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G PROTEIN $\beta\gamma$ DIMER EXPRESSION IN CARDIOMYOCYTES; DEVELOPMENTAL ACQUISITION OF $G\beta_3$

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Abstract

Heterotrimeric G proteins are comprised of a guanine nucleotide binding $G\alpha$ subunit and the $G\beta\gamma$ dimers that link G protein-coupled receptors (GPCRs) to effectors. This study focuses on the expression and localization patterns for certain $G\beta$ and $G\gamma$ subunits in neonatal and adult cardiomyocytes. We identify developmental downregulation of $G\beta_1$, $G\beta_2$ and $G\gamma_2$, and a switch in the molecular form of $G\gamma_3$, in cardiomyocytes. $G\beta_1$ is highly localized to caveolae membranes, whereas $G\beta_2$ is identified in caveolae and other membrane fractions. $G\beta_3$ is not detected in neonatal cardiomyocytes, but rather $G\beta_3$ is upregulated in adult cardiomyocytes and detected in the caveolae and soluble fractions. The observation that cardiomyocytes co-express multiple $G\beta$ and $G\gamma$ subunits in a developmentally regulated manner, and that these $G\beta$ and $G\gamma$ subunits assume distinct subcellular localization patterns, provides for a high level of signaling specificity in the heart.

Keywords

G proteins; cardiomyocytes; development; caveolae

INTRODUCTION

Heterotrimeric G proteins are a family of signaling proteins that link G protein-coupled receptors (GPCRs) to the activation of effectors [1]. G proteins are composed of a guanine nucleotide binding $G\alpha$ subunit that associates with the dimeric $G\beta\gamma$ complex; GPCR activation catalyzes GDP exchange for GTP on the $G\alpha$ subunit, resulting in the dissociation of GTP-liganded $G\alpha$ from $G\beta\gamma$. Freed $G\alpha$ subunits and $G\beta\gamma$ dimers both regulate effector responses; $G\beta\gamma$ dimers also play a role in targeting $G\alpha$ subunits to membrane and in controlling G protein interactions with GPCRs and effectors.

At present, 5 $G\beta$ subunits and more than 12 $G\gamma$ subunit genes have been identified in the human genome. $G\beta_{1-4}$ share over 80% identity with one another in their primary amino acid sequence, whereas $G\beta_5$ is an outlier by structural and functional criteria. Early studies relied largely on *in vitro* reconstitution assays and characterized β_1 – β_4 subunits as interchangeable components of the $\beta\gamma$ dimer. $\beta\gamma$ dimer signaling specificity was attributed largely to differences in the

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functional properties of the structurally divergent $G\gamma$ subunits. However, recent studies identify effects of $G\beta$ subunits to direct heterotrimeric G protein interactions with GPCRs and effectors [2]. The large number of $G\beta$ and $G\gamma$ subunits expressed by most tissues provides, at least in theory, the potential to assemble a dauntingly large number of structurally unique $\beta\gamma$ dimers. However, the number of structurally distinct $\beta\gamma$ dimers *in vivo* is limited by [1] tissue-restricted expression of certain $G\beta$ and $G\gamma$ subunits and [2] selectivity in $G\beta$ - $G\gamma$ interactions, such that only certain $\beta\gamma$ combinations form functional dimers. For example, using a yeast two-hybrid system, Yan *et al.* published that most $G\gamma$ subunits interact well with $G\beta_1$ and $G\beta_2$ subunits, but poorly with $G\beta_3$ and $G\beta_4$ subunits [3]. This is consistent with studies in transfected cells or *in vitro* translation systems, where all $G\gamma$ subunits interact with $G\beta_1$, most $G\gamma$ subunits (with the notable exception of $G\gamma_1$, and the related $G\gamma_{11}$) interact with $G\beta_2$, but no $G\gamma$ subunit binds to $G\beta_3$ [4–6]. However, these $\beta\gamma$ dimer pairs forming during reconstitution experiments in cell-free systems (or following heterologous overexpression in undifferentiated cell lines) may not necessarily faithfully mimic $\beta\gamma$ dimer formation in native tissues (at endogenous levels of protein expression and with potential differences in the subcellular localization of individual $G\beta$ and $G\gamma$ subunits). Of note, there is still only limited information on $G\beta\gamma$ dimer expression in heart and $\beta_3\gamma$ interactions in native tissues have not been examined. The absence of information on $G\beta_3\gamma$ dimer expression is frustrating in view of evidence that a polymorphism in the $G\beta_3$ subunit gene (the *GNB3* 825T allele) has been associated with several metabolic and cardiovascular disorders [7].

$G\beta$ and $G\gamma$ subunit expression in ventricular myocardium (or isolated cardiomyocytes preparations) is reported to change during development. Hansen *et al.* identified $G\beta_1$, $G\beta_2$, $G\gamma_3$, $G\gamma_5$, and $G\gamma_7$ expression in cholera extracts of membranes prepared from neonatal ventricles (and neonatal rat cardiomyocyte cultures), with lower levels of $G\beta_2$, $G\gamma_5$, and $G\gamma_7$ (and no $G\beta_1$ or $G\gamma_3$) in adult ventricular preparations; $G\beta_3$ and $G\gamma_2$ were not detected in the ventricle at either age [8]. Since recent studies identified caveolae (or lipid rafts) as membrane subdomains that spatially organize GPCR-activated signaling pathway, and G protein $\beta\gamma$ dimers expressed at low levels (or compartmentalized to lipid rafts) might have evaded detection in previous studies, we examined G protein β and γ subunit expression in ventricular cardiomyocytes. This study identifies a striking developmental switch in $G\beta$ and $G\gamma$ subunit expression in the ventricle that (in theory) provides a novel mechanism to specify GPCR signaling pathways in the heart.

METHODS

Cardiomyocytes were isolated from the hearts of 2-day-old Wistar rats by a trypsin dispersion procedure according to a protocol that incorporates a differential attachment procedure to enrich for cardiomyocytes followed by irradiation [9]. Cells were plated at a density of 0.5×10^6 cells/ml (high-density, to generate a confluent monolayer) or 0.25×10^6 cells/ml (low-density, conditions associated with markedly reduced cell-cell contacts) on protamine sulfate-coated culture dishes and cultured in MEM (Gibco BRL) with 10% fetal calf serum, 5×10^{-6} M hypoxanthine, and 12 mM NaHCO_3 . Adult rat ventricular myocytes were disaggregated according to methods described previously and used within 1–6 hr of isolation [10].

Caveolin-rich membranes were prepared according to a detergent-free purification scheme described previously [9]. Briefly, cells from five 100-mm diameter dishes were scraped into 0.5 M sodium carbonate, pH 11.0 (0.5 ml per dish) and combined for each preparation. The extract was sequentially disrupted by homogenization with a Dounce homogenizer, a Polytron tissue grinder, and a tip sonicator. The homogenate was adjusted to 40% sucrose by adding an equal volume of 80% sucrose prepared in Mes-buffered saline (MBS; 25 mM Mes, pH 6.5, 0.15 M NaCl), placed on the bottom of an ultracentrifuge tube, overlaid with a 5–35%

continuous sucrose gradient, and centrifuged at 38,000 rpm for 16–18 hrs in a SW40 rotor (Beckman). After centrifugation, aliquots of fractions were dissolved in sample buffer containing SDS and 2-mercaptoethanol and heated prior to electrophoresis in SDS-PAGE gels. Samples were then transferred to nitrocellulose and immunoblotted with anti-caveolin-3 (mAb 26; BD Transduction Laboratories). The polyclonal anti-G β 1, -G β 2, -G β 3, -G γ 2 and -G γ 3 were from Santa Cruz. Immunoblot analysis was limited to these proteins as preliminary studies indicated that the commercially available reagents for other G β or G γ subunits do not detect endogenous levels of G β and G γ subunits in heart. Immunodetection was with chemiluminescence.

Results

Developmental changes in G β and G γ subunit expression in ventricular myocardium

G β and G γ subunit expression generally has been examined at the mRNA level, since antibodies that are sufficiently sensitive/specific to detect the endogenous proteins at physiologically relevant levels of expression are relatively recent. Figure 1A shows that G β 1, G β 2, and G β 3 proteins are detected in a developmentally regulated manner in extracts from post-natal day 2 and adult cardiomyocytes; high levels of G β 1 and G β 2 (but not G β 3) also are detected by immunoblot analysis in extracts from rat brain (included as a control preparation in the experiments). In each case immunoreactivity is specific; bands are not detected when immunoblot analysis is performed with antibodies preadsorbed with competing peptide antigen. G β 1 and G β 2 are readily detected in neonatal cardiomyocytes. G β 2 expression also is detected in adult cardiomyocytes, although at considerably lower levels; G β 1 expression is at the limits of detection in extracts from isolated adult cardiomyocytes. While immunoblotting on extracts from intact ventricular tissue also shows a developmental decline in G β 1 and G β 2 protein expression, these differences are rather modest when compared to the more striking developmental decreases in G β 1 and G β 2 protein expression in purified cardiomyocyte preparations (Figure 1B). These results suggest that the significant amounts of G β subunits detected in the adult ventricle derive from contaminating cell types (such as fibroblasts). In striking contrast, G β 3 expression is confined to adult cardiomyocytes; G β 3 is not detected in neonatal cardiomyocytes. G β 3 is detected only at trace levels in post-natal day 2 ventricles; G β 3 expression increases by post-natal days 8–11, reaching adult levels by 2 weeks of age.

G β subunit expression also was tracked in neonatal cardiomyocytes maintained in culture for 10–14 days, to determine whether G β subunit expression is regulated *in vitro*. The observation that G β 1 and G β 2 expression is maintained at high levels and G β 3 expression is not induced when cardiomyocytes are aged *in vitro* (for an interval that would be associated with downregulation of G β 1/G β 2 and the induction of G β 3 *in vivo* in the intact ventricle) indicates that the developmental programs that regulate G β expression *in vivo* are not triggered when cardiomyocytes are aged *in vitro* (and that neonatal cardiomyocyte cultures are a valid surrogate model for studies of G β subunit function in the neonatal ventricle).

Certain developmental changes in gene expression have been attributed to the postnatal surge in thyroid hormone secretion that regulates the expression of thyroid hormone-responsive gene products. Given the marked effects of thyroid hormone on autonomic (and GPCR) responsiveness, we tracked G β expression in neonatal cardiomyocytes cultured for 5 days in serum free medium containing a range of thyroid hormone concentrations (10^{-12} to 10^{-8} M tri-iodothyronine). The observation that stepwise increments in thyroid hormone concentrations lead to the predictable increase in β 1-adrenergic receptor expression, without a fall in G β 1/G β 2 expression or the induction of G β 3 effectively excludes a role for thyroid hormone as a major mediator of developmental changes in cardiomyocyte G β subunit expression (data not shown).

$G\gamma$ subunits that introduce an additional level of complexity to signaling pathways also were examined. Figure 1A shows that $G\gamma_2$ and $G\gamma_3$ are detected at high levels in brain. $G\gamma_2$ is detected in neonatal cardiomyocytes, and at much lower levels in the adult cardiomyocytes. $G\gamma_3$ is resolved as an epitope specific doublet in brain and neonatal cardiomyocytes; similar molecular heterogeneity for $G\gamma_3$ (and other $G\gamma$ subunits) has been identified in studies on endogenous proteins in tissues, but its significance remains uncertain. Both forms of $G\gamma_3$ are detected in equal amounts in neonatal cardiomyocytes; the slower migrating form of $G\gamma_3$ predominates in adult cardiomyocytes.

β and γ subunit targeting to lipid raft/caveolae

$G\beta$ subunit partitioning between soluble and particulate fractions was examined as an initial strategy to identify differences in $G\beta\gamma$ dimer localization in cardiomyocytes. Figure 2 shows that $G\beta_1$ and $G\beta_2$ are recovered exclusively in the particulate fraction of neonatal and adult cardiomyocytes; no $G\beta_1$ or $G\beta_2$ immunoreactivity is detected in the soluble fractions (even with increased protein loading or long exposures of the gel). In contrast, $G\beta_3$ (which is confined to adult cardiomyocytes) partitions to both particulate and soluble fractions.

Recent studies identify caveolae (or lipid rafts) as structures that spatially organize certain components of GPCR-activated signaling pathways [11–13]. Caveolae are 50–100 nm flask-shaped invaginations of the plasma membrane that are particularly abundant in terminally differentiated cells (including cardiomyocytes) and provide a mechanism to dynamically regulate specialized functions at the cell surface. We previously demonstrated that β_2 -adrenergic receptors and pertussis toxin-sensitive $G\alpha$ subunits are confined to the caveolae fraction of quiescent neonatal and adult cardiomyocytes [9;14]. In contrast, $G\alpha_s$ and $G\beta$ (identified with an antibody that does not discriminate between individual $G\beta$ isoforms) partition between caveolae and other cell fractions [14]. We examined the subcellular distribution of individual $G\beta$ subunits using a similar biochemical fractionation scheme that involves equilibrium centrifugation through a discontinuous sucrose gradient to separate buoyant lipid vesicles (F4-7 of the gradient, that represents ~0.5% of total cell protein and is enriched in the muscle-specific caveolae marker protein caveolin-3) from other cell membranes and cytosolic proteins (that are recovered in the heavy sucrose gradient fractions and pellet [P]).

Figure 2 shows that $G\beta_1$ is recovered exclusively in the low-density buoyant vesicle fraction isolated from neonatal and adult cardiomyocytes. $G\gamma_3$ also is recovered mostly in the caveolin-3-enriched F4-7 fraction. In contrast, $G\beta_2$ (in neonatal and adult cardiomyocytes) and $G\beta_3$ (in adult cardiomyocytes) distribute to both low-density caveolin-3-enriched membranes and heavy sucrose gradient fractions (which contain the bulk of the cellular protein).

Discussion

This study demonstrates that cardiomyocytes co-express multiple $G\beta$ and $G\gamma$ subunits in a developmentally regulated manner. We identify a developmental downregulation of $G\beta_1$, $G\beta_2$ and $G\gamma_2$, a switch in the molecular form of $G\gamma_3$, and a developmental induction of $G\beta_3$. There is little-to-no information on developmental controls of $G\beta$ and $G\gamma$ subunit expression (and the available information has focused mainly on $G\gamma_2$, which increases during the late embryonic period in the brain and is induced in human leukemia HL-60 cells during differentiation into granulocyte [15]). The molecular mechanism underlying developmental changes in $G\beta\gamma$ dimer expression remain uncertain; while certain age-dependent changes in gene expression can be attributed to a perinatal surge in thyroid hormone, the $G\beta\gamma$ subunits examined in this study do not appear to be thyroid hormone-responsive gene products. However, developmental differences in $G\beta$ and $G\gamma$ expression are predicted to lead to the formation of $\beta\gamma$ dimer pairs of varying composition in distinct subcellular compartments (caveolae vs. non-caveolae membranes) in neonatal and adult cardiomyocytes. Current

concepts regarding the role of G $\beta\gamma$ dimers in the regulation of GPCR signaling pathways is largely based upon studies that pair many G γ subunits with a single G β subunit (or a single G γ with structurally/functionally diverse G β 's such as G β_1 and G β_5). Reconstitution experiments that examine the signaling repertoire of a particular cell type (i.e., that address physiologically relevant questions related to G $\beta\gamma$ dimer assembly and function in a particular tissue), based upon the G β and G γ subunits that are expressed and co-localize in any particular cell type have not been attempted. Studies reported herein, which identify G β and G γ subunit expression and localization in neonatal and adult cardiomyocytes, provide the basis for such an analysis in future studies.

This study identified distinct expression patterns for the structurally related G β_1 , G β_2 , and G β_3 proteins; technical constraints (the lack of a sufficiently sensitive/specific antibody) precluded studies of G β_4 ; G β_5 is an outlier by structural and functional criteria and was not considered. While G β_1 and G β_2 share considerable structural homology, and these G β subunits function interchangeably in the regulation of a range of effectors (including G protein-activated inwardly rectifying potassium channels and high-voltage-activated calcium channels), G β_1 and G β_2 display distinct expression and localization patterns in cardiomyocytes. G β_1 is highly localized to caveolae and undergoes a pronounced developmental down-regulation. Of note, our previous studies showed that β_2 -ARs also localize to caveolae membranes. The co-localization of β_2 -ARs and G β_1 subunits to caveolae may be significant, given recent evidence that β_2 -adrenergic receptor activation leads to the internalization of G α_s -G β_1 -G γ_7 complexes from the plasma membrane to the cytoplasm [16] and that G β_1 -containing dimers are more potent than G β_2 -containing dimers at activating the G α_s -adenylyl cyclase pathway [2]. These results suggest that caveolae may play a particularly important role as nucleation centers for a β_2 AR-G $\beta_1\gamma$ -AC pathway. Studies from the Robishaw laboratory suggest that G γ_7 is G β_1 's preferred dimerization partner in the β_2 -AR signaling pathway [17;18]. On the basis of these studies, we would predict that G γ_7 also localizes (with β_2 -ARs and G β_1 subunits) to caveolae membranes, but available anti-G γ_7 antibodies were not sufficiently sensitive/specific to recognize native G γ_7 proteins at physiologic levels of expression to test this hypothesis (data not shown).

G β_2 shows a considerably more modest developmental downregulation and a different localization pattern; G β_2 partitions to both to caveolae and non-caveolae membranes. The distinct subcellular localization patterns for G β_2 and G β_1 may be significant, given recent evidence that even the highly structurally homologous G β_1 and G β_2 subunits are not necessarily functionally redundant. For example, while G β_1 and G β_2 act interchangeably to regulate many effectors, only G β_2 regulates low-voltage-activated Ca²⁺ currents carried by α_1H Ca²⁺ channels (due to a cluster of surface-exposed residues that are unique to G β_2 and form a surface contact point for α_1H channels [19]).

Finally, we show that G β_3 is detected only in the adult heart. The developmental upregulation of G β_3 is unusual; most developmentally regulated signaling proteins (such as G β_1 and G β_2) are abundant in the neonatal (less differentiated) heart and undergo a developmental down-regulation. While G β_3 expression has been detected in retinal cone cells, brain, heart, skeletal muscle, platelets, liver and lung, developmental regulation of G β_3 expression has not previously been reported. G β_3 also displays a unique subcellular distribution, relative to other G β subunits; G β_3 is not exclusively a membrane protein, but is recovered in substantial amounts in the cytosolic fraction. A similar cytosolic localization pattern for G β_3 has been reported previously, although a unique functional role for cytosolic G β_3 (distinct from other G β subunits, not necessarily requiring dimerization with G γ subunits) has not been considered. Rather, attempts to delineate G β_3 function have used reconstitution approaches focusing on traditional GPCR signaling mechanisms. Most attempts to identify G β_3 dimerization partners have been thwarted by the generally weak interaction between G β_3 and most G γ subunits [3–6]; G β_3 does

not mimic the actions of $G\beta_1$ and $G\beta_2$ to interact with $G\gamma_2$ or $G\gamma_3$ or to support signaling by $G\alpha_s$ [20]. However, effects of $G\beta_3$ to reconstitute some traditional GPCR signaling functions have been identified. For example, $G\beta_3\gamma_4$ dimers mediate mAChR-dependent calcium channel inhibition, $G\beta_3\gamma_5$ dimers (but not $G\beta_1\gamma_5$ dimers) support α_2A -AR-coupling to $G\alpha_i$, and $G\beta_3$ translocates from the cytosol to the membrane fraction in response to β AR activation in rat heart [21;22]. These results are most consistent with the notion that $G\beta_3$ plays a unique role (distinct from $G\beta_1$ or $G\beta_2$) and that $G\beta_3$ may preferentially participate in signaling pathway mediated by PTX-sensitive G proteins.

Recent studies identify a polymorphism in the human $G\beta_3$ gene (the GNB3 825T allele) associated with a complex phenotype consisting of essential hypertension, obesity, diabetes and other metabolic disorders, and altered drug responses [7;23]. $G\beta$ subunits are comprised of seven WD repeating motif proteins that define a seven blade propeller-like structure. The GNB3 825T allele encodes an alternatively spliced (41 amino acid shorter) variant of the β_3 subunit; this in-frame deletion results in the expression of a protein that lacks the equivalent of one entire WD repeat domain (i.e., a $G\beta_{3s}$ subunit with only 6 propeller blades). The Siffert laboratory has published evidence that this truncated $G\beta_3$ protein is functional, with evidence that $G\beta_{3s}$ dimerizes with certain $G\gamma$ subunits ($G\gamma_5$ and the related $G\gamma_{12}$, as well as $G\gamma_8$ in retinal cone cells) and it enhances signaling by PTX-sensitive heterotrimeric G proteins [24;25]. Based upon these findings, the enhanced chemotaxis and cardiac potassium channel regulation that has been identified in individuals carrying the 825-T allele has been attributed to dimers containing truncated $G\beta_{3s}$ subunits (that are believed to interact with enhanced efficacy with effectors, compared to dimers containing full-length $G\beta_3$). However, other investigators have failed to identify $G\beta_{3s}$ dimerization with $G\gamma$ subunits (or $G\beta_{3s}$ modulation of channel function), and have argued that the C825T-allele produces a 'functional $G\beta_3$ knockout' by expressing a 'junk $G\beta_{3s}$ mRNA' that is not translated into protein. While our studies do not address this controversy, the observation that $G\beta_3$ is developmentally-induced in the ventricle (and therefore may subserve a unique function in the mature differentiated heart) provides an additional rationale to resolve the functional role of this somewhat eccentric signaling protein.

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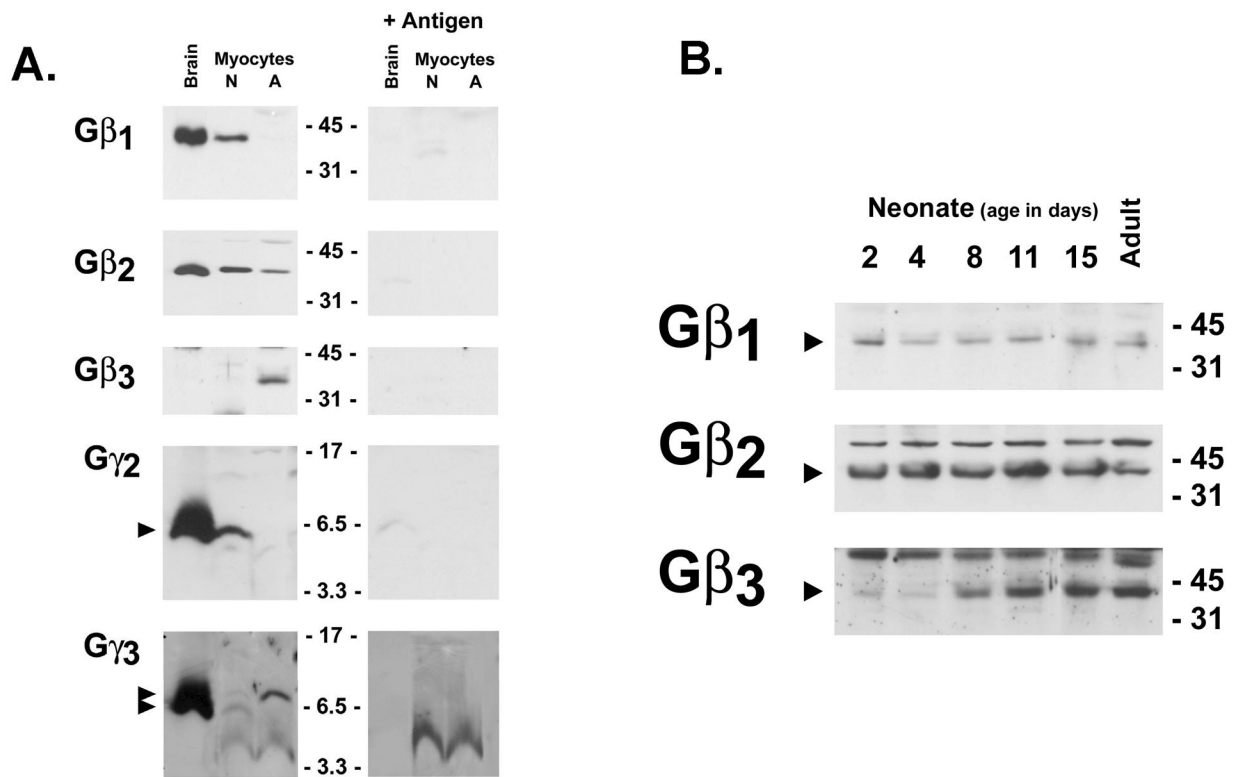


Figure 1. Developmental changes in Gβ and Gγ expression in the ventricle

100 μg of total cell protein extracted from day 5 neonatal cardiomyocyte cultures, or freshly isolated adult rat cardiomyocytes (Panel A) or from ventricles from rats at the indicated ages (Panel B) or were subjected to SDS-PAGE and immunoblot analysis with the indicated antibodies. An extract from brain (100 μg) was included as a positive control in Panel A. Epitope specific immunoreactivity was established by immunoblotting with antibody complexed with competing antigen peptide; note smaller proteins detected by the Gγ₃ antibody are non-specific. Arrow denote epitope specific bands, with positions of the molecular weight standards (in kDa) indicated.

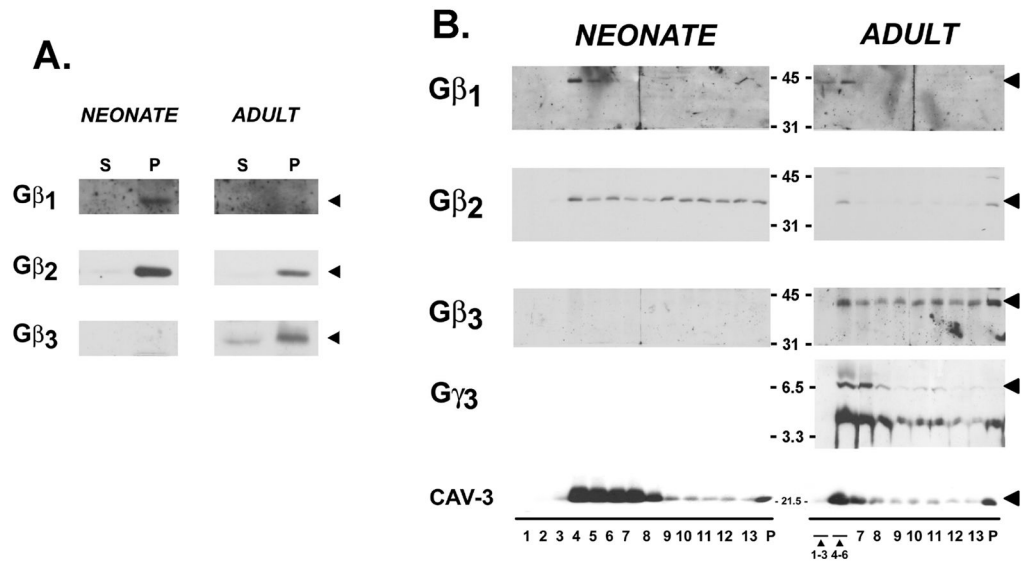


Figure 2. Gβ and Gγ partitioning to membranes and low-density caveolae in cardiomyocytes
Panel A: Neonatal cardiomyocyte cultures and acutely isolated adult cardiomyocytes were partitioned into soluble and particulate fractions and then subjected to immunoblot analysis for Gβ subunits as indicated. *Panel B:* Neonatal cardiomyocyte cultures and isolated adult cardiomyocytes were homogenized in sodium carbonate buffer and subjected to sucrose gradient centrifugation as described in methods. Fractions were collected from the top of the gradient and analyzed by SDS-PAGE and immunoblot analysis with the indicated antibodies. Fractions 1–3 and 4–6 in profiles from adult cardiomyocytes were pooled, due to the limiting amounts of protein recovered in these fractions. Immunoblot analysis was on 35 μg of protein from each fraction. Results are representative of data from three separate experiments.