

# The Insulin-Like Growth Factor System in Vascular Smooth Muscle: Interaction With Insulin and Growth Factors

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Vascular smooth muscle cells (SMCs) occur throughout the vascular tree and have important physiological functions. They are also involved in pathological processes such as development and progression of atherosclerotic lesions, restenosis following angioplasty, and in hypertension. This review is focused on the role of the insulin-like growth factor (IGF) system in proliferation, migration, and hypertrophy of vascular SMCs and its interaction with insulin and other growth factors. The IGF-I receptor is highly expressed in SMCs in intact arteries and in cultured SMCs and is activated by binding of IGF-I to the two  $\alpha$ -subunits. Insulin and IGF-II from the circulation can interact with the IGF-I receptor at higher concentrations. Insulin receptors are few or absent in SMCs and circulating insulin concentrations in vivo are probably too low for a direct action of insulin on the IGF-I receptor in SMCs. Receptor activation initiates a number of signal transduction pathways. Increased phosphatidylinositol turnover and calcium mobilization correlates with actin filament reorganization and stimulation of directed migration of the SMC in a gradient of IGF-I. The effects of IGF-I receptor activation on signal transduction pathways (eg, the MAP kinase cascade) implicated in DNA synthesis and proliferation are weak and this correlates with the meager mitogenic activity of IGF-I in SMC. Several components of the IGF-system in SMC are regulated by growth factors such as platelet-derived growth factor (PDGF)-BB and basic fibroblast growth factor (bFGF). IGF-I is downregulated by decreased metabolism (eg, diabetes and fasting) and in these states levels of IGF-I mRNA and IGFBP-2 and -4 mRNA are decreased. On the contrary, SMC hypertrophy is associated with increased levels of IGF-I, IGFBP-2, and IGFBP-4 mRNA. In conclusion, the IGF-system in SMCs is likely to play an important role in SMC migration and the response of the SMCs to metabolic deprivation, and hypertrophy.

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VASCULAR SMOOTH MUSCLE CELLS (SMCs) occur throughout the vascular tree, and are the only cell type present in the media of mammalian arteries. In the young growing organism, the vascular SMC proliferates, migrates, and synthesizes extracellular matrix components such as collagen, elastin, fibronectin, and proteoglycans.<sup>1,2</sup> This state of the SMC is referred to as the "synthetic phenotype." As the vessel matures, the vascular SMC enters a quiescent state. The quiescent SMC (the "contractile phenotype") is filled with myofilaments and takes part in regulation of blood pressure and flow. Many pathological conditions are associated with conversion of the quiescent SMC to a more synthetic phenotype that is able to proliferate, migrate, and secrete proteins such as extracellular matrix components in the adult vessel wall. This process has been shown to occur in development and progression of atherosclerotic lesions<sup>3,4</sup> and in restenosis following angioplasty.<sup>5,6</sup> Less well studied are the changes in SMCs that occur during hypertension and hypertrophy.<sup>7</sup> The phenotypic state of the vascular SMC is believed to be induced and regulated by locally produced autocrine/paracrine molecules such as growth factors and cytokines, circulating hormones, and hemodynamic factors.<sup>1,2,3,7</sup> SMCs in the synthetic phenotype can respond to a number of growth-regulatory molecules, growth factors, and chemoattractants, such as platelet-derived growth factor (PDGF) isoforms, basic fibroblast growth factor (bFGF), interleukin-1, transforming growth factor- $\beta$ , and insulin-like growth factor-I (IGF-I).

This review is focused on the role of the IGF system in proliferation, migration, and hypertrophy of vascular SMCs and its interaction with insulin and other growth factors.

## COMPONENTS OF THE IGF SYSTEM IN VASCULAR SMOOTH MUSCLE

### Receptors

Specific receptors for IGF-I are abundant in plasma membranes from intact bovine arteries,<sup>8</sup> in cultured rat<sup>9</sup> and bovine<sup>10</sup> aortic SMCs, as well as in human vascular SMCs.<sup>11</sup> Human SMCs from newborn aorta express approximately 15,000 high-affinity IGF-I-binding sites per cell.<sup>12</sup> The  $K_d$  for IGF-I interaction with its receptor is in the range of 0.1 nmol/L in vascular SMCs.<sup>9,10,13</sup> The molecular size of the vascular SMC IGF-I receptor  $\alpha$ -subunit (135 to 145 kd) has no apparent difference from that of the  $\alpha$ -subunit expressed in other tissues.<sup>13-15</sup> The  $\alpha_2\beta_2$ IGF-I receptor dimer binds only one IGF-I molecule with high affinity, but a second IGF-I molecule can bind to the receptor dimer with a lower affinity, a phenomenon referred to as negative cooperativity (for review, see De Meyts<sup>16</sup>). High-affinity binding of IGF-I to the IGF-I receptor involves cross-linking of two distinct areas of the two  $\alpha$ -subunits brought together by one IGF-I molecule in human SMCs and other cell types.<sup>17</sup> This process is similar but not identical to the interaction of insulin with the insulin receptor.<sup>16</sup>

### Local Production

IGF-I mRNA is expressed in quiescent vascular SMCs in vivo and in cultured vascular SMCs in vitro.<sup>18-22</sup> Secretion of IGF-I protein has been shown in cell cultures of vascular SMCs.<sup>23,24</sup> Size distributions of SMC IGF-I mRNA transcripts are similar to those in other tissues,<sup>25</sup> with a relative expression of IGF-Ia and IGF-Ib mRNA of 1:10.<sup>26</sup>

Compared with the expression of IGF-I mRNA, expression of IGF-II mRNA is considerably lower in SMCs such

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0026-0495/95/4410-4010\$03.00/0

as rat bladder SMCs and rat aortic SMCs, and is under the limit of detection in our solution hybridization assay (H.J. Arnqvist, unpublished, January 1995).

An interesting aspect is that other cell types such as macrophages and monocytes, which are present at high numbers in the vascular wall during formation and progression of atherosclerotic lesions, secrete IGF-I, which may interact with the surrounding SMCs.<sup>27,28</sup> Furthermore, IGF-I is released from the  $\alpha$ -granules of platelets following degranulation.<sup>29</sup> Thus, SMCs express IGF-I receptors and the IGF-I gene and produce IGF-I both in the quiescent vascular wall and in cultured vascular SMCs. During pathological conditions, other cell types may contribute to IGF-I interaction with SMCs in a paracrine manner.

### *Binding Proteins*

Six binding proteins for IGFs (IGFBPs) have been characterized.<sup>30</sup> Affinity of the binding proteins for IGFs is on the same order of magnitude (nanomolar range) as the affinity of the receptors.<sup>31</sup> The two major forms of IGFBPs produced and secreted by SMCs are IGFBP-2 and IGFBP-4. Thus, mRNA for IGFBP-2 and IGFBP-4 can be detected in rat aortic SMCs, in intact-rat aorta, and in rat urinary bladder SMCs.<sup>32,33</sup> IGFBP-2 and IGFBP-4 are secreted in the culture medium by porcine vascular SMCs.<sup>34</sup> There is evidence that rat aortic SMCs also can express IGFBP-3.<sup>35</sup>

The function of IGFBPs is still largely unknown. IGFBP-1 has been found to enhance the effect of IGF-I on DNA synthesis under certain conditions in vascular SMCs,<sup>36</sup> an effect that depends on serine phosphorylation of IGFBP-1 and might involve an increased binding of IGF-I to its receptor in the presence of IGFBP-1<sup>37</sup> (for review, see Clemmons<sup>38</sup>). The two SMC-derived IGFBPs do not seem to potentially alter the action of IGF-I in vascular SMCs. A high concentration (500 ng/mL) of IGFBP-4 has a slight inhibitory (15% decrease) effect on IGF-I-induced DNA synthesis in vascular SMCs, whereas exogenously added IGFBP-2 is without effects.<sup>39</sup> Some reports show that IGFBPs can exert effects independently of IGF-I. For example, IGFBP-1 has recently been shown to enhance cell migration via interaction with  $\alpha_5\beta_1$ -integrins.<sup>40</sup> Other effects of IGFBPs may include protection of IGF-I from degradation, or localization of IGF-I at its site of action.<sup>38</sup>

### **IGF-I IS A WEAK VASCULAR SMOOTH MUSCLE GROWTH FACTOR IN VITRO AND IN VIVO**

#### *DNA Synthesis and Proliferation In Vitro*

IGF-I stimulates DNA synthesis in vascular SMCs of rat, bovine, porcine, or human origin.<sup>9-12,23</sup> Nanomolar or lower concentrations are required to produce half-maximal stimulation of DNA synthesis. Stimulatory effects of IGF-II and insulin on SMC DNA synthesis can be demonstrated, but the potency of these factors is 10- to 1,000-fold lower than IGF-I, suggesting that the effects are mediated mainly through the IGF-I receptor.<sup>9,10</sup>

Following addition of IGF-I to human newborn aortic SMCs, DNA synthesis in the major population of the responding cells peaks at 14 hours,<sup>12</sup> which indicates that

the effect is due to a direct effect of IGF-I receptor stimulation and is not a secondary effect due to secretion of other mitogens. Interestingly, in these cells, the time required for maximal stimulation of DNA synthesis seems to be shorter in a population of SMCs stimulated with IGF-I, as compared with a population stimulated with PDGF-BB.<sup>12</sup> This suggests that the mechanisms of IGF-I-induced DNA synthesis differ from those of PDGF-induced DNA synthesis, or that different populations of cells respond to IGF-I and PDGF-BB. It should be noted that the maximal DNA synthesis induced by IGF-I is in general considerably lower than the maximal DNA synthesis induced by PDGF or serum.<sup>12,13</sup>

The meager stimulation of DNA synthesis by IGF-I seems too weak to produce a measurable and consistent increase in cell number, as has been reported in human aortic SMCs<sup>12</sup> and myometrial SMCs.<sup>41</sup> Accordingly, PDGF-BB increases the cell number of human aortic SMCs 3 days after addition, whereas IGF-I does not.<sup>12</sup> The cell number increase following IGF-I stimulation of rat aortic SMCs is in the range of 10% to 20% as compared with controls, whereas PDGF-BB produces a 60% increase in cell number during the same conditions.<sup>13</sup>

Taken together, these observations show that IGF-I is a weak growth factor when added in the absence of other growth factors to SMCs from various origins.

#### *Lack of Effects on the Mitogen-Activated Protein Kinase Cascade*

Many growth factor tyrosine kinase receptors activate a signal transduction pathway that includes recruitment of growth factor receptor-bound protein-2 (GRB-2) and the *ras*-GTP exchange molecule SOS through a *src*-homology 2 (SH2) domain in GRB-2 that interacts with the activated, phosphorylated receptor. These events further lead to conversion of inactive *ras*-GDP to active *ras*-GTP, activation of *raf*, mitogen-activated protein (MAP) kinase kinase, MAP kinase, and transcription factors, and eventually DNA synthesis and proliferation on differentiation.<sup>42</sup> The IGF-I receptor does not seem to bind GRB-2 directly, but receptor activation leads to phosphorylation of insulin receptor substrate (IRS)-1 or -2, which binds various SH2-containing proteins.<sup>43</sup> Thus, the IGF-I receptor may activate the MAP kinase cascade, at least partly, through phosphorylation of IRS, which subsequently binds GRB-2 and activates SOS, *ras*, and downstream enzymes.<sup>43</sup> However, although PDGF evokes a marked activation of MAP kinase kinase and MAP kinase (Erk1 and Erk2) in human SMCs, IGF-I is unable to induce activation of the MAP kinase cascade in these cells.<sup>12</sup> The meager ability of IGF-I to activate the MAP kinase cascade in SMCs is probably not due to the lower number of IGF-I receptors per cell as compared with the number of PDGF receptors per cell, but to a different signaling capacity of IGF-I as compared with PDGF. IRS isoforms expressed in SMCs have not yet been identified, and it is possible that the levels of these signal transduction molecules are low in SMCs, making the subsequent activation of the MAP kinase cascade weak. However, activation of the MAP kinase cascade has been

demonstrated to be 100- to 1,000-fold more efficiently coupled to PDGF receptor activation as compared with IGF-I receptor activation in cells expressing IRS-1,<sup>44</sup> suggesting that the signaling capacity of the PDGF receptor and the IGF-I receptor is truly different in this respect.

#### *DNA Synthesis in Normal and Diabetic Rat Aorta*

So far, there are few data on the *in vivo* effects of IGF-I in SMCs. A commonly used *in vivo* model of SMC proliferation and migration is balloon injury, in which balloon catheterization of rat aorta or carotid artery injures the endothelium and the underlying SMCs and induces proliferation and migration of medial SMCs, followed by formation of neointima and intimal proliferation.<sup>45,46</sup>

After balloon catheterization of rat aorta, DNA synthesis in the media peaks at 2 days after the injury.<sup>47</sup> This procedure is accompanied by an increased IGF-I receptor gene expression that peaks at 24 hours after injury and increased IGF-I gene expression that peaks at 48 hours after injury.<sup>47</sup> Treatment of rats with exogenous IGF-I (35 nmol/d) following balloon catheterization does not lead to increased DNA synthesis in the media, and doses of 150 nmol/d are required to increase DNA synthesis in medial SMCs (Y. Chen et al, unpublished results). Metabolic deprivation of SMCs in the artery, induced by diabetes on fasting, is associated with decreased IGF-I gene expression,<sup>18</sup> as well as decreased levels of IGFBP-2 and IGFBP-4 mRNA.<sup>33</sup> Levels of IGF-I receptor mRNA do not change during these conditions.<sup>48</sup> Furthermore, balloon catheterization of arteries in diabetic or fasted rats results in significantly lower DNA synthesis as compared with that observed in normal rats.<sup>47,49</sup> Treatment of diabetic rats with 35 nmol/d exogenous insulin decreases blood glucose, increases plasma levels of IGF-I, and significantly increases DNA synthesis in medial SMCs following balloon catheterization.<sup>47</sup> However, treatment of diabetic rats with exogenous IGF-I increases SMC medial DNA synthesis to the same extent as an equimolar dose of insulin without improving the diabetic state.<sup>47</sup> These results suggest that IGF-I has a direct effect on SMC DNA synthesis, whereas insulin may increase DNA synthesis indirectly through increased levels of circulating IGF-I.

Thus, diabetic vascular SMCs are more sensitive to IGF-I than nondiabetic vascular SMCs. This may indicate that IGF-I increases DNA synthesis more efficiently when the SMC is in a metabolically deprived state.

#### IGF-I INDUCES DIRECTED MIGRATION OF VASCULAR SMOOTH MUSCLE

##### *Migration and Chemotaxis Mediated Through the IGF-I Receptor*

Directed migration of vascular SMCs is a key event in formation and progression of atherosclerotic lesions and in restenosis following balloon catheterization. PDGF has long been known to stimulate directed migration and chemotaxis of vascular SMCs,<sup>50</sup> and PDGF-BB is the strongest known chemoattractant for SMCs.

In contrast to its weak mitogenic effects, IGF-I acts as a

potent chemoattractant for cultured human SMCs of newborn or adult origin.<sup>12,51</sup> In fact, IGF-I is typically able to induce 50% of the maximal migratory effect observed with PDGF-BB in a Boyden-chamber assay. This is significant, since the PDGF receptor outnumbers the IGF-I receptor by approximately sixfold. The concentration of IGF-I required to produce half-maximal stimulation of migration ranges from 0.08 to 0.2 nmol/L. The effect of IGF-I on migration and chemotaxis is mediated through the IGF-I receptor, with no apparent contribution from the IGF-II receptor or insulin receptors. The migratory effect of IGF-I can be inhibited by an IGF-I receptor-blocking antibody ( $\alpha$ IR-3). However, IGF-II and insulin can induce migration through interaction with the IGF-I receptor when present in higher concentrations.<sup>12</sup> Thus, IGF-I is a potent chemoattractant for vascular SMCs, and the effects are comparable to the effects of PDGF-BB. Induction of migration of SMCs can be considered a potentially important biological function of IGF-I in the vascular wall.

##### *Induction of Migration Correlates With Stimulation of Calcium Mobilization and Phosphatidylinositol Turnover*

Phospholipase C (PLC) catalyzes hydrolysis of phosphatidylinositol-4,5-bisphosphate (PIP<sub>2</sub>) to inositol-1,4,5-trisphosphate (IP<sub>3</sub>) and diacylglycerol (DAG). Generation of IP<sub>3</sub> leads to mobilization of calcium from intracellular stores, whereas DAG activates different isoenzymes of protein kinase C (PKC). IGF-I is a potent inducer of phosphatidylinositol turnover in human aortic SMCs.<sup>12</sup> Accordingly, an early decrease in PIP<sub>2</sub> lipid mass with a reciprocal increase in DAG lipid mass is observed within 30 seconds following IGF-I stimulation. Consistent with the hydrolysis of PIP<sub>2</sub>, IGF-I causes an early dose-dependent increase in intracellular calcium levels in human arterial SMCs. The maximal effects of IGF-I on early PIP<sub>2</sub> hydrolysis, DAG formation, and calcium mobilization are comparable to the maximal effects induced by PDGF-BB.<sup>12</sup> The fact that increased phosphatidylinositol turnover is a common element of signal transduction for chemoattractants in SMCs and that inhibition of PLC activation blocks migration<sup>52</sup> indicates that this signal transduction pathway is involved in migration and chemotaxis. PIP<sub>2</sub> hydrolysis and calcium mobilization induced by IGF-I may result in a localized transient actin filament reorganization (for review, see Stossel<sup>53</sup>). This reorganization of actin filaments is probably required for protrusion of filopodia in the gradient of IGF-I.

#### INTERACTION BETWEEN THE IGF SYSTEM AND OTHER GROWTH FACTORS

##### *IGF-I Enhances DNA Synthesis Induced by PDGF*

Although the mitogenic effect of IGF-I in the absence of other growth factors is weak, the effects of PDGF or bFGF on DNA synthesis can be enhanced by IGF-I in SMCs.<sup>11,13,54-56</sup> Furthermore, the effects of IGF-I and PDGF on induction of *c-myc* are additive in cultured aortic SMCs, suggesting different mechanisms of action of IGF-I and PDGF to induce DNA synthesis and proliferation.

These observations indicate that IGF-I may play a role in

proliferation of SMCs when present with growth factors such as PDGF, and the presence of IGF-I may be required for a maximal proliferative response.

#### *Growth Factor Regulation of IGF-I, IGF-I Receptors, and Binding Proteins*

IGF-I gene expression in SMCs is regulated by different growth factors. Results on the effects of growth factors on IGF-I mRNA levels are inconsistent and may reflect different states of the cultured SMCs. PDGF and bFGF have been reported to cause a rapid (within 4 to 6 hours) and sustained (at least 24 hours) decreased IGF-I gene expression and a decreased secretion of IGF-I in rat aortic SMCs.<sup>21,56</sup> The decrease may be mediated through increased levels of intracellular calcium following stimulation with PDGF or bFGF, since an increase of intracellular calcium levels has been found to have a similar effect.<sup>58</sup> Furthermore, protein synthesis seems to be required for the inhibitory effect of PDGF isoforms on IGF-I gene expression.<sup>56</sup> In contrast to these findings, Delafontaine et al<sup>59</sup> reported an increased level of IGF-I mRNA following stimulation of rat aortic SMCs with PDGF isoforms. The discrepancies of these results and other studies may be due to differences in confluency of the SMCs or in the ability of PDGF to induce calcium mobilization and/or protein synthesis. PDGF has also been shown to increase radioimmunoassayable IGF-I in culture media from porcine aortic SMCs.<sup>54</sup>

IGF-I is able to increase levels of IGF-I mRNA in rat aortic SMCs under conditions in which PDGF causes decreased levels of IGF-I mRNA.<sup>21</sup> The effect of IGF-I on IGF-I mRNA is observed 3 hours after addition of IGF-I, and is sustained for up to 24 hours. High concentrations of insulin (10  $\mu\text{mol/L}$ ) produce a similar effect on IGF-I mRNA, most likely through interaction with the IGF-I receptor. Growth hormone, a well-known regulator of IGF-I gene expression in other tissues,<sup>60</sup> does not regulate levels of IGF-I mRNA in cultured rat aortic SMCs.<sup>21</sup> Angiotensin II has been found to increase IGF-I mRNA in SMCs.<sup>61</sup> Thus, it appears that mitogenic growth factors, ie, PDGF and bFGF, at least under some conditions, result in decreased levels of IGF-I mRNA, whereas weak growth factors, ie, IGF-I and angiotensin II, result in increased levels of IGF-I mRNA. The biological significance and the cause of the inconsistency of results related to IGF-I gene expression need further study.

The complexity of growth factor regulation of the IGF system in SMCs is further enhanced by the ability of the same growth factors to regulate IGF-I receptors and IGFBPs. Several growth factors modify levels of IGF-I receptors on SMCs, thereby modifying the biological effects of IGF-I. For example, addition of PDGF or FGF to cultured rat aortic SMCs results in an increased number of IGF-I receptors 2 to 3 hours later,<sup>55</sup> in what seems to be a PKC-dependent manner.<sup>62</sup> In other studies, PDGF has been shown to increase promoter activity of the IGF-I receptor gene.<sup>63</sup>

Further, the number of IGF-I receptors per SMC can be

increased by angiotensin II, through a mechanism that differs from the mechanism used by PDGF.<sup>62</sup>

Another point of interaction of growth factors with the IGF system in vascular SMCs is regulation of IGFBPs. IGF-I and insulin have been described to increase IGFBP-4 expression (protein and mRNA) in porcine SMCs, and the subsequent binding of IGF-I to IGFBPs results in degradation and appearance of IGFBP-4 proteolytic fragments.<sup>39</sup> Since insulin does not bind to IGFBPs, IGFBP-4 induced by insulin is not degraded. However, no significant effect of IGF-I on levels of IGFBP-4 mRNA were found in another study on rat aortic SMCs.<sup>35</sup> PDGF has been shown to increase IGFBP-4 gene expression and secretion from rat aortic SMCs.<sup>56</sup> Levels of IGFBP-2 do not seem to be regulated to the same extent as IGFBP-4 by growth factors.

### THE IGF SYSTEM IN SMOOTH MUSCLE HYPERTROPHY

#### *Metabolic Effects of IGF-I in Smooth Muscle*

Hypertrophy is characterized by increased cell size without appreciable increase in cell number. Thus, amino acid uptake and protein synthesis are required for hypertrophy. This is perhaps where IGF-I has its strongest effects as compared with other growth factors. For example, IGF-I is generally a more potent inducer of protein synthesis as compared with DNA synthesis in SMCs. Low (nanomolar) concentrations of IGF-I stimulate amino acid uptake, glucose metabolism, and protein synthesis in intact bovine arteries,<sup>64</sup> and metabolic effects are also induced by IGF-I in cultured vascular SMCs (K.E. Bornfeldt et al, unpublished, January 1995). This suggests that the IGF-I receptor is more efficiently coupled to intracellular signal transduction pathways involved in anabolic effects as compared with those induced by mitogenic growth factors such as PDGF. IGF-I also potentially stimulates production of extracellular matrix components in SMCs, such as fibronectin<sup>65</sup> and elastin.<sup>66,67</sup>

#### *IGF-I and IGFBP-2 and IGFBP-4 Are Regulated in Hypertrophy*

Hypertrophy of vascular SMCs is associated with changes in the IGF system. In the rat portal vein, expression of IGF-I mRNA and IGF-I protein is increased in hypertrophy induced by partial ligation of the portal vein.<sup>32</sup> Increased levels of IGF-I and IGFBP-4 mRNA are also observed in rat aorta subjected to coarctation.<sup>68,69</sup> In a urinary-bladder model of SMC hypertrophy induced by partial outlet obstruction, the developing hypertrophy is associated with a transient increase in IGF-I mRNA and pronounced, sustained increases of mRNA encoding IGFBP-2 and IGFBP-4.<sup>70</sup> Accordingly, levels of IGFBP-2 protein are increased in hypertrophying bladder (Y. Chen et al, unpublished results, January 1995). The induction of IGF-I mRNA in hypertrophy is approximately sixfold the increases of IGF-I mRNA observed during SMC proliferation induced by balloon catheterization, suggesting that the IGF system plays a more important role in hypertrophy as compared with hyperplasia. IGF-I expression is increased in several other models of hypertrophy, such as during

increased vascular load in rat femoral artery<sup>71</sup> and during hypertrophy of skeletal muscle and heart muscle.<sup>72-74</sup> Regression of hypertrophy after removal of the outlet obstruction of the bladder is associated with decreased levels of mRNA for IGF-I, IGFBP-2, and IGFBP-4, whereas levels of IGF-I receptor mRNA do not change during development and regression of hypertrophy.<sup>70</sup>

Finally, infusion of exogenous IGF-I exaggerates hypertrophy of the kidney in diabetic rats.<sup>75</sup> In summary, the IGF system appears to play an important role in hypertrophying tissues.

## INTERACTIONS BETWEEN INSULIN AND THE IGF SYSTEM

### *Receptor Interaction*

Expression of insulin receptors is low or absent in vascular SMCs.<sup>9,10,15</sup> When present in sufficient concentrations, insulin is able to interact with the IGF-I receptor in SMCs. The concentrations of insulin required for IGF-I receptor interaction are 100- to 1,000-fold those of IGF-I in cultured SMCs<sup>9-11,15</sup> and in plasma membranes from arteries.<sup>8</sup> Insulin analogs such as B10 Asp, in which a basic amino acid (histidine) in position B10 has been replaced with an acidic amino acid (aspartic acid), are more potent than native insulin in interacting with the insulin receptor and have a higher mitogenic effect as compared with native insulin.<sup>9,16,76</sup> In rat aortic SMCs, which are devoid of insulin receptors, the insulin analog B10 Asp is more potent than native insulin in interacting with the IGF-I receptor and stimulating DNA synthesis through activation of the IGF-I receptor.<sup>9</sup> This may be explained by the fact that IGF-I has an acidic amino (glutamic acid) acid in the corresponding position, and the single amino acid substitution makes the insulin molecule chemically and biologically more similar to IGF-I. This modification may enhance binding of the B10 Asp insulin analog to the IGF-I receptor in SMCs.

Since such high concentrations of insulin are required for IGF-I receptor interaction, and since SMCs are essentially devoid of insulin receptors, the main effects of insulin on the IGF system in SMCs may be through regulation of circulating IGF-I and IGFBPs.

### *Insulin Regulation of Circulating IGF-I and IGFBPs*

Circulating IGF-I is regulated by growth hormone, insulin, and nutrition.<sup>77,78</sup> In insulin-deficient states such as diabetes, levels of circulating IGF-I are low. The liver is considered the major source of circulating IGF-I, and in the rat expression of IGF-I mRNA in liver is approximately 100-fold higher than in peripheral tissues.<sup>18</sup> However, in man, there is little difference in the tissue level of IGF-I gene expression between liver and peripheral tissues.<sup>79</sup> It is therefore conceivable that the liver is not the main source of circulating IGF-I, and this is also suggested by direct measurements of liver IGF-I production in man.<sup>80</sup> The major part of circulating IGF-I is bound to IGFBP-3, whereas the free biologically active fraction is regulated by IGFBP-1. IGFBP-1 is to a large extent produced in the liver, and is directly and acutely (within hours) regulated by

insulin.<sup>77,80</sup> Insulin is thus an important regulator of IGF-I activity. The ratio of portal insulin concentration to peripheral insulin concentration differs between healthy subjects and insulin-treated diabetic patients, and the route of insulin delivery may determine how IGF-I activity is affected by insulin.

### *Insulin Resistance, Hyperinsulinemia, and Cardiovascular Risk Factors*

There is some epidemiological evidence that in nondiabetic and glucose-intolerant individuals, hyperinsulinemia is associated with cardiovascular disease.<sup>81-84</sup> Furthermore, insulin resistance with compensatory hyperinsulinemia is associated with risk factors for cardiovascular disease such as hypertension, dyslipidemia, and decreased fibrinolysis.<sup>85-88</sup> Thus, insulin by itself has been suggested to promote atherosclerosis.<sup>89</sup> However, this association is not strong and consistent,<sup>90</sup> and hyperinsulinemia as a causative factor for atherosclerotic disease has accordingly been questioned.<sup>91,92</sup> Today, no firm evidence on a mechanism for an atherogenic action of insulin exists.<sup>91,93</sup> No consistent direct effect of insulin in concentrations observed in vivo in insulin-resistant states or during insulin treatment has been found in vascular SMCs.<sup>13</sup> Insulin treatment of patients with non-insulin-dependent diabetes mellitus (NIDDM) and secondary treatment failure on oral agents markedly increases peripheral insulin concentrations and at the same time improves both glycemic control and other cardiovascular risk factors such as dyslipidemia and albuminuria.<sup>94-98</sup> Furthermore, insulin treatment of NIDDM patients after an acute myocardial infarction has been shown to reduce mortality.<sup>99</sup> These findings argue against insulin as a cause of cardiovascular morbidity in patients with NIDDM. Increased proinsulin and split-proinsulin concentrations have also been found to correlate with certain cardiovascular risk factors.<sup>100</sup> It is not known if this is a reflection of increased proinsulin release from  $\beta$  cells under stress in patients with varying degrees of insulin resistance, or if it has any pathogenetic meaning. Proinsulin does not seem to affect SMCs directly, except at extremely high concentrations,<sup>13</sup> and no mechanism whereby proinsulin could promote atherosclerosis has been identified.

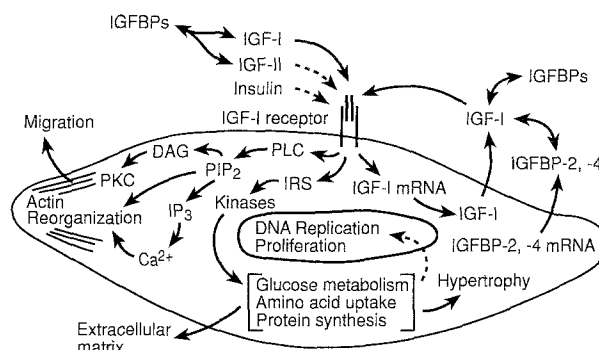
### *Endogenous and Exogenous Hyperinsulinemia*

In an insulin-resistant patient, the pancreas tries to overcome insulin resistance by increasing insulin production.<sup>85</sup> This increases the supply of insulin to the liver, where a large proportion of it, approximately 50%, is extracted and will also increase peripheral insulin concentrations.<sup>101</sup> Treatment with sulfonylureas also increases insulin supply to the liver (unless it causes blood glucose levels to decrease sufficiently to decrease the glucose stimulus for insulin secretion) and will thereby result in endogenous hyperinsulinemia. In contrast, treatment with subcutaneous insulin in patients with NIDDM primarily results in peripheral hyperinsulinemia, and endogenous insulin secretion is decreased.<sup>102</sup> This means that, for example, fat tissue, vasculature, and liver are exposed to

different levels of insulin during endogenous hyperinsulinemia in insulin-resistant states such as NIDDM combined with obesity than in exogenously produced hyperinsulinemia caused by insulin treatment. It is therefore conceivable that endogenous and exogenous hyperinsulinemia may have qualitatively different effects on lipoprotein metabolism and other processes of importance for atherosclerotic disease.

### SUMMARY

Our current understanding of some of the actions and biological effects of the IGF system in a SMC is shown schematically in Fig 1. Locally produced IGF-I or IGF-I from the circulation binds to the two  $\alpha$ -subunits of the IGF-I receptor, which is highly expressed in SMCs in the intact artery and in culture. Insulin and IGF-II can interact with the IGF-I receptor at high concentrations. Insulin receptors are few or absent in SMCs, and circulating insulin concentrations in vivo are probably too low for a direct action on the IGF-I receptor in SMCs. Receptor activation initiates a number of signal transduction pathways. Increased phosphatidylinositol turnover and calcium mobilization correlates with actin filament reorganization and stimulation of directed migration of the SMC in a gradient of IGF-I. Phosphorylation and activation of various kinases (and IRS-1 or -2) are likely to be important in the increased metabolism (amino acid uptake, protein synthesis, and glucose metabolism) of the SMC. The effects of IGF-I receptor activation on signal transduction pathways (eg, the MAP kinase cascade) associated with DNA synthesis and proliferation are weak, and this correlates with the meager mitogenic activity of IGF-I in SMCs. In contrast to the potent mitogen PDGF, the weaker mitogenic effects of IGF-I may be dependent on the basal metabolic state of the SMC (in culture or in the vascular wall) and may preferentially be due to the ability of IGF-I to potently increase metabolism in SMCs. The increased metabolic state of the SMC following stimulation with IGF-I may thus be responsible for the increased DNA synthesis in cultured cells and in diabetic aortic smooth muscle. Activation of the IGF-I receptor leads to increased levels of IGF-I mRNA, which may contribute to further IGF-I receptor activation through an autocrine loop. Several components of the IGF system in SMCs are regulated by growth factors such as PDGF-BB



	PDGF-BB	IGF-I	Diabetes/ Fasting	Hypertrophy
IGF-I mRNA	↑/↓	↑	↓	↑
IGF-I	↑/↓	N.A.	↓	↑
IGF-I receptor mRNA	↑	?	—	—
IGF-I receptor	↑	N.A.	—	—
IGFBP-2 mRNA	—	—	↓	↑
IGFBP-2	—	—	?	↑
IGFBP-4 mRNA	↑	↑/—	↓	↑
IGFBP-4	↑	↑/↓	?	?

**Fig 1. Components and regulation of the IGF system in SMC.** Some of the fundamental mechanisms involved in regulation of the SMC IGF-system are shown in the table. ↑, Increased levels; ↓, decreased levels; —, no significant effect; ?, not determined; N.A., not applicable.

and bFGF. These include IGF-I expression, IGF-I receptor expression, and IGFBP-4 expression.

The IGF system is downregulated by states characterized by decreased metabolism (eg, diabetes and fasting), and in these states, levels of IGF-I mRNA and IGFBP-2 and -4 mRNA are decreased. In contrast, SMC hypertrophy is associated with increased levels of IGF-I, IGFBP-2, and IGFBP-4 mRNA.

In conclusion, the IGF system in smooth muscle is extensively regulated and is likely to play an important role in SMC migration, response of the SMC to metabolic deprivation, and hypertrophy.

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