

# Insulin Receptor Isoforms and Insulin Receptor/Insulin-Like Growth Factor Receptor Hybrids in Physiology and Disease

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In mammals, the insulin receptor (IR) gene has acquired an additional exon, exon 11. This exon may be skipped in a developmental and tissue-specific manner. The IR, therefore, occurs in two isoforms (exon 11 minus IR-A and exon 11 plus IR-B). The most relevant functional difference between these two isoforms is the high affinity of IR-A for IGF-II.

IR-A is predominantly expressed during prenatal life. It enhances the effects of IGF-II during embryogenesis and fetal development. It is also significantly expressed in adult tissues, especially in the brain. Conversely, IR-B is predominantly expressed in adult, well-differentiated tissues, including the liver, where it enhances the metabolic effects of insulin.

Dysregulation of IR splicing in insulin target tissues may occur in patients with insulin resistance; however, its role in type 2 diabetes is unclear.

IR-A is often aberrantly expressed in cancer cells, thus increasing their responsiveness to IGF-II and to insulin and explaining the cancer-promoting effect of hyperinsulinemia observed in obese and type 2 diabetic patients. Aberrant IR-A expression may favor cancer resistance to both conventional and targeted therapies by a variety of mechanisms.

Finally, IR isoforms form heterodimers, IR-A/IR-B, and hybrid IR/IGF-IR receptors (HR-A and HR-B). The functional characteristics of such hybrid receptors and their role in physiology, in diabetes, and in malignant cells are not yet fully understood. These receptors seem to enhance cell responsiveness to IGFs. (*Endocrine Reviews* 30: 586–623, 2009)

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Abbreviations: APS, Associate protein substrate; AT, ataxia telangiectasia; ATM, AT mutated; AT/RT, atypical teratoid/rhabdoid tumors; BRET, bioluminescence resonance energy transfer; CR, cysteine-rich region; dmpk, dystrophin myotonia protein kinase; E, embryonic day; EGF, epidermal growth factor; ER, estrogen receptor; FAK, focal adhesion kinase; FnIII, fibronectin type III; FoxO, forkhead box 'other'; HR, hybrid receptor; HR-A, HR containing IR-A hemidimers; HR-B, HR containing IR-B hemidimers; ID, insert domain; IGFBP, IGF binding protein; IGF1RKO, *Igf1r* knockout; ILP, insulin-like peptide; IR, insulin receptor; IR-A, IR isoform A; IR-B, IR isoform B; IRS, IR substrate; MBNL, muscleblind; MD1, myotonic dystrophy type 1; MEK1, MAPK kinase 1; MPO, myeloperoxidase; mTOR, mammalian target of rapamycin; PCOS, polycystic ovary syndrome; PI3K, PI3-kinase; PPP, picropodophyllin; raptor, regulatory-associated protein of mTOR; SH2, Src homology 2; T2DM, type 2 diabetes mellitus; TSC2, tuberous sclerosis complex 2.

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## I. Introduction

In 1985, two different groups reported cloning of the insulin receptor (IR) cDNA. These cDNAs were of slightly different lengths (1, 2), indicating that the IR exists in two isoforms. These two isoforms were found to be IR isoform A (IR-A), lacking exon 11, and IR isoform B (IR-B), including exon 11. Several subsequent studies were performed to correlate IR isoform expression with insulin resistance/type 2 diabetes mellitus (T2DM) (3–5). The role of IR isoforms in T2DM has remained elusive because the data obtained by different groups conflicted (6–9). Further studies indicated subtle differences between IR-A and IR-B in terms of receptor activation and signaling, suggesting different functions for each IR isoform (10–12). This concept was confirmed by the observation that IR-A, but not IR-B, is a high-affinity receptor for IGF-II (13). These studies placed IR-A in the IGF system, which regulates several biological events, including cancer, aging, and diabetes (14–16). IGF system dysregulation frequently occurs in malignancies and includes IGF-IR overactivation, by both receptor overexpression and autocrine/paracrine overproduction of IGF-I and IGF-II (17, 18). In this system, IR-A overexpression may contribute to modulation of tissue responses to insulin and IGF-I/II (16, 19).

Herein, we review data indicating that IR splicing is an evolutionary conserved mechanism in mammals that is responsible for the specificity of insulin and IGF signaling. Indeed, IR-A up-regulation is associated with decreased metabolic insulin signaling and increased IGF signaling, whereas IR-B up-regulation is associated with predominant metabolic insulin signaling. Predominant IR-A expression may therefore be important in embryonic life for growth and fetal development, whereas predominant IR-B expression has a role in metabolic insulin action in adult

life. Dysregulation of IR splicing, *i.e.*, increased IR-A expression in adult life, may play an underestimated role in cancer progression and the aging process.

## II. Insulin Receptor Structure and Signaling

### A. Insulin receptor gene

#### 1. IR gene structure

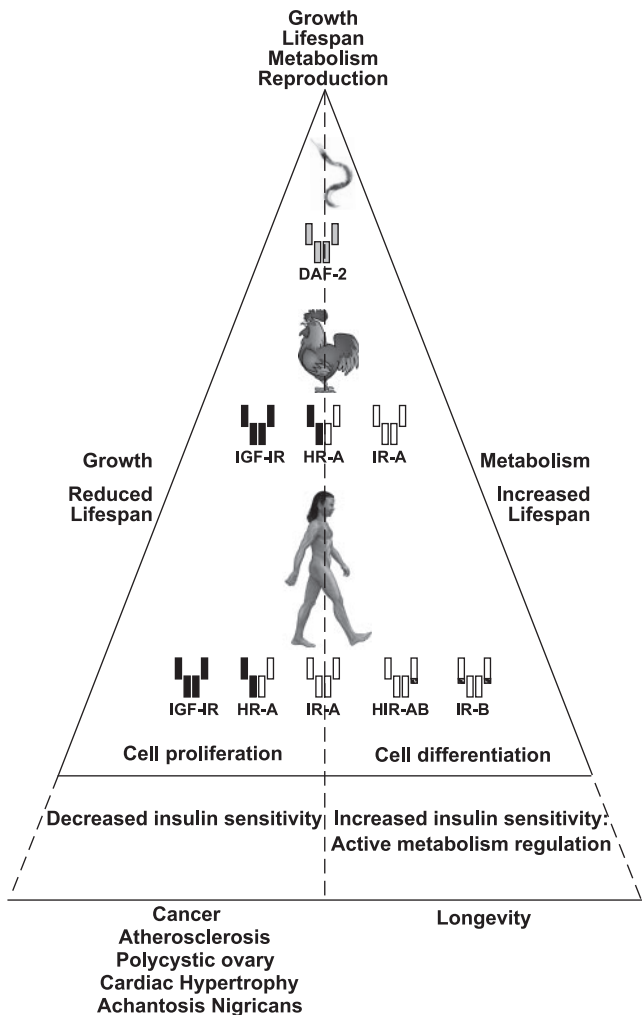
The human IR is encoded by a 22-exon gene (*Ir*) spanning 120 kb that is located on chromosome 19. Isolation and characterization of the human IR cDNA (approximately 5 kb) by the groups of Axel Ullrich (2) and Bill Rutter (20) in 1985 revealed predicted human insulin pro-receptor sizes of 1343 and 1355 amino acids, respectively. The difference in size was found to be due to exclusion or inclusion of a 12-amino acid segment at the C-terminal end of the IR  $\alpha$ -subunit. Studies on the exon-intron organization of *Ir* indicated that the 12-amino acid region is encoded by exon 11, spanning 36 bp, that could be alternatively spliced, thus generating two IR isoforms (21).

Homology between IR and IGF-IR is high, ranging from 45–65% in the ligand binding domains to 60–85% in the tyrosine kinase and substrate recruitment domains (22, 23). Indeed, *Ir* and *Igf1r* have evolved from an ancestral gene and are part of a system that is highly conserved in vertebrates and invertebrates, which coordinates metabolic, growth, and differentiation responses to environmental conditions and nutrient availability (24, 25) (Fig. 1). Although only one receptor protein is present in invertebrates (26, 27), three distinct receptors have been identified in vertebrates: IR (1, 2) IGF-IR (23), and an orphan receptor named the IR-related Receptor (IRR) (28, 29). The observation that the triple *Ir/Igf1r/Irr* knockout, at variance with the single and double knockouts, does not develop the male phenotype suggests that the IRR signaling pathway is required for male sexual differentiation (30).

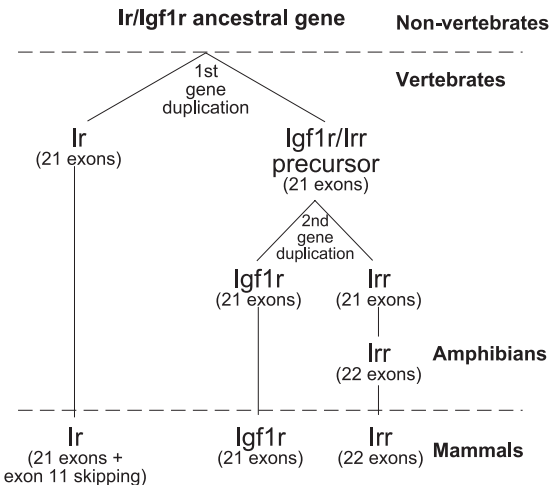
#### 2. Phylogeny of the *Ir* gene family

The first duplication of the ancestral *Ir-like* gene led to the *Ir* paralog and the common ancestral gene of both *Igf1r* and *Irr*, which were generated in a second round of duplication (23, 29, 31) (Fig. 2). Approximately 20% of all sites in *Ir* transcripts are invariant across vertebrates (31). Such conserved sites are abundant in the tyrosine kinase domain (32), indicating that this domain is under strong selection pressure to maintain the general IR signal transduction functions.

In contrast, only 2% of the overall *Ir* transcript is specific and not shared by *Igf1r* or *Irr*. IR-specific sites are mainly located in the extracellular portion of the receptor, suggesting that differences in the function of paralogs in



**FIG. 1.** Signaling diversification in the IGF system, a key regulator of metabolism and life span. In invertebrates (*C. elegans*; top of the triangle), only one receptor of the IGF system is present (DAuer Formation-2). Nutrient availability activates DAuer Formation-2 and elicits coincident biological functions, including activation of metabolism and growth, reproduction, and death. In contrast, low nutrient availability causes poor DAuer Formation-2 activation. In this case, *C. elegans* will neither grow nor reproduce, and it becomes a long-lived dauer larva. In vertebrates (chicken; middle of the triangle), the presence of two different receptors of the IGF system leads to functional diversification: whereas IR-A mainly regulates glucose metabolism, IGF-IR regulates growth and survival. HRs (HR-A) may have some overlapping functions, including the proliferative effects of insulin and proinsulin. In mammals (*Homo sapiens*; bottom of the triangle), the appearance of IR-B, a receptor with exquisite metabolic functions, makes the scenario even more complex. The assumption that IGF system down-regulation is coincident with a prolonged life span becomes less evident. Despite receptor subtype complexity, however, functional studies on receptor subtypes maintain the validity of this paradigm. The key for interpretation of such receptor complexity is IR-A; overactivated/overexpressed IR-A leads to a reduced metabolic effect of insulin and increased activation of IGF-like signaling (left side of the triangle). As a consequence, increased cell proliferation, atherosclerosis and cancer may be promoted. In contrast, decreased IR-A signaling is associated with restrained IGF signaling and increased insulin metabolic effects, as observed in healthy centenarians. In light of this view, human longevity is inversely related to insulin/IGF signaling promiscuity.



**FIG. 2.** Schematic representation of IR phylogeny. An ancestral gene exists in nonvertebrates (DAuer Formation-2), which encodes for a common receptor for insulin-like peptides. A gene duplication occurred in vertebrates, resulting in two 21-exon genes, one encoding the *Ir* and the other one a precursor of the *Igf1r* and *Irr*. A second gene duplication resulted in the formation of two separate genes for the IGF-IR and the IRR, both formed by 21 exons. In amphibians, the *Irr* gene acquired one more exon, becoming a 22-exon gene. Moreover, in mammals, the *Ir* gene also acquired an additional exon (exon 11) together with the ability to skip the exon in a developmental and tissue-specific fashion.

the family have been evolutionarily achieved more through changes in ligand-binding affinity (33) than by modifications in the intracellular tyrosine kinase domain (31).

At variance with *Igf1r*, *Ir* and *Irr* include exon 11. Interestingly, *Ir* exon 11 is found exclusively in mammals (31). This finding implies that functional diversification of the *Ir* family during evolution was achieved through alternative splicing (Fig. 2).

Alternative splicing of *Ir* exon 11 in mammals and its physiological implications will be discussed in the next paragraphs.

### 3. IR promoter

The *Ir* promoter spans 2000 bp (21). It contains many GCs, no TATA or CAAT boxes, and multiple transcription initiation sites (34). It contains a largely GC-rich region, located between –1818 and –288 bp (35). The region spanning –646 to –489 bp is important for activity of the proximal promoter (36). A positive regulatory element is localized between –1823 and –1311 bp, whereas a negative regulatory element is found between –1311 and –877 bp (37). This organization suggests that IR expression is highly regulated in different tissues. In tissues that are typical targets of insulin action, like hepatocytes, *Ir* promoter activity may be regulated by the HT-FIR transcription factor (38), IRNF-I, and IRNF-II (IR nuclear factors I and II) (39). Also, the nuclear protein HMGA1, which is up-regulated in embryonic tissues and human malignancies (40), may activate *Ir* promoter (41).

Interaction of Sp1 with wild-type p53 reduces *Ir* promoter activity, whereas p53 mutants may directly bind and stimulate the *Ir* promoter. This effect of p53 mutants may be responsible for IR overexpression in human cancer (42). Estrogen receptors (ERs) bound to estrogens may also inhibit *Ir* promoter activity. Indeed, two estrogen response elements were found in the *Ir* promoter (43). The existence of these modulatory mechanisms suggests that IR expression is highly regulated in cells in a development- and tissue-specific manner.

## B. Insulin receptor expression

### 1. *IR expression in physiological conditions*

Although the major insulin target tissues are liver, adipose tissue, and skeletal muscle, IRs have also been found in the brain, heart, kidney, pulmonary alveoli, pancreatic acini, placenta vascular endothelium, monocytes, granulocytes, erythrocytes, and fibroblasts (44). The observation that IRs are not restricted to insulin target tissues suggests that IRs may be functionally linked to multiple systems, in addition to their known role in the metabolic actions of insulin. The findings of both metabolic and non-metabolic effects of IRs are supported by the effects of insulin on embryonic development. Briefly, pancreatic islet  $\beta$ -cell secretory granules have been observed in the human fetus at 14 wk gestation, and IRs have been detected in the liver as early as 15 to 18 wk gestation. Furthermore, monocytes and erythrocytes from human cord blood have higher IR content than similar cells harvested from adult individuals (44). Moreover, the fetal IR is not down-regulated by hyperinsulinemia (44); rather, hyperinsulinemia is associated with increased IR content in cord blood monocytes. In accordance with the notion that insulin may regulate fetal growth, fetal hyperinsulinemia leads to macrosomia, whereas insulin deficiency leads to growth impairment (44). After birth, IR expression in monocytes and erythrocytes decreases, remains unchanged until puberty (44), and then increases in adult life (44). In accordance with the inhibitory effect of estrogens on *Ir* promoter activity, monocyte IR content is higher during the luteal phase in adult females (43). This elevation is abolished by use of oral contraceptives (44) or pregnancy (45). Moreover, glucocorticoids and thyroid hormones have been reported to enhance IR expression (46).

Finally, nutrition and exercise have been reported to influence IR expression (47), although the data obtained in experimental animals were not always confirmed in humans (48).

### 2. *IR expression in various tissues*

IR expression in mammalian tissues has been determined by both binding assays and selective immunopre-

cipitation. The highest expression of IR protein was found in adipose tissue. Relative IR expression in liver, heart, and lung tissue was approximately 30% of that in adipose tissue, whereas it was approximately 10% in muscle, brain, spleen, placenta, and kidney tissue (49). Quantification of IR isoforms has been determined by both RT-PCR and Western blot using antibodies specifically recognizing the IR-B protein. IR-B expression accounted for approximately 80% of total IR expression in liver, 60% in muscle and adipose tissue, 40% in placenta, and 0% in lymphocytes (6).

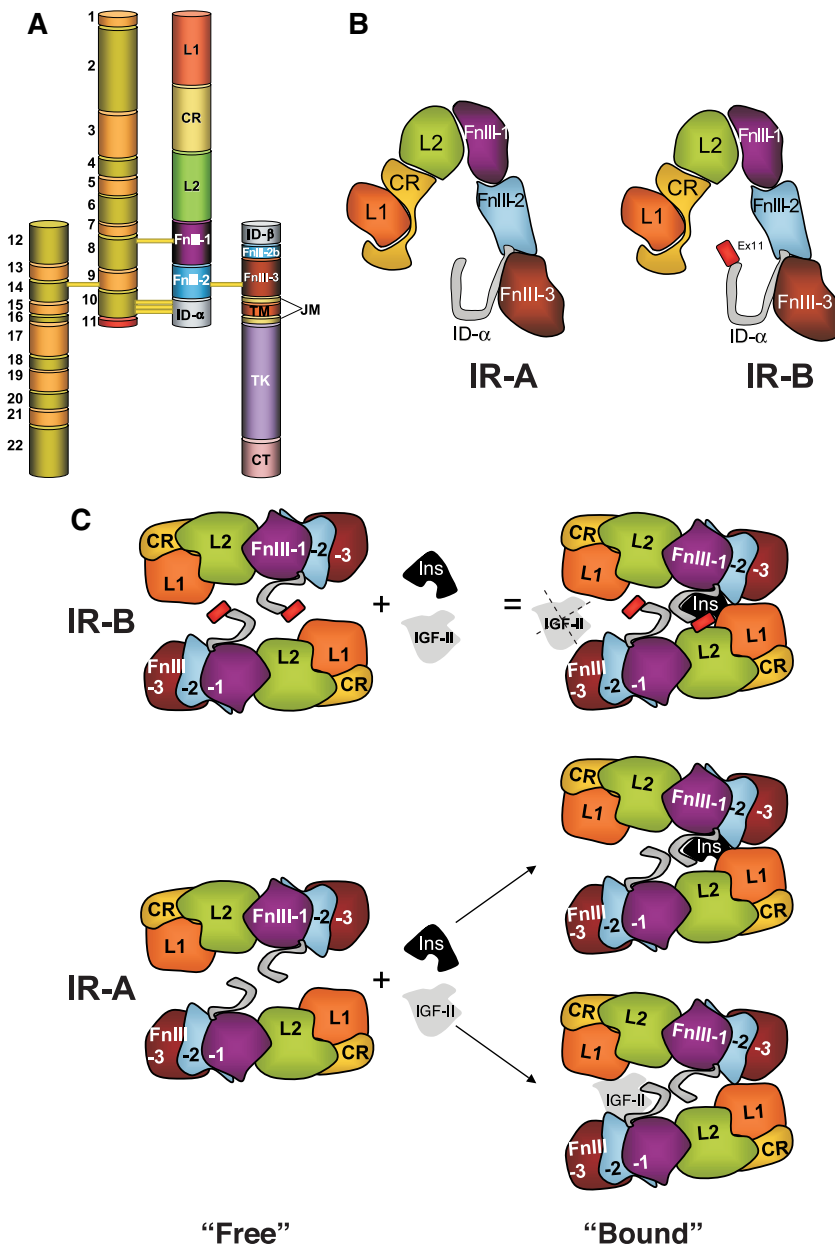
In the brain and pancreas, the IR expression level is much lower than that in typical insulin-responsive tissues. Moreover, the effect of insulin is typically not metabolic in these organs. Recent data support a specific role of IR isoforms in the biology of these tissues.

### 3. *IR expression in brain*

Both IR and insulin are present in the brain (50, 51). Cerebral insulin is transported from the plasma into the cerebrospinal fluid (52) through IR-based, saturable transport (53), occurring mainly in the olfactory bulb and hypothalamus (53). Synthesis of insulin has likewise been detected in neuronal tissue, including neonatal rabbit and adult rat brain (52, 54). Cerebral IRs and insulin are present in the olfactory bulb, hypothalamus, cerebral cortex, cerebellum, hippocampus, and pituitary intermediate lobe (55, 56). The increase in circulating insulin is associated with an increase in insulin in the cerebrospinal fluid (57). Persistent hyperinsulinemia down-regulates IR-mediated insulin transport to the brain (57). In mammalian brain, two IR types are present. In addition to the typical IR present in glial cells, a brain-specific IR is present in neurons (52). This brain-specific IR is mainly the IR-A isoform with a lower molecular weight as a result of differential glycosylation. Brain insulin is believed to have a role in neuronal survival, learning, memory, regulation of energy homeostasis, and reproduction (58). It is also involved in the control of energy balance in mammals because delivery of insulin to the brain is anorexigenic and reduces body weight (58). Accordingly, mice with a brain conditional knockout of IR (NIRKO mice) are insulin resistant, glucose intolerant, and overweight (59). The reduction of food intake caused by centrally administered insulin is lower in overweight animals compared with lean and normal-weight animals, suggesting that insulin resistance in the brain may contribute to weight gain (60).

Brain IR also regulates cognitive functions. Patients with type 1 or 2 diabetes have been found to have diminished mental performance (61). Moreover, patients with T2DM are at higher risk for cognitive decline and Alzheimer's disease (62). In Alzheimer's patients, the activity of brain IR is reduced (60) and insulin concentrations in the





**FIG. 3.** Modular structure of IR isoforms. **A**, Diagram of the  $\alpha 2\beta 2$  structure of the IR. On the left half of the figure, the IR is represented by the 22 exon-encoded sequence. On the right half, predicted protein modules are indicated. L1, Large domain 1; CR, cysteine-rich domain; L2, large domain 2; Fn, fibronectin type III domains; TM, transmembrane domain; JM, juxta membrane domain; TK, tyrosine kinase domain; CT, C-terminal domain. **B**, Schematic side view of the 3-D structure of the IR isoform  $\alpha$ -subunit (L1, CR, L2, FnIII-1/2) and part of the extracellular portion of the  $\beta$ -subunit (FnIII-3). The gray loop indicates the insert domain (ID- $\alpha$ ). The red fragment on top of ID- $\alpha$  is encoded by exon 11 and is present in IR-B, but not in IR-A. **C**, Schematic top view of the 3-D structure of the IR heterotetramer extracellular portion. Insulin (black molecule) binds to one site of IR-B. The presence of the red fragment encoded by exon 11 does not allow for binding of IGF-II (gray molecule) to IR-B. Both insulin and IGF-II may bind to IR-A, due to the absence of the red fragment.

cerebrospinal fluid are lower than normal, indicating impaired insulin transport to the brain (56). Notably, insulin treatment ameliorates cognitive impairment in diabetic patients (57). These observations are in accordance with data obtained in animals. Additionally, insulin-deficient rats display reduced performance in

complex tasks (63). Overall, animal and human studies indicate that insulin may affect cognitive processes (52).

#### 4. IR expression in endocrine pancreas

Both IR and IGF-IR have been shown to be present in  $\beta$ -cells (64, 65). IGF-I acts as a negative regulator of insulin secretion, whereas the role of IR in  $\beta$ -cells remains controversial because IGF-IR activation by insulin may interfere with the evaluation of IR function (66, 67). Recent studies that circumvent the confounding presence of the IGF-IR have concluded that insulin is a positive regulator of its own production (68, 69).

The relative role of IR and IGF-IR in  $\beta$ -cells has been investigated in transgenic models. The  $\beta$ -cell-specific *Ir* knockout (*BIRKO*) (70) manifests progressive glucose intolerance, as well as reduced islet size and insulin content. *Igf1r* knockout ( *$\beta$ IGFRKO*) mice (71, 72) display normal  $\beta$ -cells and islets but show defects in glucose-stimulated insulin secretion (71, 72). At 2 months of age, they display hyperinsulinemia, in accordance with the inhibitory effect of IGF-I on insulin secretion (73, 74). Remarkably, both *BIRKO* and  *$\beta$ IGFRKO* mice show a loss of acute phase insulin secretion, probably due to common defects in signaling downstream IR and IGF-IR (75, 76). Although IR and IGF-IR are unlikely to play a critical role in islet development, they are important for the islet hyperplastic response to insulin resistance (77) and pancreatic injury (78).

The predominant isoform in human pancreatic  $\beta$ -cells is IR-B (79), suggesting that the IGF-II/IR-A interaction does not play a major role in  $\beta$ -cell physiology and that the effects of IGF-II in  $\beta$ -cells are mediated by IGF-IR, as suggested by the  *$\beta$ IGFRKO* phenotype.

#### 5. IR expression in malignant cells

An unexpected observation was the ability of mitogens, such as concanavalin A and Epstein-Barr virus, to increase IR expression in lymphocytes (80). Moreover, human lymphocyte-derived malignant cells, such as the IM-9 cells (B-type lymphoblasts derived from a subject with multiple

myeloma), are abundantly endowed with high-affinity IRs (80). IR up-regulation in these cells has no major effect on cell metabolism, but coincides with the development of increased sensitivity to the nonmetabolic effects of insulin. A role for IR in tumor progression was suggested by studies indicating that IR is overexpressed in several tumors, including breast, colon, lung, ovary, and thyroid carcinomas (13, 81, 82). The biological relevance and the putative mechanisms involved in IR overexpression in malignant cells will be discussed below (see *Section V.C*).

## C. Insulin receptor structure, ligand binding, and autophosphorylation

### 1. IR protein: structure and glycosylation

The IR protein is a heterotetramer consisting of two extracellular  $\alpha$ -subunits and two transmembrane  $\beta$ -subunits held together by disulfide bonds (83, 84). The  $\alpha$ -chain and 194 residues of the  $\beta$ -chain form the extracellular portion of the IR; in the  $\beta$ -chain, there is a single transmembrane sequence and a 403-residue cytoplasmic domain containing the tyrosine kinase activity (Fig. 3). Ligand binding to the IR  $\alpha$ -subunit stimulates tyrosine kinase activity intrinsic to the  $\beta$ -subunit of the receptor (84–86). The  $\alpha$ - and  $\beta$ -chains are both synthesized from a unique mRNA, which is constituted by 22 exons. *Ir* mRNA encodes for a protein of 1370 amino acids, indicating a predicted molecular mass of 153,917 Da. The protein is cleaved by furin into  $\alpha$ - and  $\beta$ -subunits. The  $\alpha$ -subunit contains 723 amino acids, with a molecular mass of 130 kDa (83, 84). The  $\beta$ -subunit contains 620 amino acids, with a molecular mass of 95 kDa (83, 84). Both subunits are glycosylated, thus accounting for most or all of the molecular mass difference in the observed *vs.* predicted values in various tissues and cells (87).

Comparative sequence analyses have shown that the IR family members are composed of a number of different, repeated structural units (83, 84). The N-terminal half of each ectodomain monomer consists of two homologous leucine-rich repeat domains (L1 and L2) of approximately 150 amino acids each, separated by a cysteine-rich region (CR), consisting of seven smaller repeats, also containing approximately 150 residues, with one or two disulfide bonds (83, 84) (Fig. 3). The C-terminal half of each ectodomain monomer (approximately 460 residues) consists of three fibronectin type III domains (FnIII-1, FnIII-2, and FnIII-3). They are relatively small (approximately 100 amino acids) and form a seven-stranded  $\beta$ -sandwich. The FnIII-2 domain of IR contains a large, 120-amino acid residue fragment, termed the insert domain (ID) (83, 84), and the furin cleavage site (83, 84) (Fig. 3).

The IR splice variant IR-B differs from IR-A by the presence of a 12-amino acid segment (coded by exon 11)

inserted between IR-A residues 716 and 717, three residues before the C-terminus of the  $\alpha$ -chain (84).

The intracellular part of each IR monomer contains a tyrosine kinase domain flanked by two regulatory regions (the juxtamembrane region and the C-tail) that contain the phosphotyrosine binding sites for signaling molecules. In particular, the juxtamembrane region is involved in docking IR substrates (IRS) (88) 1–4 and Shc, as well as in receptor internalization (85, 86, 89).

### 2. IR binding and phosphorylation

Analysis of insulin binding to IR reveals curvilinear Scatchard plots and negative cooperativity (84), thereby implying the existence of both low-affinity and high-affinity insulin binding sites. These two different ligand-binding regions are termed site 1 (low-affinity site) and site 2 (high-affinity site) (83, 84, 86, 89). Photo-affinity labeling and alanine scanning data indicate that insulin binds to the site composed of the L1 domain and  $\alpha$ -subunit C-terminal peptide sequence (amino acids 704–715, CT domain) (Fig. 3). A second binding site exists within the C-terminal part of L2 and the first FnIII domain (Fn0) (84). Insulin binds first to the low-affinity site (site 1) on one  $\alpha$ -subunit and then to the second site (site 2) of the other IR  $\alpha$ -subunit (84, 90). A second insulin molecule bridging both leftover sites 1 and 2 accelerates dissociation of the first bound insulin molecule (84). This behavior explains the bell-shaped curve and negative cooperativity and provides a molecular basis for receptor tyrosine kinase activation, by approximating the two-kinase domains and permitting transphosphorylation. The biological role of IR-negative cooperativity is an interesting issue. The acceleration of the dissociation rate of the IR complex by increased insulin concentration is important for insulin actions. Indeed, the mitogenic effects of insulin are disproportionately enhanced by insulin analogs that have slower dissociation rates relative to native human insulin, suggesting that the negative cooperativity is important for limiting the mitogenic effects of insulin (84). Computational Boolean analyses have demonstrated that ligand residence time on the IR may indeed determine choices in branching signaling pathways (85, 86, 89).

The three-dimensional structure of the IR ectodomain dimer (90) has allowed for better understanding of the localization of insulin binding sites 1 and 2. Each monomer of the IR ectodomain exhibits an inverted-V arrangement relative to the cell membrane, with the L1-CR-L2 domains forming one leg and the three FnIII domains forming the other one (90). In the dimer, the second monomer is related to the first by a 2-fold rotation around the axis of the inverted V, with the L1-CR-L2 domains of one monomer packed against the three FnIII domains of the other (Fig. 3B). At the apex of the inverted V, the L2 do-

main of each monomer contacts the FnIII-1 domain of the other, whereas the base of the C terminus of the FnIII-3 domains is oriented in such a way that it is capable of being extended through the cell membrane to the kinase domains of the intact receptor. The first component of site 1 in both  $\alpha$ -subunits is the central  $\beta$ -sheet of L1 (91, 92). The second component of site 1 is formed by the central modules of the CR. The larger size of this module in IR is partly responsible for the lower IR affinity of the bulkier IGF-I and IGF-II ligands compared with its affinity for insulin (Fig. 3C). The third component of site 1 is the CT peptide, as demonstrated by chemical cross-linking. The CT peptide sequence, belonging to the other IR monomer, is closely juxtaposed to the L1 domain of the contralateral IR monomer and contacts amino acid B25 of the insulin molecule (93) (Fig. 3C). It is reasonable to suppose that the exon 11-encoded 12-amino acid peptide present in IR-B may contribute, together with the CR module, to reduce the affinity of IR-B for IGF-II by further restraining the site 1 pocket. Site 2 is formed by the C-terminal loops of FnIII-1 and the N-terminal loops of FnIII-2 that are adjacent to the L1 face (90). The three-dimensional structure of the IR may explain the contribution of each domain to insulin binding and the complexity of the binding characteristics of the IR isoforms and IR/IGF-IR hybrids.

In the insulin-free state, the inhibitory IR conformation maintains a minimum separation between the two intracellular tyrosine kinases. This distance between the tyrosine kinases prevents the tyrosine kinase activation loop (94) of one tyrosine kinase from reaching the catalytic transphosphorylation site of the other tyrosine kinase (Fig. 3). Binding of a single insulin molecule joins the two ectodomains with a consequent reduction of separation between the associated tyrosine kinase domains, thereby allowing transphosphorylation of the tyrosine kinase activation loops at the catalytic loci of the opposing tyrosine kinase domains. Phosphopeptide mapping techniques (95, 96) have resolved tyrosine kinase residues (in the juxtamembrane region: amino acids 953, 960, and/or 972; in the catalytic domain: 1146, 1151, and 1152; and in the carboxyterminal domain: 1316 and 1322) (1, 2) (Fig. 3). The most important domain for auto- and transphosphorylation is the catalytic domain (amino acids 1146, 1151, and 1152). Phosphorylation of these sites correlates with the acquisition of transphosphorylation activity (97, 98).

Carboxyterminal deletions lacking either 43 amino acids (99) or mutants with tyrosine residues 1316 and 1322 changed to phenylalanines (100, 101) have normal tyrosine kinase activity and diminished autophosphorylation due to loss of the two tyrosine residues. However, these mutants, when transfected into the fibroblast cell

line Rat1, show diminished (102, 103) or unchanged (104) glucose uptake and glycogen synthase activity (“metabolic signaling”).

In the juxtamembrane region of the  $\beta$ -subunit, Tyr-960 is important for IRS-1 phosphorylation and for metabolic and mitogenic responses to insulin (96), whereas Tyr-953 and Tyr-960 play a role in receptor endocytosis (105, 106) because they exist within consensus endocytosis signals for internalization via clathrin-coated pits (94, 107).

#### D. Insulin receptor signal transduction pathways

Insulin binding to the IR extracellular  $\alpha$ -subunit induces a conformational change in the receptor molecule, which brings the two  $\beta$ -subunits into close opposition. Crystallographic studies of the IR kinase domain in the unphosphorylated and phosphorylated states indicate that autophosphorylation activates the IR tyrosine kinase due to a series of alterations in the  $\beta$ -subunit conformation that facilitate ATP binding,  $\beta$ -subunit phosphorylation, recruitment of membrane and cytosolic protein substrates, and their subsequent phosphorylation.

The activated IR tyrosine kinase phosphorylates several intracellular substrates, including the most extensively characterized IR substrates (IRS-1, -2, -3, and -4), IRS-5/DOK4, IRS-6/DOK5, Shc, Gab1, Cbl, associate protein substrate (APS), and the signal regulatory protein family members (85, 86, 108). Each of these phosphorylated proteins provides specific docking sites for effectors containing Src homology 2 (SH2) domains that specifically recognize different phosphotyrosine residues, including the regulatory subunit p85 of type 1A PI3-kinase (PI3K); the protein tyrosine phosphatase SHP2; the Src family of non-receptor-type tyrosine kinases, including Fyn and Csk; the adaptor proteins Grb2; and the GTPase activating protein (109) of Ras. Some of these molecules contain SH3 domains that bind proline-rich regions with the consensus sequence PXXP and thereby provide additional sites for protein-protein interactions with additional downstream intracellular effectors. In this complex cascade of biochemical signals, two major signaling pathways have been recognized, mediating either prevalent metabolic or mitogenic effects and originating by the activation of PI3K or Ras, respectively.

##### 1. The PI3K pathway

In the PI3K pathway, a regulatory p85 subunit and a catalytic p110 subunit phosphorylate phosphatidylinositol-(4, 5)-bisphosphate (PIP2), thereby generating phosphatidylinositol-(3, 4, 5)-trisphosphate (PIP3). PIP3 recruits and activates pleckstrin homology domain-containing proteins, including enzymes, substrates, adaptors, and cytoskeletal molecules. Among these, phosphoinositide-de-

pendent kinase-1 phosphorylates and activates several downstream enzymes, including the serine/threonine kinase Akt (protein kinase B) and protein kinase C (110). In addition, PIP3 directly facilitates Akt activation by mediating its translocation to the membrane via the pleckstrin homology domain. Akt activation regulates metabolic enzymes, such as glycogen synthase kinase 3 and 6-phosphofructo-2-kinase, and it is involved in glucose metabolism by such activities as induction of glucose transporter (Glut-4) translocation from intracellular storage compartments to the plasma membrane (108). Activated Akt also phosphorylates the Bcl-2 family member BAD, an important proapoptotic protein (111) that, when phosphorylated, is not able to exert its proapoptotic function. Moreover, activated Akt phosphorylates forkhead box ‘Other’ (FoxO) proteins (FoxO1, FoxO3, and FoxO4), which are signaling molecules that regulate various cell functions (112), including metabolism, apoptosis promotion (*e.g.*, via the proapoptotic member of the Bcl-2 family, Bim), and inhibition of cell growth (113, 114). Upon insulin stimulation, FoxO proteins are phosphorylated by Akt and, after interaction with 14-3-3 proteins and exportins, translocate to the cytoplasm where they undergo ubiquitylation and degradation (113, 114). Therefore, IR activation suppresses the transcriptional program of FoxO proteins.

Another pathway regulated by PI3K-Akt activation is the regulatory-associated protein of mTOR (raptor)–mammalian target of rapamycin (mTOR) pathway, which regulates cell growth and metabolism (86) and integrates signals coming from insulin, as well as other growth factors, with those coming from nutrients. Activated Akt phosphorylates and inactivates TSC2 (tuberous sclerosis complex 2). TSC2 belongs to a heterodimeric complex with TSC1 (tuberous sclerosis complex 1 or hamartin) that functions as the Rheb (Ras homolog enriched in brain) GTPase-activating protein (109). Inactivation of TSC2 by Akt reduces the GAP activity of the TSC1/TSC2 complex, thus increasing the amount of GTP-bound Rheb, a ras-family GTP-binding protein that binds and activates the raptor–mTOR complex.

Two main signaling pathways downstream of the raptor–mTOR complex link IR to the control of mRNA translation: the p70S6 kinase (p70S6K) and eIF4E-binding protein-1 (4E-BP1) pathways. p70S6K is a serine/threonine protein kinase that regulates factors involved in protein synthesis, including ribosomal S6 protein and the translational regulators eukaryotic translation elongation factor 2 kinase and eukaryotic translation initiation factor-4B. When phosphorylated by raptor–mTOR, 4E-BP1 releases eIF-4E, allowing it to interact with eIF-4G, and thus activating cap-dependent mRNA translation (115).

There is also evidence of complex cross-talk between the PI3K-Akt-mTOR pathway and the p53 pathway, which suggests that regulation of cell functions by IR signaling and the p53 pathway may overlap (116).

Activated IR recruits APS (109), an adapter that contains three SH2 domains. Upon binding to the IR  $\beta$ -subunit, APS is tyrosine phosphorylated and acquires the ability to phosphorylate Cbl on three tyrosines (117). Insulin stimulation results in assembly of the Cbl/CrkII/C3G complex and its recruitment to lipid raft domains, where it catalyzes activation of the Rho family small GTP-binding proteins TC10 $\alpha$  and TC10 $\beta$  (118).

c-Abl tyrosine kinase is an important component of IR signaling. Insulin stimulates c-Abl tyrosine phosphorylation with consequent focal adhesion kinase (FAK) dephosphorylation. Dephosphorylated FAK mediates the metabolic effects of insulin. Therefore, when c-Abl tyrosine kinase is inhibited, FAK is phosphorylated in response to insulin, which promotes cell proliferation and migration, rather than cell metabolism. Indeed, FAK phosphorylation or dephosphorylation by insulin may mediate alternative mitogenic or metabolic predominance in insulin effects on target cells (119).

## 2. The Ras pathway

Grb2 is an adaptor that may bind to phosphorylated IRS proteins through its SH2 domain. Via its SH3 domain, Grb2 activates ras guanine nucleotide exchange factor mSos (Son of Sevenless), which, in turn, activates p21ras, a GTP-binding protein with GTPase activity toward active (GTP-bound) or inactive (GDP-bound) p21ras form (120). Phosphorylated IR may also activate p21ras through Shc proteins. In particular, Tyr-972 of IR binds to the N-terminal phosphotyrosine binding domain of Shc. As a consequence, both 52- and 46-kDa isoforms of Shc are phosphorylated at Tyr-317, which recruits the Grb2/Sos/p21ras complex. Therefore, both phosphorylated IRS and Shc bind to Grb2, although the Shc/Grb2/Sos complex is predominantly involved in the activation of p21ras and sustained ERK1/2 activation in response to insulin.

Active p21ras recruits and activates the serine/threonine kinase Raf, which, in turn, phosphorylates the dual specificity kinase MAPK kinase (MEK1), which then phosphorylates ERK1/2, a kinase of the MAPK family. In its inactive form, ERK1/2 is mainly located in the cytoplasm, where it binds to MEK1 to form an MEK/ERK heterodimer (85, 108). When phosphorylated, ERK1/2 dissociates from MEK1 and translocates to the nucleus, where it phosphorylates a number of substrates (SRC-1, Pax6, NF-AT, Elk-1, MEF2, c-Fos, c-Myc, and STAT3) involved in the activation of a complex transcriptional program (120, 121). Moreover, activated ERK1/2 phosphorylates numerous substrates in the cytoplasmic com-



partment. Given that ERK1/2 shuttles between the cytoplasm and the nucleus and has numerous targets in both compartments, its spatial distribution is crucial for determining the biological response.

Other MAPKs, such as Jun N-terminal kinase and p38 kinase, are also activated by insulin and contribute to the complexity of its biological responses (121). Both p70S6K and Jun N-terminal kinase participate in a negative feedback loop involved in the termination of insulin signaling by phosphorylation of serine residues in IRS proteins (85, 108).

### III. The Biology of Insulin Receptor Isoforms

#### A. IR isoform generation

Further insights on IR function were provided by studies on IR isoforms. Indeed, the mature IR exists as two isoforms, IR-A and IR-B, which result from alternative splicing of the primary transcript. IR-B differs from IR-A by the inclusion of exon 11, which encodes 12 amino acid residues (residues 717–728) at the carboxyl terminus of IR  $\alpha$ -subunit. Inclusion of this exon is differentially regulated in various tissues. In adult life, IR-A is ubiquitously expressed, whereas IR-B is predominantly expressed in liver and also substantially expressed in muscle, adipose tissue, and kidney, which are all target tissues of the metabolic effects of insulin (10, 122). Moreover, IR-A is predominantly expressed in fetal and cancer tissues. A high IR-A:IR-B ratio has been implicated in the insulin resistance of patients with myotonic dystrophy and possibly in patients with T2DM (123).

The sequences involved in IR exon 11 splicing are only partially known. Transient transfection experiments in human hepatoblastoma cells (HepG2) with minigenes spanning from exon 10 to 12 allowed for identification of a 48-nucleotide purine-rich sequence at the 5' end of intron 10 that functions as a splicing enhancer and increases exon 11 inclusion (124). Moreover, a 43-nucleotide sequence that favors skipping of exon 11 has been mapped upstream of the break point sequence of intron 10. Mutation studies have also indicated the existence of exon 11 sequences that play a role in determining the degree of exon inclusion in both a positive and negative manner. Further minigene analysis indicated that sequences in exons 10, 11, and 12 regulate the splicing process, perhaps because they are recognized by specific splicing factors including U1 snRNP, SF1, and U2AF65/35. In particular, strengthening of either the 5' or 3' splice sites in exon 11 by mutagenesis leads to its constitutive inclusion. In contrast, strengthening of upstream and downstream splice donor and acceptor sites on the neighboring exons (10 and 12) leads to a decreased exon 11 inclusion. Moreover, the interplay of splicing factors involved in the regulation of

tissue-specific or developmental-related exon 11 skipping remains unclear (125). Studies of the rat clathrin light chain B and the rat  $\beta$ -tropomyosin genes have shown that overexpression of SF2/ASF proteins induces the use of a proximal splice site, either 5' or 3', over a distal site (126, 127). This activity is antagonized by the splicing factor hnRNP-A1, which favors the use of distal splice sites over proximal sites. Hence, the alternative choice of splice sites reflects a balance between SF2/ASF and hnRNP-A1 proteins. These results are in accordance with the observation that cancer cells, which express mostly IR-A, overexpress hnRNP-A1 proteins as well (128).

More recently, a mechanism favoring a high IR-A:IR-B ratio has been described to operate in skeletal muscles of myotonic dystrophy type 1 (MD1) patients. MD1 is caused by an expanded CUG trinucleotide repeat in the 3' untranslated region of the dystrophin myotonia protein kinase (*dmpk*) gene transcript (129). As a consequence of CTG expansion, mutant DMPK RNA accumulates in the nucleus, causing *dmpk* haploinsufficiency (130). Moreover, nuclear accumulation of CUG-containing RNA alters the levels of certain splicing factors and inactivates muscleblind (MBNL) 1 proteins, which are required for inclusion of IR exon 11 in the IR-B transcript (131, 132). In contrast, other splicing factors are abnormally expressed in MD1 myoblasts, including the CUG-binding protein (CUG-BP1), a component of the CELF family of splicing regulators, and hnRNP H proteins (133, 134).

Elevated levels of both hnRNP H and CUG-BP1 result in formation of an RNA-dependent complex that inhibits IR exon 11 inclusion, which results in a predominance of IR-A. This inhibitory effect cannot be blocked by MBNL1 proteins, which normally bind hnRNP and CUG-BP1, because of their nuclear sequestration and inactivation. Studies of a human IR minigene encoding *Ir* exons 10, 11, and 12 have demonstrated that CUG-BP1, hnRNP H and MBNL1 are all able to directly bind RNA sequences encoded by this *Ir-b* minigene (135), but the binding sites remain unknown. These results suggest that the fine-tuning of IR isoform expression may be regulated by a balance between MBLN, CELF, and hnRNP H proteins.

#### B. IR isoforms and ligand specificity

The alternative splicing of exon 11 in the expression of IR-A and IR-B results in structural and functional differences between the isoforms. Therefore, the two isoforms have unique properties (10–12). Indeed, IR-A displays approximately 1.7-fold higher affinity for insulin than IR-B (10). Moreover, Yamaguchi *et al.* (11) observed that insulin association and dissociation from IR-A is faster than from IR-B. These findings are counterintuitive, given the expectation that receptors with higher binding affinity usually have slower ligand dissociation kinetics. This ap-

parent contradiction might be an artifact of the procedure that was employed in the dissociation studies, given that it was measured in the absence of unlabeled insulin. Negative cooperativity does not occur, and potential changes in receptor site-site interactions are not taken into account under such conditions. Increased IR-A internalization and recycling time (see *Section III.C*) may also contribute to the results obtained in intact cells.

In contrast to the very modest difference in insulin steady-state binding affinity, we found that the two isoforms markedly differ in their IGF-II binding affinity. Bound labeled insulin was displaced from IR-A by low concentrations of IGF-II ( $ED_{50} = 2.5$  nM), whereas high IGF-II concentrations were necessary for displacement from IR-B ( $ED_{50} > 100$  nM). These results were obtained in IGF-IR knockout mouse embryo fibroblasts that had been transfected with either human IR-A or IR-B cDNA (R<sup>-</sup>/IR-A and R<sup>-</sup>/IR-B, respectively) and in transfected NIH-3T3 and CHO cells (13) (Table 1). Moreover, the ability of IGF-I to compete with <sup>125</sup>I-insulin binding differs between the two IR isoforms, although much less markedly than IGF-II (Table 1). Half-maximal binding inhibition for IGF-I was about 10-fold higher in cells expressing IR-A than in cells expressing IR-B ( $41 \pm 15$  vs.  $390 \pm 50$  nM for CHO/IR-A and CHO/IR-B, respectively) (11). Similar differences were found in immunocaptured receptors (136). These data indicate that residues encoded by exon 11 exert a major effect on the conformational state of the IR  $\alpha$ -subunit binding site.

As previously described, the insulin binding site on the L1 domain (“classical binding site”) of both IR isoforms depends on two functional epitopes. However, the quantitative contribution of single amino acids to insulin affinity differs significantly for each IR isoform. In particular, mutation of Asn<sup>15</sup> to alanine in IR-A results in a receptor that is completely devoid of insulin binding activity, whereas a similar mutation in IR-B results in a 63-fold decrease in affinity. Mutation of Leu<sup>37</sup> to alanine in

IR-B produces a 40-fold affinity reduction (137). In the C-terminal domain of the  $\alpha$ -subunit, alanine mutations of Tyr<sup>708</sup> or Asn<sup>711</sup> have a greater effect on the affinity of the B isoform with respect to the A isoform, whereas the reverse occurs for alanine mutations of Leu<sup>709</sup>, Asp<sup>707</sup>, Val<sup>713</sup>, Val<sup>715</sup>, and Phe<sup>714</sup> (137).

Recently, Denley *et al.* (138) evaluated regions of IGF-II that may determine its high affinity for IR-A. Studies with chimeras, where the C and D domains of IGF-II were exchanged with the analogous domains of IGF-I, indicated that C and D domains of IGF-II are involved in high-affinity binding to IR-A and low-affinity binding for IR-B. A and B domains of IGF-II and IGF-I are apparently not important for binding specificity (138).

Taken together, these data indicate that the binding site structures of IR-A and IR-B are quite different. Importantly, a direct interaction of either insulin or IGF-II with the peptide encoded by exon 11 has not yet been demonstrated.

C. IR isoforms and signaling specificity

Exon 11 inclusion in the IR transcript determines differences in ligand binding affinity, receptor internalization, and recycling time and intracellular signaling. The faster internalization and recycling time (12, 139) of IR-A has been attributed to the CEACAM1 protein, which selectively increases IR-A internalization despite being equally phosphorylated by both IR isoforms (140).

Differences between IR isoforms regarding signaling activation have been reported in pancreatic  $\beta$ -cells. In these cells, insulin gene transcription is promoted by signaling through IR-A/PI3K class 1A/p70S6K, whereas  $\beta$ GK gene transcription is regulated through IR-B/PI3K class II-like/protein kinase B (141). These signaling differences have been attributed to different localization of IR isoforms at distinct plasma membrane subdomains, thereby allowing for partitioning of adaptor proteins and subsequent activation of selective signaling pathways (142). Although distinct localization of the two isoforms has not been independently confirmed, examples of differences in signaling between IR isoforms have been reported in other models, including neonatal hepatocytes. Indeed, neonatal hepatocytes expressing IR-A, but not IR-B, have increased basal glucose uptake that does not correlate with insulin stimulation (143). In addition, neonatal hepatocytes expressing IR-B alone have increased caspase-8 and caspase-3 activation and increased apoptosis, whereas the mitochondrial branch of apoptosis is activated in neonatal hepatocytes expressing IR-A. Only co-expression of both IR isoforms protected the hepatocytes from apoptosis (144). Data obtained in murine 32D hemopoietic cells indicated that IR-A preferentially induces mitogenic and antiapoptotic signals, whereas IR-B predominantly induces cell differentiation signals (145).

**TABLE 1.** IC<sub>50</sub> values (nM) for insulin, IGF-II, and IGF-I, as measured by either ligand competition assay or BRET, using intact cells or immunopurified receptors

	Insulin	IGF-II	IGF-I	First author, year (Ref.)
IR-A	0.9		41.0	Yamaguchi, 1993 (11)
	0.9	2.5	>30.0	Frasca, 1999 (13)
	0.2	2.2	9.0	Benyoucef, 2007 (136)
IR-B	1.6		390.0	Yamaguchi, 1993 (11)
	1.0	>20.0	>30.0	Frasca, 1999 (13)
	0.5	10.0	90.0	Benyoucef, 2007 (136)
HIR-AB	1.0	10.0	>50.0	Blanquart, 2008 (224)
IGF-IR	>30.0	0.6	0.2	Pandini, 2002 (184)
	>100.0	4.4	0.8	Denley, 2004 (138)
	>1000.0	0.5		Benyoucef, 2007 (136)

HIR-AB, IR-A/IR-B hybrid receptor.

Moreover, in  $R^-/IR-A$  cells, activation by either insulin or IGF-II induces nuclear translocation of IRS-1, whereas neither insulin nor IGF-II is able to induce IRS-1 nuclear translocation in  $R^-/IR-B$  cells (146).

Finally, the abnormally high IR-A:IR-B ratio in muscle cells of patients with myotonic dystrophy seems to play an essential role in the insulin resistance of these patients, suggesting a substantial difference in signaling capability between IR-A and IR-B in muscle cells (see Section V.A).

Besides functional differences from IR-B, IR-A may differentially elicit biological effects and intracellular signaling upon insulin or IGF-II binding.  $R^-/IR-A$  cells preferentially undergo proliferation when stimulated with IGF-II, whereas they preferentially activate glucose uptake when stimulated with insulin (13, 147). These different effects are coincident with quantitative and temporal differences in the phosphorylation of intracellular substrates in response to either insulin or IGF-II binding. In particular, IGF-II is less effective than insulin in stimulating the IRS/PI3K pathway, rather than the Shc/ERK pathway (13), and it induces higher p70S6K:Akt and ERK1/2:Akt ratios than insulin (148). In SKUT-1 human leiomyosarcoma cells, which express IR-A and not IR-B and lack functional IGF-IR, IGF-II is a more potent activator of the Shc/ERK pathway and stimulator of cell migration than insulin, whereas insulin is a more potent stimulator of the PI3K/Akt pathway and a better protector from apoptosis than IGF-II (148). This differential IR-A signaling activation elicited by insulin and IGF-II is reflected by differential global gene expression in response to treatment with insulin or IGF-II. Microarray technology performed in  $R^-/IR-A$  cells stimulated with either insulin or IGF-II indicated that 214 transcripts were similarly regulated by insulin and IGF-II, whereas 45 genes were differentially regulated. Among them, 12 genes were responsive only to insulin, whereas six genes were responsive only to IGF-II. The other 27 transcripts were regulated by both ligands, but with a significant difference in response kinetics, because the effect of IGF-II was generally stronger and more persistent than that of insulin (149).

Recently, we showed that IGF-I may induce remarkable activation of intracellular signaling in  $R^-/IR-A$  cells characterized by a high p70S6K:Akt ratio, despite eliciting only modest IR-A autophosphorylation (150). These studies await independent confirmation.

## IV. Insulin Receptor Isoforms in Physiology

### A. Role of IR isoforms in development

Insulin and IGFs are important for development in both vertebrates and invertebrates. Genetic studies in *Drosophila*

*melanogaster* have shown that insulin-like peptides (ILPs) regulate development, longevity, metabolism, and female reproduction by acting through a conserved insulin signaling pathway (151, 152). Indeed, altered expression of genes encoding ILPs in this conserved pathway has phenotypic effects on the growth and organogenesis of *D. melanogaster*. In particular, overexpression of *d-ilp* genes results in bigger flies in a *Drosophila* IR-dependent manner (25). In contrast, genetic ablation of *d-ilp* genes causes a development delay and growth retardation (153). These phenotypes are similar to those observed in flies homozygous for a partial loss-of-function mutation in *Drosophila* IR (25).

In vertebrates, IR and IGF-IR are expressed early in fetal tissues (44). IR-A is the predominant IR isoform in fetal tissues, whereas IR-B appears in postnatal life in insulin-target tissues (13). These data suggest that, in fetal tissues, IR-A may play a role in mediating some of the effects of IGF-II. The contribution of IR-A to embryo development has been mainly studied in mice, where IGF-II acts as an IR ligand in the promotion of embryonic growth (154). Mice lacking IR are born with 10–20% growth retardation (154) without apparent metabolic abnormalities; metabolic abnormalities appear after birth. The growth-promoting role of IR in embryos is indicated by studies in mice with combined alterations in various elements of the IGF system. These experiments document that IGF-II induces signals through IR to stimulate embryonic growth. Single mutations that ablate *Ir* function result in embryos that are approximately 80–90% of normal size, whereas single *Igf1r* mutations result in smaller embryos (45% of normal size). Combined ablation of *Ir* and *Igf1r*, however, results in even smaller embryos (30% of normal size). The same “30% phenotype” (155) is brought about by double mutations inactivating *Igf2* and *Igf1r*, but not by inactivating mutations of *Igf1* and *Igf1r*. The latter double mutants have the same phenotype as single *Igf1r* mutants (156), suggesting that IGF-I signals exclusively through IGF-IR. In contrast, the growth retardation observed in *Igf2/Igf1r* double mutants is greater than that observed in *Igf1r* single mutants, indicating that IGF-II signals through an additional receptor besides IGF-IR. Because *Igf2/Igf1r* and *Ir/Igf1r* double mutants have the same phenotype as *Igf2/Igf1r/Ir* triple mutants, the additional receptor for IGF-II is IR. Biochemical evidence that the IR-A is indeed a high-affinity IGF-II receptor (13) supports this conclusion.

The analysis of growth retardation onset in mouse embryos lacking *Ir*, or *Igf1r*, or both indicates that during midgestation [embryonic day (E) 12.5 to 15.5] IGF-IR is the main IGF-II receptor, whereas, starting at about E15.5, the IGF-II/IR interaction becomes quantitatively more important (154).



Unlike mice, humans lacking IRs show more severe intrauterine growth retardation (157–160). Indirect evidence suggests that growth retardation is present as early as 27 wk gestation (161). This discrepancy with *Ir*-deficient mice is probably due to differences in development timing and to a compensatory increase in IGF-IR expression (154). Indeed, rodents are born at a developmental stage corresponding to approximately 26 wk of human gestation. Therefore, the IR-dependent phase of embryonic growth is temporally limited in mouse embryos, whereas it is more extended in humans. This distinction explains why the growth retardation defect in *Ins1/Ins2*- or *Ir*-deficient mice is not as severe as the growth retardation of children with leprechaunism characterized by IR mutations that impair insulin binding.

Moreover, IGF-II expression declines after birth in mice. Therefore, the growth-promoting effect of the IR is mediated by insulin after birth (162). In contrast, IGF-II secretion persists throughout adult life in humans (163), providing an additional element of differentiation between the two species (164).

The IGF system may also influence placental development. Although IGF-I expression is low in the placenta, IGF-II expression is abundant in most species (165). The role of IGF-II in placental development has been confirmed in mice lacking the type 2 IGF receptor (mannose 6-phosphate receptor), which is responsible for IGF-II degradation. These animals have a placental mass that is 25% greater than normal (162). These data suggest an important role for IR-A in mediating the effect of IGF-II on placental development.

Because reduced placental development may result in reduced fetal growth (166), it has been suggested that IGF-II and IR-A may influence fetal growth by promoting normal placental development. This conclusion is supported by the reduced placental and fetal size of the IGF-II knockout mice (155). Accordingly, placental growth is reduced in mice lacking the placental specific *igf-II* gene transcript (postnatal day 0); as a consequence, fetal size is also reduced (167). In contrast, placental weight is normal in IGF-I-deficient mice (156).

IGF-I and IGF-II likely play different roles in placental development and function. Data indicate that IGF-I regulates the differentiation of cytotrophoblast into syncytiotrophoblast (168) and extravillous cells (169). In contrast, IGF-II appears to have a role in regulating nutrient exchange. More specifically, in mice with specific placental IGF-II knockdown, the placenta has significantly reduced diffusional exchange surface area and nutrient permeability (170). The different effects of IGF-I and IGF-II on placental development are compatible with the possi-

bility that IGF-II acts via a different receptor (IR-A) than IGF-IR.

Interestingly, IR-A may contribute to vertebrate fetal development by mediating the growth promoting effects of proinsulin. In several vertebrate species, proinsulin mRNA is first detected before formation of the endocrine pancreas (171) and later in development, in extrapancreatic tissues (172). Although extrapancreatic proinsulin gene expression is much lower than in the pancreas (171), proinsulin mRNA can be detected in the chick embryo as early as d 0.5 of development, (173), as well as in the retinal neuroepithelium at E3 (174). Although proinsulin protein is detected in the three embryonic layers, it is mainly detected in the neuroepithelium (173). Remarkably, the presence of proinsulin can be detected before IGF-I expression (173). Because functional IRs and IGF-IRs are both expressed at early developmental stages (175, 176), it is possible that proinsulin may indeed act via both IR and IGF-IR. Because the only IR isoform expressed in chicken is IR-A (31), this isoform may also act as a receptor for proinsulin, although proinsulin was found to be a weak competitor of  $^{125}\text{I}$ -insulin for binding to IR on IM-9 cells, which exclusively express IR-A (177).

Binding studies in the chick neuroretina revealed that proinsulin may act through IR/IGF-IR hybrids [hybrid receptors (HRs)]. Indeed, in the neuroretina, heterodimeric receptors are found at early stages, when the homodimeric IR was apparently absent. The proportion of HRs decreases and that of homodimeric IRs increases as retinal development proceeds (178). Interestingly, binding-displacement studies in this chick neural tissue revealed that HRs bind not only insulin and IGF-I with similar high affinity but also proinsulin (approximate  $\text{EC}_{50} = 10^{-8} \text{ M}$ ) (178). These data suggest that IR-A hemidimers may confer to HRs the ability to bind proinsulin and to cross-talk with the IGF-IR signaling pathway in the early development of vertebrate embryos.

## B. IR isoforms and cell differentiation

IR isoform switching to predominant IR-B expression has been found to be associated with cell differentiation in several models.

### 1. Adipocyte differentiation

Differentiation of brown preadipocytes into mature adipocytes is associated with a dramatic increase in total IR content and with a marked IR isoform switch from IR-A to IR-B (179). In addition, IR-deficient brown preadipocytes are unable to undergo differentiation. However, excessive IR expression is also associated with the inability to differentiate, suggesting that a high IR:IGF-IR ratio may also inhibit the ability of cells to differentiate (179). Indeed, high



IR levels appear to impair IGF-IR signaling, probably by competing for intracellular substrates (180).

IR isoform switching to IR-B also occurs in 3T3-L1 cells induced to differentiate into adipocytes by dexamethasone (181). In these cells, isoform switching persists up to 8 d after dexamethasone removal, indicating that it directly correlates with cell differentiation. Inactivation of one *Ir* allele by homologous recombination reduced IR expression level by approximately 50% and inhibited the differentiation process (182).

Differentiation of stromal-vascular preadipocytes isolated from rat epididymal white adipose tissue yielded similar results. During preadipocyte differentiation, the proportion of IR-B expression level increases, whereas that of IR-A decreases significantly (183).

Taken together, these results suggest that an increase in the IR-B:IR-A ratio, as well as a certain IR/IGF-IR ratio, is important for adipocyte differentiation.

## 2. Hepatocyte differentiation

Human hepatoblastoma (HepG2) cells, when cultured in standard conditions, express approximately 80% IR-A and show a fetal phenotype, including increased synthesis of  $\alpha$ -fetoprotein. However, in the presence of low serum and dexamethasone, they differentiate and acquire approximately 80% IR-B expression, a percentage similar to that of adult hepatocytes (181, 184). Whether a high IR-B:IR-A ratio is a prerequisite for hepatocyte differentiation remains to be clarified.

## 3. Hematopoietic cell differentiation

Studies in 32D cells have provided further insights into the role of IR isoforms in cell differentiation (145). 32D cells are murine hematopoietic cells that have an absolute requirement of IL-3 for cell survival (185). 32D cells differentiate into granulocytes when shifted from IL-3 to IGF-I, a process that can be monitored by evaluating the expression of myeloperoxidase (MPO) (186). Transfection of 32D cells with an IR-B expression plasmid resulted in MPO mRNA up-regulation, regardless of the presence of ligands, suggesting that IR-B can initiate a differentiation program. This phenomenon was not observed in cells transfected with an IR-A expression plasmid (145). Cotransfection with an IRS-1 expression plasmid inhibited MPO mRNA expression in both IR-A- and IR-B-transfected cells, suggesting that IRS-1 interferes with the IR-driven differentiation program.

## 4. The thyroid cancer model

As mentioned in Section V.C, thyroid cancer occurs in different histotypes with a variable degree of differentiation. IR-A predominance is directly related to the degree of thyroid cancer dedifferentiation (81).

Taken together, these studies indicate a positive correlation between predominant IR-B expression and cell differentiation. These data fit well with the high IR-A:IR-B ratio observed in poorly differentiated cells, both in physiology (embryonic and fetal cells) and in disease (cancer cells). The molecular bases underlying IR isoform switching and cell differentiation are, however, largely unknown.

## C. Role of IR isoforms in aging

Several pieces of evidence suggest that the IGF system is important in the regulation of life span (108) because a variety of biological models indicate that inhibition of insulin/IGF signaling results in increased life span. In *Caenorhabditis elegans* (187), disruption of *daf-2* (the ortholog of the *Ir/Igf1r* gene family) prolongs life by 50% (188). Similar genetic manipulations in *D. melanogaster* result in increased life span (189). Similarly, ablation of *chico* (*Irs1*-like gene) also increases the life span (190).

The IGF system is involved in the control of vertebrate longevity (15, 191, 192) by modulating the levels of antioxidative defense molecules (193). Mice that overexpress GH/IGF-I exhibit 50% life span reduction, and exogenous administration of GH/IGF-I decreases the levels of antioxidative defense molecules (194). In contrast, hemizygous *Igf1r* knockout mice (191) display decreased growth and body weight and increased life span. It is reasonable to suppose that IGF-I may affect life span extension by regulating glucose metabolism because calorie restriction increases life span (195) and reduces plasma levels of GH, IGF-I, and insulin (196). Calorie-restricted animals, dwarf mice, and IGF-I-deficient mice share increased insulin sensitivity (197).

Studies in vertebrates suggest that reduced IGF-I signaling could extend life span in humans. However, in humans, GH and IGF-I deficiency are associated with growth disorders, insulin resistance, increased risk of cardiovascular disease, and atherosclerosis. On the other hand, phenotyping of human centenarians revealed that insulin sensitivity, which is a key feature of long-lived mutant mice (198), is strictly associated with exceptional longevity in humans (199). However, whereas decreased IGF-I levels are associated with increased morbidity and mortality in advanced age, increased IGF-I levels do not promote longevity due to the greater risk of developing certain cancers, including those of the prostate, breast, lung, and colon (200). Therefore, human longevity may be regulated by an optimal IGF system set point (201) that is permissive for optimal insulin sensitivity. A clear-cut interpretation of the role of the IGF system in human longevity has been provided by studies that have identified new nonsynonymous mutations in *Igf1r* in centenarians. These mu-

tations resulted in reduced IGF-I signaling in transformed lymphocytes (202).

These findings suggest a more complex relationship between IGF signaling and longevity in humans. Because insulin and IGF signaling are more convergent in lower animals, longevity in those animals is more directly related to the reduction of common insulin/IGF signaling, regulating both metabolism and growth. Because insulin and IGF signaling have developed more specific and distinct functions in humans, due also to the expression of specific receptor subtypes (see *Section II.A*), human longevity may result from attenuation of IGF signaling (specific growth signaling) and the enhancement of insulin sensitivity (specific metabolic signaling). In this respect, the relative expression of IR-A might contribute to regulate this set point and the predominance of either IR or IGF-IR signal branching.

Indeed, in vertebrates such as rats, advanced age is associated with isoform switching to IR-A (183) and an increased IR-A:IR-B ratio. These changes may contribute to the insulin resistance observed among aged animals, together with other changes, such as decreased IRS proteins. These observations are in accordance with other studies in aged rats, showing an association between insulin resistance/glucose intolerance (203, 204) and decreased IR-B expression in the liver, heart, adipose tissue, and skeletal muscle. It is reasonable to speculate that the same isoform switch may occur in humans with age, although no experimental data are available.

In conclusion, data obtained using experimental models indicate that an increased relative abundance of IR-A and insulin resistance usually occurs in advanced age. Increased IR-A expression may enhance IGF signaling via IR-A/IGF-IR hybrids (184) (see *Section VII.A–B*). In addition, compensatory hyperinsulinemia increases IGF bioavailability by decreasing IGF binding protein (IGFBP)-1 and IGFBP-2 (205). Moreover, *in vitro* data indicate that IR-A activation by IGF-II results in preferential activation of the IRS-2 pathway (13, 206). Brain IRS-2 (207) plays a crucial role in nutrient homeostasis (108), and reduced IRS-2 signaling may result in increased life span (207). Thus, one might speculate that enhanced IRS-2 signaling due to an increased relative abundance of IR-A and increased IGF-II action may play a role in reducing life span in vertebrates.

## V. Insulin Receptor Isoforms in Disease

### A. Insulin resistance and altered IR-A/IR-B ratio: the model of myotonic dystrophy

MD1 has been used as a model to study the factors involved in aberrant IR mRNA splicing and its possible

role in determining insulin resistance. MD1 is a disorder characterized by skeletal muscle abnormalities, such as myotonia, weakness, and atrophy (208). However, several extramuscular abnormalities, including cardiac conduction defects and neuropsychiatric and endocrine abnormalities, are also observed in MD1 patients (208). In particular, these patients show peripheral insulin resistance with glucose intolerance, hyperinsulinemia, and an increased risk of developing type II diabetes (209). As discussed in *Section III.A*, muscleblind proteins that are necessary for inclusion of IR exon 11 are functionally inactivated in MD1 patients (131, 132), thus impairing IR-B expression. Indeed, Savkur *et al.* (210) observed an increased IR-A:IR-B ratio in the skeletal muscle of MD1 patients and provided evidence suggesting that this abnormality may play a role in peripheral insulin resistance.

Similar abnormalities have been observed in myotonic dystrophy type II (MD2), which is caused by accumulation of transcribed but untranslated CCTG expansion and consequent CUG repeat-containing RNA in ribonuclear inclusions (211, 212). As in MD1, the IR-A:IR-B ratio is significantly increased in the muscle of MD2 patients. In both MD1 and MD2 patients, IR abnormalities appear very early and precede the development of dystrophic changes (210, 213).

Taken together, studies on MD1 and MD2 have identified a mechanism of predominant IR-A expression in muscle and other tissues caused by the defective interplay of at least three families of splicing factors. They have also confirmed that predominant IR-A expression in muscle may cause peripheral insulin resistance.

### B. Insulin resistance and type 2 diabetes mellitus: a pathogenic role for differential splicing of IR?

In Western countries, more than 6.5% of the adult population and up to 15% of the elderly population is affected by T2DM. The pathogenesis of T2DM includes a variable degree of insulin resistance in muscle, liver, and fat tissues and increasingly impaired insulin secretion.

Whether an altered balance of IR isoforms is involved in insulin resistance and T2DM is unclear. In contrast with results obtained in MD1 and MD2 patients, Mosthaf *et al.* (3) found reduced IR-A expression in skeletal muscles of T2DM patients compared with control subjects and suggested that the reduced expression of this high-affinity isoform could be pathogenetically associated with insulin resistance and T2DM. Importantly, the reduced IR-A:IR-B ratio found in adipocytes and muscle of T2DM patients was confirmed by some (4, 5, 9), but not all studies (6–8).

To address this discrepancy found in human studies, studies in animal models were performed. In pancreatectomized insulin-resistant diabetic Sprague-Dawley rats, no alterations in *Ir* splicing were observed, compared with

control rats (204, 214), suggesting that diabetes, *per se*, does not alter relative IR isoform abundance.

In contrast, studies performed in spontaneously obese and diabetic rhesus monkeys indicated that hyperinsulinemia is associated with preferential IR-A expression. Indeed, hyperinsulinemic monkeys (either normoglycemic or at early-stage diabetes) were found to express a higher proportion of IR-A in skeletal muscle and liver, compared with the normal controls (normoglycemic and hyperinsulinemic) and late-stage diabetic monkeys (hyperglycemic and hypoinsulinemic) (215, 216). This observation was in accordance with the finding that IR-A expression is necessary for the increased insulin secretion observed in early stages of T2DM because insulin gene transcription by pancreatic  $\beta$ -cells requires IR-A signaling (141).

Increased relative abundance of IR-A has been reported in a T2DM patient with extreme insulin resistance and hyperinsulinemia (217). Whether insulin resistance and hyperinsulinemia *per se*, in the absence of T2DM, are associated with altered IR splicing remains unclear. A study carried out in a small series of obese nondiabetic patients did not find any significant changes in IR isoform expression (7). In contrast with data obtained in monkeys, a study carried out in nondiabetic obese and insulin-resistant Pima Indians found that the relative abundance of IR-A in skeletal muscle was reduced compared with matched non-insulin-resistant controls (218). Moreover, patients with insulinoma, characterized by hyperinsulinemia and non-genetically determined insulin resistance, were also found to have reduced IR-A expression in skeletal muscle compared with controls (219).

It is important to understand IR isoform regulation in nonclassical insulin target tissues of insulin-resistant patients because these tissues may respond with hyperplastic or neoplastic changes (220). Currently available data are not sufficient to resolve this issue. In one study, IR isoforms were measured in granulosa cells of insulin-resistant patients with polycystic ovary syndrome (PCOS) (221). IR-A was predominantly expressed (approximately 80%) in granulosa cells of both normal and PCOS patients. Total IR was significantly higher in granulosa cells of PCOS patients than in controls, despite increased intrafollicular insulin levels in PCOS patients (no down-regulation effect) (221).

A conclusive interpretation of data concerning the role of IR isoform regulation in insulin resistance and insulin secretion in T2DM patients is not possible at the moment. T2DM is a complex and heterogeneous syndrome, and IR splicing can be affected by several variables, including hyperinsulinemia, hyperglycemia, age, disease stage, and genetic alterations underlying T2DM. Interpretation of data is also made difficult by the different models and meth-

odologies used and by the limitation that most studies have not measured total IR content. Although it seems unlikely that altered IR splicing plays a major role in insulin resistance in T2DM, insulin resistance, hyperinsulinemia, and altered glucose tolerance are associated with an increased IR-A:IR-B ratio in certain genetic syndromes, both in animals (spontaneously diabetic monkeys) and in humans (patients with MD1 and MD2). Indeed, when studies in humans were reanalyzed, taking the T2DM stage into account, data appeared to be mostly consistent with those obtained in monkeys (215). However, some data obtained in T2DM, in Pima Indians, and in patients with insulinoma do not fit this model.

With regard to potential explanations for the contribution of an increased IR-A:IR-B to insulin resistance, IR-A has a slightly higher binding affinity for insulin than IR-B, but also a lower signaling potential (222, 223). Moreover, because IR-A and IR-B may heterodimerize, IR-A overexpression can cause a significant reduction in IR-B homodimers and an increase in IR-A/IR-B heterodimers, which have high affinity for IGF-II (215, 224). This shift may result in increased IR availability for IGF-II binding and reduced IR availability for the metabolic effects of insulin.

### C. Aberrant expression of IR-A in cancer

In the last few decades, accumulating evidence has established that IRs are usually abnormally expressed in cancer cells, where they mediate both the metabolic and nonmetabolic effects of insulin. Most recently, it was observed that *Ir* splicing is altered in cancer cells, thus increasing IR-A:IR-B ratio, which profoundly affects the cell response to circulating insulin and IGFs. These observations may have important implications in cancer biology and treatment.

#### 1. Aberrant IR expression in cancer cells

IR expression has been evaluated in a variety of human malignancies. Papa and colleagues (225, 226) found that IRs were overexpressed in a large series of human breast cancer specimens. Mean IR content was more than 6-fold higher in cancer specimens compared with normal breast tissue ( $P < 0.001$ ) (225). Approximately 80% of breast cancer samples had an IR content higher than the mean value  $+2$  SD in normal breast, and approximately 20% had IR values over 10-fold higher than mean value in normal breast (225). Functional studies indicated a higher IR responsiveness to insulin in breast cancer (227) than in normal breast cells.

Further insights into the role of IR overexpression in cancer were provided by data indicating that IR-A is also an IGF-II receptor (13). IR-A was found to be the pre-

dominant IR isoform expressed in a variety of carcinomas, including carcinomas of the breast, colon, and lung (13).

In particular, IR-A was found to be the predominant IR isoform in a panel of breast cancer cell lines (ranging from 64–100% of total IR) and in a series of breast cancer tissue specimens (ranging from 40–80%) (228) (Fig. 4). In contrast, IR-A represented 30–50% of total IR content in normal breast cells and tissue specimens (228). Interest-

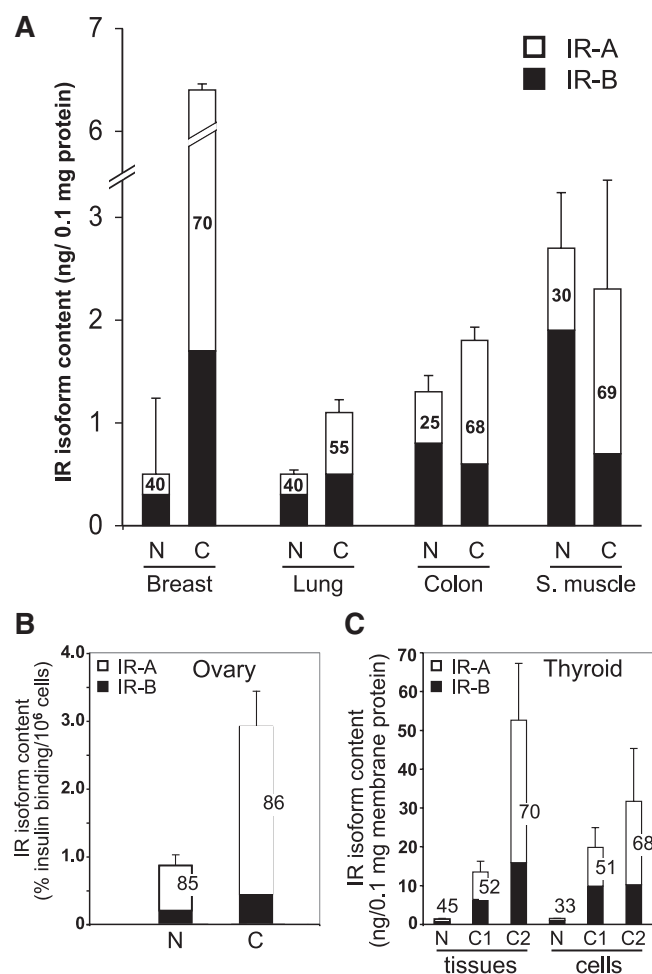
ingly, in several breast cancer cell lines (especially in ER-negative cells), as well as in approximately 40% of breast cancer specimens, IR expression predominates over IGF-IR expression (228, 229). Breast cancer cells produce IGF-II in an autocrine manner. In cells with a high IR-A:IGF-IR ratio, such as the ER-negative breast cancer cell line MDA-MB-157, autocrine production of IGF-II stimulates cell growth through IR-A stimulation. In MDA-MB-157 cells, blocking either IGF-II or the IR markedly inhibited growth, demonstrating the relevance of this loop in cell growth (228).

Both IR and IGF-IR were also found to be overexpressed in well-differentiated thyroid carcinomas (81). In particular, the IR-A:IGF-IR ratio progressively increased in the less-differentiated carcinomas (81). Also, thyroid cancer cell lines, especially when undifferentiated, produce autocrine IGF-II, which can phosphorylate the IR at nanomolar concentrations. The ability of IGF-II to phosphorylate the IR is in close relation with IR-A relative abundance ( $r = 0.628$ ;  $P = 0.0001$ ). Similar data were reported in ovarian cancer cells, in which IR-A is preferentially expressed and mediates mitogenic signaling in response to low doses of insulin and IGF-II (230) (Fig. 4).

The relative contribution of IR-A and IGF-IR to the biological effects of IGF-II was evaluated in thyroid cancer cells, B-CPAP, overexpressing IR-A. In these cells, IGF-II stimulation was similarly inhibited by either an IR-blocking antibody, MA-51, or an IGF-IR-blocking antibody,  $\alpha$ IR3 (81, 231). Combination of the two antibodies was the most effective at inhibiting IGF-II stimulation (81). These results indicate that both IR-A and IGF-IR are involved in mediating the effects of IGF-II.

Taken together, these studies indicate that IR-A is aberrantly expressed in breast and thyroid cancer cells. The IR-A:IGF-IR ratio is substantially increased in ER-negative breast cancer cells and in less-differentiated thyroid cancer cells. The ratio correlates with autocrine IGF-II production. Moreover, IR-A significantly contributes to the biological effects of IGF-II. To fully inhibit the biological effects of autocrine IGF-II, both IR-A and IGF-IR need to be blocked (81).

An important role of the IGF-II/IR-A loop has also been observed in gestational trophoblastic neoplasias, including hydatidiform moles, invasive moles, choriocarcinomas, and placental site trophoblastic tumors (232). These findings are in accordance with the notion that IGF-II plays an important role in normal placental development and is expressed in both hydatidiform moles and choriocarcinomas (17). Both IGF-I and IGF-II stimulated choriocarcinoma cell invasion, although they signal through different receptors: IGF-I through IGF-IR, and IGF-II through IR-A. In JEG-3 choriocarcinoma cells, which pre-



**FIG. 4.** IR isoform content in various cancer tissues (C), compared with the corresponding normal tissues (N). A, Data pertaining to breast, lung, and colon cancer were acquired by analysis of surgical tissue specimens (13). Data on skeletal muscle (s. muscle) were obtained by analysis of human rhabdomyosarcoma cells (148) and were compared with values obtained by analysis of human muscle specimens (our unpublished data). IR isoform content has been calculated by determining the total IR protein content, as measured by ELISA, and the relative IR isoform transcript abundance, as measured by RT-PCR. B, Data from ovaries have been obtained by analysis of transformed and nontransformed cultured cells. IR isoform content has been calculated by determining the total IR protein content, as measured by a binding assay, and the relative IR isoform transcript abundance, as measured by real time RT-PCR (230). Numbers indicate percentage of IR-A isoform expression. C, IR isoform content in surgical specimens and cultured cells of the normal thyroid compared with differentiated (C1) and undifferentiated (C2) cancer (81). IR isoform content has been calculated by determining the membrane IR protein content, as measured by ELISA, and the relative IR isoform transcript abundance, as measured by RT-PCR.



dominantly express IR-A, IGF-II stimulated cell invasion more potently than insulin, although both ligands signaled through IR-A (233). These data are reminiscent of those obtained in leiomyosarcoma cells (148). One possible explanation for the stronger effect of IGF-II on cell migration is its ability to bind vitronectin, a ligand of integrin  $\alpha V\beta 3$  (234), and therefore to integrate different signaling through this pathway.

IR-A overexpression is not limited to malignancies derived from epithelial cells. Both leiomyosarcoma and rhabdomyosarcoma cells were found to express IR-A and IGF-IR in variable amounts, with IR-A often exceeding IGF-IR. These cells also secrete IGF-II. Moreover, the importance of the IGF-II/IR-A loop is recapitulated in SKUT-1 leiomyosarcoma cells that express high IR-A levels and are almost null for IGF-IR. In these cells, IGF-II was able to elicit its biological effects exclusively via IR-A, whereas IGF-I was totally ineffective due to the absence of functional IGF-IR (148). Similar results were reported for solitary fibrous tumors, which are mesenchymal tumors that are frequently associated with hypoglycemia. More specifically, IR-A was constitutively activated, whereas IGF-IR and IGF-I were not expressed (235).

A peculiar and so far unique role of the insulin/IR/autocrine loop in cancer progression has been reported in atypical teratoid/rhabdoid tumors (AT/RT) (236), a group of highly malignant pediatric tumors of the central nervous system (237). Many AT/RT cell lines not only overexpress IR but also produce insulin, which is able to stimulate an autocrine loop that is biologically relevant for cell proliferation. Insulin activates both the PI3K/Akt/mTOR and the ERK pathways. Furthermore, studies with either pharmacological inhibitors or small interfering RNAs indicated that the IR/PI3K/Akt/mTOR pathway is crucial for AT/RT cell proliferation in response to autocrine insulin (236). Although the IR isoform expressed by AT/RT cells was not investigated, it has been previously reported that central nervous system cells predominantly express IR-A (10). This study, therefore, suggests that a unique insulin/IR-A autocrine loop may contribute to cancer cell proliferation and survival.

## 2. Mechanisms of aberrant IR-A expression in cancer

The mechanisms responsible for aberrant IR-A expression in human cancer are largely unknown and may share similarities with the mechanisms operating during embryonic and fetal development, which are also characterized by increased IR expression and increased IR-A:IR-B ratio. As mentioned above (see *Section III.A*), we do not know the molecular mechanisms of tissue-specific and development-driven IR isoform regulation. Similarly, we do not know the mechanisms involved in IR exon 11 skipping in cancer. Alternative IR splicing is only one of the several

examples of alternative splicing that may occur both in human development (238) and in cancer cell “retro-differentiation” (239) due to either mutations or cell stressors, such as hypoxia or altered pH (239). As far as IR is concerned, exon 11 skipping may be regulated by hormonal factors, such as dexamethasone and insulin (181). Increased cancer incidence has been observed in individuals with insulin resistance and hyperinsulinemia, consequent to obesity and/or T2DM (240). However, because contradictory data exist on the role of hyperinsulinemia and IR splicing, it seems unlikely that hyperinsulinemia plays a role in IR exon 11 skipping in cancer.

As far as IR overexpression in cancer is concerned, IR gene amplification seldom occurs, and IR gene rearrangement has not been reported. In 96 primary breast carcinomas with high IR expression, only 8% showed IR gene amplification, and none showed IR gene rearrangement (241).

An important mechanism for IR overexpression in cancer may be p53 protein inactivation. Wild-type p53 specifically acts as a repressor of the IR promoter, as indicated by studies in p53 knockout mice that have a higher liver IR content in respect to controls (42). Inactivating mutations of the p53 gene occur in approximately 50% of all human malignancies (242) and may account for decreased p53 inhibition at the IR promoter. In agreement with this hypothesis, undifferentiated thyroid carcinomas, which frequently carry a mutant p53, have higher IR levels than well-differentiated carcinomas carrying a wild-type p53 gene (81). p53 may be functionally inactivated by nonmutational mechanisms. For instance, high levels of HMGA1 proteins may reduce p53 DNA-binding activity by interacting with the p53 oligomerization domain (243). Actually, HMGA1 levels are low in normal differentiated cells, whereas they are high in embryonic and malignant cells (244). In addition, HMGA1 proteins may directly regulate IR gene transcription (see *Section II.B*). Indeed, HMGA1 proteins interact with two Adenine and Thymine-rich sequences of the IR promoter in a multi-protein complex involving Sp1 transcription factor, CCAAT/enhancer binding protein, and AP-2 transcription factor. All of these factors are required for full transactivation of the IR gene (245), and they may be dysregulated in cancer.

Finally, IR up-regulation is present in breast cancers that have been initiated in transgenic mice by various oncogenes, including Wnt, Neu, and Ret (246).

In conclusion, aberrant IR-A expression is strictly bound to cancer development and progression, both as a cause and an effect.

## 3. Aberrant IR-A expression in cancer: mechanisms of altered signaling and implications for cancer progression

Aberrant IR-A expression may contribute to the dysregulated response of cancer cells to insulin and IGFs in many ways. First, IR overexpression sensitizes cancer cells

to the pleiotropic effects of circulating insulin, especially in hyperinsulinemic patients. Tissue resistance to insulin associated with obesity or T2DM is essentially restricted to metabolic effects, whereas nonmetabolic effects are relatively unimpaired. For instance, hyperinsulinemia in insulin-resistant patients is often associated with increased proliferation of ovary theca cells and keratinocytes, causing PCOS and acanthosis nigricans. Circulating insulin levels in these patients are particularly high (0.2–0.6 nmol/liter), reaching a concentration that is similar to that required for half maximal IR autophosphorylation in breast cancer tissue (227). As already mentioned, the IR is not restricted to mediating metabolic activity; when overexpressed in NIH 3T3 fibroblasts or immortalized human breast epithelial cells at a level similar to that found in some breast carcinomas, IR-A induced a ligand-dependent transformed phenotype, an effect that could be inhibited by an IR-blocking antibody (247, 248). These cells, however, were not able to form tumors in nude mice, suggesting that other factors are required for full malignant transformation. The potential transforming effect of IR is also suggested by the observation that a 24-month treatment of female rats with a AspB10, an insulin analog with enhanced affinity for the IR, induced the formation of both benign and malignant mammary gland tumors (249).

As a second mechanism, IR-A overexpression expands the pool of IGF-I binding sites by forming HRs with the homolog IGF-IR. HRs containing IR-A (HR-A) may bind insulin, although with relatively low affinity (184) (see *Section VII*).

As previously mentioned, a third mechanism favoring IR-driven tumor promotion is the high affinity of IR-A for IGF-II, which is frequently produced by cancer cells.

Moreover, aberrant IR-A expression induces high IR-A:IR-B and IR-A:IGF-IR ratios, causing subtle but biologically significant differences in ligand-stimulated signaling.

As discussed in *Section III.C*, signaling differences between IR-A and IR-B in response to insulin have been previously described (11, 139, 141). IR-A binding to IGF-II is associated with stimulation of growth and cell invasion (13), whereas IR-B, which does not bind IGF-II, is associated with differentiation and metabolic signals (145). On the other hand, a high IR-A:IGF-IR ratio may favor the effects of IGF-II over the effects of IGF-I. Studies in brown adipocytes suggest that alteration of the IR-A:IGF-IR ratio in favor of IR-A may impair the ability of the cell to undergo a differentiation program (179).

Recent epidemiological studies have demonstrated that both T2DM and obesity are associated with an increased risk for many forms of cancer, including cancer of the breast, colon, liver, pancreas, kidney, and others (250,

251). These studies, together with the finding that IR-A is often aberrantly expressed in cancer cells, have strengthened the hypothesis that insulin resistance and compensatory hyperinsulinemia are a major link between diabetes and cancer (240).

Hyperinsulinemia may indirectly contribute to cancer cell proliferation by a variety of mechanisms, including reduced IGFBP-1 and -2 production (with increased availability of IGF-I and IGF-II) and reduced SHBG. The reduction in SHBG increases the sex steroid-free fraction, which, in turn, increases IGF-IR expression in cancer cells, thus providing an additional indirect mechanism for the mitogenic effect of hyperinsulinemia (252–254).

#### **D. IR isoforms and cancer risk in type 2 diabetes patients treated with insulin or insulin analogs**

It is well known that insulin treatment of diabetic patients does not closely mimic endogenous insulin secretion and leads to peripheral tissue hyperinsulinization and liver hypoinsulinization. Although liver cells predominantly express IR-B, most peripheral tissues also express IR-A at a variable degree and may be abnormally stimulated by exogenous hyperinsulinemia. An additional matter of concern is the use of insulin analogs that have been recently developed to improve glycemic control and favor compliance in diabetic patients (255). Today, three short-acting (insulin lispro, insulin aspart, and glulisine) and two long-acting insulin analogs (insulin detemir and insulin glargine) are available for the treatment of diabetic patients (255). Although most of these analogs have been used for over a decade, their long-term safety profile has not been firmly established. Even subtle modifications of the insulin structure may affect receptor specificity and association/dissociation rate, thereby resulting in abnormal signaling and an abnormal mitogenic:metabolic ratio. Both of these mechanisms received experimental support by preclinical studies carried out with the insulin analog AspB10, which was not released for use in humans (256–258). In a variety of cell lines, AspB10 has an increased mitogenic effect (257, 259), a consequence of both concomitant IR and IGF-IR activation (257) and AspB10 slow dissociation from the IR (257, 260). When injected *in vivo*, AspB10 induced mammary tumors in female rodents (261). Studies on commercially available insulin analogs are limited (258, 262, 263). As far as short-acting analogs are concerned, most data indicate that their mitogenic potency is not different from that of insulin, although some divergent data have been reported. For instance, lispro was found to have a slightly reduced affinity for IR-A (264), but an increased (+50%) affinity for IGF-IR, as compared with native insulin (258). This characteristic, however, did not result in an increased mitogenic effect (264). Insulin aspart was reported to give a slight growth

advantage over native insulin to cancer cells (265), whereas insulin glulisine was less potent than native insulin in stimulating growth in nonmalignant MCF-10 mammary cells (266). Moreover, the limited available data do not indicate an increased carcinogenic effect of insulin aspart (data available on [http://www.accessdata.fda.gov/drugsatfda\\_docs/label/2008/020986s0471bl.pdf](http://www.accessdata.fda.gov/drugsatfda_docs/label/2008/020986s0471bl.pdf) or glulisine (266) in mice compared with native insulin.

More controversial data have been published on the long-acting insulin analogs. A higher mitogenic:metabolic ratio of glargine compared with native insulin has been reported (258, 267) and attributed to increased affinity for IGF-IR. Other studies have found only minor differences in the mitogenic effect between glargine and native insulin (268). The other long-acting analog, insulin detemir, which does not have an altered amino acid sequence but is acylated at B29Lys, has been reported to have a reduced mitogenic:metabolic ratio (258) (data also available at: [http://www.accessdata.fda.gov/drugsatfda\\_docs/nda/2005/021-536\\_Levemir\\_pharmr.pdf](http://www.accessdata.fda.gov/drugsatfda_docs/nda/2005/021-536_Levemir_pharmr.pdf)).

While this review was in preparation, four large retrospective studies in humans have addressed the issue of cancer risk in diabetic patients being treated with the long-acting insulin analog glargine (269–272). The effect on cancer risk of insulin detemir, which was introduced only recently, was not addressed by these studies. Three of these studies indicated that treatment with insulin glargine might be associated with a higher risk of cancer than native insulin. However, because of the retrospective, observational characteristics of all three studies, the possible effect of allocation bias and other confounders cannot be ruled out, and they should be regarded as inconclusive. A further small randomized study comparing insulin glargine and neutral protamine Hagedorn (NPH) insulin found no increase in cancer risk associated with the use of glargine (273).

Only limited data are available regarding analog interaction with IR isoforms. Studies have been carried out in cells expressing IR-B (263) or IR-A (258) or variable amounts of the two isoforms (262, 264). In general, only small differences in terms of binding affinity, association, and dissociation were found among native insulin, short-acting insulin analogs, and insulin glargine. We have preliminary data, obtained by analysis of an engineered mouse cell model expressing either human IR-A or IR-B, indicating that long-acting insulin analogs preferentially activate the mitogenic ERK pathway, an effect that is more evident with the IR-A isoform (Sciaccia L, Cassarino M, Genua M, Pandini G, Le Moli R, Squatrito S, Vigneri R unpublished data). The issue of the specific insulin analog effect on IR isoform activation requires further study.

## VI. Possible Implications of the Aberrant IR-A Expression for Cancer Therapy

### A. Role of the IGF system in mediating resistance to anticancer therapies

The crucial role of IGF-IR in promoting resistance to cancer cell killing by conventional anticancer treatments, such as radiation and chemotherapy, is well documented. IGF-IR down-regulation by antisense nucleotides or its inhibition by tyrosine kinase inhibitors increases cancer cell sensitivity to both radiation and chemotherapy in a variety of malignancies (18, 274, 275). Activation of the MEK/ERK pathway or, alternatively, of the PI3K pathway is involved in various cell models of radioresistance (276).

IGF-IR also plays a role in radiosensitivity of patients affected by ataxia telangiectasia (AT) (277), a rare disease resulting from inactivating mutations of the AT mutated (ATM) gene. ATM protein is a sensor of DNA damage and stimulates repair of double-stranded DNA breaks, such as those caused by ionizing radiations (278). Therefore, cells from AT patients are characterized by extreme radiosensitivity. Interestingly, AT cells express low levels of IGF-IR compared with control cells, and IGF-IR forced expression restores radioresistance in AT cells at near normal levels (277). The *Igf-Ir* gene, therefore, is a downstream target of the response pathway of ATM-mediated DNA damage (279). These studies indicate an important role of IGF-IR in several pathways involved in the induction of radioresistance.

So far, studies aiming to evaluate the possible role of IR-A in the regulation of radioresistance and/or resistance to chemotherapy have not been carried out. Given the similarities between IR and IGF-IR regarding both signaling pathways and biological effects, we hypothesize that aberrant IR-A expression in cancer cells may contribute to resistance to both radiation and chemotherapy, especially if the cancer cells have a high IR-A:IGF-IR ratio.

In recent years, a number of approaches have been established to block various growth factor receptors and growth-related signaling pathways in cancer cells. For some of these targeted therapies, a role of the IGF system in mediating cancer resistance has been documented.

#### 1. Therapies targeted to mTOR

The mTOR is a serine/threonine kinase that regulates cell growth and metabolism by affecting multiple pathways involved in ribosome biogenesis, translation initiation, and nutrient uptake (280). When associated with raptor, mTOR forms a complex (TORC1) that induces phosphorylation of p70S6 kinase (p70S6K) and the translation inhibitory factor 4EBP1 (eukaryotic translation initiation factor 4E binding protein 1), thus regulating the



translation of critical mRNAs involved in cell cycle progression and cell proliferation. mTOR is regulated by insulin/IGFs and other growth factors through the PI3K–Akt pathway (281) and is abnormally activated in most cancer cells. TORC1 inhibitors, such as rapamycin and its derivative analogs, have been tested for their anticancer activity. Furthermore, select rapamycin analogs are currently under evaluation in phase I–II clinical trials. Currently available clinical trial results indicate that cancer responsiveness to mTOR inhibitors is variable and somewhat disappointing (282). At least one mechanism of cancer cell resistance to mTOR inhibitors involves Akt activation. Cell pretreatment with an IGF-IR blocking antibody (h7C10) (283) resulted in prevention of Akt activation and improved inhibition of rhabdomyosarcoma cell growth and survival. Treating acute myeloid leukemia (AML) cells with the rapamycin analog everolimus (RAD001) caused IGF-IR-dependent Akt activation in addition to autocrine production of IGF-I (284). Also, in AML cells, coinhibition of the IGF-IR/PI3K/Akt pathway enhanced the antineoplastic effects of the mTOR inhibitor. Whether aberrant IR-A expression in cancer cells may mimic the IGF-IR effect and provide resistance to mTOR inhibitors deserves further study.

## 2. Therapies targeted to the epidermal growth factor (EGF) receptor family

The receptors of the EGF family and their ligands are frequently overexpressed in advanced malignancies and have been implicated in poor prognosis and resistance to chemotherapy. A variety of approaches have been developed for targeting EGF receptor (EGFR) and human EGFR 2/erythroblastic leukemia viral oncogene homolog 2 (HER2/ErbB2), such as blocking antibodies and small molecules with tyrosine kinase-inhibiting activity. However, only a small proportion of cancer patients receive significant benefit from these therapies, because of either primary or acquired resistance to these agents (274, 285). Mechanisms of resistance are various and not fully elucidated. One mechanism may involve increased IGF-IR signaling, as described for breast cancer cells resistant to the anti-HER2/ErbB2 monoclonal antibody, trastuzumab (286), and for colorectal cancer cells resistant to anti-EGFR monoclonal antibody 225 (287). Moreover, in a variety of cell models, IGF-IR also mediates resistance to EGFR tyrosine kinase inhibitors, such as AG1478 (288) and gefitinib (Iressa) (289, 290). In tamoxifen-resistant breast cancer cells, IGF-IR may modulate EGFR phosphorylation via a mechanism that involves c-Src activation (291).

Recently, Jones *et al.* (292) analyzed a human cancer cell line (LoVo) that expresses IR-A and IGF-II but lacks mature IGF-IR and found that IR-A is involved in *de novo*

resistance to gefitinib. Cell exposure to insulin or IGF-II caused EGFR phosphorylation at Tyr845, Tyr1068, and Tyr1173. Treatment with gefitinib had a very small effect on LoVo cell proliferation and caused phosphorylation of both IR-A and Akt. Inhibition of IR-A with a specific inhibitor (ABDP) reduced EGFR phosphorylation and markedly potentiated the antiproliferative effect of gefitinib.

These studies clearly indicate that IGF-IR overactivation is an important mediator of resistance to therapies targeted to receptors of the EGFR family and that IR-A may have a similar role, especially in cells with a high IR-A:IGF-IR ratio.

## B. Role of IR and hyperinsulinemia in resistance to IGF-IR or IGF-targeted therapies

### 1. Therapies targeted to IGF-IR

The most promising approaches to block the effects of IGF-IR in cancer cells include the use of blocking antibodies and small molecules with tyrosine kinase-inhibiting activity. Accumulating *in vitro* and *in vivo* evidence indicate that these therapeutic strategies may indeed inhibit tumor growth and are especially effective at sensitizing cancer cells to conventional anticancer therapies, such as radiation and chemotherapy (293).

Recently, some studies raised the possibility that therapies targeted at IGF-IR may increase IR sensitivity, at least *in vitro* (Table 2). Also, selective IGF-IR down-regulation with small interfering RNAs resulted in increased

**TABLE 2.** Putative mechanisms involving IR, namely IR-A, which may account for cancer resistance to therapies specifically targeting IGF-IR signaling

Mechanism	Effect	Refs.
Typical cancer features		
Aberrant IR-A expression and activated IGF-II/IR-A loop	Enhanced response to IGF-II and insulin	13, 81, 148, 228
Increased IR-A	Enhanced IGF signaling	184, 231, 301
Possible consequences induced by selective IGF-IR signaling blockade		
Increased IR-mediated IRS-1/Grb-2/ERK activity and/or increased IR-mediated Akt activity	Increased IR-A responsiveness	295, 337
Increased IR-A homodimer formation	Increased IR-A responsiveness	294
Increased circulating GH	Compensatory hyperinsulinemia	302



sensitivity to insulin in cultured MDA-435 breast cancer cells (294). In this case, however, IGF-IR down-regulation caused a decrease of IR/IGF-IR hybrids and, as a consequence, reduced sequestration of IR moieties in hybrids and enhanced IR homodimer formation. Similar data were obtained in primary cultures of osteoblasts subjected to conditional disruption of IGF-IR (295). In these IGF-IR knockdown osteoblasts, increased IRS-1 phosphorylation, ERK/Akt activation, proliferation, and glucose uptake were observed in response to insulin. Insulin also induced the expression of several genes downstream the ERK pathway, such as *Glut-1* and *c-fos*, and genes related to angiogenesis, such as *Vegf* and *iNos*. Also, in this case, the hypothesized mechanism was reduced engagement of IR moieties in IR/IGF-IR hybrids and a consequent increase of IR homodimers. These *in vitro* studies suggest that anticancer therapies targeting IGF-IR may have the unwanted consequence of enhancing IR signaling, which may provide an important mechanism of resistance to IGF-IR-targeted therapies and may favor the selection of cancer cell clones with activated IR-A (Table 2).

Phase II clinical trials with anti-IGF-IR antibodies in patients with various malignancies are under way. It is too early to establish whether these treatments induce enhanced IR-A signaling and clonal selection of IR-A over-expressing cells. Preliminary results indicate that the use of anti-IGF-IR antibodies is associated with insulin resistance and hyperinsulinemia. The mechanism(s) involved may be related to increased circulating GH, a consequence of reduced IGF-I feedback at the pituitary level.

Taken together, *in vitro* and *in vivo* studies strongly suggest that a major mechanism of resistance to IGF-IR-targeted therapies in cancer may involve enhanced IR-A homodimer formation and GH-mediated development of hyperinsulinemia, both of which contribute to IR-A activation (Table 2).

Small molecules with tyrosine kinase inhibitory activity selective for IGF-IR have been studied. These therapeutics are intended to avoid inhibition of the metabolic effects of IR. One such therapeutic is picropodophyllin (PPP), a non-toxic cyclolignan found to be a potent inhibitor of IGF-IR, but ineffective on homologous IRs (296). In mice, PPP selectively inhibited and killed transformed cells overexpressing IGF-IR, as well as a variety of cancer cells (296). Mice treated with PPP did not develop hyperglycemia. Rather, serum glucose slightly decreased in PPP-treated animals. This finding is not fully understood. PPP is thought to interfere with phosphorylation at the substrate level, and its selective effect toward the IGF-IR is probably explained by differences of amino acid sequences outside of the activation loop region, which is identical for IGF-IR and IR. To our knowledge, PPP has never been tested in

humans, and therefore its anticancer efficacy, metabolic effects, and adverse effects are unknown. Moreover, selective small molecule inhibitors have the limitation that they leave the IGF-II/IR-A loop intact, which is the principal mechanism of IGF system activation in certain malignancies.

## 2. Therapies targeted to IGFs

As already mentioned, another strategy for blocking the effects of IGF system dysregulation in cancer involves blockade of the IGF-I and IGF-II ligands using antibodies.

Limited data exist pertaining to antibodies that block both IGF-I and IGF-II. Such antibodies have been shown to reduce cancer progression and metastatic spread of prostate and liver cancer in an animal model (297, 298). Using the mouse monoclonal antibody KM1468, which blocks both IGF-I and IGF-II, a dose-dependent inhibition of human prostate cancer metastasis growth was observed in bone, and a marked reduction of liver foci development was observed in animals injected with human colorectal cancer cells. However, this antibody did not block colorectal cancer cell metastases in the lung, which contains fewer IGFs than bone and liver, suggesting that paracrine IGFs may play a relevant role in metastatic cancer spread. Because KM1468 neutralizes only free/bioactive IGFs, it has been speculated that this antibody is active only in the limited area in which free/bioactive IGFs are released by IGFBP (*e.g.*, in the tumor microenvironment). Although this point was not addressed in the animal model, it is expected that reduced free/bioactive IGF-I stimulates feedback activation of pituitary GH secretion, which, in turn, may adversely affect tumor growth and progression by direct stimulation of cancer cells by GH (299) and by causing insulin resistance with compensatory hyperinsulinemia. Stimulation of cancer-expressed IR-A by hyperinsulinemia may induce partial resistance to this treatment (Table 2).

In contrast, selective inhibition of IGF-II should not affect GH secretion, which is under negative feedback by IGF-I. Feng *et al.* (300) have developed three human monoclonal antibodies that specifically recognize IGF-II and do not cross-react with IGF-I or insulin. Treatment with the most potent of these antibodies (m610) inhibits IGF-IR phosphorylation and downstream kinases, Akt and MAPK, with an IC<sub>50</sub> on the order of 1 nmol/liter and inhibits growth of prostate cancer cells and migration of breast cancer cells. The same antibody inhibits IR and IGF-IR phosphorylation induced by IGF-II with approximately the same efficiency. These IGF-II specific antibodies have not been tested in humans and, therefore, their anticancer efficacy is unknown. This strategy seems to be promising in view of the fact that the serum IGF-II concentration in humans is approximately 3-fold higher than

that of IGF-I (700 *vs.* 200 ng/ml, respectively), and given that several malignancies overexpress IGF-II and IR-A.

However, it is expected that antibody efficacy will be variably affected by the presence or absence of autocrine IGF-II and by IGF-IR and IR-A expression levels in malignant cells.

A combined approach using a blocking antibody for IGF-IR and HRs together with a blocking antibody for IGF-II may be the most effective approach. This combined therapy would have the advantage of blocking the activities of IR-A and IR-B in response to IGF-II. It is not expected to block the possible development of insulin resistance and hyperinsulinemia caused by the increased GH associated with the use of anti-IGF-IR antibodies.

### C. Targeting IR-A signaling in cancer

As previously mentioned, aberrant IR-A signaling may represent an important mechanism of resistance to various anticancer therapies and should be considered an important target in cancer therapy. However, generalized IR inhibition would induce insulin resistance, compensatory hyperinsulinemia, and possibly T2DM. One strategy would be to target only IR-A, leaving the metabolic insulin effects in insulin target tissues, which predominantly express the IR-B isoform, relatively unaffected. However, selective immunological blockade of IR signaling is unlikely to be achieved because no isoform-specific antibody is currently available. Furthermore, it is expected that specific antibodies to IR-A will be difficult to obtain.

A possible targeted strategy would be to block aberrant IR-A expression in cancer by inhibiting the splicing process involved in abnormal IR exon 11 skipping. However, the factors involved in this process in cancer are probably multiple and not yet characterized.

An alternative immunological strategy may take into account the abundance of HR-A in cancer cells. Anti-IGF-IR antibodies, recognizing not only IGF-IR homodimers but also HRs, are expected to reduce HR-A signaling. In fact, in cancer cells with a low IR:IGF-IR ratio, most IR moieties are assembled in HRs. In contrast, in cancer cells with a high IR:IGF-IR ratio, the majority of IRs occur as homodimers and not as HRs. In these cells, IR-A will not be substantially blocked by anti-HR antibodies. Double blockade of IGF-IR and HRs is, in any case, advantageous over simple IGF-IR blockade because most IGF-IR occur as HRs. We have previously obtained evidence that the IR:IGF-IR ratio is an important determinant of the cancer cell response to blocking antibodies. In fact, IR blockade was able to inhibit cancer cell proliferation in response to exogenous and/or autocrine IGF-II in cancer cells with a high IR:IGF-IR ratio (81, 228). In these cells, IR and/or HR blockade is often more useful than IGF-IR blockade (301).

Another possible immunological strategy that will inhibit, at least partially, IR-A signaling is the use of IGF-II blocking antibodies. In cancer cells with a high IR-A:IGF-IR ratio, IR-A will be the most important receptor for IGF-II signaling. Importantly, IR-A and IGF-IR have similar affinity for IGF-II (see *previous paragraph* and *Section III.B*).

A different approach to IR-A blocking is based on the use of small molecules with nonselective tyrosine kinase-inhibiting activity for both IGF-IR and IR, such as BMS-554417 (302). At submicromolar concentrations, BMS-554417 inhibits both IR and IGF-IR with similar potency and with 5-fold selectivity over other kinases. However, variable results were obtained with this compound in various cancer cell lines. In mice, BMS-554417 administration induced a small but statistically significant increase in serum glucose, especially after a glucose load. Moreover, serum insulin markedly increased at 2 h after a glucose load in BMS-554417-treated animals compared with control animals ( $67.7 \pm 10.3$  *vs.*  $0.152 \pm 0.08$  ng/ml, respectively;  $P = 0.0001$ ) (302). It is possible that this striking serum insulin increase may overcome IR inhibition in cancer cells overexpressing IR-A, causing tumor resistance to the drug. Moreover, no data on serum GH are available after chronic use of BMS-554417, which is expected to increase serum GH by inhibiting negative feedback of IGF-I on the pituitary.

In summary, the role of IR-A as an important factor for resistance to anti-cancer therapies is just becoming recognized. So far, the attention of researchers has focused on targeting the homolog IGF-IR or IGFs. In light of the recent literature, cancers with a high IR:IGF-IR ratio are unlikely to greatly benefit from this approach. Rather, some evidence suggests that these treatments may increase IR-A signaling and possibly lead to the development of resistant clones. An additional adverse effect of these treatments is the rise of GH with consequent development of insulin resistance and compensatory hyperinsulinemia, which, in turn, can stimulate cancer cell growth. The anti-tyrosine kinase small molecule approach faces a similar problem. If the inhibitors have an elevated selectivity for the IGF-IR, they leave intact or enhance IR-A signaling. In contrast, if they have low selectivity and inhibit IR, they may cause insulin resistance with compensatory hyperinsulinemia.

In any case, future clinical trials using these targeted therapies should be designed to evaluate the effects on IR-A signaling in cancer cells and on circulating levels of GH and insulin. Finally, the efficacy of these therapies should be evaluated in relationship to the IR-A:IGF-IR ratio in cancer cells.

TABLE 3. Receptor subtypes of the IGF system in mammals

Receptor	Homotetramers			Heterotetramers (hybrids)		
	IR-B/IR-B	IR-A/IR-A	IGF-IR/IGF-IR	IR-B/IR-A	IR-B/IGF-IR	IR-A/IGF-IR
Name	IR-B	IR-A	IGF-IR	HIR-AB	HR-B	HR-A
Ligand(s)	Insulin	Insulin IGF-II	IGF-I IGF-II	Insulin IGF-II	IGF-I IGF-II	IGF-I IGF-II Insulin

Variable tetrameric assembly of IR isoforms and IGF-IR moieties confers different ligand binding preferences and different signaling capabilities.

VII. IR Isoforms and Hybrid Receptors

A. IR-A/IR-B hybrids

Both IR isoforms are coexpressed in most cells; therefore, the isoforms are expected to homodimerize (forming IR-A/IR-A and IR-B/IR-B homodimers) and heterodimerize (forming IR-A/IR-B hybrids). It would be important, therefore, to assess the functional characteristics of IR-A/IR-B hybrids (Table 3); however, these studies have been hampered by the lack of adequate methodologies.

Recently, Uhles et al. (142) suggested that *Ir* exon 11 may act as a sorting signal that sorts the two IR isoforms into different lipid raft microdomains of the plasma membrane. This differential localization provides a molecular basis for differential signaling by the two isoforms and should prevent heterodimerization of IR-A and IR-B moieties. It is unclear at which stage this targeting process would operate, but it should occur in the endoplasmic reticulum at a very early posttranslational stage, before dimerization of proreceptors and disulfide bond formation between  $\alpha$ -subunits (303).

Two recent studies using bioluminescence resonance energy transfer (BRET) (304) technology have independently shown that IR-A and IR-B moieties heterodimerize and that IR-A/IR-B hybrids are randomly formed in cells (136, 224). This finding indicates that the previous negative data obtained in a pancreatic  $\beta$ -cell line is not of general relevance.

One of the two studies compared BRET signals from IR-B homodimers and IR-A/IR-B heterodimers and concluded that their EC<sub>50</sub> values for insulin stimulation are not significantly different (136).

The other study (224) showed that IR-A/IR-B hybrids are capable of recruiting intracellular partners upon insulin and IGF-II stimulation with the same affinity as IR-A homodimers. IGF-I also activated IR-A/IR-B hybrids, but with a lower affinity. These data suggest that, in the presence of predominant IR-A expression, IR-B moieties are mostly incorporated into IR-A/IR-B hybrids with the consequence that most insulin binding sites will behave as IGF-II binding sites.

B. IR/IGF-IR hybrids: functional characteristics and the role of IR isoforms

As mentioned above, in cells expressing both IR and IGF-IR, IR hemireceptors may heterodimerize with IGF-IR hemireceptors, leading to the formation of HRs (11, 305–308) (Fig. 5). The existence of HRs was first hypothesized by Kasuga et al. in 1983 (309). Six years later, Soos and Siddle (306) identified HRs from the human placenta, thus confirming their existence. In accordance with their high affinity for IGF-I, HRs have been measured as the proportion of total <sup>125</sup>I-labeled IGF-I that may be immunoprecipitated with an anti-IR antibody. Heterodimerization of the two receptors is due to the high degree of homology between IR and IGF-IR, which ranges from 27 to 84% depending on the region that is compared (310, 311). Heterodimerization is believed to occur with a similar efficiency as homodimerization. Therefore, the proportion of hybrids is a function of the mole fractions of each receptor (49) and the expected proportion of HRs can be calculated as follows: HRs = 2√IR√IGF-IR (49, 229). According to this model, in a study carried out in differentiated 3T3-L1 adipocytes, a marked IR increase caused most IGF-IR hemidimers to form HR rather than IGF-IR homodimers. In these cells, IGF-I fully stimulated glucose uptake through IR  $\beta$ -subunit activation (312). However, in some cancer tissues, an HR content higher than predicted has been observed (229), suggesting that unknown

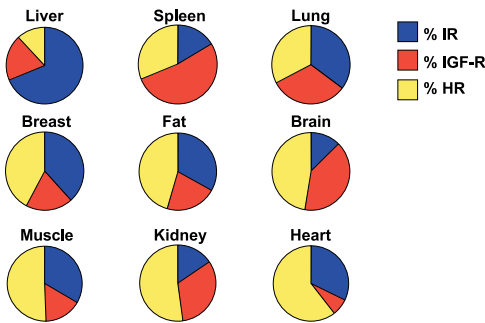


FIG. 5. Expression of IR (blue), IGF-IR (red), and HRs (yellow) in rabbit tissues. Hybrid receptor content was determined by polyethylene glycol assay, as the aliquot of <sup>125</sup>I-IGF-I radioactivity that was immunoprecipitated by an anti-IR antibody (49). In most tissues, HRs represent approximately one half of the total amount of IGF system receptors present in the cell.



factors may modulate the assembly of either homodimers or heterodimers.

The physiological role of HRs is still unclear. Studies in cells are complicated by the concomitant variable expression of IRs and IGF-IR with HRs and by the unavailability of specific antibodies recognizing only HRs (11, 305, 308, 313, 314). Moreover, affinity chromatography-purified HRs may have altered functional characteristics and are often contaminated with variable amounts of both homodimeric IR and IGF-IR. Early studies carried out with purified HRs indicate that these receptors mostly bind IGF-I and that they bind insulin with a much lower affinity (305) (Table 3).

When hybrids composed of intact IGF-IR or IR hemidimers plus kinase-inactive IR hemidimers were prepared, both insulin and IGF-I stimulated phosphate incorporation into both  $\beta$ -subunits to a similar extent (315), providing evidence that HR autophosphorylation occurs by intramolecular transreaction independent of which hemireceptor  $\alpha$ -subunit is ligand-occupied. Others have confirmed these findings, although IGF-I was found to be more efficient than insulin (307, 316–318).

At variance with homodimeric receptors, HRs have peculiar binding properties. When labeled IGF-I was used as a tracer, binding was displaced by low IGF-I concentrations, but only by high insulin concentrations. In contrast, labeled insulin bound to HRs was displaced by low concentrations of both insulin and IGF-I, with IGF-I being more effective. These data are consistent with a model in which IGF-I allosterically inhibits insulin binding to HR via interaction with the IGF-I hemidimer  $\alpha$ -subunit. Similar data were obtained by Soos *et al.* (305), who found high affinity binding to HRs by both insulin and IGF-I, but a limited ability of insulin to displace labeled IGF-I. Labeled insulin, in contrast, was displaced by both insulin and IGF-I (305).

Further studies were designed to evaluate HR characteristics according to whether they incorporate IR-A or IR-B hemidimers. First, experiments carried out in transfected cells indicated that both IR-A and IR-B are able to form hybrids with IGF-IR with the same efficiency (136, 184, 319) and in close agreement with the random assembly model (49, 229). Therefore, the proportion of HR-A (HR containing IR-A hemidimers) or HR-B (HR containing IR-B hemidimers) depends on the relative abundance of the two IR isoforms (Table 3).

To address the functional characteristics of HR-A and HR-B, we studied transfected cells expressing similar amounts of either HR-A or HR-B (184) and evaluated ligand-stimulated receptor autophosphorylation. Experiments were carried out in the presence of a molar excess of an IR-blocking antibody to avoid interference by the ho-

modimeric IR. We found that IGF-I, IGF-II, and insulin were able to stimulate HR-A phosphorylation, although insulin was less effective. In regard to HR-B phosphorylation, IGF-II and insulin were much less effective than IGF-I. We also found that all three ligands, including insulin, were able to induce *in vitro* phosphorylation of specific IGF-IR substrates, such as Crk-II, when binding to HR-A (184). In contrast, in cells expressing HR-B, only IGF-I and IGF-II, but not insulin, were able to phosphorylate Crk-II. Indeed, available studies indicate that Crk-II, a SH2-SH3 adapter protein, is phosphorylated *in vitro* only by IGF-IR tyrosine kinase and not by IR (320). When the binding abilities of HR-A and HR-B were measured in competition-inhibition experiments using HRs that had been immunocaptured with 83-7, an anti-IR antibody recognizing HRs, both IGF-I and IGF-II displaced  $I^{125}$ -IGF-I binding. For HR-A, the  $ED_{50}$  values were 0.5 and 0.7 nM for IGF-I and IGF-II, respectively, whereas for HR-B, they were somewhat lower, especially for IGF-II ( $ED_{50} = 2.5$  and 15.0 nM for IGF-I and IGF-II, respectively). Insulin was able to displace  $I^{125}$ -IGF-I from HR-A ( $ED_{50} = 3.7$  nM), but not from HR-B ( $ED_{50} > 100$  nM insulin) (184). These studies suggest that HR-A could be considered a low specificity receptor, which may be activated by high-affinity ligands, IGF-I and IGF-II and, under certain conditions (*e.g.*, hyperinsulinemia), by the low-affinity ligand, insulin (184).

Two recent studies addressed HR-A and HR-B ligand specificity (136, 319) and found that both HR subtypes have a very low affinity for insulin. Relevant differences in the calculation of  $ED_{50}$  values and in the displacement efficiency of either IGF-I or IGF-II toward the  $I^{125}$ -IGF-I tracer in competition-inhibition experiments in the two studies were reported. The reasons for these discrepancies are unclear and may reflect differences both in the assay procedure and in the cell models that were used (136, 184, 319). The most important difference may be our use of transfected R<sup>-</sup> cells, which are devoid of endogenous IGF-IR, whereas the other two studies used transfected CHO (hamster) cells, in which endogenous hamster IGF-IR homodimers may be captured by the anti-IR antibody that is used to immunopurify HRs (321). Moreover, subtle changes in posttranslational processing may occur in different cell types after transfection with the human IR and IGF-IR cDNAs. In this regard, an interesting model is presented by the developing chick neuroretina (178, 322), where both IR and IGF-IR coexist, but IGF-IR is the predominant receptor. Therefore, in this model, most IRs occur as HRs. Because the chick only expresses the IR-A isoform, only HR-A is present. In this model, whereas IGF-I bound mostly to IGF-IR homodimers, insulin bound



preferentially to HR, which had similar binding affinity for insulin and IGF-I (178).

In summary, available data indicate that both HR-A and HR-B bind IGF-I with high affinity. Some, but not all reports indicate that, by binding to HRs, both IGF-I and insulin may activate autophosphorylation of IR and IGF-IR  $\beta$ -subunits, suggesting that the signaling pathway activated by HR is unique. Whether the IGF-II binding affinity for HRs is similar or lower than that of IGF-I is unclear. IGF-I is able to displace insulin, whereas the opposite does not hold true for HR-B, and it is a matter of discussion for HR-A. As a consequence, whether HR-A functions as a receptor with broader binding specificity than HR-B awaits further study.

### C. IR/IGF-IR hybrids and cancer

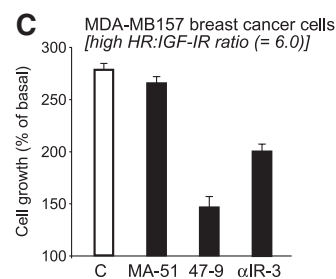
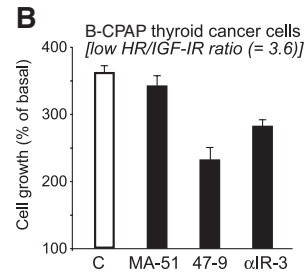
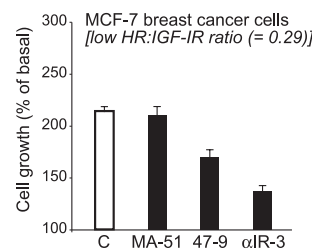
Most human cancers overexpress both IGF-IR and IR (82, 229, 323). Therefore, it is reasonable to expect that they also overexpress HRs. In the majority of breast cancer specimens (>75%), HRs exceeded IGF-IR in terms of content (229). Upon IGF-I stimulation of breast cancer cells overexpressing HRs, HR autophosphorylation exceeded IGF-IR autophosphorylation, suggesting that most of the IGF-I effect was mediated by HRs. In breast cancer, the measured content of HRs was directly related to the molar ratio of both IRs and IGF-IRs, suggesting that HR formation occurred by random assembly of IR and IGF-IR moieties.

Cell growth studies with specific monoclonal antibodies blocking either HRs or IGF-IR homodimers indicated that, in a given cell type, the IGF-I mitogenic effect occurred predominantly via the receptor type that was more abundant. Thus, an antibody to IGF-IR was a stronger growth inhibitor in breast cancer cells with a low HR:IGF-IR ratio (229) (Fig. 6A). In contrast, an HR blocking antibody markedly inhibited growth in thyroid and breast cancer cells with high HR:IGF-IR ratios (Fig. 6, B and C). When MDA-MB-231 breast cancer cells, which are characterized by a high HR:IGF-IR, were xenografted in mice, a more potent antitumoral response was obtained with h7C10, a monoclonal antibody with neutralizing activity against both IGF-IR and HRs, as compared with antibodies targeting solely IGF-IR or HRs (301) (Fig. 6D).

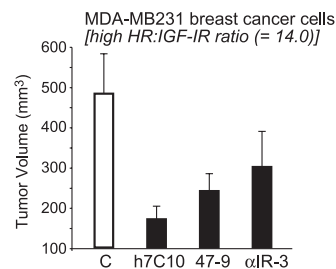
Because both IR-A and IR-B can form hybrids with IGF-IR with the same efficiency (184), cancer cells overexpressing IR-A are expected to overexpress HR-A.

In thyroid carcinomas, IR-A and, consequently, HR-A are expressed in poorly differentiated histotypes (81, 231). As mentioned above, in these cancer cells, an antibody with blocking activity against both HRs and IGF-IR is a more potent antiproliferative agent than a selective anti-IGF-IR antibody (231) (Fig. 6B). In thyroid cancer specimens, the measured HR content often exceeded HR content calculated on the basis of the random assembly model,

### A In vitro



### D In vivo



**FIG. 6.** Effect of IGF-IR or HR targeting in cancer cells with different IGF-IR:HRs ratios. Human breast cancer cells, MCF-7 (A) or MDA-MB157 (C), and papillary thyroid cancer cells, B-CPAP (B), were incubated with IGF-I (10 nM) in the presence of an unrelated antibody (control) or in the presence of antibodies inhibiting IGF-IR ( $\alpha$ IR-3), IR (Ab MA-51), or both IR and HRs (Ab 47-9). Cell growth was most greatly inhibited by blocking IGF-IR in MCF-7 cells (high IGF-IR:HRs ratio), whereas it was most greatly inhibited by blocking HRs in MDA-MB157 and B-CPAP cells (both with low IGF-IR:HRs ratios) (229, 231). D, Antitumor activity of antibodies that inhibit IGF-IR with poor (Ab  $\alpha$ IR3) or high affinity (Ab h7C10) for HRs as compared with an antibody targeting both IR and HRs (Ab 47-9) using an established xenograft tumor model. Athymic nude mice engrafted with MDA-MB-231 cells were treated for 26 d with a loading dose of 1 mg of antibody. The control group received PBS. Ab h7C10 significantly inhibited tumor growth, whereas Ab  $\alpha$ IR3 showed significant minor activity. Ab 47-9 had intermediate activity on tumor growth (301).

suggesting the presence of mechanisms favoring HR over homodimer assembly (231).

In prostate cancer cells, HR formation is favored by nongenomic activity of both androgen and estrogen re-

ceptors, both of which selectively up-regulate IGF-IR but not IR (252, 253). Although IGF-IRs were similarly expressed in benign prostate hyperplasia and cancer tissues, IRs and HRs were more intensely expressed in prostate cancer tissues. In addition, IR and HR expression increased with Gleason score (324), suggesting that the HR:IGF-IR ratio is increased in advanced prostate carcinomas.

High IR-A and HR-A expression levels were also found in human myosarcomas (148) and osteosarcomas (325), which are malignancies that produce autocrine IGF-II. In patients with osteosarcoma, tumor-derived circulating IGF-II was significantly associated with decreased disease-free survival. Simultaneous inhibition of IR-A, HRs, and IGF-IR proved to be a more efficient strategy than selective IGF-IR inhibition (325).

Recently IR-A, IR-B, and HRs were found to coexist with IGF-IR in human papillomavirus-positive cervical cancer cells (326). Although these receptors were found to mediate an IGF-I antiapoptotic effect, full understanding of the biological significance of HRs in these cells requires further study.

In conclusion, a well-defined finding of these studies is that HRs, especially HR-A, should be taken into account for analyses of therapies designed to target the effects of IGFs in cancer.

#### D. IR isoforms in the regulation of the IGF system

Available data on the functional characteristics of IR isoforms and *Ir* splicing regulation in physiology and disease suggest the hypothesis that a major physiological role of *Ir* splicing is to provide an additional step for IGF system regulation. The insulin/IGF-I signaling pathway is a conserved pathway from yeast to mammals. However, noticeable differences exist between the invertebrate and vertebrate due to an increased number of ligands and receptors (192). Coevolutionary analysis of receptor and ligand transcripts across different species indicates that the IR has a higher coevolutionary relationship with insulin than with IGF-I or IGF-II. Likewise, IGF-IR has a higher coevolutionary relationship with IGF-I than with insulin (327). Interestingly, both IR and IGF-IR share a similar and relatively lower evolutionary relationship with IGF-II (327).

These studies suggest that evolution has separated signaling pathways devoted either to metabolism regulation (insulin/IR) or growth regulation (IGF-I/IGF-IR) but has conserved some cross-talk between the two pathways (IGF-II/IR-A, IGF-II/IGF-IR). By increasing IR-A abundance, the growth pathway is enhanced by various mechanisms. The first mechanism is represented by IGF-II binding to IR-A. The second mechanism is activated by IGF-II binding to IR-A/IR-B hybrids, which may have similar binding characteristics as IR-A homodimers (328). In this

case, IGF-II would induce simultaneous phosphorylation of IR-A and IR-B  $\beta$ -subunits. The third mechanism, by which IR-A may enhance the growth pathway, is through formation of HR-A, which may have increased ligand affinity compared with HR-B. Although the increased affinity of HR-A for insulin has been questioned (136), this putative characteristic of IR-A may have considerable relevance because it provides an explanation for activation of the IGF-IR pathway by insulin (184) in hyperinsulinemic patients.

Taken together, these data indicate that *Ir* exon 11 skipping and increased IR-A relative abundance may provide a method by which to enhance the biological effects of IGF-II and favor cross-talk between the IR and IGF-IR signaling pathways, mechanisms that appear to play a role in embryogenesis and fetal development. Conversely, *Ir* exon 11 inclusion and consequent increased relative abundance of IR-B leads to reduced exposure to IGF-II and favors the specific metabolic effect of insulin in differentiated target tissues.

### VIII. Summary, Conclusion, and Perspectives

#### A. The physiological role of IR isoforms

The physiological role of the two IR isoforms is not completely established. Their physiological roles are likely based on their different binding affinities for IGF-II, rather than on their slightly different binding affinities for insulin. Low-specificity receptors, such as IR-A and perhaps HR-A, that are able to bind insulin and IGFs are important for mediating growth and cell metabolism during embryogenesis and fetal life, resembling the promiscuous ancestral receptor of invertebrates. It is reasonable to assume that IR-B, which is predominantly expressed at high levels in differentiated insulin target tissues and selectively binds insulin, mediates metabolic effects in a tissue-specific manner, in relation to the enzymatic machinery for nutrient utilization. On the other hand, it is relatively unclear why IR-A is expressed at variable levels in adult differentiated tissues. It may maintain a “trophic” effect by mediating the effects of both circulating and locally produced IGF-II.

In any case, the fact that mammals have acquired a new *Ir* exon and the ability to skip it by alternative splicing in a developmental and tissue-specific manner suggests that alternative splicing is employed to regulate the IGF system by fine-tuning of ligand specificity.

#### B. Implications for type 2 diabetes and associated disorders

Studies that have aimed to evaluate whether IR isoform regulation could be associated with insulin resistance and T2DM have yielded inconsistent results, possibly because

T2DM is a heterogeneous and complex disease with variable levels of insulin resistance. Patient age and body mass index, as well as drug therapies, might also influence IR isoform expression. Given this level of complexity, we believe that available data are insufficient to draw a firm conclusion on the role, if any, of IR isoforms in diabetes and insulin resistance. Studies in pancreatic  $\beta$ -cells showing that IR-A promotes insulin gene transcription, whereas IR-B promotes  $\beta$ GK gene transcription, would support a possible role of IR isoforms in type II diabetes development.

Whether IR-A and HR-A may be aberrantly expressed in micro- and macrovessels of diabetic patients, contributing to micro- and macrovascular complications, remains an experimental hypothesis that may be worth testing in future studies.

### C. Implications for oncology

Strong evidence suggests that most common malignancies are associated with subtle derangements of the IGF system that are caused by drastic changes in nutrition habits and lifestyle. Systemic disorders, such as obesity, diabetes, and metabolic syndrome, are associated with an increased risk for cancer (240, 250, 251, 329), whereas weight control is associated with a decreased cancer risk (330, 331). Hyperinsulinemia, which is a common characteristic of all of these conditions, seems to be the predominant pathogenetic factor associated with cancer (59, 332–334). The recognition that IR-A and HR-A are aberrantly expressed in cancer cells has provided a framework for better understanding of the cancer-promoting effects of hyperinsulinemia. Moreover, both insulin and IGFs synergize with sex steroids in the promotion of sex steroid-sensitive tumors (254, 335, 336).

Taken together, these studies underscore the utility of preventing the development of obesity and T2DM and consequent hyperinsulinemia as an effective cancer prevention strategy.

As far as cancer therapy is concerned, available evidence indicates that normalization of insulin levels through weight control or insulin sensitizers may improve a cancer prognosis.

It is known that IRs are overexpressed in many cancers and that IR-A is often the prevalent IR isoform in tumors. Aberrant IR-A expression is more pronounced in dedifferentiated cancer and, therefore, IR-A and HR-A overexpression in cancer may be an important factor for tumor resistance to anticancer therapies, including therapies targeting the IGF-IR.

### D. Perspectives

Many questions pertaining to IR isoforms remain unanswered, especially with regard to their physiological role and the role of IR-A expression in adult differentiated cells. Whether IR isoforms are located in different membrane subdomains and whether they elicit different signaling pathways in response to insulin remains to be better established. In addition, the possible role of IR isoforms in the regulation of tissue-specific insulin sensitivity remains to be clarified. Clearly, more work is needed to understand the binding affinity of IR isoforms and HRs for synthetic insulin analogs (especially long-acting analogs) used in the treatment of diabetic patients. It is now clear that modifications of the insulin structure may differentially affect both the binding and intracellular signaling of insulin analogs.

There is also an urgent need to fully understand the mechanisms that lead to aberrant IR-A overexpression in cancer cells and the possible ways to block it to overcome IR-A-dependent tumor progression and resistance to anticancer drugs.

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