,146]. Recently infusion of IGF I into the brachial artery in humans has been shown to increase forearm blood flow [147]. Consistent with those findings is the report that insulin-induced vasodilation in humans is blocked by the NO-synthase inhibitor, L-NMMA [148]. It is of note that contrary to its effect on endothelial cells, IGF I inhibits cytokine-induced production of NO in VSMC [149].

4.6. Atherosclerosis

Studies of IGF I expression in atherosclerosis are limited. A recent report has documented increased IGF I immunostaining in synthetic VSMC in human atherosclerotic plaque [150]. Furthermore, IGF IR mRNA expression has been demonstrated in smooth muscle cells in atherosclerotic lesions [151]. Inhibitors of the growth hormone-IGF I axis, namely the somatostatin analogs octreotide and angiopeptin, inhibit VSMC proliferation in vitro and in vivo [152–156]. A recent human trial has indicated that angiopeptin decreased clinical events during 12 months of follow-up after coronary balloon angioplasty by approximately 22% [157]. This clinical effect contrasted with the lack of any evident effect upon angiographic variables.

5. Summary and conclusion

A large body of evidence has conclusively shown that IGF I is an essential regulator of developmental growth.

Thus mice bearing a null mutation for the IGF IR gene invariably die shortly after birth, and mice bearing a null mutation for the IGF I gene have a high neonatal mortality rate and marked growth retardation [158,159]. The ubiquitous effects of IGF I make it likely that this autocrine/endocrine system plays an important role in cardiovascular development. Its potential role in cardiovascular pathophysiology has raised considerable interest over the last several years. There is strong evidence that IGF I is a critical determinant of vascular growth responses in vitro and in vivo. Regulation of VSMC IGF IR availability appears to be crucial for the control of VSMC growth, and as such is at a convergence point for the effects of multiple growth factors. Clinical studies relating to IGF I in hypertension are extremely limited but significant data from animal studies now suggest a role for IGF I as a mediator of hypertrophic/hyperplastic responses in hypertension. Furthermore, significant animal data now exist implicating IGF I as an important mediator of cardiac hypertrophic responses. The development of a specific pharmacologic inhibitor of the IGF IR should allow rational clinical trials to address the function of IGF I as a mediator of cardiovascular growth responses. Specifically, areas of great interest will include the potential prevention of post-angioplasty restenosis, of atherosclerotic lesion development and progression, and of the complications of hypertensive vascular disease. The use of IGF I to ameliorate myocardial growth and function post infarction, to promote angiogenesis and collateral artery formation in the setting of peripheral vascular disease, are other important directions for future research. The use of IGF I to improve wound healing, improve recovery from acute renal failure and improve glucose control is currently under investigation. Clearly ongoing studies addressing the mechanisms whereby IGF I interacts with its receptor and binding proteins to produce its effects in cardiovascular tissues, will provide a rationale for novel and pertinent clinical research.

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