

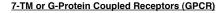


7-TM or G-Protein Coupled Receptors (GPCR)

Majority of transmembrane signaling via hormones, neurotransmitters, sight and smell mediated by GPCRs

About 2000: ~5% of worm and 3% of mammalian genomes

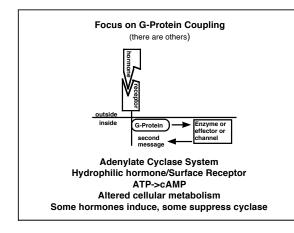
~2000 reported since 1st cloning (1983, bovine opsin). The human genome is now known to encode approximately 1000 GPCRs, ~ 400 non-olfactory receptors; ~150 orphan receptors (~2003); in last 17 years ~15 de-orphanized.

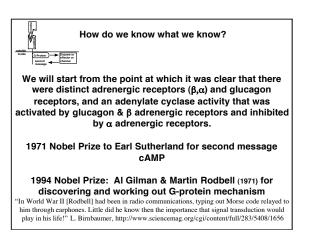


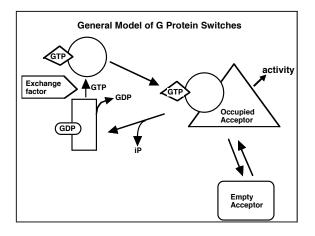
Major Drug Targets for Pharmaceutical Industry

>50% of all modern drugs (~20% of the top 50 best-selling drugs) are targeted at GPCRs (including adrenergic, histaminergic, dopaminergic, serotonergic, opiate, cholinergic, etc.) for pain, asthma, inflammation, obesity, cancer, and cardiovascular, metabolic, gastrointestinal and CNS diseases (e.g., Claritin, Zyprexa, Zantac and Cozaar).







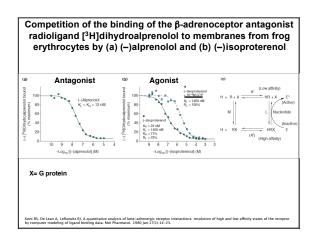


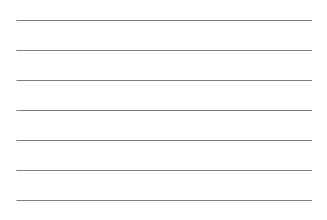


Experimental findings which have lead to the current model: 1. GTP enhanced hormone activation of cyclase and

- reduction of hormone (glucagon) binding to receptors in membrane preps. (Rodbell, 1960s) - <u>contaminant of ATP</u>! 2. GTP reduces agonist, but not antagonist binding to
- receptors (coupling important)
- 3. Nonhydrolyzable GTP analogues (GPPNP) work: (hydrolysis not required)
- 4. Nonhydrolyzable GTP analogues give permanent activation (a GTPase turns off signal)
- 5. B-adrenergic receptor-dependent slow GTPase (evidence for direct role of GTP)
- GTP binding protein purified via detergents by GTP affinity column away from cyclase, reconstitutes agonistdependent cyclase in S49 cyc⁻ membranes (receptors and cyclase, but not coupled) and GPPNP-dependent cyclase activity (separate subunits) - <u>this is first direct evidence of 3 components</u>
- Identification of GTP-binding subunit by [³²P]GTP-derived affinity label and by cholera toxin (which activates system)-catalyzed [³²P]ADP-ribosylation of GTP-binding subunit.
- Purification of receptor and cyclase came after G protein (why?), but finally all reconstituted into liposomes, fully hormone-sensitive cyclase system requires lipid bilayer.
- 9. Agonist-dependent release of [³H]GDP and binding of [³⁵S]GTPγS (agonist-bound receptor opens up G-binding site allowing exchange of GDP and GTP); Kds for various GTPases are 10⁻¹¹-10⁻⁷ M! very tight binding relative to ambient conc. [GTP]>10⁻⁴, [GDP]>10⁻⁵M; thus, not engineered to respond to GNP levels, not regulated by ratio of GTP:GDP
- 10. Kinetics of receptor/G interaction are cyclase independent (R/G & G/C independent).

- 11. Rate constant of activation of Gs-C complex linearly depends on concentration of the agonist-bound receptor : [k(on-observed) = kon(intrinsic) × [R]_{lotal} = [H]/(K₄+[H]) ; [R]_{lotal}=lotal receptor; [H]=agonist concentration; K₄=dissociation constant] receptor acts as a catalyst not permanently associated with activated complex: "collision coupling"
- 12. Gs-GDP forms complex with agonist-bound receptor, dissociates when GDP exchanged with GTP or analogue; this dissociation estimated to give 10x amplification of agonist signal in addition to 100-fold amplification due to slow GTPase activity and high activity of cyclase (similar to light and rhodopsin)
- Receptor-Gx(GDP) complex has higher affinity for agonists than receptor alone. AFFINITY OF RECEPTOR FOR <u>ANTAGONIST</u> NOT AFFECTED BY GTP OR ANALOGUE; GTP binding reduces affinity of R for <u>agonist</u> and dissociates R-G complex, permits recycling of R, lifetime of G-GTP complex before hydrolysis is many seconds (Gα^{GTP} t₁₀~10 sec)





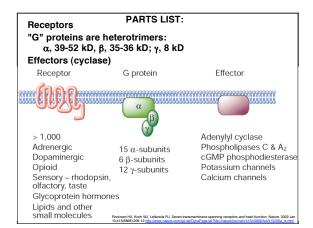
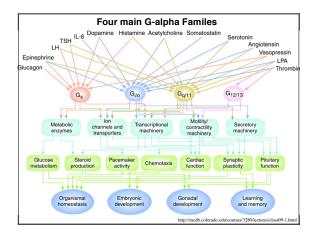
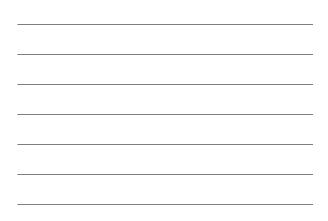


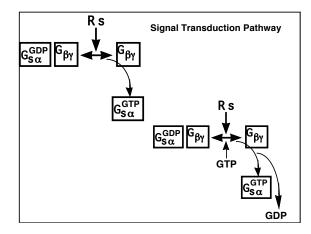


Table 1 Examples of heterotrimeric G-protein effector				
G-protein subunits	Effectors			
$G\alpha_{s}$ $G\alpha_{off}$	↑Adenylyl cyclase RGS-PX1 (GAP, sorting nexin) Calcium channels c-Src tyrosine kinases			
Gα _T (transducin) Gα _{gust} (gustducin)	↑cGMP phosphodiesterase Phosphodiesterase (bitter, sweet taste)			
Gα _{1 1, 2, 3} Gα ₀ Gα ₄	↓Adenylyl cyclase, ↑c-Src tyrosine kinases Rap1GAP1			
$G\alpha_{q}, G\alpha_{11}, G\alpha_{14, 15, 16}$	1Phospholipase C LARG RhoGEF			
Gα ₁₂ , Gα ₁₃	p115 RhoGEF, PDZ-RhoGEF, LARG RhoGEF (Rho activation, stress-fibre formation) E-Cadherin (β-catenin release)			
Gβγ	KIR3.1–3.4 (GIRK K* channels) GRKs 1Adenylyl cyclases (ACII, ACIV) 1Phospholipases (PLC β1, β2, β3) PI3Kγ			

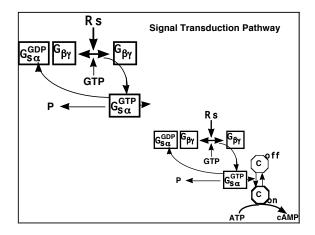
esting and an experiment and an experiment and an experiment and a second a second and a second a second and a second a second a second and a second a s



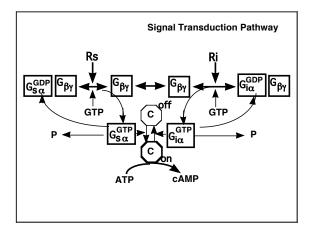








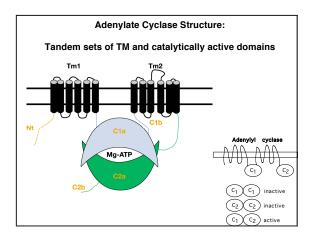




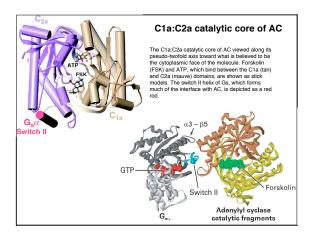


G_{α} is GTP binding protein and GTPase	G Protein's
GTP hydrolysis used as a timing device	Features
For B-AR: H:R ($t_{1/2}$ >1 sec), G α^{GTP} $t_{1/2}$ ~10 sec	
k _{catGTPase} (for Gα)~2-4/min-slow!, but much faste	er than ras:
k _{automana} (ras)~0.02/min. almost off	

- thus, ras needs GTPase Activating Protein: GAP
- $k_{\textit{diss GDP}}(ras) {\sim} 0.008/min$ about the same as $k_{\textit{diss GDP}}(G\alpha\gamma\beta$ complex)~0.01/min; both need GNRP (G nucleotide releasing protein), more commonly called GEF (exchange factor).
- βy subunits:
- GDP dissociation from $G\alpha\gamma\beta$ complex is 100x slower than for α subunit alone..... thus, $\beta\gamma$ keeps system inactive until hormone hits the
- receptor
- $\beta\gamma$ required for $G\alpha$ interaction with the receptor and for other regulatory steps
- $G\alpha GDP$ can be thought of as inhibitor of $\beta\gamma$









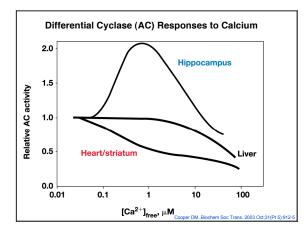
Multiple adenylate cyclases:

Adenylyl Cyclase I-IX, (all Gs α stimulated)

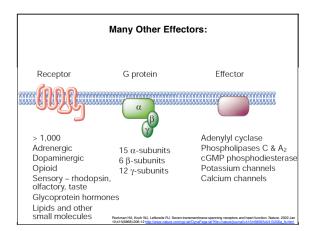
Type I:	Ca/calmodulin-sensitive, α_s stimulates,
	$\beta\gamma$ inhibits indirectly in presence of α_s
Type II:	Ca/CalM insensitive, α_s stimulates, $\beta\gamma + \alpha_s$
	stimulates!, PK-C regulated
Type III:	little sensitivity to By
Type IV:	similar to type II
Type V, V	l: not regulated by βγ
	shares sequence with II&IV& BARK etc.
	associated with βγ regulation

Non-classical, cytoplasmic (not integral membrane) bicarbonate-activated AC

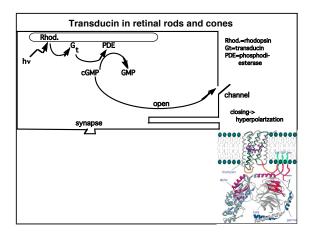
Cyclase regulation (AC1-AC9)				
Gsα	All are stimulated			
Giα	Gi Gi, Gz, Go inhibit calmodulin- and FSK-stimulated AC1			
	activity; Gi inhibits AC5 & AC6; No effect on AC2			
Gβγ	AC2, AC4, & AC7 stimulated; AC1 inhibited; AC5 & AC6			
	maybe inhibited by the $\beta 1\gamma 2$			
	All except AC9 are stimulated			
PKA	AC5 & AC6 are inhibited			
PKC	Stimulates AC1, AC2, AC3 & AC7; also AC5 by PKC- α & - ζ			
Calcium				
Inhibits: all cyclases at high concentration; AC5 & AC6 at				
micromolar; AC1 via calmodulin kinase(CaMK) IV, AC3 via CaMK				
II; AC9 via calcineurin				
Stimulates: AC1 & AC8 via calmodulin; AC5 via PKC-α, AC2 &				
AC7 via PKC				
No effect on AC2, AC4, and AC7				
FSK, forskolin; PKA, protein kinase A; PKC, protein kinase C				
1' SN,	ioiskoiiii, FRA, pioleiii kiilase A, FRO, pioleiii kiilase C			









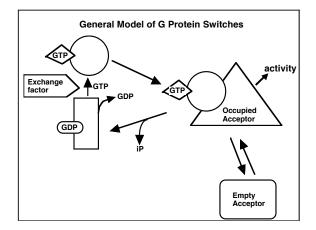




Other classes of "G" protein

GTPase functions: Protein synthesis (EF-tu), Signaling (GPCR, heterotrimeric) ER-translocation (SRP, SRP-R) Differentiation and proliferation (ras) Vesicular traffic (rabs) Cytoskeleton (rac and rho)

> $\frac{Not \ Identical:}{G\alpha = 350-400 \ amino \ acids}$ ras-like = 200 aa EF-Tu 400-900 aa





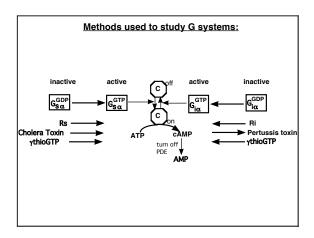
Methods used to study G systems:

** <u>Cholera toxin</u> ADP-ribosylates arginine (from NAD+) Gs -, inhibits GTPase activity

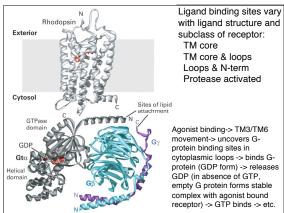
** Pertussis toxin ADP-ribosylates cys near C-terminus of Gi [whooping cough] inactivates, blocks Gi interaction with receptors

ARF: ADP-ribosylating factor required for toxin activities,

- ** Forskolin directly activates cyclase
- **<u>γτhio-GTP</u>, non-hydrolyzable analogue, activates
- ** F_4AI^2 , with GDP mimic γ phosphate group of GTP-trimeric







with ligand structure and subclass of receptor: TM core & loops Loops & N-term Protease activated

Agonist binding-> TM3/TM6 movement-> uncovers Gprotein binding sites in cytoplasmic loops -> binds G-protein (GDP form) -> releases GDP (in absence of GTP, empty G protein forms stable complex with agonist bound receptor) -> GTP binds -> etc.

<u>Desensitization</u>: tendency of biological responses to wane over time despite continuous presence of stimulus of constant intensity.

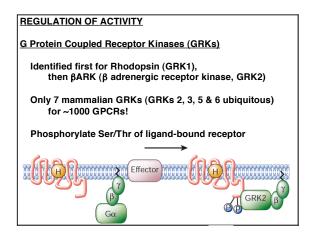
<u>Homologous</u> desensitization : Receptor ligand induces the loss of that receptor's activity (but not the activity of other receptors)

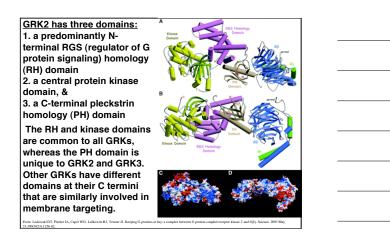
<u>Heterologous</u> desensitization: Stimulation of one receptor induces the loss of a different receptor's activity.

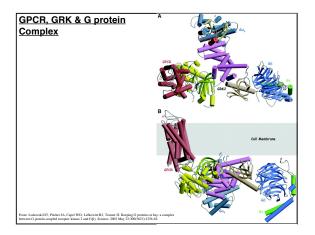
Phosphorylation on 5-6 loop and C-terminus

Activity Switching

Receptor Homo- and Heterodimerization









Regulators of G-protein signaling (RGS)

Identified in yeast and worms first

GTPase activating proteins (GAPs) for G α 's

~100-fold increase in GTPase rate (lower activation energy)

controled by 14-3-3 proteins (P-ser/thr binding proteins)

REGULATION OF ACTIVITY

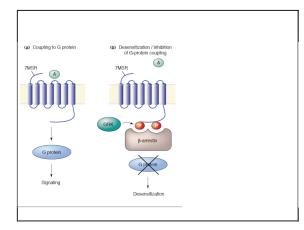
Arrestins

Identified first for Rhodopsin (retinal arrestin), then β Adrenergic Receptor (βarrestin-1, βarrestin-2)

Only 3 mammalian arrestins for ~1000 GPCRs! (retinal arrestin, βarrestin-1, βarrestin-2)

Bind to Phosphorylated GPCRs

Mediate multiple activities



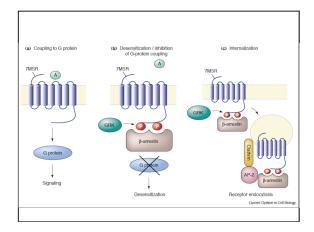


β<u>Arrestins</u>

Block Receptor/G Protein Interaction (desensitize)

Agonist-dependent Adaptor proteins:

Endocytosis (Clathrin, AP2, ARF6, ARNO, NSF), arrestin ubiquitination for endocytosis



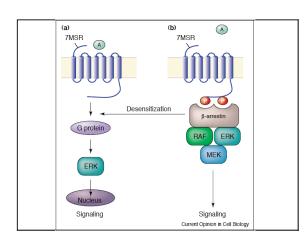


β<u>Arrestins</u>

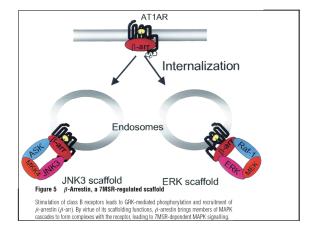
Block Receptor/G Protein Interaction (desensitize)

Agonist-dependent Adaptor proteins:

Endocytosis (Clathrin, AP2, ARF6, ARNO, NSF), arrestin ubiquitination for endocytosis Multiple kinase pathways (MAPK, src, RTKs), scaffold function for assembly of complexes (src, MAPK, P38, JNK, AKT, etc.)









β<u>Arrestins</u>

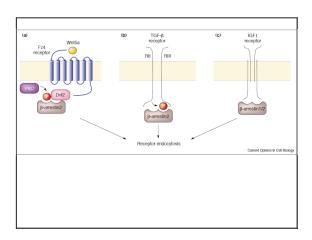
Block Receptor/G Protein Interaction (desensitize)

Agonist-dependent Adaptor proteins:

Endocytosis (Clathrin, AP2, ARF6, ARNO, NSF), arrestin ubiquitination for endocytosis Multiple kinase pathways (MAPK, src, RTKs), scaffold function for assembly of complexes

Activate cAMP Phosphodiesterase (desensitization)

Non-GPCR receptor/channel modulation

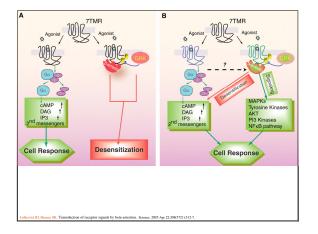


binding protein	p-Arrestin isolom	i i unetionat consequence	
		Trafficking proteins	
Clathrin	β-Arrestin 1, 2	Endocytosis	
AP2	β-Arrestin 1, 2	Endocytosis	Table 1. A list of β-
NSF	β-Arrestin 1	Endocytosis; recycling	
		Small G/GEFs	arrestin-interacting
ARF6	β -Arrestin 2 \gg 1	Endocytosis	•
ARNO	β-Arrestin 2	Endocytosis	proteins.
Ral-GDS	β-Arrestin 1, 2	Ral-mediated cytoskeletal changes	-
RhoA	β-Arrestin 1	Angiotensin II-dependent stress	ARF, ADP ribosylation factor;
		fiber formation	
		Signaling proteins	ARNO, ARF nucleotide
MAPK cascade			exchange factor; IkBa, inhibitor
components			of nuclear factor kB; PDE4D,
ASK1	β-Arrestin 1, 2	JNK3 and p38 activation	phosphodiesterase 4D; PP2A,
c-Raf-1	β-Arrestin 1, 2	ERK activation	
JNK3	β-Arrestin 2≫>1	Stabilization of pJNK on endosomes	protein phosphatase 2A; Ral,
ERK2	β-Arrestin 1, 2	Stabilization of pERK on endosomes	members of the Ras superfamil
Nonreceptor			of small guanosine
tyrosine kinases			triphosphatases (GTPases);
c-Src	β-Arrestin 1, 2	Endocytosis, ERK activation	Ral-GDS, Ral guanosine
Yes	β-Arrestin 1	Gaq activation and GLUT4	
		transport	diphosphate (GDP) dissociation
Hck	β-Arrestin 1	Exocytosis of granules in neutrophils	stimulator; RhoA, a small
Fgr	β-Arrestin 1	Exocytosis of granules in neutrophils	GTPase; small G/GEFs, small
Others			GTPase and guanine nucleotid
Mdm2	β-Arrestin 1, 2	Ubiquitination, endocytosis	
ΙκΒα	β-Arrestin 1, 2	Stabilization of IκBα upon β2AR and TNFR stimulation	exchange factors.
DDF (D (0.4		
PDE4D family Dishevelled	β-Arrestin 1, 2 β-Arrestin 1	cAMP degradation Increase in TCF/LEF transcription	Lefkowitz RJ, Shenoy SK.
Dishevelled	β-Arrestin 1 β-Arrestin 2	Endocytosis of Frizzled4	Transduction of receptor signals by
PP2A	β-Arrestin 1	Ser ⁴¹² dephosphorylation	beta-arrestins. Science. 2005 Apr
FFER	p-Arrestin T	ser ···· depriosphorylation	22;308(5721):512-7.

Functional cons

B-Arrestin isoform







Desensitization: tendency of biological responses to wane over time despite continuous presence of stimulus of constant intensity.

Homologous desensitization : β-adrenergic receptor kinase (BARK) moves from cytoplasm to complex with Gβγ, binding site overlaps with C-terminal PH domain . BARK phosphorylates receptor and lowers activity, after phosphorylation, β -arrestin binds and really drops activity. BARK member of the GRKs

Heterologous desensitization: stimulation of other receptors, PKA plays a role, PKA is about 6x slower than BARK, arrestin independent.

Phosphorylation on 5-6 loop and C-terminus

Activity Switching

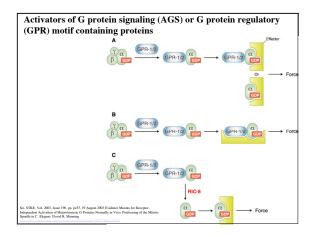
REGULATION OF ACTIVITY

Activators of G protein signaling (AGS) or G protein regulatory (GPR) motif containing proteins

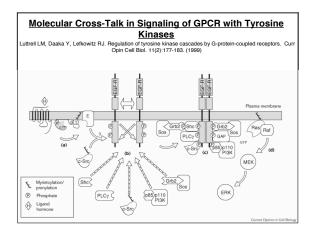
Receptor-independent activation of heterotrimer G proteins

Lanier SM. AGS proteins, GPR motifs and the signals processed by heterotrimeric

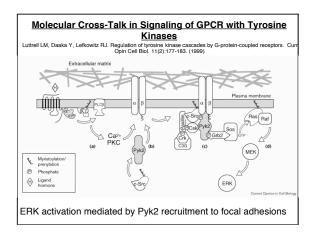
Cannet Sin, ACG proteins Biol Cell. 2004 Jun;96(5):360-72 http://www.sciencedirect.com/science?.ob=ArticleURL&_uid=86VRK-4CDJ867-1 Ls_user=5010455_coverDate=06X27305272004220058_uid=202402799&_rdoc=18_fmt=full&_orig=search&_qd= 18_cdi=62378_ost=36_docanchor=&iww=c&_acct=C000022659&_version=18_urtVersion=0&_userid=5010 458md5=015556a565b5d854a1016056aacatimigpref=f



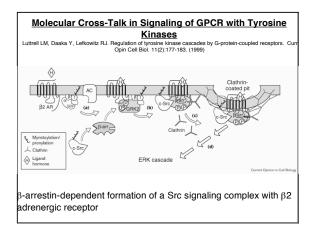














Diseases and G Proteins: Both loss of function and gain of function mutations

•Pseudohypoparathyroidism type la (PHP-la) has 30-50% Gs activity, appears to be autosomal-dominant, primary defect not always certain

·Cholera (salt secretion) and whooping cough

-Lithium at therapeutic concentrations (0.6 mM) blocks coupling of muscarinic and β - adrenergic receptors to G proteins, may be basis of some of Li⁺ effects in manic depression, although PIP₂ effect may be far more important

•Growth hormone-secreting pituitary tumors with somatic mutations in Gs, Gαs activated by mutation inhibiting GTPase, same defect in 3/11 adrenal cortex and 3/10 ovarian endocrine tumors in Gi2 chain and in autonomously functioning thyroid adenoma

Diseases and G Proteins: Both loss of function and gain of function mutations

-Acromegaly-hypersecretion of growth hormone by somatotrophs in pituitary, very small tumors, two classes of tumors, one is a $G_{s\alpha}$ defect -> Growth hormone constitutively secreted, adenylate cyclase only needs GTP, GHRH independent cAMP, Gln 227 and Arg 201 mutations

--Chemokine receptor CCR5, co-receptor fo HIV, mutation prevents binding of HIV to target cells; homozygotes protected from HIV

--Combined testotoxicosis and pseudohypoparathyroidism type Ia (PHP-Ia) - rare

P, Nakamoto JM, van Dop C, Bourne HR Bapid GDP n (6493)-164-169

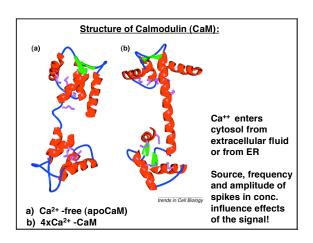
Other Second Message Systems:

Ca++: intracellular [Ca2+] usually 10-7->10-5M

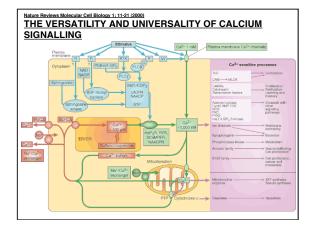
Transient increases (sparks, waves)-quickly pumped out or binding proteins sequester. Some effectors bind Ca⁺⁺ directly (PK-C). Many use intermediates: troponin C (muscle), S100 family, recoverin, frequenin, and best understood...

<u>Calmodulin</u> (17kD,4 binding sites, K_d for 2 carboxy-term= 10⁻⁷ M, for 2 N-term=2.4x10⁻⁶)

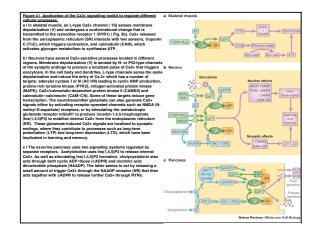
Ca²⁺ Binding exposes hydrophobic side chains:



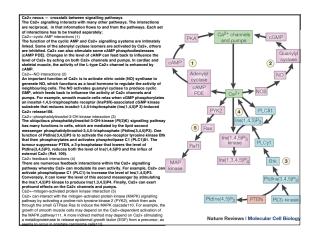




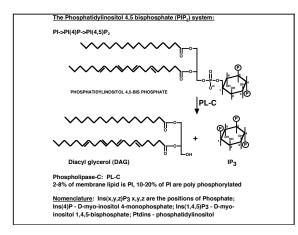




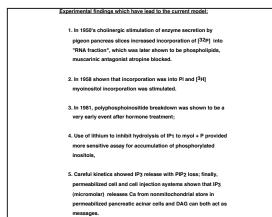


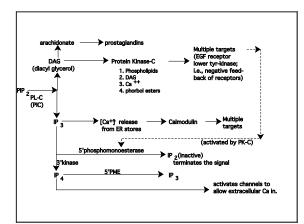




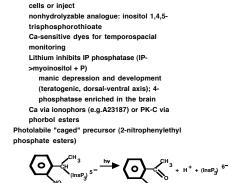












Systems studied: add IP3 to permeabilized

Methods:



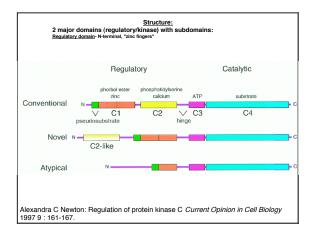
Protein Kinase C (PKC)

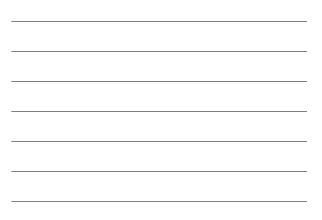
single chain of **77 kD**

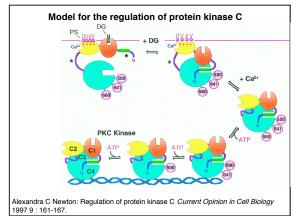
- ***Discovered by Nishizuka and colleagues 1977
- ***cytoplasmic-inactive // translocated to plasma membrane on binding DAG-active
- ***DAG induces translocation to membrane and increases affinity for Ca** to normal physiologic levels, DAG binds stoichiometrically and steriospecifically (sn12, not sn2,3)
- ***Requires acidic phospholipid (probably PS), 4-10 per enzyme ***multiple isozymes -11 identified by cDNA screening,
- ***phorbol esters and other tumor promoters bind at diglyceride site and activate PK-C, more potent than DAG and not readily metabolized

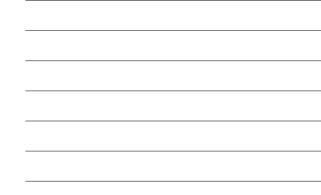
nhibitors: cationic amphipathic, e.g., chlorpromazine, trifluoperazine and sphingosine

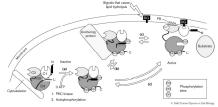
Multiple Isoforms of PL-C: 56.6 kD (PLC-α),138.2 kD (PLC-β), 148.4 kD (PLC-γ) 85.8 kD (PLC-δ)











**pseudosubstrate site in aa19-36 (R¹⁹-F-A-R-K-G-<u>A</u>²⁵-L-R-G-K-N-V-H-D-V-K-N³⁶) peptide is antagonist (Ki=147 nM, inhibits, substitution of A25 for Ser gives good substrate)

**removed by Ca-dependent protease (Calpain I) in presence of TPA, DAG etc. -> <u>51 kD (</u>constitutively active, unstable) and <u>26 kD</u> (regulatory) fragments

<u>experimental trick</u>: treat cells with high levels of TPA, short term increase in PK-C activity, but overnight functionally PK-C depleted

NOTE COMMON REGULATORY MECHANISM: Built-in inhibitor is released on activation

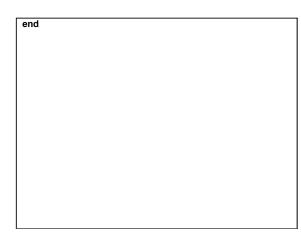
PK-C (covalently associated inhibitory domain)-pseudosubstrate

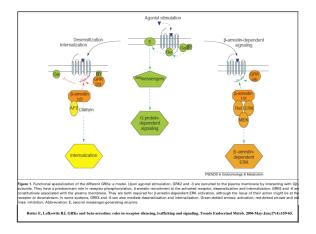
cAMP-dependent PK (regulatory subunits released by cAMP binding) also inhibitor protein which contains pseudosubstrate R-R-N-<u>A</u>-I; substrate is R-R-X-<u>Ser(P)-</u>X

cGMP-PDE of ROS (γ inhibitory subunit released by T_{α} of transducin)

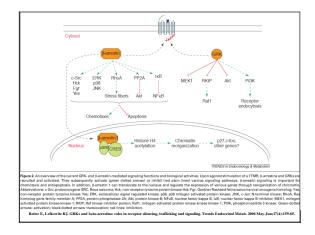
myosin light chain kinase (substrate-like inhibitory tail, calmodulin binds to release)

Ca/Calmodulin-dependent protein kinase: hexamer, internal pseudosubstrate inhibits, Ca/calmodulin binding allows autophosphorylation and Ca/Calmodulin independence

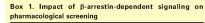












pharmacological screening Pharmacological screening Pharmacological agents acting via 7TMRs have traditionally been discovered through the screening of numerous chemical structures in biological systems. Clearly, the type of receptor screen employed to detect biologically active molecules will greatly define the types of molecules detected. For many years, these functional high-thrus G protein activation, as the read-out. The drugs detected by such screens have been agonists, partial agonists, antagonists or inverse agonists for G protein activation. However, the recent demonstration that specific ligands are able to activate β-arrestin-dependent, G protein-independent signaling implies that multiple discrete 'active' receptor conformations coexist (48.50.54.68). It is now possible to develop assays to screen compound libraries systematically using β-arrestin recruitment (e.g. confocal microscopy, fluorescence resonance energy transfer- or biolumines-cence resonance energy transfer-based assays) or β-arrestin redouts for 7TMR activation. This new generation of high throughput screens will potentially lead to the identification of new pathousy-selective drugs that might have valuable therapeutic properties.