

Heterotrimeric G Proteins and the Single-Transmembrane Domain IGF-II/M6P Receptor: Functional Interaction and Relevance to Cell Signaling

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Abstract The G protein-coupled receptor (GPCR) family represents the largest and most versatile group of cell surface receptors. Classical GPCR signaling constitutes ligand binding to a seven-transmembrane domain receptor, receptor interaction with a heterotrimeric G protein, and the subsequent activation or inhibition of downstream intracellular effectors to mediate a cellular response. However, recent reports on direct, receptor-independent G protein activation, G protein-independent signaling by GPCRs, and signaling of nonheptahelical receptors via trimeric G proteins have highlighted the intrinsic complexities of G protein signaling mechanisms. The insulin-like growth factor-II/mannose-6 phosphate (IGF-II/M6P) receptor is a single-transmembrane glycoprotein whose principal function is the intracellular transport of lysosomal enzymes. In addition, the receptor

also mediates some biological effects in response to IGF-II binding in both neuronal and nonneuronal systems. Multidisciplinary efforts to elucidate the intracellular signaling pathways that underlie these effects have generated data to suggest that the IGF-II/M6P receptor might mediate transmembrane signaling via a G protein-coupled mechanism. The purpose of this review is to outline the characteristics of traditional and nontraditional GPCRs, to relate the IGF-II/M6P receptor's structure with its role in G protein-coupled signaling and to summarize evidence gathered over the years regarding the putative signaling of the IGF-II/M6P receptor mediated by a G protein.

Keywords G protein-coupled receptor · IGF-II/MGP · Heterotrimeric G protein

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Introduction

The family of classical G protein-coupled receptors (GPCRs) constitutes the largest class of cell-surface receptors with an essential role in almost all physiological processes in both mammalian and nonmammalian species. These receptors are recognized and bound by a diverse category of ligands, including odorants, taste ligands, light, metals, nucleotides, lipids, photons, ions, biogenic amines, amino acids, proteins, and peptides [1–5]. Current estimates indicate that more than 800 genes within the mammalian genome code for GPCRs, some of which still remained orphaned, with no known ligand or function. Given the association of GPCRs to a broad range of physiological functions, this family of receptors represents one of the most important drug targets for the pharmaceutical industry. Indeed, by some estimates, nearly 45% of the marketed drugs are known ligands of

approximately 30 members of the GPCR family [2, 6]. To fully exploit therapeutic potential further, considerable effort is being made to identify cognate ligands for the remaining GPCRs and to characterize their functional relevance in human physiology.

The main structural characteristic of GPCRs is a seven-transmembrane-helix core domain that is capped on the extracellular side by a ligand-binding domain and on the cytoplasmic side by a domain that interacts with heterotrimeric G proteins composed of α , β , and γ subunits. The $G\alpha$ subunit binds to and hydrolyzes guanosine 5'-triphosphate (GTP), whereas the $G\beta\gamma$ subunits form an undissociable functional unit. In the resting state, the $G\alpha$ subunit is bound to guanosine 5'-diphosphate (GDP) and is associated with the $G\beta\gamma$ subunit complex. Upon ligand binding, a conformational change is induced within the intracellular domains of the receptor, which promotes receptor interaction with the heterotrimeric G protein [1, 3, 4]. Subsequently, GDP on the $G\alpha$ subunit is exchanged for GTP, triggering a conformational change in the heterotrimer that results in dissociation of the GTP-bound $G\alpha$ subunit from the $\beta\gamma$ subunits. The released G protein subunits then either positively or negatively regulate a diverse array of effector enzymes and ion channels, leading to a cellular response to the ligand-initiated signal [1, 2, 7]. It has now become clear that in addition to the GTP-bound $G\alpha$ subunit, free $\beta\gamma$ subunits can also bind to and regulate the activity of a great variety of effector molecules. Signaling is terminated after hydrolysis of GTP to GDP by intrinsic GTPase activity of the $G\alpha$ subunit. The resulting GDP-bound inactive $G\alpha$ subunit undergoes a conformational change that allows it to reacquire affinity for the $G\beta\gamma$ subunits, and the heterotrimer thus returns to the basal state, ready to respond to a new cycle of receptor binding. Each receptor can activate a large number of G proteins before the signal is terminated by receptor internalization. All GPCRs use the same basic mechanism to act on a wide spectrum of signal transduction pathways in mediating a variety of cellular responses [3–8]. Interestingly, however, recent data obtained from cross-linking and fluorescence resonance studies indicate that dissociation of the G protein subunits may not be required for downstream signaling by the GPCR [5, 9].

The heterotrimeric G protein subunits, which interact with effector molecules to transduce extracellular signals into cellular responses, display significant homology in both their primary sequence and tertiary structure. To date, 27 distinct $G\alpha$ subunits, 5 forms of $G\beta$ subunits, and 14 forms of $G\gamma$ subunits have been cloned and characterized [2, 7]. The various permutations of $G\alpha$, $G\beta$, and $G\gamma$ subunit combinations provide a large diversity for signaling via heterotrimeric G proteins. G proteins are classified into four families, Gs, Gi/o, Gq, and $G_{12/13}$, based on the sequence homology of the α subunits and their associated effects on a

selective effector [7, 10, 11]. In general, G α s proteins activate, whereas G α i proteins inhibit, adenylyl cyclase (AC) activity and modulate cAMP levels, although both families can also regulate src tyrosine kinases and phosphodiesterases. Stimulation of G α q proteins, on the other hand, can activate phospholipase C β (PLC β) and increase protein kinase C (PKC) activity, whereas $G_{12/13}$ proteins can mediate signals by activating Rho GTPases and proteins from the ezrin/radixin/moesin family [7, 12, 13].

In addition to the various $G\alpha$ protein subunits, $G\beta\gamma$ dimers can also mediate signaling by regulating the activity of PLC β , AC, potassium channels, Cav $_2$ calcium channels, and phosphoinositide 3'(PI-3)-kinase γ . Some recent evidence indicates that the $G\beta$ subunit plays a critical role in determining the specificity of signaling induced by the $G\beta\gamma$ complex [3, 4, 7, 14]. It is also of interest to note that although most GPCRs are preferentially coupled to a certain subfamily of G proteins, they can activate other classes of G protein with reduced efficiency. Given the diversity of G protein subunits and downstream effector molecules, the pattern of responses of a cell/tissue to a particular GPCR can be complex. The specificity of the cellular response to GPCR stimulation depends on the G protein heterotrimers recognized by the receptor, specific effector molecules expressed in the cells/tissue, and the relative concentrations of the various components in the signaling pathways [3, 7, 14, 15]. Additionally, as the modulation of second messengers often results in measurable intracellular/biochemical changes such as alterations in cAMP or inositol 1,4,5-trisphosphate (IP $_3$) levels, it is possible to screen the specific receptor-G protein coupling using both functional and nonfunctional assays.

Characterization of GPCRs

Over the years, several methods, ranging from simple receptor ligand-binding assays to high-throughput technologies, have been developed to characterize receptor–protein interactions. More recently, the advancement of high-resolution visualization techniques has provided an additional tool to view the *in vivo* effects of agonist stimulation on GPCRs [1, 3, 5, 6, 16, 17]. Some of the basic procedures that are typically used for the characterization of several GPCRs are based on the ligand-induced activation of the $G\alpha$ protein and its interaction with GTP analogues.

Receptor-binding Assays Some of the most straightforward procedures for determining a putative receptor-G protein interaction are receptor-binding assays performed in the presence of nonhydrolyzable GTP analogues such as GTP γ S and Gpp(NH)p, which act to permanently activate the targeted G protein and thereby promote a reduction in affinity of ligand/receptor-binding. In this approach, tissue/

cells or plasma membrane preparations incubated with radiolabeled or fluorescently labeled ligands in the presence of increasing concentrations of nonhydrolyzable GTP analogues show a dose-dependent decrease in the binding of the ligand to the receptor if the receptor does indeed interact with a G protein. In addition, the general subclass of G protein associated with a given receptor can also be determined by examining ligand-binding profiles in the presence of different G protein-selective toxins, such as *Bordetella pertussis* toxin (PTX, which inhibits Gi proteins) and cholera toxin from *Vibrio cholerae* (CTX, which affects Gs proteins) [4, 16, 17]. More recently, the [³⁵S]GTPγS-binding assay has been used to measure the level of G protein activation after agonist occupation of a GPCR. In this assay, [³⁵S]γGTPS replaces endogenous GTP and binds to the Gα subunit after activation of the receptor to form a Gα-[³⁵S]γGTPS complex. Because the γ-thiophosphate bond is resistant to hydrolysis by the GTPase of Gα, the G protein is prevented from reforming as a heterotrimer, and thus, [³⁵S]γGTPS-labeled Gα subunits accumulate and can be measured by counting the amount of [³⁵S]-label incorporated [18–20]. A nonradioactive GTPγS-binding assay, using europium (Eu)-labeled GTP derivatives in which the amount of Eu-GTP remaining after filtration is quantified by time-resolved fluorometry, has also been developed for a variety of GPCRs [21].

Biochemical/structural Assays Another experimental approach that is used to investigate G protein–receptor coupling is the examination of their physical interaction. This can be done by performing co-immunoprecipitation experiments, in which the receptor protein is pulled down from the tissue homogenates using a receptor-specific antibody and then probed by Western blotting for an associated G protein [22–24]. Although these experiments are useful in recognizing the G protein subclass (e.g., Gs, Gi, Gi2, etc.) associated with a specific GPCR, this procedure cannot conclusively determine a direct physical interaction between the two proteins. To resolve this issue, fluorescence resonance energy transfer (FRET) and bioluminescence resonance energy transfer assays, based on the principle of resonance energy transfer between chromophores carried by two moieties/proteins residing within 100 Å of each other, have been developed [17, 25–27]. Both techniques have been successfully used to study GPCR oligomerization, as well as to demonstrate GPCR interactions with associated kinases and β-arrestins in living cells [13, 17, 28–30]. Although studies involving a direct demonstration of interaction of a GPCR with G proteins have not yet been published, GPCR-mediated dissociation of the Gα and Gβ subunits has been investigated using FRET [31, 32]. More recently, Hoffman et al. [33] have developed the use of fluorescein arsenical hairpin binder-

based FRET assay, using a smaller fluorescent moiety that interferes less with normal GPCR functioning during imaging, to determine GPCR activation. The continued development of new technologies will undoubtedly improve the resolution and real-time examination of G protein–receptor interactions in living cells.

Functional Assays Another way in which receptor–G protein interactions may be measured is to assess the functional outcome of receptor stimulation/antagonism using second messenger or reporter gene assays. For example, intracellular cAMP levels, which are modulated by Gi/Gs proteins, can be measured using a variety of methods including anti-cAMP antibody-mediated competition assays, forskolin-stimulated agonism/antagonism assays, reporter gene assay systems, time-resolved fluorescence, and amplified luminescence proximity assays [13, 34–40]. Other assays used to measure GPCR function include commercially available radioligand kits, which detect changes in IP₃ production after GPCR-initiated activation of PLC activity, as well as melanophore-based pigment dispersion/aggregation assays, which reflect the activation of AC or PLC [41]. Alterations in the flux of intracellular calcium, as measured by Ca²⁺-sensitive fluorescent dyes, bioluminescent indicators, or reporter gene assays, can also be used as a GPCR screening technique [13, 42, 43]. Clearly, the choice of appropriate functional GPCR assay will depend on considerations of tissue, G protein type, feasibility, and scale of detection.

Novel Regulators of G Protein Signaling

Although receptor coupling to trimeric G proteins is a central event in GPCR-mediated signaling, recent data obtained using a variety of experimental approaches have provided a glimpse into the inherent complexity of G protein signaling by demonstrating that (1) G proteins can be directly activated without receptor involvement and (2) nonclassical GPCRs can mediate signaling via trimeric G proteins [2, 3, 15, 44, 45]. Two general types of direct G protein regulators have been identified that either accelerate the GTPase activity of the Gα subunit or alter G protein signaling by influencing nucleotide exchange or G protein subunit interactions. Thus, these proteins provide alternative binding partners for G protein subunits and enable them to serve functions independent of GPCRs, such as the regulation of cell polarity and cell division [45–47]. On the other hand, a number of studies have indicated that nonclassical GPCRs can also mediate some of their biological effects via possible activation of heterotrimeric G proteins. These include receptor tyrosine kinases, which mediate the actions of certain growth factors

such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), and fibroblast growth factor (FGF) as well as receptors for atrial natriuretic peptide, integrins, and insulin-like growth factor-II (IGF-II). A number of recent reviews have highlighted the paradigms by which tyrosine kinase receptors can evoke cellular effects via activation of G proteins [2, 15, 44, 48, 49], but very little information is currently available on the implication of an interaction between the IGF-II receptor and a G protein. This review aims to provide an overview of our current knowledge about the IGF-II receptor and its possible significance in regulating neuronal function in the central nervous system (CNS) by activating a trimeric G protein.

Insulin-like Growth Factor-II Receptor

The IGF-II receptor, which is identical to the cation-independent mannose 6-phosphate (M6P) receptor (hereafter referred to as the IGF-II/M6P receptor), is a multifunctional single pass transmembrane glycoprotein with no intrinsic tyrosine kinase activity (Fig. 1). The receptor binds IGF-II with higher affinity than IGF-I and does not bind insulin [50–54]. It also interacts, via distinct sites, with various M6P-containing ligands, such as transforming growth factor- β (TGF- β) [55], leukemia inhibitory factor (LIF) [56], proliferin [57], thyroglobulin [58], *Chlamydia pneumoniae* [59], and *Listeria monocytogenes* [60], as well as the non-M6P-containing retinoic acid [61]. Accumulated evidence suggests that the IGF-II/M6P receptor is expressed in most cell types, where it plays a role in lysosomal enzyme trafficking, clearance and/or activation of a variety of growth factors, and endocytosis-mediated degradation of IGF-II. In addition, a growing body of evidence supports a role for this receptor in transmembrane signaling in both neuronal and nonneuronal systems possibly via activation of heterotrimeric G protein, although this remains controversial [51–54].

Structurally, the human IGF-II/M6P receptor is composed of four distinct domains: a 40-residue amino-terminal signal sequence, an extracytoplasmic domain of 2,264 residues, a single, 23-residue transmembrane region, and a carboxy-terminal cytoplasmic tail of 164 residues (Fig. 1). The extracytoplasmic domain, i.e., the receptor region that protrudes into the extracellular space or the lumen of vesicles and intracellular organelles, is composed of 15 repeating segments, which share 14–38% sequence identity [50–54, 62, 63] (see Fig. 1). The cytoplasmic domain contains four regions that are substrates for various protein kinases including PKC, cAMP-dependent protein kinase, and casein kinases I and II [50, 51, 53, 54]. The receptor may exist as a dimer under both in vitro and in vivo conditions, and dimerization has been shown to alter the

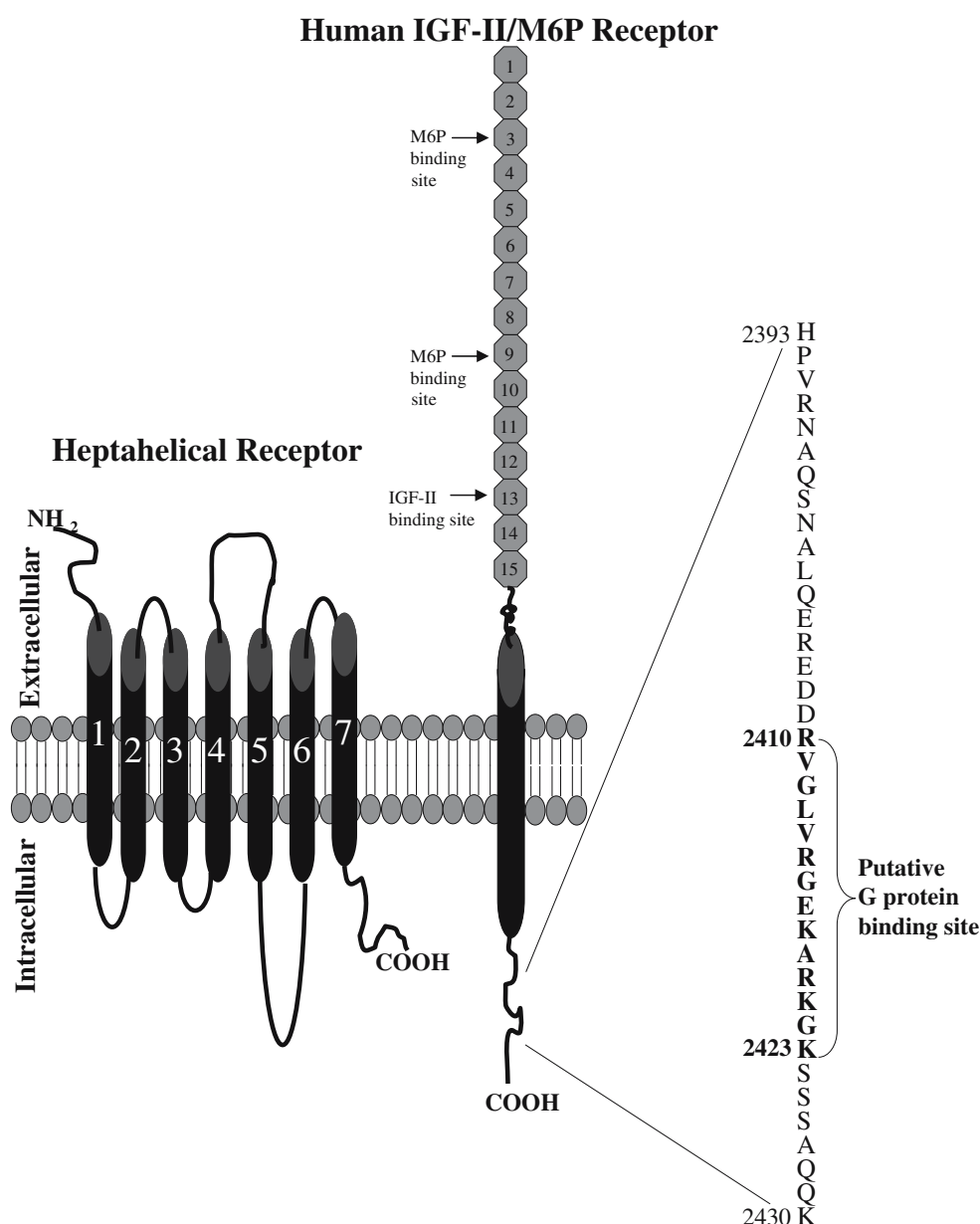
kinetics of IGF-II/M6P receptor internalization at the cell surface [64–66]. A truncated form of the receptor lacking the intracellular and transmembrane domains has also been identified in bovine serum and in the serum, urine, and amniotic fluid of rats and humans [51, 67–70].

The truncated receptor represents the product of proteolytic cleavage of the receptor's extracytoplasmic domain, which is subsequently released from the cell surface as a result of normal receptor turnover [69, 71]. Although high levels of the truncated receptor can interfere with IGF-II action by sequestering IGF-II away from the IGF-I receptor [72–74], it is not known whether the concentrations achieved physiologically have significant biological function.

IGF-II/M6P Receptor Ligand-binding Properties The IGF-II/M6P receptor binds three general categories of ligands at two distinct sites—IGFs, M6P-containing molecules and retinoic acid [50–54]. Two high-affinity M6P-binding sites are localized to repeats 1–3 and 7–11 within the extracytoplasmic region, whereas a third lower-affinity M6P recognition site within receptor domain 5 has recently been identified [75] (Fig. 1). In mammals, IGF-II binds the receptor at a primary site localized to the amino-terminal portion of extracytoplasmic domain 11, although sequence elements within domain 13 have been suggested to contribute an approximately five- to tenfold enhancement to the binding affinity of the receptor for IGF-II [76–81]. IGF-II and M6P-containing peptides are able to bind simultaneously to the IGF-II/M6P receptor, and binding of one ligand has been shown to reciprocally modulate receptor affinity for the other [82–85].

IGF-II/M6P Receptor Distribution The IGF-II/M6P receptor plays a critical role in prenatal tissue growth. It is therefore not surprising that receptor expression is developmentally regulated, with high-prenatal levels preceding a sharp postnatal decline, which is less acute in humans than in other mammals [86–91]. In adult, the receptor is ubiquitously expressed in various tissues including the heart, lung, muscle, intestine, kidney, liver, spleen, thymus, testis, ovary, and brain [92–94]. Within the CNS, IGF-II/M6P receptor mRNA and/or protein has been detected across all major regions of the brain and spinal cord, with particular enrichment in cortical areas, hippocampus, hypothalamus, and cerebellum as well as in certain brainstem and spinal motor nuclei [89, 95–100]. In general, high receptor immunoreactivity has also been found in the striatum, deep cortical layers, pyramidal and granule cell layers of the hippocampus, thalamic nuclei, cerebellar Purkinje cells, and in motor neurons of the brainstem and spinal cord [100]. Although IGF-II/M6P receptor expression has not been detected on microglia or astrocytes in the adult rat brain,

Fig. 1 Diagram of the structures of a heptahelical G protein-coupled receptor and the IGF-II/M6P receptor. Traditional G protein-coupled receptors have a transmembrane core composed of seven membrane-spanning domains (*black cylinders*) capped on the extracellular side by a ligand-binding domain and on the cytoplasmic side by a domain that interacts with heterotrimeric G proteins composed of α , β , and γ subunits. By contrast, the IGF-II/M6P receptor is a type I single-transmembrane glycoprotein consisting of four structural domains, including an amino-terminal signal sequence, which is not shown because it is subsequently cleaved during the formation of the mature receptor. The large extracytoplasmic domain is made up of 15 structurally homologous repeat domains, indicated as *grey octagons*. The receptor has a single-transmembrane domain and a carboxy-terminal cytoplasmic tail. G protein binding to the IGF-II/M6P receptor is believed to occur within a 14-amino-acid segment (RVGLVRGEKARKGK) within the cytoplasmic tail, which does not have a kinase domain



receptor immunoreactivity has been reported on glial cells of the adult mouse brain under normal conditions [100, 101]. Additionally, receptor levels are differentially altered in response to ischemic [102, 103], electrolytic [104], and chemical [105, 106] brain trauma, suggesting the receptor might have a role in neurodegeneration or regeneration after brain lesion/trauma.

IGF-II/M6P Receptor Functions The majority of IGF-II/M6P receptors are located intracellularly, where they function principally in the trafficking of M6P-containing lysosomal enzymes from the trans-Golgi network (TGN) to the endosomal-lysosomal system. After receptor binding to soluble lysosomal enzymes within the Golgi complex, clathrin-associated proteins bind to an acidic-cluster-dileucine

amino acid motif within the cytosolic tail of the IGF-II/M6P receptor, and the receptor–enzyme complex is carried to early endosomes via clathrin-coated vesicles [53, 107–110]. Previously, the interaction between clathrin adaptor protein 1 (AP-1), ADP-ribosylation factor, and the IGF-II/M6P receptor was thought to mediate clathrin-coat assembly on vesicles budding from the TGN [53, 111–113]. However, several recent studies have indicated that members of the clathrin-associated Golgi-localized, γ -ear-containing, ADP-ribosylation factor-binding (GGA) protein family, rather than AP-1 alone, participate in IGF-II/M6P receptor movement out of the Golgi [108, 114–119]. Receptor–enzyme complexes dissociate within the acidic pH of the endosomes, after which receptors are either recycled back to the TGN or trafficked up to the plasma membrane. Cell surface receptors

(~10% of the total receptor population) mediate the binding and internalization of a number of extracellular growth factors and peptides, including IGF-II, proliferin, LIF, renin, and EGF, for their subsequent degradation. IGF-II/M6P receptor-mediated internalization is also believed to facilitate activation of the latent TGF- β to the active factor [55, 120, 121], which regulates differentiation and growth of many cell types.

Latent pro-TGF- β , which bears an M6P-tagged N-linked oligosaccharide side chain, is secreted from cells and stored in the extracellular matrix as an inactive precursor, which is activated after cleavage by proteases such as plasmin [55, 120, 121]. The ability of plasminogen and the urokinase-type plasminogen activator receptor (uPAR) to bind the IGF-II/M6P receptor at regions distinct from its M6P-binding sites supports a putative model in which binding of urokinase plasminogen activator to uPAR complexed to the IGF-II/M6P receptor facilitates conversion of plasminogen to plasmin, which in turn proteolytically activates the receptor-bound TGF- β precursor [108, 122].

The importance of IGF-II/M6P receptor-mediated regulation of extracellular IGF-II concentrations is underscored by gene targeting studies that have shown that deletion of the IGF-II/M6P receptor gene results in excess IGF-II levels, organomegaly, and perinatal death, which can be rescued when expressed in an IGF-II or IGF-I receptor-deficient background [123, 124]. A number of studies have also reported that expression of the IGF-II/M6P receptor can stimulate apoptosis or suppress proliferation and tumorigenesis in cultured cell model systems using SW 48 colorectal cancer cells [125], JEG-3 choriocarcinoma cells [126], and PC-3 prostate cancer cells [127]. Accordingly, decreased IGF-II/M6P levels provoke increased proliferation *in vitro* or enhanced tumorigenesis upon injection of the altered cells into animals [128–131]. The mechanisms by which the IGF-II/M6P receptor acts to suppress cell growth and inhibit apoptosis, both in the universal sense and as they apply to individual types of cells, are still not entirely clear. It is possible that both major ligand-binding functions of the receptor—IGF-II binding and phosphomannosyl ligand binding—may contribute to the receptor's growth-suppressive activity. An important recent example illustrating this problem can be found in the elegant study of Li and Sahagian [132] that showed that expression of the IGF-II/M6P receptor in receptor-deficient 66c14 mouse mammary tumor cells blocked the ability of the cells to proliferate and form tumors in mice, despite having no apparent effect on the *in vitro* rate of proliferation or invasiveness. It was unclear whether this effect was due to enhanced internalization of IGF-II, increased activation of TGF- β , or decreased secretion of lysosomal enzymes in the IGF-II/M6P receptor-expressing cells.

Several studies suggest that in addition to its trafficking role, the IGF-II/M6P receptor also mediates transmembrane signaling after IGF-II binding, including increased amino acid uptake in muscle cells [133], glycogen synthesis in hepatoma cells [134], exocytosis of insulin from pancreatic cells [135], cell proliferation in K562 erythroleukemia cells [136], increased gene expression in spermatocytes [137], motility of human rhabdomyosarcoma cells [138], migration of human extravillous trophoblasts [139], stimulation of Na⁺/H⁺ exchange and inositol triphosphate production in canine kidney cells [140], calcium influx (but not cell proliferation) in primed BALB/c3T3 fibroblast cells [141–143], increased choline acetyltransferase (ChAT) activity in septal cultured neurons [144], and potentiation of acetylcholine (ACh) release from the adult rat hippocampus [145]. Receptor specificity in most cases was confirmed by the use of IGF-II analogues, receptor antibodies that mimic/block IGF-II effects, or by evaluating biological effects in a cellular model system lacking IGF-I receptors [135, 136, 139, 145].

Despite the evidence that a variety of cellular/biological effects are being mediated by the IGF-II/M6P receptor, not much is known about the intracellular mechanisms by which the receptor regulates such effects. The single-transmembrane domain structure of the receptor and the lack of a kinase domain in its cytoplasmic tail suggest that components of its downstream signaling pathways likely differ from those of the IGF-I and insulin receptors, which usually mediate their effects by triggering intrinsic tyrosine kinase activity that interfaces with an array of intracellular signaling cascades, such as mitogen-activated protein (MAP) kinase and PI-3-kinase pathways. Evidence demonstrating that the effects of IGF-II are PTX sensitive and are mediated either by a decrease in AC activity [139, 146], increased IP₃ production [140], or stimulation of PKC activity [147] has raised the intriguing possibility that the IGF-II/M6P receptor might mediate signaling via a G protein-coupled mechanism. Although this suggestion has been met with some skepticism in the past, the identification of other single-transmembrane domain receptors coupling to G proteins, together with a growing number of recent studies on IGF-II in both neuronal and nonneuronal systems, indicate that IGF-II/M6P receptor–G protein coupling may constitute a genuine physiologically important interaction.

IGF-II/M6P Receptor–G Protein Interaction

Over the last two decades, a variety of experimental approaches under both *in vivo* and *in vitro* conditions have indicated that the single-transmembrane domain IGF-II/

M6P receptor may be associated either directly or indirectly with a heterotrimeric G protein (Table 1). Evidence for such an interaction was first suggested in 1987 by Ikuo Nishimoto and colleagues [142, 148, 149] when they reported that IGF-II-induced Ca^{2+} influx in competent BALB/c3T3 cells primed with EGF was inhibited by PTX in a concentration-dependent manner and that [^{125}I] IGF-II binding was inhibited in the presence of GTP γ S. Low concentrations of IGF-I and insulin did not alter Ca^{2+} levels, suggesting that this effect was possibly mediated via the IGF-II/M6P receptor. The authors further strengthened the notion of an IGF-II/M6P receptor–G protein interaction with their finding that IGF-II attenuated PTX-catalyzed ADP ribosylation in mouse BALB/c3T3 fibroblast cell membrane, an effect that was significantly attenuated when IGF-II was washed out, but mimicked by aluminum fluoride (i.e., 10-mM NaF+100- μM AlCl_3) and GTP γ S [150]. Additionally, when phospholipid vesicles were reconstituted with purified rat IGF-II/M6P receptor and Gi_2 protein, there was a resulting decrease in [^{125}I]IGF-II binding in the presence of GTP γ S; moreover, IGF-II facilitated [^{35}S]GTP γ S binding to Gi_2 in a PTX-sensitive manner. The specificity of the IGF-II/M6P receptor was indicated by the continued effectiveness of IGF-II in IGF-I receptor-deficient membranes and by the attenuation of IGF-II-induced effects in IGF-II/M6P receptor-free membranes, as well as in the presence of an anti-IGF-II/M6P receptor blocking antibody [150]. It was further demonstrated that the stimulatory effect of IGF-II on [^{35}S]GTP γ S binding

and GTPase activity in phospholipid vesicles expressing the human IGF-II/M6P receptor and Gi proteins can be regulated by M6P, although binding of M6P-bearing ligand to the receptor itself is not altered by GTP γ S [151] (Table 1).

By comparing the primary sequence of the human IGF-II/M6P receptor with that of known GPCRs and mastoparan, a wasp venom peptide belonging to the activators of G protein signaling protein (AGS) family [152], Nishimoto and colleagues [153, 154] have identified a 14-residue sequence (Arg 2410 -Lys 2423) within the cytoplasmic region of the IGF-II/M6P receptor that shares structural homology with both the venom peptide and the terminal portion of the third cytoplasmic loop of GPCRs. When the synthesized peptide sequence (RVGLVRGEKARKGK) was tested in an aqueous system, it was found to stimulate [^{35}S]GTP γ S binding to $\text{G}\alpha_{i2}$, induce GTPase activity, and increase GDP release, all of which were sensitive to both PTX treatment and Mg^{2+} concentrations. Furthermore, in phospholipid vesicles reconstituted with the human IGF-II/M6P receptor and $\text{G}\alpha_{i2}$, administration of an antibody raised against the 14-residue sequence attenuated the IGF-II-induced stimulation of [^{35}S]GTP γ S binding to soluble $\text{G}\alpha_{i2}$ proteins [154–156]. To examine this effect under more physiological conditions, COS cells stably expressing constitutively activated $\text{G}\alpha_i$ proteins were transfected with human IGF-II/M6P receptor cDNA. In these cells, IGF-II significantly impaired CTX- or forskolin-stimulated AC activity, whereas no effect was observed in cells transfected with empty vector, or in cells expressing truncated IGF-II/M6P recep-

Table 1 Evidence supporting IGF-II/M6P receptor–G protein interaction

Cell type	Evidence of interaction with G protein	References
BALB/c3T3 cells	PTX-blocked IGF-II-mediated increase in Ca^{2+} mobilization PTX-catalyzed ADP ribosylation is abolished by IGF-II and mimicked by GTP γ S GTP γ S inhibition of [^{125}I]IGF-II binding	[142, 148–150]
Phospholipid vesicles expressing IGF-II/M6P receptor and Gi_2 protein	[^{35}S]GTP γ S binding to Gi_2 is facilitated by IGF-II and is sensitive to PTX and an antibody against the 14 a.a. tail sequence GTP γ S-sensitive decrease in [^{125}I]IGF-II binding	[150, 151, 154–156]
COS cells stably transferred with full length IGF-II/M6P receptor and $\text{G}\alpha_{i2}$ protein	CTX and forskolin-stimulated increase in AC activity is impaired by administration of IGF-II	[157]
CHO cells	PTX-blocked IGF-II-mediated increase in Ca^{2+} influx	[159]
Rabbit chondrocytes	IGF-II-mediated increase in Ca^{2+} influx abolished in the presence of PTX	[160]
Bovine capillary endothelial cells	PTX treatment prevents Leu^{27} IGF-II and proliferin-induced chemotaxis	[161]
Mouse pancreatic β cells	IGF-II-mediated insulin exocytosis is sensitive to PTX	[135]
Human extravillous trophoblasts	Decreased AC activity and increased migration in the presence of IGF-II and Leu^{27} IGF-II	[139]
Rat hippocampal neurons and dissociated basal forebrain cholinergic neurons	[^{125}I]IGF-II binding inhibited in the presence of Gpp(NH)p, GTP γ S, and PTX Co-immunoprecipitation of IGF-II/M6P receptor with $\text{G}\alpha_{i2}$ protein; sensitive to PTX treatment Leu^{27} IGF-II-induced ACh release inhibited in the presence of PTX PTX-abolished reduction in whole cell current and increased depolarization induced by Leu^{27} IGF-II	[145]

tors without the Arg²⁴¹⁰-Lys²⁴²³ sequence [157]. Furthermore, the C-terminal Ser²⁴²⁴-Ile²⁴⁵¹ region of the IGF-II/M6P receptor was found to exhibit sequence similarity with a part of the pleckstrin homology domain of several proteins that bind the G $\beta\gamma$ dimer and inhibit its stimulatory action on AC activity [157]. These results, taken together, led Nishimoto and colleagues [156, 157] to postulate that the IGF-II/M6P receptor may couple directly to the G α_{i2} protein via the identified 14-residue sequence located in the cytoplasmic domain of the receptor (Fig. 1).

Interestingly, the interaction between the IGF-II/M6P receptor and the G protein was challenged in 1995 by a report from Körner et al. [158] in which they failed to replicate the coupling of the IGF-II/M6P receptor with an inhibitory G protein.

In their paradigm, IGF-II did not alter PTX-mediated [³²P]ADP ribosylation or GTPase activity in mouse L cells (L929, a mouse embryonic fibroblast line) transfected with wild-type or truncated human IGF-II/M6P receptor cDNA.

Furthermore, IGF-II had no effect on either GTP γ S binding or GTPase activity of PTX-sensitive G proteins in phospholipid vesicles reconstituted with wild-type or truncated IGF-II/M6P receptors. In addition, IGF-II did not affect GTP γ S binding in vesicles containing purified wild-type IGF-II/M6P receptor and monomeric G α or G β and γ dimers. These results suggested that the human IGF-II/M6P receptor does not interact or couple to G proteins in mouse L cell membranes or in phospholipid vesicles [158]. Nevertheless, a number of reports over the past decade persistently suggest that IGF-II/M6P receptors expressed in various tissues across different species may couple to an inhibitory G protein. This is supported by experimental data showing that: (1) IGF-II/M6P receptor-mediated increases in Ca²⁺ influx in Chinese hamster ovary cells, as well as Ca²⁺ mobilization in articular rabbit chondrocytes, are both abolished in the presence of PTX [159, 160]; (2) chemotaxis of bovine capillary endothelial cells induced by the IGF-II analogue Leu²⁷IGF-II is mediated via an IGF-II/M6P receptor-dependent PTX-sensitive pathway [161]; (3) IGF-II, acting through the IGF-II/M6P receptor, promotes exocytosis of insulin from mouse pancreatic β cells via a PTX-sensitive, PKC-dependent pathway [135]; and (4) IGF-II/M6P receptor stimulation by IGF-II, Leu²⁷IGF-II, or a related analogue, QAYL-Leu²⁷IGF-II, decreases AC activity and promotes migration of human extravillous trophoblasts [139] (Table 1).

Although most of the results on IGF-II/M6P receptor signaling have been obtained from nonneuronal systems, an accumulating body of evidence indicates that IGF-II/M6P receptors expressed in the brain may also utilize G proteins to transduce extracellular signals across the plasma membrane. Earlier studies have shown that IGF-II/M6P receptors exhibit a distinct distributional profile from that of the IGF-I receptor in the adult rat brain and respond differen-

tially to various pharmacological/surgical manipulations [104, 105, 110, 162], thus raising the possibility that this receptor may have a unique role in the normal maintenance and activity-dependent functioning of the adult brain. This is substantiated, in part, by our previous results that showed that IGF-I inhibits, whereas IGF-II potentiates, endogenous ACh release from the rat hippocampal formation [163, 164]. Tetrodotoxin, a sodium channel blocker, suppressed the effects of IGF-I but not those of IGF-II, suggesting that IGF-I acts indirectly via the release of other transmitters/modulators, whereas IGF-II may act directly on, or in close proximity to, cholinergic terminals [164, 165]. Our report of a widespread distribution of the IGF-II/M6P receptor throughout the brain, including its expression on cholinergic cell bodies and fibers, provided a neuroanatomical foundation to support this idea. However, in light of the evidence that high concentrations of IGF-II can bind to the IGF-I receptor, it was not initially apparent whether the effects of IGF-II on ACh release were mediated via activation of the IGF-I receptor or the IGF-II/M6P receptor. To address this issue, we used Leu²⁷IGF-II, an IGF-II analogue that binds rather selectively to the IGF-II/M6P receptor [143, 145, 166, 167], and demonstrated that this analogue can potentiate ACh release from adult rat hippocampal slices in a TTX-insensitive manner, as observed for IGF-II. Additionally, treatment with Leu²⁷IGF-II caused a reduction in whole-cell currents and depolarization in acutely dissociated rat cholinergic basal forebrain neurons [145].

To determine if these effects of IGF-II/M6P receptor stimulation were mediated via an interaction with a G protein, we first performed competition binding experiments in rat hippocampal membrane preparations and showed that (1) GTP γ S and Gpp(NH)p inhibited [¹²⁵I] IGF-II interaction with its receptor and (2) the Gi-sensitive toxin PTX inhibited [¹²⁵I]IGF-II receptor binding. Subsequently, we demonstrated that the G α_i protein, but not G α_s or G α_q proteins, co-immunoprecipitated with the IGF-II/M6P receptors and was sensitive to PTX treatment, thus suggesting an association between hippocampal IGF-II/M6P receptors and an inhibitory G protein. The functional relevance of this interaction was confirmed by our findings that pretreatment with PTX abolished Leu²⁷IGF-II-mediated ACh release, as well as the electrophysiological effects of this peptide in isolated cholinergic neurons [145]. Additionally, we showed that the G α_i protein-IGF-II/M6P receptor coupling resulted in the activation of PKC α , possibly through either IGF-II/M6P receptor-mediated increase in IP₃ levels via PLC [168, 169] or by direct activation of PLC by the $\beta\gamma$ subunits of the G protein [170, 171]. Subsequently, phospho-PKC α was found to phosphorylate and activate two of its downstream effectors, myristoylated alanine-rich C kinase substrate (MARCKS) and growth-associated protein-43 (GAP-43; see Fig. 2).

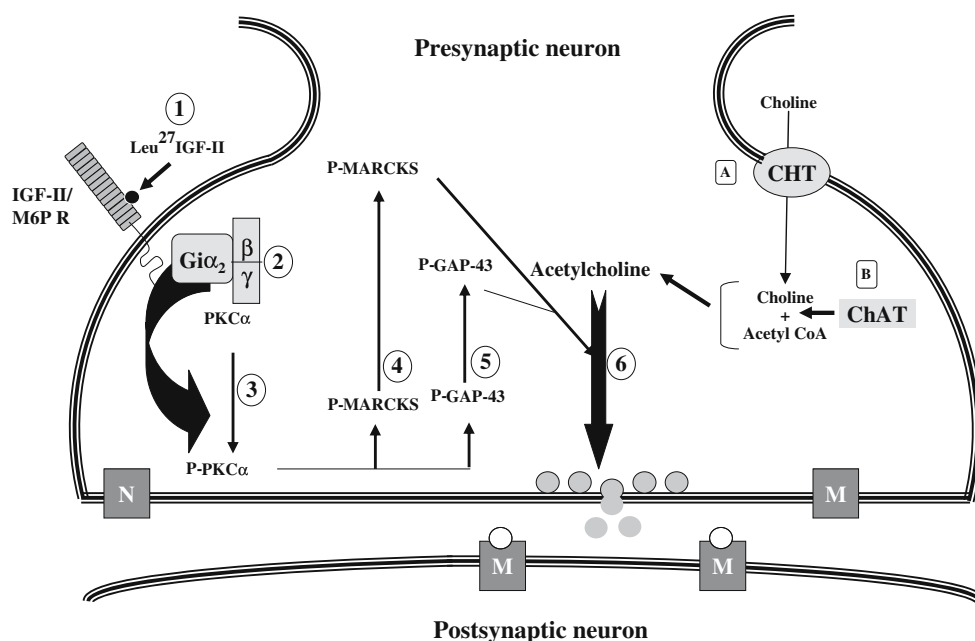


Fig. 2 Schematic representation of the events that are proposed to mediate Leu²⁷IGF-II-induced potentiation of ACh release from cholinergic terminals. Leu²⁷IGF-II binds IGF-II/M6P receptors located on cholinergic terminals (1). Activated IGF-II/M6P receptors couple to a Gi protein (2), which recruits cytosolic PKCα for subsequent phosphorylation (3). Activated PKCα phosphorylates membrane-associated MARCKS (4) and GAP-43

effectors (5), causing translocation of phospho-MARCKS into the cytoplasm and resulting in increased ACh release from synaptic terminals (6). Leu²⁷IGF-II-induced potentiation of ACh release is not associated with alterations in ACh synthesis, including high-affinity choline uptake (A) or ChAT enzyme activity (B). CHT High-affinity choline transporter, M muscarinic ACh receptor, N nicotinic ACh receptor

MARCKS and GAP-43 are well-established mediators of neurotransmitter/ACh release, as the phosphorylation and subsequent translocation of both molecules are important for actin cytoskeleton barrier breakdown at the active zone, as well as calcium/calmodulin-dependent kinase activation, respectively [172]. Collectively, these results suggest that IGF-II/M6P receptors expressed in the adult rat brain are coupled to an inhibitory G protein and that this association may be involved in mediating the effects of IGF-II on neurotransmission in the CNS (Table 1). However, it should be noted that there is still no tangible evidence to indicate whether the IGF-II/M6P receptor interacts directly or indirectly with a G protein. Certainly more work is needed to determine the nature of neuronal IGF-II/M6P receptor–G protein interaction and its relevance to the normal operation of the developing and adult brain.

Other Non-GPCRs and G Protein Interaction

It has become apparent over the last decade that certain tyrosine kinase receptors such as the EGF receptor, the IGF-I receptor, and the insulin receptor may also interact with G proteins to mediate some of their pleiotropic effects [2, 15, 44, 48, 49] (Table 2). The EGF receptor consists of an extracellular ligand-binding domain, a single-transmembrane

domain, and a cytosolic domain that encompasses its tyrosine kinase activity.

It has been reported that EGF-induced increases in intracellular Ca²⁺ in hepatocytes are mediated by EGF receptor stimulation of a G protein that modulates PLC activity [173–175].

Additionally, activation of the EGF receptor in cardiac myocytes, parotid glands, and pancreatic cells has been shown to enhance cAMP levels by stimulating AC via a stimulatory G protein [44, 176]. Studies designed to unravel the mechanism(s) involved in EGF receptor-mediated activation of Gs have shown that a 13-amino-acid sequence (Arg⁶⁴⁶–Arg⁶⁵⁸) in the cytosolic, juxtamembrane region of the EGF receptor is sufficient to activate the G protein. However, this peptide did not stimulate GTP binding to Gi but increased the GTPase activity of this protein [44, 177].

Unlike the EGF receptor, the insulin and IGF-I receptors consist of two extracellular α chains that are connected to each other by disulfide bridges and to two β chains that traverse the membrane. Although these receptors usually mediate their actions by intrinsic tyrosine kinase activity, some earlier reports indicated that insulin-dependent lipolysis and inhibition of glucose oxidation in adipocytes may be mediated by activation of a Gαi protein [178, 179]. There is also evidence that insulin receptor-mediated upregulation of GLUT4 transporters in NIH 3T3 adipocytes may depend on Gα_{q/11} proteins, whereas in rat fibroblasts,

Table 2 Other nonheptahelical receptors that interact with G proteins

Nonheptahelical receptor	Associated G protein	References
EGF receptor	Gs	[173–177]
Insulin receptor	Gi/o, Gq/11	[178–180, 183]
IGF-I receptor	Gi, Gβγ	[151, 160, 184–186]
Kainate receptor	Gi/o	[187]
AMPA receptor	Gi	[188–191]
PDGF receptor	Gi	[192, 193]
FGF receptor	Gs	[194]
Thrombospondin receptor	Go, Gs	[195, 196]
Zona pellucida glycoprotein receptor	Gi/o	[197, 198]
C-type natriuretic peptide receptor	Gi	[199–202]
T cell receptor	Gq/11	[203–206]

Note that some receptor–G protein interactions, including that of the thrombospondin receptor, are believed to be indirectly mediated.

the receptor can stimulate Gs proteins [44, 180]. However, more recent work on the mechanism of cross talk between insulin signaling through its intrinsic tyrosine kinase and potential activation of a G protein-regulated pathway has revealed some details of the process. Analysis of insulin action in cells from transgenic mice having inducible antisense RNA to *Gia2* showed that knockdown of *Gia2* expression impaired insulin action on a variety of processes [181]. It was found that this effect was due to a *Gia2*-mediated increase in activity of protein tyrosine phosphatase 1B, which interfered with insulin signaling by dephosphorylation of insulin receptor substrate-1 [181, 182]. Thus, it does not appear that the point of cross talk between the pathways in this case involves direct interaction between the insulin receptor and *Gia2*. This conclusion is supported by another study in human umbilical vein endothelial cells, in which insulin stimulated cyclic GMP production in a pertussis toxin-sensitive manner [183]. This action of insulin appeared to require extracellular signal-regulated kinase (ERK1/2) phosphorylation, suggesting signaling through the Ras–MEK–ERK cascade. Finally, direct interaction between the insulin receptor and *Gia2* could not be shown by co-immunoprecipitation [183], thus indicating that many questions remain to be addressed in relation to the interaction between the insulin receptor and the G protein-regulated signaling pathway.

Similar to insulin, a number of experimental paradigms have shown that IGF-I-induced increases in Ca^{2+} influx and DNA synthesis in BALB/c-3T3 cells, as well as activation of MAP kinase in neuronal cells, are sensitive to PTX treatment [151, 160, 184, 185]. Furthermore, there is evidence that activation of the IGF-I receptor can lead to an inhibition of AC via a *Gai2* protein and activation of ERKs through Gβγ subunits in human smooth muscle cells [186]. Although these results suggest the existence of putative alternative mechanisms for insulin and IGF-I receptor signaling, the physiological relevance of these pathways remains to be established.

Within the nervous system, nonheptahelical receptors such as the glutamatergic kainate [187] and α -amino-3-

hydroxy-5-methylisoxazole-4-propionate (AMPA) receptors [188] have also been shown to interact with G proteins. Activation of the kainate receptor, a member of the cation-permeable ionotropic glutamate receptors, has been shown to inhibit γ -aminobutyric acid (GABA) release from the hippocampus in a PTX-sensitive manner. Additionally, the binding profile of [^3H](2S,4R)-4-methylglutamate, a kainate receptor-selective agonist, is shifted to the right in the presence of Gpp(NH)p and PTX, but is not affected by CTX in rat hippocampal membranes, thus suggesting a possible association between the kainate receptor and a *Gai/o* protein [187]. There is also evidence that the AMPA receptor, another member of the ionotropic glutamate receptor family, may regulate cellular mechanisms by interacting with a G protein. This is supported by experimental data that have shown that (1) AMPA receptor activation reduced PTX-mediated ADP ribosylation of the *Gai* protein and inhibited forskolin-stimulated AC activity in isolated membranes and intact cortical cultured neurons [188]; (2) in retinal ganglion cells, AMPA-induced suppression of the cGMP-gated current is blocked by PTX, but not by GTPγS, suggesting that AMPA receptor activation in these cells leads to the inhibition of cationic channels gated by cGMP through PTX-sensitive G-protein [189]; (3) a *Gi/o* protein inhibitor *N*-ethylmaleimide attenuates the AMPA receptor-mediated presynaptic inhibition at cerebellar GABAergic synapses, whereas *Gi/o*-coupled receptor agonists baclofen (GABAB receptor agonist) and DCG-IV (mGlu receptor agonist) and the P/Q-type calcium channel blocker ω -agatoxin IVA markedly occluded the AMPA receptor-mediated inhibition of GABAergic transmission [190]; and (4) AMPA receptor-mediated inhibition of Ca^{2+} channels in rat auditory brainstem neurons can be abolished in presence of the nonhydrolyzable GTP analogue GTPγS [191]. These results suggest that AMPA receptors expressed at various central synapses may influence neurotransmitter release by interacting with heterotrimeric G proteins (Table 2).

A variety of other nonclassical GPCRs that have been shown to interact with G proteins include the PDGF [192, 193] and FGF receptors [194], the thrombospondin receptor

[195, 196], the zona pellucida glycoprotein receptor [197, 198], the C-type natriuretic peptide receptor (NPR-C) [199–202], and the T cell receptor [203–206] (see reviews [2, 44]; Table 2). It is of interest to note that NPR-C, like the IGF-II/M6P receptor, is a single-transmembrane protein that was originally thought to act as a “clearance receptor” for circulating atrial natriuretic peptide involved in cardiac development and natriuresis from the kidney. Subsequently, it was shown that activation of NPR-C can decrease AC activity in a variety of tissues via stimulation of a PTX-sensitive G protein [2, 207]. Although the significance of the NPR-C/G protein interaction remains to be fully defined, these results reinforce the notion that a single-transmembrane domain receptor can indeed interact with G proteins to mediate cell signal transduction.

Conclusion

The IGF-II/M6P receptor is a widely expressed, single-transmembrane domain, multifunctional protein that is involved primarily in lysosomal enzyme trafficking, peptide internalization, and degradation of a variety of molecules including IGF-II. A growing body of evidence, including several recent reports, suggests a role for the receptor in mediating signal transduction via coupling to an inhibitory G protein. Some of these effects include exocytosis of insulin from mouse pancreatic β cells, migration of human extravillous trophoblasts, and potentiation of ACh release from adult rat brain. However, more work is needed to better characterize the interaction between the IGF-II/M6P receptor and G protein, particularly with regard to whether the receptor–G protein interaction is direct, mediated by an intermediate protein or through the formation of a heterodimer receptor complex with a classical GPCR. Future research should also attempt to differentiate whether this receptor can couple selectively to G_i or G_o protein in some systems to mediate specific effects to highlight the physiological significance of this interaction. Additionally, it would be of interest to determine whether the IGF-II/M6P receptor, apart from potentiating endogenous ACh release, can regulate the release of other neurotransmitters in the CNS by virtue of its interactions with G proteins. Nevertheless, the addition of the IGF-II/M6P receptor to the ever-growing list of putative non-seven-transmembrane receptors that can couple to G proteins, indicates that G protein-mediated signaling might not be limited to classical GPCRs. Moreover, the discovery that CNS metabotropic receptors, such as the muscarinic ACh and metabotropic glutamate receptors, can act on ion channels in a G protein-independent manner [208] has provided further evidence that classical GPCRs do not have to mediate signal transduction exclusively via heterotrimeric G proteins. Thus, the impetus

may exist to redefine the term “G protein-coupled receptor” from a structural term referring specifically to heptahelical receptors to one of a more broad functional definition.

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