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Phospholipase D – Structure, Regulation and Function

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Phospholipase D – Structure, Regulation and Function

1 Introduction

Phospholipase D (PLD) is an enzyme that is widely distributed in bacteria, protozoa, fungi, plants and animals. Its principal substrate is phosphatidylcholine (PC) which it hydrolyzes to phosphatidic acid (PA) and free choline. PA can be further metabolized to diacylglycerol (DAG) by phosphatidate phosphohydrolase (PAP, also called lipid phosphate phosphatase), and to lysophosphatidic acid (LPA) by phospholipase A_2 (PLA₂). Phospholipase D also carries out a transphosphatidylation reaction, which is unique to this enzyme. This involves the transfer of the phosphatidyl group from the phospholipid substrate to a primary alcohol to yield a phosphatidylalcohol. This reaction occurs to a very much less extent with secondary or tertiary alcohols, giving a measure of specificity.

Many PLD isoforms have been cloned from bacterial, plant, yeast and mammalian sources. All exhibit three or four highly conserved sequences. Within two of these sequences is found the highly conserved $HXKX_4DX_6GSXN$ motif, designated HKD (Ponting & Kerr 1996; Koonin 1996). This motif is found not only in the PLD isoforms, but in a PLD superfamily comprising bacterial phosphatidylserine and cardiolipin synthases, bacterial endonucleases, pox virus envelope proteins and a murine toxin from *Yersinia* (Ponting & Kerr 1996; Koonin 1996). Mutagenesis studies have shown that the two HKD motifs in PLD are required for catalysis and associate to form a catalytic center (Sung et al. 1997; Xie et al. 1998). Catalysis occurs by a two-step mechanism and involves the formation of a phosphohistidine intermediate (Waite 1999).

Some plant and most animal PLDs require phosphatidylinositol 4,5bisphosphate (PIP₂) for activity (Qin et al. 1997; Frohman et al. 1999), and mammalian PLDs are regulated by a wide variety of growth factors, cytokines, neurotransmitters and other agonists acting through G protein-coupled receptors (GPCRs) (Exton 1999). Mammalian PLD isozymes are splice variants of two major isoforms (PLD1 and PLD2) which have M_rs of 120K and 100K, respectively. They show approximately 50% amino acid sequence identity and are widely distributed (Hammond et al. 1997; Colley et al. 1997; Exton, 1998; Meier et al. 1999). PLD1 is strongly activated in vitro by conventional PKC isozymes and members of the ADP-ribosylation factor (ARF) and Rho families of small G proteins (Hammond et al. 1997; Min et al. 1998b). In contrast, PLD2 shows weak or absent responses to PKC, ARF and Rho in vitro (Colley et al. 1997; Kodaki & Yamashita 1997; Lopez et al. 1998; Slaaby et al. 2000). Mammalian cells also contain an oleate-stimulated PLD activity (Massenburg et al. 1994; Banno et al. 1997; Lee et al. 1998), but its nature is unresolved. One form is unaffected by ARF and PIP₂ (Massenburg et al. 1994; Lee et al. 1998) whereas another form found in nuclei is stimulated by ARF (Banno et al. 1997). Oleate and other unsaturated fatty acids can stimulate PLD2 and synergize with PIP₂ (Kim et al. 1999b). Three PLD isozymes that specifically act on phosphoinositides have also been discovered (Ching et al. 1999). Two of these preferentially act on phosphatidylinositol 3,4,5-trisphosphate (PIP₃), while the other acts on PIP₃ and phosphatidylinositol 3-phosphate. None of the isozymes acts on PIP₂, but this phospholipid stimulates their activity. Another PLD isozyme has been reported in neutrophils (Horn et al. 2001). This has an apparent M_r of 90K and is not recognized by antibodies to the PLD1 and PLD2 isozymes, but does interact with an antibody raised to a conserved sequence in these enzymes. It is stimulated by PIP₂ and inhibited by oleate and divalent cations.

The cellular functions of PLD remain unclear. The enzyme has been implicated in mitogenesis, endocytosis, actin cytoskeleton rearrangements, glucose transport, secretion and superoxide production. It has also been proposed to play an important role in trafficking through the Golgi. Its cellular functions relate mainly to the generation of PA, which affects the activity of many enzymes and other cellular proteins. DAG derived from PA may also activate certain isoforms of protein kinase C (PKC). LPA is a major extracellular messenger that interacts with certain types of EDG receptors. PLD is likely involved in its generation via PA formation and subsequent PLA2 action.

This review is focussed on mammalian PLDs. For consideration of plant and yeast PLDs, the reader is referred to recent review articles (Pappan & Wang 1999; Rudge & Engebrecht 1999; Munnik 2001).

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Structure of Phospholipase D

The crystal structure of PLD from *Streptomyces* has been determined and also that of the bacterial endonuclease Nuc, a member of the PLD superfamily. Nuc is a protein of small molecular mass (16 kDa) that has only one IIKD motif. It crystallizes as dimer and each monomer consists of an 8-stranded β -sheet flanked by 5 α -helices (Stuckey & Dixon, 1999; Fig. 1). Each conserved HKD sequence is positioned on two loops and, in the dimer, they lie adjacent to each other to produce a single active site. The active site residues are held in place by a network of hydrogen bonds within each monomer and between both monomers. These involve not only the conserved His, Ser and Asn, but also adjacent Glu residues. Using tungstate as a phosphate surrogate to explore residues involved in substrate binding, it was found

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Fig. 1. Domain organization of Nuc dimer. Nuc is a bacterial endonuclease that is a member of the PLD superfamily. One monomer is yellow and the other purple with the variable loop in red. The colored spheres represent residues in the HKD motif, which are identified at the bottom of the figure. From Stuckey and Dixon (1999) by permission of the authors and publisher

that the His, The Lys and Asn residues from each HKD motif were important (Fig. 2, Stuckey & Dixon, 1999). The Lys and Asn residues are postulated to be involved in binding and neutralizing the negative charge on the phosphate of the substrate and the His residues during catalysis (see below).

The structure of *Streptomyces* PLD is shown in Fig. 3 (Leiros et al. 2000). It consists of two highly interacting components of similar topology. Each component is made up of a β -sheet composed of 8 or 9 β - strands and flanked by 9 α -helices. Overall, the structure is very similar to the Nuc endonuclease dimer. Although most of the α -helices are oriented along the β -strands, some are rotated with respect to this overall direction (Leiros et al. 2000). The active center region is very similar to that in the Nuc dimer, with identical residues from each component. The rotated α -helices are distant from the active center, but probably act as scaffolding to keep the active site open and accessible to substrate (Fig. 3, Leiros et al. 2000).

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Fig. 2. Stereographic view of PLD f rom *Streptomyces* colored dark blue to red according to the sequence. Two phosphate groups are shown in red, one of which is in the catalytic center. From Leiros et al. (2000) by permission of the authors and publisher

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Fig. 3. Hydrogen bonding at the active center of tungstate-substituted Nuc dimer. The color coding of the amino acid residues of the HKD motifs is as described in Fig.1. The A and B subscripts refer to the different monomers. From Stuckey & Dixon (1999) by permission of the authors and publisher

The enzyme was crystallized using a citrate-phosphate buffer and one phosphate was bound at the active site (Leiros et al. 2000). This very probably corresponds to the phosphate head group of the phospholipid substrate and lies in close contact to His, Lys and Asn residues contributed from both domains of the enzyme as seen for the catalytic center of the Nuc dimer (Fig. 2). As discussed in more detail below, there is much evidence that the two His residues participate in the catalytic reaction. Interestingly, there are no structural similarities between PLD and other lipases, including the secretory and cytosolic forms of PLA_2 , bacterial or mammalian PI phospholipase C (PLC), and bacterial PC-phospholipase C, with the exception of a cutinase from *Fusarium* (Leiros et al. 2000). As is evident in Fig. 3, the similar topology of the two components of *Streptomyces* PLD suggests that they have a common origin. This is also suggested by the duplicated HKD motifs of the enzyme and the fact that it is possible to align the structure of the Nuc dimer against the *Streptomyces* PLD structure (Leiros et al. 2000).

The structural elements responsible for the substrate specificity of PLD remain unknown. By analogy with the structure of cytosolic PLA_2 , residues on the lip of the entrance to the active site might play a role (Leiros et al. 2000). These may be located in two flexible loops located relatively close to the active center in a region thought to make membrane contact when catalysis occurs. *Streptomyces* PLD is much smaller (54 kDa) than mammalian PLDs and lacks the N- and C-termini that contain the interaction sites for PKC, Rho and ARF. Consequently, although its structure has provided very valuable information about the catalytic mechanism, detailed information about the mechanisms by which mammalian PLD is regulated by PKC and small G proteins, will await the determination of the structure of one of these isozymes. Nevertheless, mutagenesis studies have provided much information about the mechanisms of catalysis and regulation of the mammalian PLD1 and PLD2 isozymes.

Both PLD1 and 2 show four highly conserved sequences and other motifs. A schematic representation of PLD1 is shown in Fig. 4 (Sung et al. 1999b; Frohman et al. 1999). At the N-terminus are a PX domain, which is usually involved in interactions with proteins or 3-phosphoinositides, and a pleck-strin homology (PH) domain, which is frequently involved in membrane association involving PIP₂ or PIP₃. In the second and fourth conserved domains are the N-terminal and C-terminal HKD motifs. In the center of the linear sequence is a loop region, which is absent in PLD2 and is partly missing in splice variants of PLD1. A PIP₂ binding site has been identified between the loop region and the third conserved sequence (Sciorra et al. 1999). Interaction sites for PKC and Rho have been identified in the N- and C-terminal sequences, respectively (see below).

Mutagenesis studies have shown that both HKD motifs are required for catalysis (Sung et al. 1997) and co-expression studies in COS7 cells have shown that hydrophobic domains including and surrounding the motifs associate to bring them together to form a catalytic center (Xie et al. 1998, 2000a). Conserved sequence III is required for catalysis, but its role is unknown. Because of its enrichment in aromatic residues, which are also found for the choline-binding region of the acetylcholine receptor, it has been suggested that this sequence interacts with the choline headgroup of PC (Sung et al. 1997, 1999b).



roles for the various motifs are shown. From Sung et al. (1996b) by permission of the authors and publisher

human PLD1

3 Catalytic Mechanism

As described above, the HKD motifs are essential for catalysis, and structural and other studies show that they dimerize to form the catalytic center (Sung et al. 1997; Xie et al. 1998, 2000a). Experiments with H₂¹⁸O showed that PLD catalyzes bond cleavage of P-O rather than C-O (Holbrook et al. 1991), and an early scheme for the catalytic reaction proposed a ping-pong mechanism (Stanacev & Stuhne-Sekalec, 1970) with the formation of a covalent phosphatidyl-enzyme intermediate, with the free SH group of Cys as the phosphatidate acceptor (Yang et al. 1967). However there is now strong evidence that His is the acceptor (Waite, 1999). In addition to being part of the HKD motif, His has been shown to be labeled with ³²Pi during experiments with Nuc or Yersinia murine toxin (Ymt) employing the phosphate-water exchange reaction that members of the PLD superfamily catalyze (Gottlin et al. 1998; Rudolph et al. 1999). This labeling was abolished by hydroxylamine and by mutation of either the conserved His or Lys, but was unaffected by mutation of the conserved Ser. Tungstate, which is a phosphate analogue and an inhibitor of the reaction, also binds to His, Lys and Asn in the active site of Nuc (Stuckey & Dixon, 1999), and phosphate is in close contact with His, Lys and Asn in Streptomyces PLD (Leiros et al. 2000).

A two-step catalytic mechanism has been proposed for PLD, based on studies of Nuc and Ymt (Fig. 5, Stuckey & Dixon, 1999; Rudolph et al. 1999). The first is a nucleophilic attack on the substrate phosphorus by the imidazole N of one of the active site His residues, with the second active site His acting as a general acid to donate a H^+ to the O of the leaving group. The covalent linkage between His and phosphate generates a phosphatidylenzyme intermediate.

Although the role of the HKD motifs in the catalytic mechanism is unquestioned, other regions of PLD are required for catalysis. One region is conserved sequence III and another is the extreme C-terminus, since limited



Fig. 5. Two step mechanism for catalysis by PLD involving a covalent enzyme intermediate. From Gottlin et al. 1998 by permission of the authors and publisher

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```
Rat PLD1 KEAIVPMEVWT
Human PLD1 KEAIVPMEVWT
Rat PLD2 KRGMIPLEVWT
Human PLD2 KEGMIPLEVWT
C. elegans PLD KEGLVPSAVFT
Fig. 6. Sequences of C-termini
of PLDs from various species
Yeast SP014 SDRLSPMEIYN
```

mutations of these sequences abolish catalysis (Sung et al. 1999b; Xie et al. 2000b; Liu et al. 2001). The C-terminal four amino acids are conserved in PLD1 and PLD2 and are similar to those in putative PLDs from *C. elegans* and *D. melanogaster*, but deviate from those in fungi, bacteria and plants (Fig. 6). The mammalian sequence is not required for association of the HKD motifs or for post-translational modifications such as palmitoylation or phosphorylation (Xie et al. 2000b, 2001). The activity of some forms of PLD1 with mutations in the C-terminus can be partially restored by co-expression of the C-terminal half of wild-type PLD (Xie et al. 2000b) or by addition of peptides corresponding to the C-terminus (Liu et al. 2001).

Since the phospholipid substrate of PLD is located in cell membranes, membrane association is critical for catalytic activity. Mutagenesis studies and sequence alignments have identified several sequences potentially involved in membrane interactions. One is the PH domain, which, in many proteins, is involved in binding to phosphoinositides in membranes. However, deletion of this domain in PLD does not abolish catalytic activity or membrane association (Park et al, 1998; Xie et al. 1998, 2000a; Sung et al. 1999b), implying the existence of other domains that target the enzyme to membranes. Another PIP₂ binding site has been identified in PLD1 (Sciorra et al. 1999). Mutation of this site abolishes activity, but does not alter membrane association.

4 Cellular Location of PLD1 and PLD2

Studies of the subcellular location of mammalian PLD isozymes have involved measurements of enzyme activity in subcellular fractions, Western blotting of subcellular fractions, immunocytochemistry and overexpression of PLD isozymes tagged with green fluorescent protein (GFP) or hemagglutinin (HA) in several cell types. Subcellular fractionation of liver demonstrated that the specific activity of PLD was highest in plasma membranes, Golgi and nuclei (Provost et al. 1996). Studies in other tissues or cells also revealed the presence of PLD activity in plasma membranes, Golgi and nuclei (Liscovitch et al. 1999). However, these reports did not define the distribution of PLD1 or PLD2. Because the affinity and specificity of most antibodies to these isozymes are generally not sufficient for use in subcellular fractionation or immunofluorescence studies, researchers have mainly relied on the expression of GFP- or HA-tagged PLD1 and PLD2 in cell types such as COS, RBL, CHO, 3Y1 and REF-52 cells. However, there has been one report of the intracellular localization of endogenous PLD1 in GH₃ pituitary and NRK kidney cells. This utilized highly sensitive antibodies together with immunofluorescence, immunogold electron microscopy and cell fractionation to localize PLD1 to the Golgi apparatus (Freyberg et al. 2001). Although the enzyme was concentrated in this organelle, it exhibited a diffuse reticular staining pattern with some localization in late endosomes and lysosomes. Disruption of the Golgi with brefeldinA (BFA) or 1-butanol caused release of PLD1. Interestingly, overexpression of PLD1 led to its mislocalization in a heterogenous population of small vesicles.

Other studies using GFP- or HA-tagged PLD1 have localized PLD1 to vesicular structures in the perinuclear region (Fig. 7), but have given variable results with respect to the plasma membrane or Golgi (Colley et al. 1997; Brown et al. 1998; Kim et al. 1999b; Sugars et al. 1999; Emoto et al. 2000; Lee et al. 2001; Kam and Exton 2001). Surprisingly, this approach has localized PLD2 primarily to the plasma membrane (Colley et al. 1997; Emoto et al. 2000; Lee et al. 2001) even though this isozyme appears less likely than PLD1 to be involved in signal transduction. Some studies have reported constitutive association of PLD2 and PLD1 with growth factor receptors (Slaaby et al. 1998; Min et al. 1998a). Western blotting has shown marked PLD1 immunoreactivity in the plasma membranes of chromaffin cells (Vitale et al. 2001) and 3Y1 fibroblasts (Kim et al. 1999b), with significant amounts also in the Golgi and endoplasmic reticulum fractions of the fibroblasts. Immunofluorescence and confocal microscopy studies have also shown that expressed PLD1 is localized to the periphery of chromaffin cells (Vitale et al. 2001). On the other hand, strong PLD2 immunoreactivity has been reported in cardiac sarcolemma (Park et al. 2000) and in the periphery of PC12 cells transfected with PLD1 (Lee et al. 2001). Recently PLD activity has been identified in caveolae, and both PLD1 and PLD2 have been reported to be present (Czarny et al. 1999, 2000; Iyer & Kusner, 1999; Sciorra & Morris 1999; Y. Kim et al. 1999, 2000). Some studies, but not all (Vitale et al. 2001), have reported translocation of PLD1 in response to cell stimulation (Brown et al. 1998; Emoto et al. 2000). However, because of the strong association of PLD with membranes, these changes probably involve the relocalization and/or



Fig. 7a-c. Cellular location of PLD1 in COS-7 cells. The cells were transfected with constructs for Xpress-tagged rPLD1 and EGFP-tagged rPLD1. Panel a shows the location of Xpress-tagged rPLD1 using a monoclonal antibody to Xpress. The EGFP fluorescence is shown in panel b, and the merged image is shown in panel c. From Kam & Exton (2001) by permission of the authors and publisher

40 µm

fusion of membranes rather than movements of PLD1 per se. A recent report has shown co-localization of PLD1 and PLD2 with the actin cytoskeleton in the periphery of COS7 and PC12 cells expressing these PLD isozymes (Lee et al. 2001) and a functional interaction with this cytoskeleton has been proposed. As noted in the next section, phosphorylation and palmitoylation of PLD alter its association with membranes.

5 Posttranslational Modification of PLD

Several studies have demonstrated that PLD1 and yeast PLD (Spo14) are phosphorylated on Ser/Thr residues in unstimulated cells (Rudge et al. 1998; Y. Kim et al. 1999, 2000; Xie et al. 2000a, 2001). This results in the appearance of slower migrating bands on SDS polyacrylamide gel electrophoresis (Fig. 8, Rudge et al. 1998; Xie et al. 2000a; Kim et al. 2000). These bands are lost by treatment of the enzyme with alkaline phosphatase or with protein phosphatases1and 2A, which are specific for phosphorylated Ser or Thr residues (Rudge et al. 1998; Xie et al. 2000a). However, the endogenous phosphorylation appears to have little effect on the catalytic activity of the enzymes (Xie et al. 2000a). In contrast, it influences their subcellular localization (Fig. 8, Rudge et al. 1998; Xie et al. 2000a). The phosphorylated form of PLD1 is found exclusively in membranes in COS7 cells in which it is over-



Fig. 8. Phosphorylated PLD1 is associated with membranes. COS-7cells coexpressing the N- and C-terminal halves of rPLD1 or full-length rPLD1 were fractionated into membrane (M) and cytosol (C) fractions and Western blotted with antibodies against these proteins. The upper bands (slower migration on SDS polyacrylamide gel electrophosis) seen in the membrane fractions represent the phosphorylated enzyme. From Xie et al. (2000a) by permission of the authors and publisher

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expressed (Xie et al. 2000a; Kim et al. 2000). Phosphorylation of Spo14 is required for its relocalization during meiosis, where it participates in spore formation (Rudge et al. 1998). The nature of the protein kinase(s) responsible for the endogenous phosphorylation of PLD1 and Spo14 is unknown. There has been one report that PLD2 is phosphorylated on Ser/Thr residues and that this inhibits its activity (Watanabe & Kanaho 2000). Modification of PLD isozymes by tyrosine kinases and PKC will be discussed below in the relevant sections.

PLD1 has been reported to be palmitoylated when expressed in COS-7 cells (Manifava et al. 1999; Sugars et al. 1999; Xie et al. 2001). This occurs on Cys residues 240 and 241 in hPLD1 and rPLD1 (Sugars et al. 1999; Xie et al. 2001). The effect of palmitoylation on the catalytic activity of PLD1 is un-



Fig. 9A, B. PLD2 is palmitoylated on cysteines 223 and 224. The incorporation of $[{}^{3}H]$ palmitate into rPLD1 and the alanine mutants is shown by fluorography. Palmitoylation was totally lost in the C223A, C224A double mutant. From unpublished studies by Z. Xie,W.-T. Ho and J.H. Exton

clear. Although palmitoylation is eliminated when the two Cys residues are mutated to Ala, the enzyme is fully active in vitro (Sugars et al. 1999). When expressed in COS-7 cells, there is a partial loss of catalytic activity (Sugars et al. 1999; Xie et al. 2001), but it is not clear that this is due to the loss of palmitoylation or to the Cys mutations per se. This is because mutant forms of PLD1 in which the palmitoylation sites have been deleted show high catalytic activity (Xie et al. 2000). Loss of palmitoylation does, however, weaken the association of PLD1 with membranes (Xie et al. 2000) and causes its relocalization within COS-7 cells (Sugars et al. 1999). rPLD2 is also palmitoylated when expressed in COS-7 cells (Fig. 9) and the modification is eliminated by mutations of Cys 223 and Cys 224 (corresponding to Cys 240 and 241 in rPLD1). Although this results in a loss of basal catalytic activity, the activity in the presence of phorbol ester is not decreased as seen also for PLD1. As in the case of PLD1, mutations of the palmitoylation site reduces the membrane association of PLD2.

There has been one report that PLD1 expressed in Sf9 cells is glycosylated and that this determines its distribution between the membrane and soluble fractions (Min et al. 1998b). There have been no reports of this posttranslational modification in mammalian cells. Neither PLD1 nor PLD2 has the consensus sequences for modification by myristoylation or prenylation.

6

Regulation of Phospholipase D

The PLD activity of many cell types is increased by a variety of hormones, neurotransmitters, growth factors and cytokines (Exton 1997; Exton 1999). Many of the agonists act through membrane receptors coupled to hetero-trimeric G proteins e.g. G_q , G_i , G_{13} , but there is no evidence that these G proteins activate PLD directly. In contrast, they act on the enzyme via signaling cascades. Likewise, the tyrosine kinase activity of growth factor receptors does not appear to regulate PLD by *direct* phosphorylation and the regulation again appears to be indirect.

6.1 Role of Phosphatidylinositol 4,5 Bisphosphate

Many factors have been shown to affect PLD activity directly. One factor that is essential for catalytic activity of many isozymes in animals, plants and protozoa is PIP_2 (Brown et al. 1993; Liscovitch et al. 1994; Hammond et al. 1995; Pappan et al. 1997; Wang et al. 2001). PIP_3 is also effective and phos-



Fig. 10. PLD1 activity is stimulated in vitro by PI 4,5-P₂ and PI 3,4,5-P₂, but not by other phospholipids. In vitro PLD assays were carried out with recombinant rPLD1 in the presence of myristoylated ARF3 and GTP γ S. Where indicated PIP₂ was replaced by other lipids in the substrate PL vesicles by other lipids. From Min et al. (1998b) by permission of the authors and publisher

phatidylinositol 4-phosphate (PIP) can have an effect, but all other phospholipids are ineffective (Fig. 10, Brown et al. 1993; Liscovitch et al. 1994; Schmidt et al. 1996b; Pappan et al. 1997; Hammond et al. 1997; Min et al. 1998b; c.f. Hodgkin et al. 2000). A binding site for PIP₂ on PLD2 has been located between conserved sequences II and III by the use of a photoreactive PIP₂ derivative, and by the demonstration that the site contains amino acid residues that are required for PLD activity (Sciorra et al. 1999). The sequence contains multiple residues that are conserved between PLD1, PLD2 and Spo14. Although mutation of these residues in PLD2 and Spo14 causes loss of PIP₂ binding and catalytic activity, it does not affect the cellular localization of these enzymes, indicating that other sequences are involved in membrane association (Sciorra et al. 1999). Another study has localized another

 PIP_2 binding site in PLD1 to the isolated PH domain using surface plasmon resonance (Hodgkin et al. 2000). Mutagenesis of conserved residues in this domain caused a loss of PLD activity. However, these results must be interpreted with caution since another study showed that deletion of the PH domain produced little effect on activity (Hoer et al. 2000) and other studies have shown that deletion of the N-terminal 319 residues of PLD1 or PLD2, which contain the PH domain, results in an enzyme that is still active (Park et al. 1998; Xie et al. 1998; Sung et al. 1999a,b).

Evidence that PIP₂ is required for the activity of PLD in vivo has come from several studies utilizing permeabilized cells. These have included examinations of the effects of neomycin, which binds PIP₂ and inhibits PLD activity stimulated by MgATP and GTPyS or by PKC and PMA (Liscovitch et al. 1994; Pertile et al. 1995; Ohguchi et al. 1996; Schmidt et al. 1996b). The Clostridium difficile Toxin B which inactivates Rho proteins reduces PIP₂ levels in cells (Schmidt et al. 1996b). This is because Rho stimulates PIP₂ synthesis through its action on PI 4-P 5-kinase via Rho-kinase (Oude Weernink et al. 2000). The decrease in PIP₂ is associated with decreased membrane-associated PLD activity and this can be reversed by adding PIP₂ to the membranes (Schmidt et al. 1996b). Both Toxin B and the C3 exoenzyme of C. botulinum, which also inactivates Rho, inhibited the ability of carbachol or AlF₄⁻ to activate PLD in HEK cells expressing the M3 muscarinic cholinergic receptor (Schmidt et al. 1996a). However, these results can also be explained by inhibition of the direct effect of Rho on PLD (see below).

Another line of support for the dependence of PLD on PIP₂ for activity comes from studies of the interaction and co-localization of Type I α PI 4-P 5-kinase and PLD (Divecha et al. 2000). These have utilized co-expression of PLD2 and the kinase in COS-7 cells and have shown by co-immunoprecipitation that the two proteins associate. Furthermore, they co-localized in a submembranous vesicular compartment whenexpressed in PAE cells. Local control of the activity of PLD2 by PIP₂ was indicated by the finding that PLD activity was reduced when a kinase-dead mutant of PI 4-P 5-kinase was transfected in place of the wild-type enzyme (Divecha et al. 2000). Control of PLD activity by changes in the level of PIP₃ seems unlikely in view of the much higher level of PIP₂ in cells. Accordingly, concentrations of wortmannin that greatly decrease the level of PIP₃ are without effect on basal and GTP γ S-stimulated PLD activity in permeabilized HL-60 cells (El Hadj et al. 1999).

6.2 Role of Protein Kinase C

PKC is an important mediator of agonist activation of PLD in some cell lines, but may play a minimal role in other cell types. In most cells, treatment with 4 β -phorbol 12-myristate 13- acetate (PMA) or related phorbol esters stimulates PLD markedly, but agonist effects are often of less magnitude (Fig. 11A). The role of PKC in the effects of agonists has generally been explored by testing the effects of inhibitors of the kinase action of PKC. These have included a variety of non-specific and specific inhibitors e.g. staurosporine, H-7, sphingosine, Ro-31-8220, bisindolylmaleimide I, Gö6076, chelerythrine, bryostatin 1 and calphostin C. Most of these inhibitors target the ATP-binding site of PKC, whereas sphingosine, bryostatin1 and calphostin C interact at the DAG/phorbol ester binding site (Nixon 1997). They generally inhibit the effects of PMA on PLD almost completely, but have partial or, in some cases, no effects on natural agonists (Exton 1997), implying the existence of other mechanisms of PLD activation not involving PKC.

Other approaches have been used to define the role of PKC in agonist activation of PLD. A common one is prolonged treatment of cells with phorbol ester to down-regulate PKC. This procedure results in a time-dependent loss of the Ca²⁺-dependent and -independent typical PKC isozymes, but no loss of the atypical isozymes (Kiley et al. 1990; Olivier and Parker 1992). Except in a few cases, PKC down-regulation results in complete or partial inhibition of the effects of growth factors or G protein-linked agonists on PLD (Exton 1997). The usual mechanism by which these factors and agonists activate PKC is by stimulating the hydrolysis of PIP₂ to generate DAG. This involves the β -isozymes of phospholipase (PLC) in the case of agonists that activate G_q and G_i , and the γ -isozymes of PLC in the case of growth factors that induce autophosphorylation of their receptors. In the case of platelet-derived growth factor (PDGF), the evidence for the involvement of PLC is very strong. For example, in cells expressing mutant receptors that are unable to induce activation of PLC, PDGF was incapable of activating PLD (Fig. 12, Yeo et al. 1994). On the other hand, the PLD response was restored with receptors that mediate PLC activation, but do not elicit other PDGF signaling pathways (Yeo et al. 1994). In another study utilizing fibroblasts overexpressing PLC-y, the PLD response to PDGF was greatly enhanced, except when tyrosine kinase activity was inhibited (Lee et al. 1994). Overexpression of the α - and β 1-isozymes of PKC also enhanced the PLD responses to PMA, G protein-linked agonists or PDGF (Pai et al. 1991; Pachter et al. 1992; Eldar



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Fig. 12. Activation of PLD by PDGF in TRMP kidney epithelial cells expressing mutated PDGF receptors. Cells were labeled with $[^{3}H]$ myristic acid and PLD measured by $[^{3+}H]$ PtdBut formation. Mutant receptors were: F5, lacking all tyrosines required for signaling; PLC-lacking the tyrosine required for coupling to PLC; PLC⁺, having only the tyrosine for coupling to PLC. The other mutants (PI3K⁺, GAP⁺, p64⁺) having the tyrosines for coupling to other signals. From Yeo et al. by permission of the authors and publisher

et al. 1993), while depletion of PKC- α by antisense methods decreased activation of the enzyme (Balboa et al. 1994).

An interesting approach to exploring the role of PKC isozymes in regulating PLD has involved the use of a peptide which binds to the receptor for activated PKC (RACK1) (Thorsen et al. 2000). Cell lines expressing this peptide showed inhibition of cell functions mediated by conventional (Ca^{2+} dependent) isozymes of PKC. Thus these cell lines showed a great loss of PMA-stimulated PLD activity, whereas the parental cells did not. On the other hand, the peptide-expressing cells showed normal uptake of choline

Fig. 11A, B. Correlation of activation of PLD with membrane translocation of PKC α . A. Time courses of activation of PLD in NIH3T3 fibroblasts by PMA, LPA and PDGF. Cells were labeled with [³H]myristic acid and PLD measured by [³H]PtdBut formation. B. The presence of PKC α and PKC ε in the cytosolic (C) and membrane (M) fractions at various times was determined by Western blotting. From unpublished studies by F.G. Buchanan, M. McReynolds and J. H. Exton

and its incorporation into PC (Thorsen et al. 2000). These data provide strong evidence for a role of α -and β -isozymes of PKC in PMA activation of PLD, possibly involving RACK1.

Activation of PKC isozymes by agonists is usually associated with their translocation from the cytosol to the plasma membrane and other intracellular membranes (Jaken 1997) The movement to the plasma membrane occurs presumably because the DAG generated by PIP₂ breakdown remains in the plasma membrane until it is metabolized. Thus the simplest scheme for the activation of PLD by agonists that stimulate PLC is that there is translocation of typical PKC isozymes to the plasma membrane where they interact with PLD to cause its activation and possibly phosphorylation. In support of this scheme, studies of the relationship between PMA- or agonist-induced membrane translocation of PKC isozymes and PLD activation have shown a good correlation (Fig. 11A & B, Kim et al. 1999b). One of these studies identified plasma membranes as the site of PKC α -PLD1 interaction (Kim et al. 1999b) and more recently, caveolae have been proposed to be the site (Kim et al. 1999b, 2000).

As described in detail below, deletion of the first 319 or 325 amino acids of PLD1 yields an enzyme that is unresponsive to PKC, but is still activated by Rho or ARF (Park et al. 1998; Sung et al. 1999b). Insertion of 5 amino acids at Glu 87 of PLD1 also renders the enzyme unable to be activated by PKC, but it remains normally responsive to Rho and ARF (Zhang et al. 1999). Expression of N-terminally truncated PLD1 in COS-7 cells results in a PLD activity that is no longer responsive to constitutively active $G\alpha_q$ which is a G protein α -subunit that activates PLC and hence PKC (Exton 1996). Likewise, cells expressing PLD1 with an insert at Glu87 show greatly impaired responses to agonists that activate the M1-and M3-muscarinic and bombesin receptors (Zhang et al. 1999) which are known to couple to G_q (Exton 1996). These results with mutant PLD1 enzymes strongly support a role for PKC in the activation of PLD1 by agonists whose receptors are linked to G_q.

A major issue in studies of the activation of PLD by PKC is the role of phosphorylation. As noted below, there is strong evidence that the α - and β isozymes of PKC can directly activate PLD1 in vitro by a non-phosphorylation mechanism (Fig.13, Conricode et al. 1992, 1994; Singer et al. 1996; Hammond et al. 1997; Min et al. 1998; Sciorra et al. 2001). However, numerous studies with inhibitors of the kinase activity of PKC have shown inhibition of the activation of PLD by PMA and agonists in many cell lines (Exton, 1997). Some investigators have also reported phosphorylation of PLD1 in response to PMA in COS or Sf9 cells overexpressing this enzyme (Min &



Fig. 13. PKC α and PKC β directly activate PLD1. Increasing concentrations of recombinant PKC α and PKC β II were incubated with recombinant rPLD1 and PLD activity measured in vitro in the absence of ATP, with (•) and without (o) PMA. PKC ζ and all other PKC isozymes (not shown) were ineffective. Adapted from Min et al. (1998b) by permission of the authors and publisher

Exton 1998; Y. Kim et al. 1999, 2000). However, there has been only one report of PMA-stimulated Ser/Thr phosphorylation of *endogenous* PLD in cells (Y. Kim et al. 1999). Furthermore, although PLD1 can be phosphorylated by PKC α in the presence of ATP in vitro (Min et al. 1998b) its activity is actually inhibited (Hammond et al. 1997; Min et al. 1998b). Three residues (Ser 2, Thr 147 and Ser 561) have been identified as sites of phosphorylation on PLD1 by PKC α (Kim et al. 2000) and single or triple mutations of these residues to Ala reduced the activation by PMA in COS cells to approximately

50% of that seen with wild type PLD1 (Y. Kim et al. 1999, 2000). Since the mutations abolished the phosphorylation of PLD1 induced by PMA in COS cells overexpressing this enzyme, as indicated by the disappearance of slower migrating bands on polyacrylamide gel electrophoresis (Kim et al. 2000), these findings suggest that both phosphorylation and non-phosphorylation mechanisms of activation of PLD were operative in these cells.

Concerning the in vivo effects of PKC inhibitors which block the kinase activity by interacting at the ATP-binding site in the catalytic domain, there are several possible explanations. One obvious explanation is that these compounds block the phosphorylation of PLD by PKC. However, although it has been shown that mutation of the phosphorylation sites of PKC on PLD1 partially blocks the activation of the enzyme by PMA in intact cells (Kim et al. 2000), it has not been shown that these mutations inhibit the ability of PKC α to activate PLD1 in vitro. As noted above, PKC-induced phosphorylation of the PLD1 in vitro actually causes a decrease in activity (Hammond et al. 1997; Min et al. 1998b). Thus the relationship between the phosphorylation of PLD by PKC and its activation by the kinase remains unclear.

Another explanation is that another protein(s) that regulates PLC activity is phosphorylated by PKC. Pretreatment of plasma membranes from neutrophils with PKC, ATP γ S and PMA to phosphorylate endogenous proteins resulted in stimulation of subsequently added PLD (Lopez et al. 1995). The effect was blocked by staurosporine, required Ca²⁺, and was observed with the α -, β 1- and γ - isozymes of PKC, but not the Ca²⁺-independent and atypical isozymes. The nature of the phosphorylated PLD regulator was not defined.

A third possibility is that PKC inhibitors block the interaction between PKC and PLD. Against this hypothesis are studies of PLD activation by PKC α in vitro which reported no inhibition by staurosporine (Singer et al. 1996) and showed, by cleavage of PKCa by trypsin into its regulatory and catalytic domains, that the regulatory domain alone could activate PLD (Singer et al. 1996). However, it was not clear whether or not the holoenzyme was more effective than the regulatory domain, i.e. whether or not the catalytic domain also played some role in the interaction of PKCa with PLD. Although most studies indicate that PKC interacts with the N-terminal 325amino acids of PLD (Park et al. 1998; Xie et al. 1998; Min & Exton 1998; Sung et al. 1999b), there is some evidence from co-immunoprecipitation studies of additional interaction sites (Min & Exton 1998; Sung et al. 1999b). These could possibly involve the catalytic domain of PKC. In support of this idea, unpublished studies in the author's laboratory have shown that Ro-31-8220 and bisindolylmadeimide inhibit the interaction of endogenous PKCa with endogenous PLD in NIH3T3 cells.

In addition to the in vivo evidence for a role of PKC in PLD regulation, many in vitro studies have shown direct activation of PLD1 by PKC isozymes (Fig. 13, Singer et al. 1996; Hammond et al. 1997; Min et al. 1998b; Sciorra et al. 2001). Several interesting features have arisen from these studies. The first is that ATP is not required for the effect and that inhibitors of PKC kinase activity are without effect, thus confirming earlier reports of a nonphosphorylation mechanism for PLD activation by PKC (Conricode et al. 1992, 1994). The second is that the response is elicited only by the α - and β isozymes of PKC (Conricode et al. 1994; Ohguchi et al. 1996; Min et al. 1998b; Sciorra et al 2001). The conclusion that the kinase activity of PKC is not needed for the in vitro activation of PLD is supported by the observation that the regulatory domain of PKC alone is capable of activating the enzyme, although it is less effective than the holoenzyme (Singer et al. 1996; Sciorra et al. 2001). Surprisingly, addition of ATP to incubations of recombinant PLD1 with PKC- α results in phosphorylation and inhibition of the phospholipase (Hammond et al. 1997; Min et al. 1998b). These data indicate that direct phosphorylation of PLD by PKC in vitro does not lead to activation. Whether or not the phosphorylation leads to alterations in the effects of activators or inhibitors of the enzyme remains to be determined. In contrast to PLD1, PLD2 is weakly or not activated by PKC in vitro (Colley et al. 1997; Slaaby et al. 2000; Sciorra et al. 2001), although it responds well to PMA when expressed in COS-7 or Sf9 cells (Siddiqi et al. 2000; Slaaby et al. 2000). This implies that PKC can activate the enzyme in vivo through indirect mechanisms. In HEK cells transfected with cDNAs for the insulin receptor and PLD2 or PLD1, insulin stimulation of PLD activity was enhanced by cotransfection with PKCa plus PLCy (Slaaby et al. 2000). Co-immunoprecipitation studies also showed a physical association between PLD2 and PKCa.

Mutagenesis and binding studies have located a major site of interaction of PLD1 with PKC α in the N-terminal sequence of the phospholipase. Thus, deletion of the first 319 or 325 amino acids of PLD1 results in an enzyme that is no longer responsive to PKC α in vitro or PMA in vivo (Fig. 14, Park et al. 1998; Sung et al. 1999b; Xie et al. 1998). Binding studies using PLD sequences fused to GST have also shown strong interaction of PKC(with the first 318 amino acids of PLD1 (Min & Exton 1998). However, the protein kinase could also associate with a mutant PLD1 in which the first 325 amino acids were deleted (Sung et al. 1999b), indicating that there was an additional interaction site(s).



Fig. 14. N-terminal deletion mutants of rPLD1 have increased basal activity, but do not respond to PKC. Wild-type and N-terminally truncated forms (169–1036 and 320–1036) of rPLD1 were expressed in COS7 cells which were labeled with $[^{3+}H]$ myristic acid for measurement of PLD activity by $[^{3}H]$ PtdBut formation. The figure shows that both truncated enzymes had increased basal activity but totally lost their response to PMA (compare values in the presence and absence of PMA). Adapted from Xie et al. 1998 with permission of the authors and publisher



Phospholipase D - Structure, Regulation and Function

Another feature that has emerged from in vitro studies of PLD1 is that PKCE interacts synergistically with RhoA (or Cdc42) and ARF to activate the enzyme (Singer et al. 1996; Ohguchi et al. 1996; Hammond et al. 1997; Hodgkin et al. 2000). This synergism is quite striking, and is also observed when Rho (or Cdc42) and ARF are combined. The mechanistic basis for these synergisms is unknown. The synergism between PKC and RhoA could explain why the stimulation of PLD by phorbol esters in some cell types is partly inhibited by inactivation of RhoA (Malcolm et al. 1996; Senogles 2000).

Although the conventional isozymes of PKC are usually stimulatory to PLD, the situation with PKC(in vitro is unclear. An early report indicated that this isozyme mediated the effect of extracellular ATP on PLD in mesangial cells (Pfeilschifter & Huwiler 1993). A role for PKCE was later supported by a study of the effects of D2 dopaminergic stimulation of PLD in GH4 pituitary cells (Senogles 2000). On the other hand, stable overexpression of PKCE and its regulatory domain in fibroblasts was observed to inhibit the effects of PMA and PDGF on PLD activity (Kiss et al. 1999). However, caution must be used in interpreting this type of study since a high level of expression of PKCE may induce effects that are not seen with endogenous levels of the enzyme.

A recent report has shown that the PKC-related protein kinases PKN α and PKN β can interact with PLD1 as shown by co-immunoprecipitation studies in COS7 cells (Oishi et al.2001). The binding site was localized to residues 228–598 of PLD1. PKN α stimulated the activity of the enzyme, whereas PKN α had a modest effect. Another Ser/Thr kinase (casein kinase 2-like serine kinase) has been reported to phosphorylate PLD1, with Ser⁹¹¹ being one site of phosphorylation (Ganley et al. 2001). However, no change in in vitro catalytic activity was observed.

6.3

Role of Rho Family GTPases

Studies of the in vitro regulation of purified or membrane-associated PLD first demonstrated that the enzyme could be directly stimulated by members of the Rho and ARF families of small GTPases (reviewed in Exton 1997, 1999). It was subsequently shown that the PLD1 isozyme responded to Rho GTPases, but the PLD2 isozyme did not (Hammond et al. 1997; Colley et al. 1997; Lopez et al. 1998; Min et al. 1998b; Kodaki & Yamashita 1997). All members of the Rho family that were tested (RhoA, RhoB, Rac1, Rac2,





Fig. 15. Effects of different Rho family members on PLD1 activity. Recombinant rPLD1 was incubated with two different concentrations of GTPyS-liganded prenylated Rho proteins and H-Ras. PLD activity was measured by the release of [³H]choline from [³H]choline-labeled PC. From Bae et al. (1998) by permission of the authors and publisher

Cdc42Hs) stimulated PLD1, but with differing efficacies (Fig. 15, Hammond et al. 1997; Bae et al. 1998). Several studies have localized the interaction site for RhoA to the C-terminal sequence of PLD1 (Sung et al. 1997; Yamazaki et al. 1999; Du et al. 2000b; Cai & Exton 2001). Thus active V¹⁴RhoA was found to bind to a C-terminal fragment of hPLD1 including amino acids 663-1074 or 674-1074 using the yeast 2-hybrid system (Sung et al. 1997; Yamazaki et al. 1999). A similar, but shorter sequence in rPLD1 was found to bind activated RhoA utilizing phage display (Cai & Exton 2001). These findings were reinforced by co-immunoprecipitation or "pull down" studies, which showed that the interaction was GTP-dependent (Yamazaki et al. 1999; Cai & Exton 2001). Peptides corresponding to the C-terminal sequence of PLD1 also blocked the ability of RhoA to stimulate the catalytic activity of the enzyme (Yamazaki et al. 1999; Cai & Exton 2001). Mutagenesis studies have revealed that certain residues are required for the interaction. One study showed that mutations in four amino acids in the Lys⁹⁴⁶ to Lys⁹⁶² sequence in rPLD1 inhibited the activation of rPLD1 by V¹⁴RhoA, but not PMA, in COS7 cells,

and blocked the binding of the enzyme to GTP γ S-liganded RhoA as shown by co-immunoprecipitation studies (Cai & Exton 2001). Another study indicated the importance of Ile⁸⁷⁰ in hPLD1 (corresponding to Ile⁸⁸² in rPLD1) for binding to Rho in the yeast split-hybrid system and for activation of PLD (Du et al. 2000b). This group identified two other residues, but these required double mutations to see effects. These findings suggest that multiple residues in the C-terminus of PLD1 are involved in the RhoA interaction.

One study has examined the amino acid residues in Rho proteins required for interaction with PLD1 (Bae et al. 1998). This showed that RhoA and RhoB were more effective than Rac2 and Cdc42Hs in activating PLD1 in vitro in accord with Hammond et al. (1997). Experiments utilizing RhoA/Ras and RhoA/Cdc42 chimeras and mutagenesis revealed that residues Tyr³⁴, Thr³⁷ and Phe³⁹ in the activation loop of RhoA were required for stimulation of the phospholipase, but that other residues (Gln⁵² and Asp⁷⁶) determined the greater efficacy of RhoA compared with Cdc42Hs (Bae et al. 1998). Another study identified the insert loop of Cdc42 (amino acids 120– 139) as being required for PLD1 activation (Walker et al. 2000). Since both RhoA and Cdc42 contain this insert, the results of the two groups are not contraditory. As described above, RhoA and Cdc42 can interacts synergistically with ARF and PKC α to activate PLD1 in vitro.

Rho family members have also been shown to be involved in the regulation of PLD in vivo. Thus expression of wild-type or constitutively active V¹⁴RhoA or V¹²Rac1 in fibroblasts or COS cells increases PLD activity (Hess et al. 1997; Park et al. 1997; Zhang et al. 1999; Du et al. 2000b; Cai & Exton 2001) and dominant negative N¹⁹RhoA or N¹⁷Rac1 attenuates the activation of PLD induced by EGF, PMA or constitutively active $G\alpha_{13}$ (Hess et al. 1997; Plonk et al. 1998; Meacci et al. 1999). Another commonly used approach to reduce RhoA activity in cells is by treatment with the C3 exoenzyme of Clostridium botulinum which inactivates RhoA by ADP-ribosylation (Aktories et al. 1989). Toxin B from C. difficile which inactivates Rho, Rac and Cdc42 through monoglucosylation (Just et al. 1995) has also been employed. The C3 exoenzyme has been shown to attenuate PLD responses to agonists in several cell lines (Fig. 16, Malcolm et al. 1996; Hess et al. 1997; Plonk et al. 1998; Meacci et al. 1999; Senogles 2000; Murthy et al. 2001) and to inhibit GTPyS stimulation of PLD in membranes (Kuribara et al. 1995; Schmidt et al. 1996a). Toxin B from C. difficile has similar effects to the C3 exoenzyme on carbachol-stimulated PLD activity in HEK cells expressing M3 muscarinic receptors (Schmidt et al 1996a,b). It also inhibits IgE receptor-coupled PLD activation in RBL-2H3 cells and suppresses activation of the enzyme by GTPyS and PMA in the permeabilized cells (Ojio et al. 1996).



Fig. 16. Effect of C3 exoenzyme from C. Botulinum on the stimulation of PLD by LPA in Rat1 fibroblasts. PLD activity was measured by [³H]PtdBut formation in cells labeled with [³⁺H]myristic acid. Cells were scrape-loaded with C3 exoenzyme. From Malcolm et al. (1996) by permission of the authors and publisher

The in vivo effects of N¹⁹RhoA and the clostridial toxins can be attributed to direct inhibition of the stimulatory effects of Rho protein on PLD1. This is supported by the observations that mutations in PLD1 that block binding of RhoA also abolish the activation of the enzyme by V¹⁴RhoA in vivo. (Du et al. 2000; Cai & Exton 2001). However, indirect mechanisms for the regulation of PLD by Rho have been proposed. These include changes in PIP₂ (Schmidt et al. 1996b) since *C. difficile* Toxin B lowers both PIP₂ levels and PLD activity in HEK cells and membranes, and direct addition of PIP₂ to the membranes restores activity. Furthermore, several studies have shown that Rho can control the activity of PI-4P 5-kinase (Chong et al. 1994; Ren et al. 1996; Oude Weernink et al. 2000). Although these studies show that a decrease in PIP2 can reduce PLD activity in vivo, they have not shown that agonists stimulate the enzyme by increasing the level of this lipid.

Another postulated indirect mechanism involves Rho kinase (Schmidt et al. 1999). The evidence is that transfection of wild-type or constitutively active Rho kinase into HEK cells expressing M3 muscarinic receptors enhanced the stimulatory effect of carbachol on PLD activity without changing the effect of PMA. In contrast, kinase-deficient Rho kinase was without effect (Schmidt et al. 1999). However, active Rho kinase alone had minimal effects in the intact cells. In contrast, active Rho kinase increased basal and MgATP plus GTP γ S-stimulated PLD activity in HEK cell membranes and a Rho kinase inhibitor reduced the stimulatory effect of RhoA plus GTP γ S and MgATP (Schmidt et al. 1999). The Rho kinase inhibitor also decreased the stimulatory effect of carbachol in the cells. Although these experiments point to a significant role for Rho kinase in M3 muscarinic activation of PLD, they do not clearly distinguish between Rho kinase effects on PIP2 synthesis vs. PLD activity.

Further analysis of the effects of activation of the M3 muscarinic receptor on PLD activity using overexpression of certain G protein α -subunits indicated that $G\alpha_{12}$ and $G\alpha_{13}$, but not $G\alpha_q$ enhanced the effect of carbachol, but not PMA, on the enzyme (Rümenapp et al. 2001). As expected, $G\alpha_{12}$ and $G\alpha_{13}$ did not influence the activation of PLC, whereas $G\alpha_{q}$ enhanced the effect of carbachol on this enzyme. Overexpression of two regulators of G protein signaling (RGSs) that were specific suppressors of either $G\alpha_q$ or $G\alpha_{12}/G\alpha_{13}$ signaling also indicated that cholinergic stimulation of PLD involved $G\alpha_{12}/G\alpha_{13}$ but not $G\alpha_q$, whereas the reverse was true for PLC (Rümenapp et al 2001). Since $G\alpha_{13}$ can activate Rho in many cell lines (Buhl et al. 1995; Plonk et al. 1996; Katoh et al. 1998; Hooley et al. 1996; Fromm et al. 1997; Mao et al. 1998; Murthy et al. 2001) and since Rho is an activator of PLD, this seems the probable mechanism by which the M3 muscarinic receptor activates the enzyme. Since the data of Rümenapp et al. (2001) indicate that this receptor also activates PLC via $G\alpha_q$, it is somewhat surprising that PLD is not also activated via a PKC-dependent mechanism. As also shown in earlier reports (Schmidt et al. 1994, 1996, 1998; Voss et al. 1999), PLD can be activated by PMA in these cells. Thus it seems that stable expression of the M3 receptor in the cells may have altered the ability of PLC activation to lead to stimulation of PKC.

Agents that activate Rho family proteins could increase PLD activity by inducing activation and translocation of these proteins to membranes containing PLD1. Several studies have reported rapid agonist-induced membrane translocation of RhoA (Fleming et al. 1996; Kranenburg et al. 1997; Abousalham et al. 1997; Keller et al. 1997; Fensome et al. 1998; Michaely et al. 1999; Houle et al. 1999). It has also been shown that activation of Rho proteins by GTP γ S induces their membrane association (Bokoch et al. 1994; Fleming et al. 1996). Although the specific membrane fractions to which the Rho proteins were translocated were not defined in most cases, some studies have shown that these proteins are relocalized to plasma membranes or caveolae (Kranenburg et al. 1997; Michaely et al. 1999). As noted earlier, there is evidence that both PLD1 and PLD2 are present in caveolae.
6.4 Role of ARF Family GTPases

ARF was one of the first in vitro regulators of PLD to be recognized (Brown et al. 1993; Cockcroft et al. 1994). It was recognized to be the principal component of cytosol responsible for PLD activation (Fig. 17, Cockcroft et al. 1994). It exists in six mammalian isoforms (ARF1-6) and all are capable of activating PLD (Massenburg et al. 1994; Brown et al. 1995; Tsai et al. 1998). An ARF-like protein termed hARL1, which is 57% identical in amino acid sequence to hARF1, is also able to activate PLD (Hong et al. 1998). Myristoy-lation enhances the potency of the ARFs, as seen for most actions of these small G proteins (Massenburg et al. 1994; Brown et al. 1995; Tsai et al. 1998; Fensome et al. 1998).

PLD1 is much more responsive to ARF than is PLD2 (Hammond et al. 1997; Colley et al. 1997; Kodaki & Yamashita 1997; Min et al. 1998; Lopez et al. 1998; Lee et al. 1998; Sung et al. 1999a; Zhang et al. 1999; Slaaby et al.



Fig. 17. Effects of ARF, Rho and cytosol on PLD activity of membranes from COS-7 cells expressing vector or rPLD1. Cells were transfected with pcDNA3 vector or with rPLD1 and membranes isolated. PLD activity was measured in vitro by measuring $[^{3+}H]$ PtdBut formation from $[^{3}H$ -palmitoyl]PC in PL vesicles. GTPyS was added alone or with myristoylated ARF3, prenylated RhoA or cytosol from the same cells. From Park et al. (1997) by pemission of the authors and publisher

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2000). Synergism is observed in the actions of ARF with PKC α or RhoA on the activity of partially purified preparations of PLD (Singer et al. 1996; Hodgkin et al.1999; Kuribara et al. 1995) and on recombinant PLD1 (Hammond et al. 1997).

The interaction site on ARF for PLD has been localized to its N-terminus (Zhang et al. 1994; Jones et al. 1999) including the N-terminal helix and adjacent loop, the α 2-helix and part of the β 2-strand (Jones et al. 1999). The PLD interaction region is different from that required for activation of cholera toxin (Zhang et al. 1995) or for coatamer binding (Jones et al. 1999). However, the interaction site on PLD1 for ARF has not been defined, although it is not located in the N-terminal 319 amino acids (Park et al. 1998; Sung et al. 1999). As noted above, PLD1 is much more responsive to ARF than is PLD2. However, truncation of the first 308 amino acids of PLD2 reduces its basal activity and renders it very responsive to ARF (Sung et al. 1999).

Although there have been many reports showing that ARF stimulates PLD in membranes and partially purified preparations of the enzyme, and also activates PLD1 in vitro (Brown et al. 1993; 1995; Bourgoin et al. 1995; Singer et al. 1996; Massenburg et al. 1994; Cockcroft 1994; Hammond et al. 1995, 1997; Park et al. 1997; Abousalham et al. 1997; Min et al. 1998b; Sung et al. 1999a, 1999b; Katayama et al. 1998; Rumenapp et al. 1995; Caumont et al. 1998; Hodgkin et al. 1999), the evidence that this occurs in vivo is more limited. Thus expression of constitutively active L⁷¹ARF3 in COS7 cells was observed to stimulate the endogenous PLD, but had no effect on expressed PLD1 (Park et al. 1997). This could be due to the localization of expressed PLD1 in the Golgi, which are disrupted by L⁷¹ARF3. Better evidence for ARF activation of PLD in vivo has come from studies with ARF6. This class III ARF is very effective in activating PLD (Massenburg et al. 1994) and is principally localized to the plasma membrane (Cavenagh et al. 1996) where it is involved in membrane trafficking and actin remodeling (Al-Awar et al. 2000). ARF6 cycles between plasma membranes and cytosol or a tubulovesicular compartment as determined by its GTP binding/activation state (Gaschet & Hsu, 1999; Radhakrishna & Donaldson, 1997). Stimulation of chromaffin cells with nicotine to elevate the cytosolic Ca²⁺ caused an activation of PLD and also a translocation of ARF6 to the plasma membrane fraction (Caumont et al. 1998) resulting in a concurrent increase in PLD activity in this fraction. Treatment of the permeabilized cells with GTPyS similarly caused an increase in PLD activity and a relocalization of ARF6 to the plasma membrane (Caumont et al. 1998). Further evidence for the control of PLD by ARF6 was obtained in experiments in which the activation of PLD by Ca²⁺ in permeabilized chromaffin cells was markedly inhibited by addition of a myristoylated peptide corresponding to the N-terminus of ARF6, but

not by the corresponding peptide from ARF1 (Caumont et al. 1998). Similar results with these peptides were obtained in myometrial extracts treated with GTP γ S (Le Stunff et al. 2000a). These results suggest a major role for ARF6 in regulation of PLD in some cell types. The regulation of PLD in the Golgi apparatus by Class I ARFs will be discussed below in Section 7.1.

There have been several reports implicating ARF in the regulation of PLD by certain agonists. In permeabilized HEK cells stably expressing the M3 cholinergic receptor, the activation of PLD by GTPyS was reduced by cytosol depletion and restored by ARF1 (Rümenapp et al. 1995, 1997). The activation of PLD by carbachol in these cells was inhibited by brefeldin A (BFA) (Rümenapp et al, 1995), which is a fungal metabolite inhibitor of some of the guanine nucleotide exchange factors (GEFs) for ARFs (Moss & Vaughan, 1998). Another study showed that BFA (5-50 µg/ml) inhibited PDGF and PMA activation of PLD in Rat1 fibroblasts overexpressing insulin receptors (HIRcB cells) whereas an inactive analog was without effect (Shome et al. 1998). Similarly, BFA has been reported to inhibit the effects of angiotensin II, endothelin 1 and PDGF on PLD in vascular smooth muscle cells (Shome et al. 1999; Andresen et al. 2001) and the actions of histamine, bradykinin and carbachol on the enzyme in 1321N1 astrocytoma cells (Mitchell et al. 1998). Activation of M3 muscarinic cholinergic or AT₁ angiotensin II receptors in the latter cells resulted in their co-immunoprecipitation with ARF1 and RhoA.. Co-immunoprecipitation and BFA inhibition were not observed with activation of receptors for gonadotropin-releasing hormone (GnRH) (Mitchell et al. 1998). However, these attributes could be restored by mutation of these receptors to contain the canonical Asp Pro XX Tyr sequence present in the seventh transmembrane domain in the effective receptors. Thus this motif was proposed to mediate interaction of the receptors with RhoA and ARF and hence activation of PLD (Mitchell et al. 1998).

In contract to the preceding findings, BFA has been reported to be without effect on basal PLD in A549 adenocarcinoma cells or on the stimulation of the enzyme by PMA, sphingosine1-phosphate or bradykinin (Meacci et al. 1999). In HL-60 cells, the inhibitor also did not inhibit the stimulation of PLD by formyl-Met-Leu-Phe (FMLP) or ATP at times and doses when the Golgi apparatus was completely disrupted (Guillemain & Exton, 1997). These data suggest that, if ARF is involved in agonist activation of PLD in these cells, its activation does not depend on a BFA-sensitive GEF.

There have been other reports implicating ARF in agonist activation of PLD. For example, in permeabilized HIRcB cells that overexpress insulin receptors, insulin has been reported to enhance the effect of ARF plus GTPγS on PLD (Shome et al. 1997). Insulin was also reported to promote the binding of GTPγS to ARF and the binding of ARF to cell membranes. In

another study, expression of dominant negative forms of ARF1 and ARF6 in HIRcB cells resulted in inhibition of the stimulation of PLD by PDGF and PMA (Shome et al.1998). FMLP and PMA have also been shown to promote the association of ARF to membranes in intact HL-60 cells (Houle et al. 1995, 1999), which was correlated with an increase in GTP γ S-stimulated PLD activity in the membranes.

In cytosol-depleted neutrophils stimulated with FMLP, myristoylated ARF1 restored the stimulation of PLD by GTP γ S (Fensome et al. 1998). Pertussis toxin blocked the effect of FMLP implying the involvement of G proteins of the Gi/Go family. The C3 exoenzyme of *C. botulinum* partly reduced the effect, suggesting synergism with Rho family proteins (Fensome et al. 1998). FMLP, PMA and GTP γ S also promoted the membrane translocation of both ARF and Rho in the intact or permeabilized neutrophils. In another study, subcellular fractionation of HL-60 cells revealed that ARF1-dependent and FMLP-dependent PLD activity was located in plasma membranes and endomembranes (Whatmore et al. 1996). Substantial activity of PI-4 kinase and PI 4P 5-kinase was found in plasma membranes. PIP2 was enriched in these membranes, whereas PI and PI 4-P were found predominantly in endomembranes. These findings support roles for ARF and PIP₂ in the regulation of PLD in plasma membranes in these cells.

An additional way in which ARFs could regulate PLD activity is through the effects of ARF1 and ARF6 on PI-4P 5-kinase, which synthesizes PIP₂. ARF1 directly interacts with Type I PI-4P 5-kinase and increases its activity (Jones et al. 2000). Addition of ARF1 to Golgi membranes in the presence of the type I enzyme also dramatically increases the PIP₂ level in these membranes (Jones et al. 2000). Another report has shown that ARF can recruit PI 4-P 5-kinase- β to the Golgi complex, resulting in a potent stimulation of PIP₂ synthesis (Godi et al. 1999). In both studies, the effects were independent of PLD activity. Another report has identified PI 4-P 5-kinase as a downstream effector of ARF6 (Honda et al. 1999) in brain cytosol and HeLa cells. These proteins were colocalized in membranes ruffles in cells activated with AlF₄⁻ or EGF. In contrast to ARF6, neither ARF1 nor ARF5 was colocalized with the lipid kinase, whereas PLD2 relocalized to the ruffles perhaps because of a local increase in PIP₂ (Honda et al. 1999).

Another approach to exploring the role of ARF in the activation of PLD in vivo has utilized proteins that inhibit ARF action or activation. Arfaptin an ARF binding protein (Kanoh et al. 1997) inhibited the activation of PLD by different ARFs in vitro (Fig. 18, Tsai et al. 1998; Williger et al. 1999b) and by PMA in NIH 3T3 cells (Williger et al. 1999a). Similarly, ARP an ARF-related protein inhibited the in vitro stimulation of PLD by ARF and ARNO, a GEF for ARF (Schürmann et al. 1999). The constitutively active form of ARP was



Fig. 18. Arfaptin inhibits ARF stimulation of PLD activity in Golgi. Golgi-enriched membranes were incubated with GTP(S, myristoylated ARF3 and increasing concentrations of arfaptin. PLD activity was measured by [³H]PtdBut formation from [³H-palmitoyl]PC in PL vesicles. From Williger et al. (1999) by permission of the authors and publisher

also inhibitory, but the dominant negative form was not, indicating that ARP was acting by interacting with ARNO. The active and wild-type forms of ARP also inhibited muscarinic activation of PLD and ARF translocation to membranes (Schürmann et al. 1999). These data suggest that ARP inhibits ARF-mediated PLD activation by binding to ARNO or other proteins containing the Sec7 (GEF) domain.

6.5 Role of Tyrosine Phosphorylation

Many agonists whose receptors encode tyrosine kinase activity or which activate soluble tyrosine kinases can stimulate PLD (Natarajan et al. 1996; Exton 1997, 1999). Thus growth factors acting on many cell types, and agents that activate T cell receptors or the receptors for IgE on mast cells increase the activity of the enzyme. However, the activation mechanism is indirect in most cases and may not involve phosphorylation of the enzyme. Growth

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factors can activate multiple signaling pathways leading to regulation of the enzyme by PKC, Rho family proteins and Ras family proteins (Exton 1997).

The use of inhibitors of tyrosine kinases has also implicated these kinases in the activation of PLD by agonists acting through heptahelical receptors that couple to heterotrimeric G proteins. Thus, the inhibitors decrease the activation of PLD by ATP in U937 promonocytes (Dubyak et al. 1993; Kusner et al. 1993), thrombin in platelets (Martinson et al. 1994), FMLP in neutrophils or HI.60 cells (Uings et al. 1992; Houle et al. 1999), endothelin 1, norepinephrine and angiotensin 11 in vascular smooth muscle cells (Wilkes et al. 1993; Jinsi et al. 1996; Suzuki et al. 1996b), bombesin in fibroblasts (Briscoe et al. 1995), carbachol in PC12 pheochromocytoma cells and HEK cells expressing the M3 muscarinic receptor (Ito et al. 1997a; Schmidt et al. 1994) and endothelin 1 in myometrium (Le Stunff et al. 2000b).

Another approach to identifying a role for tyrosine phosphorylation in the regulation of PLD involves the use of vanadate, which is an inhibitor of tyrosine phosphatases. Stimulation of PLD activity by vanadate or H_2O_2 alone or in combination has been demonstrated in HL-60 cells (Bourgoin & Grinstein 1992), U937 cells (Dubyak et al. 1993), endothelial cells (Natarajan et al. 1993), vascular smooth muscle (Ward et al. 1995), Swiss 3T3 fibroblasts



Fig. 19A, B. H_2O_2 stimulation of PLD activity and protein tyrosine phosphorylation in Swiss 3T3 fibroblasts. The cells were labeled with [³H]myristic acid, pretreated with vanadate and then stimulated with H_2O_2 at different concentrations. PLD was measured by [³H]PtdBut formation, and all lysates were immunoprecipitated using an anti-rPLD1 antibody then Western blotted with an anti-PTyr antibody. Adapted from Min et al. (1998a) by permission of the authors and publisher

(Min et al. 1998a) and myometrium (Le Stunff et al. 2000). A key point in the regulation of PLD activity by tyrosine kinases is whether or not the activity of the enzyme is controlled by direct tyrosine phosphorylation. On this point there is no clear evidence. Several studies have shown that H₂O₂ activates PLD and promotes the tyrosine phosphorylation of several cellular proteins including PLD (Fig. 19, Gomez-Cambronero 1995; Ito et al. 1997b; Marcil et al 1997; Min et al. 1998a). Although the tyrosine phosphorylation of cellular proteins was correlated with the activation of PLD, the tyrosine phosphorylation of PLD itself was not (Bourgoin & Grinstein 1992; Ito et al. 1997a, 1997b; Min et al. 1998a). Furthermore, the effects of PKC inhibitors and PKC down-regulation indicated that PKC mediated most of the PLD activity change seen with H_2O_2 in Swiss 3T3 cells (Min et al. 1998a) although not in endothelial cells (Natarajan et al. 1993). Another study showed that mutation of the tyrosine phosphorylation site in PLD2 did not alter the ability of EGF to activate the enzyme in HEK 293 cells expressing both PLD2 and the EGF receptor (Slaaby et al. 1998). In contrast to the marked tyrosine phosphorylation of PLD induced by H₂O₂ in Swiss 3T3 cells, that induced by PDGF was barely detectable, yet the growth factor induced a large activation of the enzyme (Min et al. 1998a).

A recent report showed that norepinephrine increased the tyrosine phosphorylation of PLD2 in vascular smooth muscle cells (Parmentier et al. 2001). The effect was blocked by U0126 a reported inhibitor of MAP kinase kinase. However, ERK2 a MAP kinase did not phosphorylate PLD2 invitro, and the kinase responsible for the in vivo phosphorylation and the effect of this phosphorylation on PLD2 activity remain unknown.

The nature of the tyrosine kinases activated by G protein-coupled receptors and H_2O_2 is not well defined, but there is evidence that they are Ca²⁺dependent (Ito et al. 1997a, 1997b). All of the G protein-coupled receptors that mediate PLD activation through a tyrosine kinase mechanism are known to activate G_q and phospholipase C, and thus increase cytosolic Ca²⁺ (Exton 1996). This would then activate any Ca²⁺-dependent tyrosine kinases. In fact, angiotensin II has been shown to increase tyrosine kinase activity in a Ca²⁺-dependent manner in liver epithelial cells and aortic smooth muscle cells (Huckle et al. 1992) and this is true for thrombin acting on BC₃H1 muscle cells (Offermanns et al. 1993) and platelet-activating factor acting on Kupffer cells (Chao et al. 1992), although with other agonists and cell lines, there is evidence that other, Ca²⁺-independent protein kinases are involved. A focal adhesion kinase homologue termed PYK2 (also known as CADTK, CAK β , RAFTK and FAK2) has been implicated in the effects of LPA, angiotensin II, cholecystokinin and PDGF in several cell lines (Yu et al. 1996; Brinson et al. 1998; Tapia et al. 1999; Tang et al. 2000), whereas focal adhesion kinase itself seems not to be involved in Ca^{2+} -mediated tyrosine phosphorylation (Sinnett-Smith et al. 1993). In the case of H_2O_2 , there is evidence that Syk is the tyrosine kinase specifically activated in a B cell line (Schieven et al. 1993), whereas in a T cell line, Lck, another Src family member is involved (Hardwick & Sefton 1997).

Another mechanism by which agonists acting through G protein-coupled receptors could act via tyrosine phosphorylation is through transactivation of the EGF receptor (Prenzel et al. 1999; Zwick et al. 1999; Keely et al. 2000). This is thought to involve Ca^{2+} activation of a metalloprotease that cleaves a membrane precursor to release HB-EGF which then acts on the EGF receptor (Prenzel et al. 1999). This mechanism has not yet been examined for the activation of PLD by G protein-coupled receptors.

6.6

Roles of Ras and Ral

Several reports have indicated that tyrosine phosphorylation or G proteinmediated signaling can regulate PLD through the low Mr GTPases Ras and Ral in some cell lines. Thus, infection of BALB/c 3T3 cells with v-Src followed by activation of its tyrosine kinase activity resulted in stimulation of PLD (Song et al. 1991) by a mechanism that was mediated by Ras (Jiang et al. 1995a), but required additional cytosolic factors. In further work, one of these factors was shown to be Ral, a member of the Ras subfamily, and this GTPase was shown to associate with PLD, but not to activate it (Jiang et al. 1995b). Thus it was proposed that Ras interacted with a GEF for Ral leading to Ral activation which, together with another factor(s), stimulated the enzyme.

Other reports showed a functional association between RalA and PLD1 in cell lysates, but this alone did not activate the enzyme (Jiang et al. 1995b; Luo et al. 1997, 1998). Further work demonstrated that ARF could also associate with active RalA-PLD1 complexes isolated from v-Src-transformed cells, and the association was increased when ARF was in the active, GTP-bound form (Luo et al. 1998). Another group found that ARF1 and RalA could bind to PLD1 and that the interaction sites were different (Kim et al. 1998). Furthermore, RalA was observed to enhance the effect of ARF1 on the activity of PLD1 (Fig. 20, Kim et al. 1998).

Another approach to exploring the role of Ral in the regulation of PLD involves the use of the lethal toxin (TcsL) from *C. Sordellii* and a variant of another toxin (TcdB-1470) from *C. difficile*. These toxins inactivate certain low Mr GTPases by monoglucosylation, includingg Rac, Ras, Ral and Rap (Popoff et al. 1996; Schmidt et al. 1998). Long-term treatment of HEK-293

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Fig. 20. RalA enhances the stimulatory effect of ARF on PLD activity. Increasing concentrations of GTP γ S-activated RalA were added to incubations of purified PLD1. PLD activity was measured in vitro by the release of [³H]choline from [³H]choline-labeled PC. From Kim et al. (1998) by permission of the authors and publisher

cells with TcsL or TcdB-1470 caused inhibition of PLD activation by PMA, but did not affect the basal activity of the enzyme or the effects of carbachol or GTP γ S, when the latter was added to the permeabilized cells (Schmidt et al. 1998). The addition of Rac1, Ras or Rap did not restore the PMAstimulated activity, but it was fully restored by RalA or RalB. These results suggest that Ral is involved in PKC stimulation of PLD in HEK-293 cells. Another group found that overnight treatment with TcsL inhibited the effect of GTP(S to stimulate PLD in permeabilized HL-60 cells (El Hadj et al. 1999). It also reduced the stimulatory effects of ARF, Rho and Rac in vitro and of PMA in intact cells. Since ARF and Rho are not targets of the toxin, these results may have been due in part to the reduction in PIP2 induced by the toxin (El Hadj et al. 1999). Experiments with TcsL toxins that were active or inactive on Ral indicated that this GTPase was involved in the stimulation of PLD by GTP γ S.

As noted above, there is evidence that constitutively active Ras activates PLD in intact cells (Jiang et al. 1995a; Carnero 1994a, 1994b; Price et al.1989b; Lucas et al. 2000). On the other hand, Ras does not directly activate PLD in vitro (Fig. 15, Quilliam et al. 1990; Hurst et al. 1991; Bae et al. 1998). Therefore the effect of Ras on PLD in vivo must involve a signaling pathway(s). As discussed above, there is evidence that one pathway involves Ral. The involvement of Ras and Ral in the regulation of PLD by growth factors and other agonists signaling through tyrosine phosphorylation has been

indicated in several studies. Thus expression of dominant negative forms of Ras and Ral inhibited the activation of PLD by epidermal growth factor (EGF) in Rat 3Y1 cells expressing the EGF receptor (Lu et al. 2000). Overexpression of wild type or activated RalA increased basal PLD activity and transformed the cells, and transformation was also observed in cells overexpressing PLD1 (Lu et al. 2000). In another report, expression of dominant negative Ras in NIH 3T3 cells completely blocked the activation of PLD by PDGF whereas expression wild type Ras in Rat 2 cells enhanced the response (Lucas et al. 2000). On the other hand these manipulations had minimal effects on the activation of PLD by phorbol ester. Expression of the adaptor molecules Shc and Grb2 in Rat 2 cells also amplified the effect of PDGF on PLD. These results support the operation of another, Ras-dependent, pathway for growth factor activation of PLD. A role for Ras and Ral in PLD activation by G protein-coupled receptors has also been indicated. In HEK-293 cells expressing the M3 muscarinic receptor, PMA-, but not carbacholinduced activation of PLD was reduced by expression of dominant negative forms of RalA and Ras, and overexpression of the Ral-specific GEF Ral-GDS enhanced PKC-induced PLD stimulation (Voss et al. 1999). The stimulatory effect of Ral-GDS was abolished by toxin TcdB-1470 from C. difficile, and the toxin and also PKC inhibition blocked the stimulation of PLD by EGF and PDGF (Voss et al. 1999). However the effects of carbachol were not modified by TcdB-1470, PKC inhibition or by expression of Ral-GDS. These data indicate that, in this cell type, PKC and Ral mediate the effects of PMA and growth factors on PLD, but that muscarinic stimulation is not dependent on PKC or Ral. Since Ral is activated by PMA or growth factors (Voss et al. 1999), it seems that this Low Mr GTPase is downstream from PKC in the signaling pathway. Other studies have implicated the Ras-Raf-MAP kinase pathway in the activation of PLD. One study found that PLD activity was elevated in v-Raf transformed cells and used dominant negative forms of Ral and Rho to indicate that these GTPases were downstream from v-Raf (Frankel et al. 1999). Another used inhibitors to implicate Ras and MAP kinase in the activation of PLD by norepinephrine (Muthalif et al. 2000). More work is needed to substantiate the role of the Ras-Raf-MAP kinase pathway in PLD regulation.

6.7

Roles of Calcium and Calmodulin

Treatment of several cell types with Ca^{2+} ionophores can activate PLD, and Ca^{2+} chelators can inhibit the stimulation of PLD by several agonists (Exton 1997). However studies of the effects of Ca^{2+} and Mg^{2+} on recombinant or

purified PLD show that the enzyme is stimulated by submicromolar concentrations of Ca²⁺, but that the stimulation is not seen in the presence of physiological concentrations of Mg²⁺ (Brown et al. 1995; Hammond et al. 1997; Min et al. 1998). These latter observations render it unlikely that Ca²⁺ *directly* activates the enzyme under physiological conditions, and indicate that Ca²⁺ stimulation of the enzyme in vivo involves other factors. Examination of the Ca²⁺-dependence of the effects of PMA, vasopressin or FMLP on PLD activity in neutrophils or hepatocytes, and of GTPγS and ARF effects in permeabilized neutrophils have indicated that increasing the cytosolic Ca²⁺ concentration from 0.1 μ M to 0.5 μ M or higher enhances basal PLD activity and also the effects of the various agents on the enzyme (Kessels et al. 1991; Gustavsson et al. 1994; Cockcroft et al. 1994). These data indicate that variations in cytosolic Ca²⁺ within the physiological range can influence the regulation of PLD.

Likely mediators of the effects of Ca^{2+} on PLD are the Ca^{2+} -dependent isozymes of PKC. This appears to be the case in hepatocytes, where PKC inhibitors reduce the stimulatory effect of Ca^{2+} (Gustavsson et al. 1994). As noted above in the section (6.2) on PKC, there is much evidence that Ca^{2+} dependent α - and β -isozymes are the major PKC isoforms that regulate PLD. Another possible mediator is calmodulin (CaM). Although PKC α and PKC β play some role in the activation of PLD by antigen in RBL-2H3 basophilic cells, the effects of CaM antagonists indicate that this Ca²⁺-binding protein also plays a role (Kumada et al. 1995). A similar situation is seen in studies with CHO cells expressing muscarinic receptors, where PLD activation by carbachol is decreased by PKC down-regulation and also by Ca²⁺ chelation and inhibition of Ca²⁺/CaM-dependent protein kinase II (Min et al. 2000).

In related studies, overexpression of a CaM binding myristoylated alanine-rich PKC substrate termed MARCKS in SK-N-MC neuroblastoma cells has been observed to increase PLD stimulation by PMA (Morash et al. 1998). PKC α , but not PKC β , was up-regulated in the cells and, like MARCKS, PKC α was lost when the cells were at a high passage number. The mechanism of the MARCKS effect is unknown, but it may act by colocalizing PKC α and PLD and/or sequestering PIP₂ (Morash et al. 1998). In further studies, MARCKS overexpression was found not to affect GTP γ S-stimulated PLD activity in the permeabilized cells (Morash et al. 2000), and the GTP γ S effect on PLD was independent of PKC. Western blot analysis of a detergentinsoluble fraction of the cells showed the presence of MARCKS, PKC α , PLD1 and PLD2, suggesting the colocalization of these proteins in caveolae.

6.8 Regulation by Other Proteins

Some early reports of the regulation of PLD by ARF indicated that other cytosolic factors were required (Houle et al. 1995; Bourgoin et al. 1995; Singer et al. 1995). One of these factors was identified as PKC((Singer et al. 1996) which is consistent with the ability of this enzyme to synergize with ARF on PLD1, as discussed in preceding sections. Protein inhibitors of the enzyme have also been described. Fodrin, a homolog of spectrin, was shown to inhibit PLD activity (Lukowski et al. 1996) and the mechanism was later ascribed to a decrease in PIP₂ (Lukowski et al. 1998). Likewise, another inhibitor of PLD (Han et al. 1996) turned out to be synaptojanin, a phosphatase that hydrolyzes PIP₂ (Chung et al. 1997). A PLD inhibitor that apparently does not act by altering PIP₂ is the clathrin assembly protein 3, which interacts with PLD directly (Lee et al. 1997). PLD2 has high intrinsic activity and it has been postulated that natural inhibitors of this enzyme exist (Colley et al. 1997). Possible inhibitors are α - and β -synucleins since these brain proteins selectively inhibit PLD2 in comparison to PLD1 (Jenco et al. 1998). Myocardial PLD2 associates with α -actinin, which exerts an inhibitory effect (Park et al. 2000). α -Actinin interacts directly with the Nterminus of PLD2 and this interaction and its inhibitory action are reversed by ARF1, which releases α -actinin from its binding site.

 β -Actin itself has recently been reported to bind directly to PLD1 and PLD2 and to inhibit their catalytic activity when stimulated by PIP₂, oleate or ARF1 (Lee et al. 2001). The binding site was localized to the 613–723 amino acid sequence of PLD2. β -Actin could displace α -actinin binding to PLD2, but had minimal effect on the ability of ARF1 to activate the enzyme. Immunoprecipitation studies demonstrated that actin interacted with both PLD1 and PLD2 in PC12 or COS7cells. Furthermore, immunocytochemical studies indicated that the two isozymes co-localized with F-actin (Lee et al. 2001). These findings indicate that actin can interact with PLD1 and PLD2 in vivo and may exert an inhibitory effect on both enzymes in intact cells.

6.9

Regulation by Ceramide

Ceramide is a product of the breakdown of sphingomyelin by sphingomyelinase, but can also be synthesized de novo or produced from sphingosine or ceramide 1-phosphate (Hannun 1996; Spiegel et al. 1996). It participates in cell signaling and plays roles in stress responses such as apoptosis, cell cycle



Fig. 21. Inhibition of PLD activity by ceramide. Membranes and cytosol from $[^{3}H]$ myristate-laabeled HL60 cells were incubated with ethanol and GTP γ S in the presence or absence of C₂-ceramide, C₈-ceramide or dihydro-C₂-ceramide. PLD was assayed in vitro by measuring $[^{3}H]$ ethanol formation. From Abousalham et al. (1997) by permission of the authors and publisher

arrest and inflammation. A large number of agonists can increase sphingomyelinase activity leading to increased levels of ceramide (Levade and Jaffrézou 1999). Cell-permeable (C2- or C6-) ceramides produce a marked inhibition of PLD activity in intact fibroblasts stimulated with PMA (Gómez-Muñoz et al. 1994) and in neutrophils stimulated with FMLP (Nakamura et al. 1994). They also inhibit the ability of exogenous PA or PLD from S. chromofuscus to stimulate DNA synthesis, and reduce the stimulation of PLD exerted by GTPyS or PMA in permeabilized fibroblasts. In a further study, the ceramides were shown to block the activation of PLD by sphingosine 1-phosphate (Gómez-Muñoz et al. 1995). Another group reported that treatment of cells with sphingomyelinase or ceramide inhibited PLD activation induced by DOG (dioctanoylglycerol) or bradykinin, but felt that this could be attributed to the inhibition of PKC(translocation (Jones & Murray 1995). Ceramide has also been shown to inhibit IgE-mediated PKC translocation and PLD activation in RBL basophilic cells (Nakamura et al. 1994) and to inhibit the stimulation of the enzyme by FMLP in intact HL-60 cells or by GTP(S in permeabilized cells (Fig. 21, Abousalham et al. 1997). As in

the report of Jones and Murray (1995), ceramide blocked the translocation of the conventional (Ca²⁺-dependent) PKC isozymes, but not that of the δ -, ϵ - or ζ -isozymes. These data suggest that in these cell lines, conventional, but not Ca²⁺-independent or atypical PKC isozymes, are involved in regulation of PLD. In the report of Abousalham et al. (1997) ceramide was also noted to inhibit the membrane association of ARF1, RhoA and Cdc42 induced by FMLP. This could partly explain the impairment of PLD activation. However, a recent report has shown that C₂-ceramide, but not C₈- or dihydro-C₂-ceramide, can directly inhibit purified recombinant PLD1 and block activation of the enzyme in permeabilized chromaffin cells (Vitale et al. 2001). Thus direct effects of ceramides are probably involved.

6.10 Role of Phosphoinositide 3-Kinase

PIP₃ can activate PLD1 directly, although it is not as efficacious as PIP₂ (Hammond et al. 1997; Min et al. 1998b). However, the cellular level of PIP₂ is so much higher than that of PIP₃ that variations in the concentration of PIP₃ per se would seem unlikely to influence PLD activity in vivo. Thus the PI 3-kinase inhibitor wortmannin has been reported to be without effect on basal and GTP γ S-stimulated PLD activity in permeabilized cells (El Hadj et al. 1999).

Studies of the regulation of PLD by PI 3-kinase in intact cells have principally utilized wortmannin and LY294002, and have given variable results. Thus, wortmannin is without effect on the stimulation of PLD by PDGF or EGF in Rat1 fibroblasts (Hess et al. 1997). Neither does it or LY294002 inhibit the activation of the enzyme by angiotensin II in vascular smooth muscle cells (Andresen et al. 2001). On the other hand, the inhibitors block the stimulation of PLD by the high affinity IgG receptor $Fc\gamma RI$ in U937 cells (Gillooly et al. 1999) and the activation of the enzyme in endothelial cells by stem cell factor (Kozawa et al. 1997). Using a different approach, namely using cells expressing wild type or mutant PDGF receptors, no evidence could be obtained for a role of PI 3-kinase in PDGF activation of PLD (Yeo et al. 1994). An obvious explanation for these divergent results is that different cells and agonists use different pathways to activate PLD and any role for PIP3 probably lies upstream from PLD.

7 Cellular Functions of Phospholipase D

Despite its widespread distribution and its regulation by many agonists, the cellular functions of PLD remain ill-defined. As described below, the effects of exogenous PLD or PA added to cells are complicated by the generation of other signaling molecules besides PA. Approaches using stable overexpression of PLD isozymes have, with a few exceptions, led to cell death, and deletion of these enzymes by antisense methods has not been very successful. There have been no reports of the knockout of either PLD1 or PLD2 by homologous recombination in mice. On the other hand, there have been a few reports of the use of catalytically inactive PLD isozymes as dominant negative alleles to reduce PLD activity in some cells. Studies of the role of PLD in specific cell functions are described below.

7.1

Role in Vesicle Trafficking in Golgi

There is much evidence that PLD and PA play roles in vesicle trafficking in the Golgi, but even this is disputed. Class I ARFs are well known to be involved in trafficking in Golgi through their roles in the recruitment of COP proteins and adaptor proteins (APs) to Golgi membranes, which results in the formation of COP-I-coated or clathrin-coated vesicles (Donaldson & Lippincott-Schwartz, 2000; Stamnes & Rothman 1993; Traub et al. 1993). ARF-stimulated PLD activity has also been reported in Golgi (Provost et al.1996; Liscovitch 1999; Ktistakis et al. 1995; Chen et al. 1997) and most immunocytochemical studies have localized PLD1 to the perinuclear region, which contains this organelle (Colley et al. 1997; Sugars et al. 1999; Kam & Exton, 2001; Freyberg et al. 2001).

The presence of ARF-stimulated PLD activity in the Golgi has given rise to the proposal that this enzyme plays a role in vesicle trafficking in this organelle (Kahn et al. 1993). In support of this, it was observed, that in a cell line with high constitutive PLD activity, ARF was not required for the formation of coatomer (COP-I)-coated vesicles (Ktistakis et al. 1996). Furthermore, ethanol inhibited the formation of coated vesicles in Golgi incubated with ARF and GTP γ S and this was attributed to inhibition of PA formation by PLD. Addition of bacterial PLD to Golgi membranes also induced coatomer binding and coated vesicle formation in the absence of ARF (Ktistakis et al. 1996). Finally, coatomer was observed to bind more avidly to vesicles containing PIP₂ and PA. In an extension of this work, primary alcohols were found to inhibit the transport of viral glycoproteins from the endoplasmic

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reticulum (ER) to the Golgi, and the block was reversed by liposomes containing PA (Bi et al. 1997).

Another group has provided evidence that PLD plays a role in the release of secretory vesicles from the trans-Golgi network. Using permeabilized GH3 pituitary cells, immunoaffinity-purified PLD1 was observed to stimulate nascent secretory vesicle budding from the trans-Golgi network, whereas 1-butanol inhibited this process (Fig. 22, Chen et al. 1997). Furthermore, generation of PA by a combination of PLC and DAG kinase also stimulated vesicle budding, and PA was found to accumulate in the Golgi during this process (Siddhanta & Shields1998). Primary butanol was also reported to disrupt the structural organization of the Golgi and to inhibit the sorting of polypeptide hormones into post-Golgi vesicles (Siddhanta et al. 2000). It was shown that inhibition of PA formation resulted in decreased PIP2 synthesis and it was suggested that this lipid was required for maintaining the structural integrity and function of the Golgi. Other work has indicated a requirement for PIP₂ in secretory vesicle formation (Fensome et al.1996; Tüscher et al. 1997; Way et al. 2000).



Fig. 22. PLD stimulates the release of nascent secretory vesicles from the trans-Golgi network. GH3 pituitary cells were labeled with an amino acid mixture containing $[^{35}S]$ methionine and permeabilized. The cells were then incubated with Sf9 cell lysates expressing hPLD1, and the supernatant and pellet fractions immunprecipitated with antibodies to growth hormone (GH) or prolactin (PRL). Vesicle budding efficiency was calculated as the immunoreactive material in the supernatant divided by that in the supernatant plus pellet. The protein concentrations refer to that of the hPLD1 preparations used. From Chen et al. (1997) by permission of the authors and publisher

In contrast to these reports, Stamnes et al. (1998) measured PA levels in Golgi membranes and found that they declined, rather than increased, during cell-free budding of coatomer-coated vesicles. Another group (Kuai et al. 2000) examined the effects of mutations in ARF3 on its ability to activate PLD1 and to recruit coatomer to Golgi membranes. They observed a very poor correlation between these effects, implying that PLD activation was not critical for Golgi vesiculation. Similarly, Jones et al. (1999) reported that an N-terminally deleted dominant negative mutant of ARF1 that did not inhibit ARF1-stimulated PLD activity effectively competed with ARF1 to prevent coatomer binding to Golgi membranes. Another study of the recruitment of AP-1 adaptors to trans-Golgi membranes reported that this was not affected by exogenous PLD or by neomycin, which is a high-affinity ligand of PIP₂ (West et al. 1997). Thus a role for PLD in Golgi trafficking remains controversial.

7.2

Role in Exocytosis and Endocytosis

PLD has also been implicated in exocytosis and endocytosis. Thus, secretion in mast cells, mammary epithelial cells, platelets, neutrophils and HL60 cells is inhibited by the addition of primary alcohols (Fig. 23, Stutchfield & Cockcroft 1993; Gruchalla et al. 1990; Lin et al. 1991; Benistant & Rubin 1990; Yuli et al. 1982; Fensome et al. 1996; Williger et al. 1999; Brown et al. 1998; Siddhanta et al. 2000; Way et al. 2000; Boisgard & Chanat 2000). However, this could be due to changes other than inhibition of PA formation by PLD. Further support for a role of PLD in exocytosis has come from several approaches. Williger et al. (1999) observed that secretion of metalloproteinase-9 from HT1080 fibrosarcoma cells could be induced by PA, but not by DAG. Subcellular fractionation studies have identified PLD activity in secretory granules in neutrophils and HL60 cells (Whatmore et al. 1996; Morgan et al. 1997) and stimulation of these cells by FMLP causes translocation of the PLD-containing vesicles to the plasma membrane. Likewise, in RBL-2H3 mast cells expressing GFP-tagged PLD1, the translocation of the enzyme from secretory granules to the plasma membrane was stimulated by crosslinking the IgE receptor (Brown et al. 1998).

The final stage in exocytosis is fusion of secretory vesicles with the plasma membrane and release of their contents into the extracellular medium. There is evidence that PLD is involved in this process. Thus in chromaffin cells, stimulation or elevation of cytosolic Ca^{2+} leads to a rapid translocation of ARF6 from secretory granules to the plasma membrane and a concomitant activation of PLD in this membrane (Caumont et al. 1998).

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Fig. 23. Ethanol inhibits β -glucuronidase secretion induced by FMLP. Metabolically inhibited HL60 cells were permeabilized with streptolysin O and incubated with and without ethanol and FMLP in the presence of different concentrations of free Ca²⁺. From Stutchfield & Cockcroft (1993) by permission of the authors and publisher

Furthermore, a myristoylated peptide corresponding to the N-terminus of ARF6 inhibited both PLD activity and the secretion of catecholamine. In later work, antibodies to ARNO, a BFA-insensitive guanine nucleotide exchange factor for ARF, were found to inhibit both PLD activity and catecholamine secretion (Caumont et al. 2000). Expression of an inactive ARNO mutant also blocked secretion of expressed growth hormone in PC12 cells. These studies implicate both ARF6 and PLD in exocytosis at the plasma membrane.

More recent work has shown a close correlation between PLD activation and catecholamine secretion in chromaffin cells stimulated with nicotine and treated with various ceramides (Vitale et al. 2001). Overexpression of wild type PLD1, but not PLD2, in PC12 cells increased exocytosis, whereas expression of catalytically inactive PLD1 inhibited this process. Inactive PLD1 also inhibited nicotine-stimulated catecholamine secretion from chromaffin cells (Vitale et al. 2001). Mutant forms of PLD that did not respond to PKC or did not interact with PIP₂ showed impaired ability to enhance exocytosis compared with wild type PLD (Vitale et al. 2001). These data provide support for a role of PLD1 in the exocytotic process and indicate supporting roles for PKC and PIP₂.

There is also evidence for a role of PLD in endocytosis. In response to stimulation, membrane receptors are endocytosed and degraded. Shen et al. (2001) have reported that the internalization and degradation of EGF receptors in rat fibroblasts is inhibited by primary, but not secondary alcohols.

Furthermore, overexpression of PLD1 or PLD2 resulted in reduced EGF receptor levels, but this was not seen with catalytically inactive mutants of these enzymes. There is evidence that EGF activation of MAP kinase depends on endocytosis of the EGF receptor (Vieira et al. 1996). In support of a role for PLD in internalization of the receptor, EGF-induced phosphorylation of MAP kinase was found to be inhibited by 1-butanol, but not 2-butanol (Shen et al. 2001). Further evidence of a role of PLD in endocytosis comes from studies of the recruitment of AP-2 proteins into the plasma membane and their targeting to endosomes (West et al 1997). These proteins are required for the formation of clathrin-coated vesicles which are involved in endocytosis. Addition of exogenous PLD to liver membranes or permeabilized NRK cells was found to promote the recruitment of AP-2 proteins to endosomes to the same extent as GTP(S, and the recruitment of AP-2 to endosomes and the plasma membrane was reduced by neomycin in the presence and absence of GTP γ S.

PLD has also been reported to be involved in the assembly of AP-2containing clathrin coats on lysosomes (Arneson et al. 1999). This is thought to be due to the effects of PA on PIP₂ synthesis. Fusion of early endosomes may also involve PLD since this process is blocked by 1-butanol, but not 2butanol, and is stimulated by exogenous PLD (Jones & Clague 1997). In contrast to AP-2 proteins, the recruitment of COP proteins to endosomal membranes does not seem to involve PLD (Gu & Gruenberg, 2000). For example, it was observed that addition of PLD or PA to endosomes did not promote COP binding, whereas GTP(S had a strong effect through activation of ARF.

An interesting proposed new role for PLD is in trafficking of the GLUT4 glucose transporter (Emoto et al. 2000). This translocation is involved in insulin-stimulated glucose transport in muscle and adipose tissue. Using Myc-tagged PLD1, the expressed enzyme was shown by immunofluorescence and confocal microscopy to partly colocalize with GLUT4 in 3T3-L1 adipocytes and CHO cells. In addition, microinjection of PLD into adipocytes markedly potentiated the effect of insulin on GLUT4 translocation to plasma membranes (Emoto et al. 2000). These results were supported by the observation that 1-butanol, but not 2-butanol, inhibited insulin-stimulated 2-deoxyglucose transport in 3T3-L1 adipocytes. The precise role of PLD in stimulating GLUT4 trafficking remains to be defined.

7.3 Role in Mitogenesis

Early studies implicated PLD and PA in the regulation of mitogenesis. However, many of these experiments involved addition of PA to cells and were complicated by the presence of LPA in the PA preparations. Some early experiments also involved incubation of intact cells with plant or bacterial PLD, but this is also problematic since it can produce LPA as a result of the action of these enzymes on LPC (van Dijk et al. 1998). Therefore these types of experiments do not provide conclusive evidence for a role of PLD or PA in cellular processes. Other approaches have examined the correlation between cellular PA levels and DNA synthesis or have manipulated the PA level through the use of primary alcohols or inhibitors of PAP e.g. propranolol. In Swiss 3T3 cells, mitogenic concentrations of sphingosine induced early increases in PA, whereas structurally related analogs did not affect either process (Zhang et al. 1990). Stimulation of Balb/c3T3 cells with PDGF caused a rapid, large and prolonged increase in PA, whereas the accumulation of DAG was biphasic (Fukami & Takenawa 1992). Propranolol enhanced the increase in PA, whereas an inhibitor of DAG kinase had no effect, indicating that the PA was produced mainly through PLD action. Treatment of the cells with exogenous PLD or PA, from which LPA had been removed, stimulated DNA synthesis (Fukami & Takenawa 1992), whereas PLC was less effective. These findings suggest that PA is more effective than DAG in regulating mitogenesis in these cells. Kondo et al. (1992) also found evidence for a role of PLD in the control of DNA synthesis in vesicular smooth muscle cells. Exogenous PLD from S. chromofuscus stimulated mitogenesis in these cells, and the effect was enhanced by insulin. Downregulation of PKC did not affect the action of PLD, suggesting that it was not due to the generation of LPA.

The proliferative action of thrombin on MC3T3-E1 osteoblasts has been proposed to involve PLD (Suzuki et al. 1996a). This is based on the observations that thrombin causes choline release from these cells and that propranolol inhibits DAG formation and DNA synthesis. However, more studies are required to support this proposal. A role for PLD in the mitogenic action of arginine vasopressin (AVP) on glomerular mesangial cells is also indicated. AVP increased mitogenesis and activated PLD in these cells (Kusaka et al. 1996). Preincubation of the cells with the putative PLD inhibitors 2,3diphosphoglycerate and carbobenzyloxy-leucine-tyrosine-chloromethylketone reduced the activation of both PLD and MAP kinase by AVP. Exogenous bacterial PLD also stimulated DNA synthesis. The stimulatory effects of AVP and bacterial PLD on thymidine incorporation into DNA were also blocked by 2,3-diphosphoglycerate. All these results support a role for PLD in the mitogenic action of AVP. However, the specificity of the PLD inhibitors may be questioned, and also the mode of action of exogenous PLD.

Another exploration of the role of PLD in mitogenesis induced by angiotensin II in vascular smooth muscle cells utilized 1-and 3-butanols to diminish PA accumulation (Wilkie et al. 1996). 1-butanol caused a significant decrease in thymidine incorporation into DNA, whereas 3-butanol was ineffective. In another exploration of the role of PLD in the mitogenic action of angiotensin II, the agonist and exogenous PLD and PA were all shown to increase DNA synthesis in vascular smooth muscle cells (Freeman 2000). However, propranolol blocked the stimulation by all these agents even though it increased PA, and an inhibitor of DAG lipase attenuated the incorporation of thymidine into DNA. Thus, in this system, DAG derived from PA may be an important signal for mitogenesis, as suggested also by the studies of Suzuki et al. (1996). In contrast, a recent report indicates the importance of PA in mitogenesis. This utilized a different approach to defining a role of PLD in mitogenic signaling, involving the use of NIH-3T3 cells stably overexpressing PLD1 (Hong et al. 2001). These cells showed enhanced PLD and MAP kinase activity in response to LPA (Fig. 24). The activation of MAP kinase was decreased by 1-butanol and enhanced by propranolol, indicating the involvement of PA, but not DAG. Evidence of the involvement of PLD



Fig. 24. Enhanced activation of MAP kinase in fibroblasts overexpressing PLD1. Vector-expressing (V) or PLD1-overexpressing (P1) NIH 3T3 cells were incubated with LPA in the presence of absence of two concentrations of 1-butanol. The activation of MAP kinase (ERK1) was assessed with phospho-specific anti-ERK antibodies. From Hong et al. (2001) by permission of the authors and publisher

and PA in the stimulation of MAP kinase by interleukin-11 in 3T3-L1 cells has also been presented (Siddiqui & Yang 1995).

A role for PA in the EGF induced transition of A431 epithelial cells from the G_2 phase of the cell cycle to mitosis has been proposed (Kaszkin et al. 1992). The cells responded to EGF with formation of PA which dosedependently correlated with a delay in transition from G_2 phase. Treatment with PMA, which increased the PA level, and with exogenous PLD also decreased the G_2 -M transition rate.

7.4

Role in Superoxide Production

Neutrophils play a major role in host defense against microorganisms. One of the responses is the generation of toxic O_2 metabolites, including the superoxide anion (O_2) , and PLD has been implicated in this process. For example, agonists that elicit this response, e.g. chemoattractants, phagocytic particles and cytokines, also stimulate PLD activity (Billah et al. 1989; Agwu et al. 1989; Pai et al. 1988). In addition, early experiments demonstrated that PA elicited NADPH-dependent production of superoxide (O⁻₂) in membrane extracts of neutrophils (Bellavite et al. 1988) or when this lipid was added to intact neutrophils (Ohtsuka et al. 1989). In neutrophils primed with tumor necrosis factor α , FMLP caused accumulation of PA and this was highly correlated with O_2^{-2} production (Bauldry et al. 1991). Through the use of neutrophils or HL60 cells labeled with [³H]hexadecyl-2-lyso-sn-glycero-3phosphocholine ([³H]alkyl-lysoPC) and alkyl-[³²P]lysoPC, the PA was shown to be formed by PLD activation (Agwu et al. 1989; Pai et al. 1988; Billah et al. 1989; Bauldry et al. 1991), and ethanol inhibition of PA formation led to a corresponding reduction of O_2^- generation (Bonser et al. 1989; Bauldry et al. 1991), Similar findings were made by Agwu et al. (1991) who also measured NADPH oxidase activity in cell-free extracts. Propranolol at low concentrations enhanced both PA accumulation and oxidase activity, but at higher concentrations the stimulation was lost (Agwu et al. 1991). Another group reported that PA produced by PLD, and not DAG, was functionally linked to the oxidase (Rossi et al. 1990). Didecanoyl PA activated NADPH oxidase in vitro, in agreement with earlier findings. In a more extensive study utilizing permeabilized neutrophils, further evidence was obtained for a role of PA (Bauldry et al. 1992).

Other studies demonstrated that DAG could also play a role in the activation of NADPH oxidase. For example, Burnham et al. (1990) observed that DAG could synergize with SDS to activate the enzyme, and Qualliotine-

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Fig. 25. PA and DAG synergize to activate NADPH oxidase in vitro. Cytosolic and membrane fractions from neutrophils were incubated with a reaction mixture containing the lipids shown. NADPH oxidase was measured as described by Qualliotine-Mann et al. (1993)

Mann et al. (1993) reported a synergism between PA and DAG (Fig. 25). This was confirmed in a later study (Erickson et al. 1999) which demonstrated that the activation of the oxidase by PA was not due to its conversion to DAG. Evidence was then presented that PA acted through a PA-regulated protein kinase (McPhail et al. 1995), which phosphorylated the p47^{phox} component of NADPH oxidase (Waite et al. 1997). In later work, the p22^{phox} subunit was also shown to be phosphorylated by the PA-activated kinase and also by conventional PKC isozymes (Regier et al. 1999). Phosphorylation of the p22^{phox} subunit was observed in neutrophils stimulated by FMLP and other agonists. Pretreatment of the cells with ethanol produced large decreases in both NADPH oxidase activity and p22^{phox} phosphorylation (Regier et al. 2000). However, these responses were not altered by ethanol in cells stimulated by PMA, indicating the existence of both PLD-mediated and PKC-mediated pathways for p22^{phox} phosphorylation and NADPH oxidase activation.

Despite the preceding evidence that NADPH oxidase can be controlled by protein kinases sensitive to PA and DAG, there is also evidence that these lipids can also act by a non-phosphorylation mechanism (McPhail et al. 1995). Thus, in a cell-free system of purified recombinant NADPH oxidase components, activation of the complex by PA plus DAG was ATPindependent and not affected by staurosporine (Palicz et al. 2001). In summary, stimulation of neutrophils by FMLP and other agonists causes PA accumulation as a result of PLD activation. This PA in combination with Phospholipase D - Structure, Regulation and Function

DAG can activate NADPH oxidase in neutrophil by phosphorylation-dependent and -independent mechanisms.

7.5 Role in Actin Cytoskeleton Rearrangements

Alterations in the actin cytoskeleton are important in cell shape changes and motility, chemotaxis, cell division, endocytosis and secretion. The changes in cell shape, motility, migration and metastasis involve activation of members of the Rho family of GTPases. For example, Rho mediates stress fiber formation and focal adhesion formation in fibroblasts and causes neurite retraction and rounding up in neurons, whereas Rac is involved in membrane ruffling and the generation of lamellipodia, and activation of Cdc42 induces filopodia formation (Nobes and Hall, 1994).

The involvement of PLD in Rho-mediated changes in the actin cytoskeleton was first suggested in studies of the effects of exogenous bacterial PLD and PA on actin polymerization and reorganization in IIC9 fibroblasts (Ha and Exton 1993a). These agents induced stress fiber formation similar to that caused by α -thrombin and also increased the F-actin content of the cells. In contrast, dioctanoylglycerol and PC-PLC from B. cereus were without effect. However, the possible role of LPA contamination or generation was not ruled out. In further work, LPA was found to cause a very rapid activation of PLD in IIC9 cells which was accompanied by an equally rapid increase in F-actin (Ha et al. 1994). However, the polymerization of actin was observed with lower concentrations of LPA than was PLD activation, suggesting that either a small increase in PA was required for the actin effect or the two processes were dissociated. Support for a role of PLD in actin stress fiber formation came from a study of cytoskeleton changes in endothelial cells (Cross et al. 1996). In agreement with Ha and Exton (1994) addition of PA induced stress fiber formation in these cells, whereas dioctanoylglycerol caused only a small effect. As expected, LPA also induced this cytoskeletal change and the effects of both PA and LPA were blocked by C3 exoenzyme, indicating the involvement of Rho. A role for PLD in regulation of the actin cytoskeleton was suggested by the observations that LPA activated PLD and that 1-butanol inhibited LPA-induced formation of both PA and actin stress fibers, whereas 2-butanol was without effect (Cross et al. 1996). In these experiments, PA was shown by thin layer chromatography to be free of LPA and not to activate PLD. Furthermore, its action on stress fibers was not inhibited by 1-butanol.



Fig. 26. Fibroblasts with reduced PLD activity show loss of stress fiber formation in response to LPA. Rat-2 fibroblast clones stably expressing inactive V5 epitope-tagged rPLD1 and showing reduced PLD activity were treated with LPA, and stress fiber formation assessed by staining with Texas red X-phalloidin and confocal microscopy. The V16, V25 and V29 clones showed expression of V5-rPLD1 and reduced PLD activity. The V20 clone did not express V5-rPLD1 and showed normal PLD activity. From Kam & Exton (2001) by permission of the authors and publisher Phospholipase D - Structure, Regulation and Function

A recent study (Kam and Exton, 2001) has provided more evidence for a role of PLD in actin stress fiber formation in cells. These workers generated Rat1 fibroblast lines stably expressing catalytically inactive V5 epitopetagged PLD1. These cell lines exhibited reduced basal and PMA- or LPAstimulated PLD activity and failed to show normal actin stress-fiber and α actinin translocation responses to LPA (Fig. 26). In contrast, the cells showed normal membrane ruffling in response to PMA and focal adhesion formation was intact, as revealed by immunostaining of vinculin. Since the activation of RhoA and of Rho kinase by LPA was unimpaired in the PLDdeficient cells, it was concluded that PLD was involved in downstream events from Rho kinase (Kam and Exton, 2001). Because PIP2 affects the function of many actin-associated cytoskeletal proteins (Sechi & Wehland 2000), the authors proposed that the role of PLD was to generate PA which then acted on type 1 PI 4-P 5-kinase (Jenkins et al. 1994; Ren et al. 1996; Moritz et al. 1992) to produce a local increase in PIP2. Further work is needed to support this hypothesis.

An association of PLD with the actin cytoskeleton was indicated by Iyer and Kusner (1999). These workers found that PLD activity was associated with the detergent-insoluble fraction of promonocytic leukocytes. This association was greatly increased by pre-incubation with GTP γ S. The fraction was enriched in the cytoskeletal proteins F-actin, talin, paxillin and α actinin, and PLD1, RhoA and ARF were also detected. A more direct interaction of PLD with actin was shown by Lee et al. (2001). Using mass spectrometry, these workers identified a major PLD2-binding protein in rat brain as β -actin. This protein was also found to bind directly to PLD2 and PLD1 and to inhibit their activity. Immunocytochemistry and co-immunoprecipitation studies showed that both PLD isozymes interacted with β actin and with the actin cytoskeleton in intact cells. In summary, all these results support a close association between PLD and the actin cytoskeleton.

7.6

Role in Lysophosphatidic Acid Formation

LPA is an intermediate in the biosynthesis of triacylglycerol and certain phospholipids. It is also an important extracellular messenger which interacts with certain EDG receptors which are present on the surface of many cells and are coupled to heterotrimeric G proteins (Contos et al. 2000). Thus LPA produces proliferative and morphological effects that are due to changes in the activity of adenylyl cyclase, PLC, PLA₂, MAP kinase and Rho (Kranenburg & Moolenaar 2001). LPA is released from activated platelets and probably other cells, and is a major mitogen in serum (Eichholtz et al. 1993).

There are several ways by which LPA could be released from cells. One is by action of phospholipase A_2 on PA to yield 1-acyl LPA, which is the major form of LPA (Fig. 27). 2-acyl LPA can also be produced through the action of PLA₁. This form is equipotent with 1-acyl LPA on EDG2 and EDG4 receptors and more potent on EDG7 receptors (Bandoh et al. 2000). An alternative pathway for LPA production is through action of lysophospholipase D on 1or 2-acyl lyso PC or other lysophospholipids to yield 1-acyl LPA or 2-acyl LPA. PLA₂ is present in numerous isoforms in mammalian cells (Dennis 1994) and PLA₁ has a widespread distribution (Pete et al. 1994). Secreted forms of PLA₂ could act on PA and other phospholipids in the outer leaflet of the plasma membranes to cause the release of LPA or formation of lysophospholipids, but it is unclear that PLA₁ could act in this manner. The nature of the lysophospholipase D that acts on lysoPC (vanDijk et al. 1998) is unclear. Bacterial forms of PLD exhibit lysophospholipase D activity, but this has not been demonstrated for mammalian PLD isoforms. If the principal route of LPA formation is from PA via phospholipase A action, then PLD is probably involved through its action on PC to yield PA.



Fig. 27. Metabolism of PA to LPA and DAG. The figure shows conversion of PA to LPA by PLA2 and the reverse reaction catalyzed by lysophosphatidate acyltransferase (LPAAT), and the conversion of PA to DAG by phosphatidate phosphohydrolase (PPH) and the reverse reaction catalyzed by diacylglycerol kinase (DGK)

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7.7 Other Cellular Roles

Many other functions have been ascribed to PLD. One is in cellular senescence (Venable et al. 1994). In this study, senescent human diploid fibroblasts were noted to have impaired DAG accumulation in response to serum. The defect was traced to an impairment in PLD activation, and it was suggested that this was due to the increase in ceramide observed in these cells.

Another role for PLD is in the turnover of PC (Tronchère et al. 1995). In neutrophils stimulated with FMLP, there was breakdown of PC to PA mediated by PLD, but no stimulation of PC synthesis. However if cytochalasin B was added with FMLP, there was conversion of PA to DAG and incorporation of choline into PC and translocation of the rate-limiting enzyme for PC synthesis (CTP: phosphocholine cytidyltransferase) from the cytosol to membranes. Further work indicated that only DAG derived from PC via PA could promote cytidyltransferase translocation and subsequent PC synthesis (Tronchère et al. 1995).

Roles for PLD-generated PA in other cellular responses have been proposed. For example, priming of neutrophils with platelet-activating factor caused PLD activation and the binding of serum-opsonized particles, whereas ethanol greatly inhibited this binding and also PA formation and the respiratory burst (Tool et al. 1999). The PAP inhibitor propranolol, enhanced the binding of the particles and addition of cell-permeant PA resulted in CD11b/CD18 integrin-dependent adhesion to the particles and fibronectin. The authors concluded that PLD-derived PA was involved in altering the affinity of the integrin for its ligands.

The role of PLD in the supply of choline for acetylcholine synthesis in the brain remains speculative. Free choline is present at low concentrations in the brain, and the turnover of acetylcholine suggests that the reuptake of choline is insufficent for continued synthesis of this neurotransmitter (Klein et al. 1995). Generation of the extra choline by PLD activity remains an attractive possibility and the agonist that stimulates PLD could be acetylcholine itself. However, the site of PLD activation and choline release, e.g. presynaptic or glial cells, and the agonists involved remain unclear.

A role for PLD in AVP-induced Ca^{2+} spiking in vascular smooth muscle cells has been proposed (Li et al. 2001). Treatment of the cells with a putative PLA₂ inhibitor (ONO-RS-082) led to inhibition of PA formation, but not that of arachidonic acid. Furthermore, exogenous PLD induced Ca^{2+} spiking, whereas arachidonic acid was without effect. 1-butanol, but not 2-butanol, suppressed the spiking caused by AVP, but had no effect on BaCl₂stimulated spiking. Based on inhibitor data PKC was proposed to be downstream from PLD in the signaling pathway involved in AVP-induced Ca²⁺ spiking.

7.8 Other Targets of Phosphatidic Acid

Cellular targets for PA have been described in some preceding sections. These include NADPH oxidase, Golgi and other membranes involved in vesicle trafficking, PI 4-P 5-kinase and protein kinases. In this section, additional PA targets will be described, but their in vivo significance remains unclear. Early work identified RasGAP as a target (Tsai et al. 1989) and the activation of Ras due to inhibition of its GAP activity by PA was thought to underlie the mitogenic action of this lipid. Inhibition of Rac interaction with Rho GDI has also been reported (Chuang et al. 1993) and *n*-chimaerin an activator of RacGAP, is stimulated by PA (Ahmed et al. 1993). However, there have been no reports of PLD action on Rac activity in intact cells. PA binds strongly and selectively to Raf 1 kinase, and inhibition of PA formation by treatment of MDCK cells with ethanol reduces membrane translocation of Raf 1 (Ghosh et al. 1996). PA-mediated recruitment of Raf 1 was reported by another group (Rizzo et al. 2000) who showed that the interaction was independent of Ras.

In HL60 cells, production of PA via activation of endogenous PLD by PMA or treatment with exogenous PA or PLD from *S. chromofuscus* results in tyrosine phosphorylation of 100-115 kDa proteins (Ohguchi et al. 1997). The phosphorylation induced by PMA is reduced by ethanol or butanol, suggesting the involvement of PLD. PA-dependent tyrosine phosphorylation of cellular proteins was also observed in studies with neutrophils (Sergeant et al.2001). Similar to what was found in HL60 cells, PMA-induced phosphorylation was decreased by primary alcohols. The tyrosine kinase(s) responsible for these effects has not been identified.

In contrast to the preceding results, PA has been found to stimulate a specific protein tyrosine phosphatase termed PTP1C (also known as SH-PTP1, HCP or SHP-1). This contains two SH2 domains and is very strongly stimulated by anionic phospholipids including PA, which is the most effective activator (Zhao et al. 1993). A later study showed that PA bound to a site at the C-terminus of the enzyme (Frank et al. 1999). PTP1C was found to be associated with the EGF receptor in A431 cells (Tomic et al. 1995), but showed little activity towards the autophosphorylated receptor unless PA was added. The lipid also enhanced the association of PTP1C with the receptor and stimulated its dephosphorylation in intact cells. The significance of these findings for EGF signaling remains to be established.

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PA can interact with certain PLC isozymes in vitro. PA was first reported to activate PLC activity associated with platelet membranes (Jackowski & Rock 1989). In a more recent study, it was found to alter the kinetics of PLC- γ l by decreasing the cooperativity index with little change in the association with substrate micelles (Jones et al. 1993). However, PA increased the activity of tyrosine phosphorylated form of the enzyme by decreasing the Km 10fold. PLC- β 1 is also stimulated by PA, which increases its association with unilamellar vesicles (Litosch 2000). PA increases the enzymatic activity in the presence of PIP₂ and Ca²⁺ and decreases the Ca²⁺ concentration required for stimulation.

Certain isoforms of cAMP-specific phosphodiesterase are regulated by PA. Thus PDE4A5 is stimulated by PA in vitro (Fig. 28), and treatment of thymocytes with DAG kinase inhibitors to decrease the PA level caused a reduction in concanavalin A-stimulated cAMP-specific PDE activity (El Bawab et al. 1997). PA extracted from ConA-stimulated cells was more effective in stimulating PDE4A5 than that extracted from unstimulated cells, and PA containing unsaturated fatty acids was more effective than that containing saturated fatty acids. PA has also been reported to bind to and activate PDE4D3 (Grange et al. 2000). Treatment of MA10 Leydig tumor cells overexpressing PDE4D3 with propranolol caused accumulation of PA. This was accompanied by an increase in PDE activity and a decrease in cAMP and protein kinase A activity. Furthermore in FRTL5 thyroid cells, which natively express PDE4D3, agents that induce PA accumulation decreased cAMP and CREB phosphorylation. These results suggest a role for PA in regulating cAMP signaling in cells.

The existence of a PA-stimulated Ser/Thr protein kinase in neutrophils was alluded to in Section 7.4. This activity was also detected in a variety of tissues and shown to be independent of Ca^{2+} and separate from PKC (Bocckino et al. 1991). Another lipid-dependent protein kinase was characterized in platelets (Khan et al. 1994). This was selective for PA and was shown to be Ca^{2+} -independent and not a PKC isozyme. Certain PKC isozymes can be activated by PA. Thus PA can substitute for PS as an activator of the enzyme (Hannun et al. 1986;

Epand and Stafford 1990). In a detailed examination of the effects of PA on different PKC isozymes, Limatola et al. (1994) observed, in the absence of Ca^{2+} , that PKC ζ was most strongly activated by PA, although PKC α was also activated by PA in the presence of Ca^{2+} . PA caused a shift in the electrophoretic mobility of PKC ζ due to its binding to the enzyme. Concerning the effects of PA on protein Ser/Thr phosphatases, this lipid has been reported to be a potent and selective inhibitor of PP1, but not of PP2A or PP2B (Kishikawa et al. 1999). PA acts on the catalytic subunit of PP1(and is able to



Fig. 28a, b. Activation of cAMP phosphodiesterase PDE4A5 by PA. Recombinant PDE4A5 prepared in Sf9 cells was incubated with different molecular species of PA and the phosphodiesterase activity measured by the conversion of $[^{3}H]$ cAMP to $[^{3}H]$ adenosine in the presence of 5'nucleotidase. Most PA species were very effective, except for distearoyl PA (Δ in panel a) and 1-palmitoyl-2-oleoyl PA and dipalmitoyl PA (Δ and in panel b). From El Bawab et al. (1997) by permission of the authors and publisher

counteract the stimulatory effects of ceramide. The possibility that PA may regulate protein phosphorylation/dephosphorylation in vivo needs further exploration.

A recent report has proposed a unique role for PA in the regulation of translation (Fang et al. 2001). This has identified the rapamycin-sensitive protein mTOR/FRAP as a target of PA. mTOR regulates translation initia-

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tion through effects on the initiation factor binding protein 4E-BP1 and the protein kinase S6K1 which phosphorylates ribosomal protein S6. PA was found to stimulate S6K1 activity and to induce 4E-BP1 hyperphosphorylation (Fang et al. 2001). Furthermore, PA interacted directly with the rapamycin binding domain of mTOR. It was proposed that PA mediates activation of mTOR by mitogenic stimuli and that rapamycin inhibits mTOR signaling by blocking PA binding. It will be interesting to see how this scheme relates to other mechanisms of mTOR regulation.

7.9

Diacylglycerol Production from Phosphatidylcholine and its Role in Protein Kinase C Regulation

An important issue in understanding PLD effects in vivo is whether PA and DAG derived from the action of PLD on PC are functionally different from those produced by PLC action on PIP₂. Banschbach et al. (1981) first noted that the DAG accumulating in mouse pancreas incubated with acetylcholine had a different fatty acid composition from that in PI, indicating that it came from another source. Although these workers suggested that this was triacylglycerol, the composition of the DAG resembled that of PC in the pancreas. Cockcroft & Allan (1984) also noted that the fatty acid composition of PA and DAG in neutrophils treated with FMLP was different from that of PI, and also suggested that these lipids were derived from another source. Bocckino et al. (1985) later demonstrated that two chromatographic peaks of DAG were produced by hepatocytes stimulated with AVP, and that these differed in their fatty acid composition. However, neither peak resembled PI in composition, and it was suggested that PC might be a source. This was confirmed in later studies of PA formation and PLD activation in hepatocytes stimulated with several agonists (Bocckino et al. 1987a; 1987b). Chemical measurements showed a rapid accumulation of PA that preceded a rise in DAG in the stimulated cells, indicating that the PA was unlikely to have arisen from DAG kinase activity. Furthermore, the fatty acid composition of the PA and DAG was noted to resemble that of PC and not PI. Studies utilizing the transphosphatidylation reaction to measure PLD activity then demonstrated that the agonists activated PLD in the cells, indicating that PLD activity was the probable source of the PA. Measurements of choline release from GTPyS- and hormone-stimulated liver plasma membranes indicated that PC was the substrate of PLD (Irving & Exton1987; Bocckino et al. 1987a). This was confirmed by isotope studies and analyses of the molecular species of DAG and phospholipids in hepatocytes stimulated with AVP (Augert et al. 1989). The major species of DAG in the stimulated hepatocytes

were found to be 16:0/18:2, 18:0/20:4, 16:0/18:1, 16:0/20:4 and 18:0/18:2 (Augert et al. 1989). This pattern resembled that of PC, but not PI, extracted from the hepatocytes. Wright et al. (1988) analyzed the kinetics of DAG production in IIC9 fibroblasts stimulated with α -thrombin and EGF. Treatment with α -thrombin induced an early phase of DAG formation peaking at 15s and a late phase peaking at 5 min. With low concentations of this agonist or with EGF, only the slow phase was observed. Since the rapid phase corresponded with IP₃ formation, it was proposed to be derived from PIP₂ hydrolysis, whereas the second phase was derived from another source. Very similar results were obtained later by Ha & Exton (1993b) who analyzed the effects of α -thrombin and PDGF on DAG levels in IIC9 fibroblasts (Fig. 29). In detailed analyses of the molecular species of DAG and phospholipids in IIC9 fibroblasts, Pessin & Raben, (1989) and Pessin et al. (1990) concluded that phosphoinositides contributed significantly to the early phase of DAG generated by a-thrombin stimulation, whereas PC contributed most of the DAG measured at 5 min and 1 h. In the case of EGF stimulation, PC was the primary source, as also indicated by the sustained release of choline. Lee et al. (1991) studying muscarinic activation of SK-N-SH neuroblastoma cells noted that the molecular species of DAG accumulating at 5s resembled those in phosphoinositides, whereas those measured at 10 min or longer resembled those in PC.

In another study of the sources of DAG in agonist-stimulated cells, Huang & Cabot (1990) incubated REF52 fibroblasts with $[^{3}H]$ myristic acid, which labels predominantly PC, and $[^{3}H]$ arachidonic acid, which is incorporated into most phospholipids. In cells labeled with arachidonic acid and stimulated with AVP, there was a rapidly generated peak of DAG and a slower increase in PA, consistent with initial formation of DAG through PIP₂ hydrolysis. On the other hand, in myristate-labeled cells, PA increased rapidly, but DAG did not change until later, in accord with PA formation from PC by PLD. Measurements of inositol phospholipid changes and of phosphatidylethanol formation from specifically labeled PC confirmed these conclusions (Huang & Cabot 1990).

Support for the view that agonists generate DAG in cells by both PLCcatalyzed breakdown of PIP₂ and PLD-mediated hydrolysis of PC has come from other studies utilizing isotopic labeling and molecular species analysis in a variety of cell types stimulated with different agonists (Martinson et al.1989; Price et al. 1989; Matozaki & Williams 1989; Kennerly 1990; Mac-Nulty et al. 1990; Lee et al. 1991; Plevin et al. 1991; Divecha et al. 1991; van Blitterswijk et al. 1991a; 1991b; Sebeldt et al. 1992; Fällman et al. 1992; Hermans et al. 1996). In general, these studies showed that DAG was derived mainly from PIP₂ in the early phase of agonist stimulation, and from PC in



Fig. 29A, B. Time courses of formation of DAG in fibroblasts stimulated with α -thrombin (A) or PDGF (B). IIC9 fibroblasts were labeled with [³H]myristic acid and incubated with α -thrombin or PDGF. [³H]DAG was measured at the indicated times by thin layer chromatography. From Ha & Exton (1993b) by permission of the authors and publisher

the late phase. Likewise PA was initially produced mainly by DAG kinase action on PIP_2 and later by PLD action on PC.

Pettit et al. (1997) also looked at the composition of DAG and PA in endothelial cells stimulated with LPA. Although these workers found that LPA produced no significant changes in individual DAG species, the pattern of molecular species was similar to that observed by Augert et al. (1989), Pessin & Raben (1989), Pessin et al. (1990), Lee et al. (1991) or Hermans et al. (1996) in cells stimulated for a short time with agonists. It reflected formation predominantly from phosphoinositides. The fatty acid composition of PA and phosphatidylbutanol in Swiss 3T3 cells stimulated with bombesin in the presence of butanol and in endothelial cells treated with LPA and butanol was also examined by Pettit et al. (1997). These workers found a predominance of 16:0, 18:0 and 18:1 fatty acids with almost undectable levels of 16:1, 18:2, 20:4 and 22:6 fatty acids, and concluded that PA and phosphatidylbutanol derived from PLD action had a very different fatty acid composition from DAG generated by PLC. Although this conclusion is correct, their data make it difficult to identify the phospholipid acted on by PLD since all mammalian phospholipids contain significant amounts of arachidonic acid and other polyunsaturated fatty acids in their sn-2position (Kuksis et al. 1968; Holub & Kuksis 1978; Smith & Jungalwala 1981; Mahadevappa & Holub 1982; Patton et al. 1982; Takamura et al. 1987; MacDonald & Sprecher 1989; Augert et al. 1989; Pessin & Raben 1989; Pessin et al. 1990; Lee et al. 1991). This presence of arachidonic acid in this position in PC is the reason why activation of PLA2 leads predominantly to the release of arachidonic acid.

The cellular role of DAG accumulating in the late phase of agonist stimulation of cells remains unclear (Wakelam 1998). It was originally postulated to produce prolonged activation of PKC, as opposed to transient activation due to PIP₂ hydrolysis (Bocckino et al. 1985; Price et al. 1989; Matozaki & Williams 1989; Exton 1990; Fällman et al. 1992). It was also proposed that the prolonged increase in DAG was related to the mitogenic action of EGF (Wright et al. 1988). The view that PC-derived DAG could activate PKC was supported by several lines of evidence including analyses of its molecular species, which were found to be effective in activating PKC in vitro (Go et al. 1987). In MDCK cells, activation of α_1 -adrenergic receptors resulted in hydrolysis of both PIP₂ and PC (Slivka et al. 1988). Treatment with neomycin to suppress PIP₂ breakdown did not significantly alter DAG production, indicating that it mainly came from PC. More importantly, neomycin did not inhibit the membrane translocation of PKC, implying that DAG derived from PC was capable of activating PKC. Furthermore, Fällman et al. (1992) showed that the sustained increase in DAG due to complement receptormediated activation of phagocytosis in neutrophils was associated with phosphorylation of MARCKS a well-known substrate of PKC. On the other hand, several groups have reported that the second phase of hormonestimulated DAG accumulation does not activate PKC (Martin et al. 1990; Leach et al. 1991; Baldassare et al. 1992). However, these investigators studied mainly conventional (Ca²⁺-dependent) PKC isozymes. In a detailed study of the activation of PKC isozymes in IIC9 fibroblasts stimulated with two different agonists Ha & Exton (1993b) showed that α -thrombin caused a rapid, but transient, translocation of PKCa to the membrane fraction



Fig. 30. Translocation of PKC isozymes induced by α -thrombin in IIC9 fibroblasts. Cells were activated with α -thrombin for the indicated times or with PMA (T) for 15 min. Cytosolic (C) and membrane (M) fractions were isolated and Western blotted for PKC α and PKC ϵ . From Ha and Exton (1993b) by permission of the authors and publisher

(Fig. 30). This coincided with transient increases in IP₃ and cytosolic Ca²⁺. PKCe was also rapidly translocated, but its membrane association persisted for 1 hr (Fig. 30). In contrast, PDGF did not cause PKC α to translocate and induced a slow membrane association of PKCe. PKC α translocation was blocked by Ca²⁺ chelators and could be induced by 1,2-dioctanoylglycerol plus ionomycin, but by neither agent alone. In contrast, the DAG alone could cause translocation of PKCe (Ha & Exton 1993b). These findings indicate that PC hydrolysis alone can activate Ca²⁺-independent PKC isozymes, whereas activation of Ca²⁺-dependent isozymes is dependent on a concurrent elevation of both DAG and cytosolic Ca²⁺ i.e. PIP₂ hydrolysis.

Some cells contain significant amounts of ether-linked phospholipids and there have been some studies of the effects of agonists on the release of 1-alkyl-2-acylglycerol and 1-alkenyl-2-acylglycerol. In pancreatic acini stimulated with cholecystokinin, 1,2-diacylglycerol and 1-alkenyl-2-acylglycerol, but not 1-alkyl-2-acylglycerol, accumulated due to hydrolysis of phosphoinositides, PC and plasmenyl-PC (Hermans et al. 1996). Due to the lower content of plasmenyl-PC, the predominant species was 1,2-diacylglycerol derived mainly from PC, but both types of diradylglycerol contained large amounts of linoleic and arachidonic acids. Stimulation of neutrophils with FMLP caused the production of both 1-alkyl-2-acylglycerol and 1,2-diacylglycerol (Dougherty et al. 1989), but their kinetics differed. The diacylglycerol was generated more rapidly than the alkyl-acylglycerol. Although alkylacylglycerol showed a greater fold-increase, its basal and stimulated levels were less than those of diacylglycerol. In a study of diradylglycerol forma-
tion in mesangial cells, Musial et al. (1995) observed that endothelin-1 generated predominantly 1,2-diacyl species, whereas interleukin-1 produced ether-linked species (alkyl-acylglycerol and alkenyl-acylglycerol).

There is still some controversy about the effects of 1-alkyl-2-acylglycerols on PKC activation. As noted above, these diradylglyerols can be generated by agonist stimulation of certain cells. Several groups have reported that they are ineffective in activating PKC (Cabot & Jaken 1984; Ganong et al. 1986; Daniel et al. 1988; Musial et al. 2001). However, their reported effects on the stimulation of PKC by PMA or 1,2-diacylglycerol have been variable. Three groups reported that 1-alkyl-2-acylglycerols inhibited the stimulatory effect of 1,2-diacylglycerols (Bass et al. 1989; Daniel et al. 1988; Musial et al. 1995). Furthermore, in mesangial cells, in which interleukin-1 generates 1alkyl-2-acylglycerol and 1-alkenyl-2-acylglycerol, the cytokine caused inhibition of PKC activation by endothelin 1 (Musial et al. 1995). 1-Alkyl-2acylglycerol also inhibited the priming of the respiratory burst induced by 1,2-diacylglycerol in polymorphonuclear leukocytes (Bass et al. 1989). In contrast to these findings, 1-alkyl-2-acylglycerol has recently been reported to enhance the activation of conventional PKC isozymes by PMA or 1oleoyl-2-acetylglycerol in vitro (Slater et al. 2001). In summary, although ether-linked diradylglycerols appear to be unable to activate PKC, their effects on the activation of the enzyme by diacylglycerols are unclear.

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Summary and Future Directions

Although much progress has been made in characterizing the enzymatic properties and regulation of mammalian PLDs, deficiencies in knowledge remain. In particular, information on the three-dimensional structure of mammalian PLDs is lacking, although the crystal structures of a plant and bacterial enzyme and of a low Mr member of the PLD superfamily have been defined. These have given information about the catalytic center and mechanism, but not how the enzyme is regulated. The catalytic center is formed by dimerization of the two HKD domains present in the enzyme, with the two histidines playing essential roles in catalysis as nucleophile and general acid in a two-step reaction. Mutagenesis studies have identified the PKC interaction site at the N-terminus and the Rho interaction site at the Cterminus, but it is not known where ARF interacts.

Both PLD1 and PLD2 are membrane-associated and appear to be localized to different regions in cells. PLD1 has a predominant perinuclear localization (?Golgi) but is located in other undefined intracellular structures and may be in the plasma membrane in some cells. PLD2 appears to be mainly in the plasma membrane. Both isozymes are subject to palmitoylation, which is not essential for activity, but is a factor in their membrane association. PLD1 is phosphorylated in unstimulated cells by an undefined Ser/Thr kinase. Phosphorylation is restricted to the N-terminal half of the enzyme and requires palmitoylation and association of the two HKD motifs. The phosphorylation has minimal effects on the intrinsic activity of the enzyme, but is involved in membrane association.

The conventional (Ca²⁺-dependent) isozymes of PKC are major regulators of PLD1 in vivo and in vitro. PLD2 can be activated by PKC-dependent mechanisms in vivo, but is not affected by PKC isozymes in vitro. Surprisingly, the activation of PLD1 by PKC in vitro does not involve phospshorylation, but occurs by a protein-protein interaction and only involves the α and β -isozymes of the kinase. The mechanism(s) by which PLD1 and PLD2 are activated by PKC in vivo have not been defined, but may or may not involve phosphorylation of the enzymes. PKC activation appears to be a major mechanism by which agonists acting on receptors coupled to G proteins or growth factors interacting with receptors encoding tyrosine kinase activity activate PLD in vivo.

Small G proteins of the Rho and ARF families activate PLD1 in vitro, but have little or no effect on PLD2. Of the Rho family, Rho is more effective than Rac and Cdc42. The G_{13} heterotrimeric G protein can activate Rho and hence PLD, and there is evidence that several agonists stimulate PLD by this mechanism. Although Rho can interact directly with PLD1 in vitro, other mechanisms of Rho activation of the enzyme may occur in vivo. PLD1 is activated by all mammalian ARFs in vitro, but the in vivo significance of ARF regulation is unclear. Class I ARFs are probably important in the regulation of the enzyme in Golgi, and ARF6 may be involved in membrane trafficking at the plasma membrane. Some reports have indicated a role for ARF in agonist regulation of PLD.

Tyrosine kinase activity plays a role in the regulation of PLD1 and PLD2, but it is unclear that this involves direct phosphorylation of the enzymes or of proteins involved in upstream events. Recently, Ral, a member of the Ras subfamily of small G proteins, has been implicated in the regulation of PLD. Ral may mediate some of the effects of Ras and growth factors on the enzyme. Ca^{2+} ions also play a role in the regulation of PLD, possibly through an action mediated by calmodulin. Ceramide, a product of sphingomyclin breakdown, is an inhibitor of PLD in vitro and in vivo. PI 3-kinase may play a role in the indirect regulation of the enzyme in some cell types.

An area needing much more work is the definition of the cellular functions of PLD. This is because many approaches have not been successful. The role of PLD in vesicle trafficking in Golgi remains controversial, although there is more support for its role in exocytosis. Evidence is also emerging for a role of PLD in endocytosis. It is still unclear what function PLD plays in the mitogenic response of cells to agonists. This is because the studies have mostly utilized inhibitors of uncertain specificity. There is more evidence that PA plays a role in superoxide production by neutrophils. Thus, PA has been reported to have in vitro and in vivo effects on the NADPH oxidase system. A role for PLD activity in the Rho-mediated rearragements of the actin cytoskeleton involved in stress fiber formation seems likely. This may involve changes in PIP₂, which is a regulator of several proteins involved in the response. It is likely, but not certain, that PA is the major source of LPA released from platelets and other cells. LPA has major effects throughout the body through its interaction with certain EDG receptors. Another product of PA metabolism is DAG. DAG derived from this source can activate novel (Ca²⁺-independent) PKC isozymes but does not act on the conventional isozymes unless cytosolic Ca²⁺ is elevated. However, it is clear that PA itself can interact with many cellular proteins and alter their activities. These involve proteins that regulate small G proteins, protein kinases, protein phosphatases, phospholipases, phosphodiesterases, phospholipid kinases and other regulatory proteins. An important element of PLD research will be to relate these and other effects of PA to the cellular changes induced by PLD activation.

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Endotoxin Tolerance – Mechanisms and Beneficial Effects in Bacterial Infection

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Endotoxin Tolerance

Endotoxin or lipopolysaccharide (LPS), a glycolipid of the cell membrane of Gram-negative bacteria, is one of the most potent known stimulators of immune responses. The immune system responds to LPS with a systemic production of proinflammatory cytokines which recruit and activate immune cells to eliminate invading pathogens (Mastroeni et al. 1999; Nakano et al. 1992). Although these cytokines are indispensible for the efficient control of growth and dissemination of the pathogen (Langermans and van Furth 1994; Nakano et al. 1992; van Furth et al. 1994), an overshooting inflammatory response is potentially autodestructive and may lead to microcirculatory dysfunction causing tissue damage, shock and eventually death (Beutler et al. 1985; Galanos and Freudenberg 1993). Injection of high dose LPS induces pathological symptoms resembling those of the septic patient (Burrell 1994).

The term "endotoxin tolerance" describes the phenomenon that immune responses and metabolic changes such as fever, inflammation or weight loss as well as lethality in response to LPS challenge are mitigated after repeated LPS administration. Prophylactic subtoxic LPS administration confers protection against inflammatory damage in a number of animal models. Intensive studies attempting to unravel the underlying mechanisms have been conducted over several decades to find a more effective prophylaxis and therapy of Gram-negative infection. In this review data are summarized on two different and apparently contrasting aspects of endotoxin tolerance, i.e. attenuation of inflammatory damage on the one hand and the concomitant modulation of anti-microbial host defense on the other hand.

In vivo Studies

The first reports on acquired resistance to endotoxin derive from physicians, who used vaccines containing whole bacteria to induce fever as a therapeutic measure. In that setting, the development of tolerance to the pyrogenicity of the vaccines was an annoying problem, as it required the infusion of steadily increasing doses to maintain elevated temperatures. Experimentally, Centanni was the first to demonstrate acquired resistance to a purified pyrogenic preparation from bacterial culture filtrate. Repeated injections of rabbits with this heat-stable, non-protein "pyrotoxina bacterica" resulted in a progressive reduction of its fever-inducing activity (Centanni 1894). In 1942, Centanni postulated that the phenomenon was due to a cellular mechanism and not based on a serological immune response (Centanni 1942). Similar results of antibody-independent desensitization to fever inEndotoxin Tolerance - Mechanisms and Beneficial Effects in Bacterial Infection 97

duction by repeated administration of fractions from Salmonella typhosa to humans were suggested by Favorite and Morgan (Favorite and Morgan 1942). In a set of experiments on pyrogenic tolerance to daily endotoxin infusions in rabbits, Beeson provided further evidence for non-immunologic mechanisms of tolerance. This conclusion was based on the findings that pyrogenic tolerance was not specific for the polysaccharide side chain and could not be transferred to naive animals. Furthermore, tolerance rapidly waned after discontinuation of the daily endotoxin infusions (Beeson 1946; Beeson 1947). Intensive studies performed by Greisman et al. led to the distinction of two phases of endotoxin tolerance (Greisman et al. 1969; Greisman et al. 1966). As reviewed in detail by Johnston et al. (Johnston and Greisman 1985), these are a nonspecific early phase, which becomes evident hours or days after endotoxin treatment and an antibody-dependent late phase tolerance induced by repeated injections of endotoxin. The early phase which lasts for about 48 h until several days is associated with hyporesponsiveness to endotoxins as a class, i.e. tolerance extends to endotoxins unrelated to the one used for desensitization. It is independent of antibody formation, as early tolerance develops equally in athymic (nude) mice, B-cell deficient (xid) mice, and splenectomized mice (Madonna and Vogel 1986). In contrast, several days after endotoxin injection, nonspecific tolerance wanes and hyporesponsiveness is restricted to the endotoxin serotype employed during the pretreatment phase. This late phase tolerance was shown to depend on the formation of LPS-specific antibodies and thus can be passively transferred with serum to naive animals (reviewed by Greisman 1985).

Early reports ascribed the diminished LPS responsiveness after endotoxin pretreatment to increased LPS clearance and degradation, e.g. by stimulation of LPS uptake by the reticuloendothelial system (RES) (Beeson 1946; Beeson 1947). This view was extended by Freedman, who demonstrated that serum transfer of tolerance to the pyrogenic and lethal activities of endotoxin was related to enhanced RES phagocytic activity of recipient rabbits, as assessed by clearance of colloidal carbon (Freedman 1960a; Freedman 1960b). Further studies in contrast demonstrated the development of pyrogenic tolerance in the absence of enhanced phagocytic activity of the RES (Greisman et al. 1964). Moreover, it was shown later on that the administration of thorothrast, used in the early experiments to demonstrate a critical involvement of the RES in mediating LPS tolerance, equally enhanced the fever response in tolerant and naive animals. Hence, a major contribution of enhanced LPS uptake by the RES is considered unlikely. An alternative explanation was suggested by Moreau et al. who demonstrated

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| Table 1. Endotoxin tolerance in vivo | Table | 1. End | iotoxin | tolerance | in vivo |
|--------------------------------------|-------|--------|---------|-----------|---------|
|--------------------------------------|-------|--------|---------|-----------|---------|

| Effect | | | References |
|----------|---------|----------|---|
| Survival | | ↑ | mouse (Beeson 1946; Freudenberg and Galanos 1988; Hill et al. 1974; Lehner et al. 2001a; Leon et al. 1992;Bundschuh et al. 1997a); rat (Sanchez-Cantu et al. 1989; Wise et al. 1983; Zingarelli et al. 1995b) |
| fever | | Ţ | human (Astiz et al. 1995; Centanni 1894; Centanni 1942; Favorite and Morgan 1942); guinea pig (Roth et al. 1997; Roth and Zeis- berger 1995); rabbit (Dinarello et al. 1968) |
| TNF | protein | ↓ ↓ | human (Astiz et al. 1995; Kiani et al. 1997; Mackensen et al. 1992); mouse (Balkhy and Heinzel 1999; Baykal et al. 1999; Erroi et al. 1993; Evans and Zuckerman 1991; Faggioni et al. 1995; Gustafson et al. 1995; Lehner et al. 2001a; Leon et al. 1992; Matsuura et al. 1994b; Mengozzi et al. 1991; Schade et al. 1996; Zuckerman and Evans 1992; Zucker- man et al. 1991); guinea pig (Roth et al. 1997); rat (Sanchez-Cantu et al. 1989); rabbit (Wakabayashi et al. 1994); pig (Klosterhalfen et al. 1992) |
| | mRNA | Ļ | mouse (Evans and Zuckerman 1991; Zuck- erman and Evans 1992); rat (Flohe et al. 1999) |
| 1L-1β | protein | ↓ ↓ | human (Kiani et al. 1997); mouse (Erroi et al. 1993); rabbit (Wakabayashi et al. 1994) |
| | | ↑ | mouse (Zuckerman et al. 1991) |
| | mRNA | ↓ | mouse (Zuckerman and Evans 1992) |
| IL-6 | protein | Ļ | human (Astiz et al. 1995; Kiani et al. 1997), mouse (Baykal et al. 1999; Erroi et al. 1993; Lehner et al. 2001a; Leon et al. 1992; Men- gozzi et al. 1991); guinea pig (Roth et al. 1997) |
| | | 1 | human (Mackensen et al. 1992) |
| IL-8 | protein | Ļ | human (Astiz et al. 1995; Kiani et al. 1997; Mackensen et al. 1992) |
| IL-10 | protein | Ļ | mouse (Baykal et al. 1999); rat (Flohe et al. 1999) |
| IL-12 | protein | \neg | mouse (Balkhy and Heinzel 1999) |

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| Effect | | | References | |
|--------------------------|-----------------|--------|--|--|
| CSF | protein | Ţ | human (Kiani et al. 1997; Mackensen et al. 1992); mouse (Erroi et al. 1993; Henricson et al. 1990; Henricson et al. 1991; Madonna et al. 1986; Madonna and Vogel 1985; Madonna and Vogel 1986; Quesenberry et al. 1975; Williams et al. 1983) | |
| lFNγ | protein | Ļ | mouse (Balkhy and Heinzel 1999; Erroi et al. 1993; Gustafson et al. 1995; Lehner et al. 2001a) | |
| chemokines | protein | ↓ ↓ | rat (Blackwell et al. 1997) | |
| arachidonic a | cid metabolites | Ļ | rat (Wise et al. 1983); pig (Klosterhalfen et al. 1992) | |
| nitric oxide derivatives | | Ļ | rat (Chamulitrat et al. 1995; Szabo et al. 1994); chicken (Chang et al. 1996) | |
| | | = | mouse (Gustafson et al. 1995) | |
| angiotensinogen | | ↓ | rat (Takano et al. 1993) | |

Table 1 (continued)

enhanced activity of serum esterases resulting in increased intravascular inactivation of endotoxin in LPS-pretreated animals (Moreau and Skarnes 1973). Nevertheless, macrophages play a cardinal role in early endotoxin tolerance as demonstrated by Freudenberg et al. in a set of adoptive transfer experiments: in the model of LPS-induced liver injury in galactosaminesensitized mice Freudenberg et al. revealed that not only LPS toxicity (Freudenberg et al. 1986), but also induction of tolerance required the presence of functional, LPS-sensitive macrophages (Freudenberg and Galanos 1988). Concomitant with the finding that most of the effects of LPS were transmitted by cytokines, several groups reported decreased levels of macrophage derived mediators in endotoxin-tolerant animals (Erroi et al. 1993; Madonna et al. 1986; Mengozzi et al. 1991) and humans (Astiz et al. 1995; Kiani et al. 1997; Mackensen et al. 1992) in response to a second LPS challenge (Table 1). Most studies focused on the production of tumor necrosis factor (TNF), which is almost completely downregulated during LPS tolerance, but other cytokines are also affected by endotoxin pretreatment. Erroi et al. established an order of cytokine inhibition in vivo within the same model of LPS tolerance in mice: TNF, interleukin-6 (IL-6) >> colony stimulating factor (CSF) > interferon gamma (IFNy) > IL-1 α and β (Erroi et al. 1993). Downregulation of TNF in spleens and peritoneal macrophages of LPS-tolerant mice appeared already at the level of mRNA production, suggesting a suppression of signaling cascades prior to transcription (Zuckerman and Evans 1992). Whereas downregulation of CSF, IFNy and IL-6 during LPS tolerance is well established, the effect of repeated LPS injections on IL-1 production is controversial. Several studies showed a partial reduction in circulating IL-1 in response to repeated LPS challenge (Zuckerman and Evans 1992; Zuckerman et al. 1991), whereas in one study IL-1 was even increased (Wakabayashi et al. 1994).

LPS tolerance develops rapidly within several hours, depending on the model. Thus, protection against liver damage of galactosamine-sensitized mice could be induced by LPS injection one hour prior to GalN/LPS challenge (Freudenberg and Galanos 1988). In contrast, suppression of cytokine production took at least five hours after a single dose of LPS (Klosterhalfen et al. 1992). Tolerance to the fever inducing activity of endotoxin even required at least 3 daily injections of endotoxin (Beeson 1947). These kinetic differences suggest distinct mechanisms of LPS-induced protection in the different models, which will be discussed later.

Ex vivo Studies

Further evidence for a contribution of macrophages to LPS tolerance stemmed from ex vivo studies showing impaired cytokine production by macrophages isolated from LPS-tolerant animals restimulated in vitro (Table 2). In 1968, Dinarello et al. already demonstrated that Kupffer cells isolated from LPS-tolerant rabbits were unable to produce endogenous pyrogen in vitro (Dinarello et al. 1968). Peritoneal murine and rat macrophages (resident or thioglycolate-elicited) isolated after in vivo administration of LPS displayed a decreased production of TNF (Gahring and Daynes 1986; Haslberger et al. 1988; Moore et al. 1990; Zuckerman et al. 1989) or IL-1 (Gahring and Daynes 1986) upon LPS restimulation in vitro. Similarly, impaired production of IL-12 and consequently of IFNy by spleen cells from endotoxin-tolerant mice was reported (Balkhy and Heinzel 1999). Additionally, these cells displayed decreased responsiveness to substitution with exogenous IL-12, arguing for a suppression of IFNy production via two distinct mechanisms (Balkhy and Heinzel 1999). Bundschuh et al. demonstrated that suppression of TNF production upon in vitro restimulation was a common feature of various macrophage populations (bone marrow cells, peritoneal cells, blood monocytes, alveolar cells and spleen cells) isolated from endotoxin-tolerant mice (Bundschuh et al. 1997b). Monocyte hyporesponsiveness was also reported after administration of endotoxin to humans (Granowitz et al. 1993; Rodrick et al. 1992). However, Mackensen et al. reported an increased capacity to release cytokines upon restimulation in vitro

| Table 2. Media | tor dysregulatic | on in en | l able 2. Mediator dysregulation in endotoxin tolerance <i>ex vivo</i> |
|--------------------------|------------------------------|----------|---|
| Effect | | | References |
| TNF | protein | → | human blood (Kimmings et al. 1996), human PBMC (Granowitz et al. 1993); mouse PMΦ (Flach, 1997 #390; Bundschuh, 1997 #288), mouse blood (Schade et al. 1996); other mouse macrophages (Bundschuh et al. 1997a); rat PMΦ (Moore et al. 1990); rat Kupffer cells (Hafenrichter et al. 1994; Hartung and Wendel 1992); rabbit PBMC (Wakabayashi et al. 1994) |
| | | Ļ | human PBMC (Mackensen et al. 1992) |
| β1-1J | protein | → | human PBMC (Granowitz et al. 1993); mouse PMФ (Gahring and Daynes 1986); rabbit PBMC (Wakabayashi et al. 1994) |
| | | ← | human PBMC (Mackensen et al. 1992) |
| 9-TI | protein | <u>→</u> | human PBMC (Granowitz et al. 1993); rat Kupffer cells (Hafenrichter et al. 1994), rat PMФ (Zingarelli et al. 1995a) |
| | | ← | human PBMC (Mackensen et al. 1992) |
| IL-10, TGFβ | protein | → | mouse PMФ (Flach and Schade 1997) |
| IL-12, IFN γ | protein | → | mouse spleen cells (Balkhy and Heinzel 1999) |
| arachidonic ac | arachidonic acid metabolites | → | mouse PMФ (Haslberger et al. 1988); rat PMФ (Coffee et al. 1992; Hafenrichter et al. 1994; Moore et al. 1990; Rogers et al. 1986; Rogers et al. 1989; Zingarelli et al. 1995b) |
| nitric oxide derivatives | rivatives | ¢ | rat PMФ (Zingarelli et al. 1995a; Zingarelli et al. 1995b) |
| superoxide | | → | rat non parenchymal cells, perfused liver (Bautista and Spitzer 1995) |
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Table 2. Mediator dysregulation in endotoxin tolerance ex vivo

of PBMC from endotoxin pretreated cancer patients, although serum cytokine levels were significantly reduced after repeated LPS injection. In contrast to the other two studies with human volunteers, Mackensen et al. isolated PBMC from cancer patients 24 hours after the last LPS injection, whereas in the other studies blood was withdrawn one hour or 6 hours, respectively, after LPS injection (Mackensen et al. 1992).

In vitro Studies

Most studies on the mechanism of macrophage desensitisation derive from experiments using primary cells or immortalized cell lines exposed to repeated LPS stimuli in vitro (Cavaillon et al. 1994; Matic and Simon 1991). As shown for macrophages isolated from endotoxin-tolerant hosts, release of various macrophage mediators in response to LPS stimulation is mitigated after repeated exposure to endotoxin in vitro. In this review we will refer to this status of macrophage hyporesponsiveness induced by repeated LPS stimulation in vitro as macrophage desensitization or refractoriness, to differentiate it from in vivo LPS tolerance, which might involve other mechanisms additional to downregulation of cytokine production. Suppression of cytokine release after LPS exposure was demonstrated for primary cells, such as peritoneal macrophages from mouse or rabbit and human monocytes as well as a variety of murine and human cell lines (Table 3). The spectrum of cytokines downregulated in desensitized macrophages in vitro involves the same mediators shown to be suppressed in vivo, although controversial data were provided for most cytokines except TNF. Thus, depending on the experimental setting, downregulation of TNF after exposure to endotoxin was associated with unchanged production as well as suppression or increase of IL-1, IL-6, IL-8, IL-10, and PGE2 release in response to a subsequent LPS stimulus (Frankenberger et al. 1995; Lepe-Zuniga and Klostergaard 1990; Mengozzi et al. 1993; Randow et al. 1995; Seatter et al. 1995; Takasuka et al. 1991). Most controversial data were obtained on the regulation of IL-1. Whereas studies performed with the human cell line THP-1 revealed a downregulation of IL-1 mRNA and protein after repeated LPS stimulation (LaRue and McCall 1994; Yoza et al. 1998; Yoza et al. 2000), data derived from experiments using human or mouse primary cells demonstrated unchanged or even increased IL-1 production in response to a second LPS stimulus (Heagy et al. 2000; Knopf et al. 1994; Kraatz et al. 1998; Li et al. 1994; Mengozzi et al. 1993; Takasuka et al. 1995; Takasuka et al. 1991). However, it is possible that despite normal or increased IL-1 levels in desensitized macrophages, the biological activity of IL-1 in the supernatant is

| Table J. Memai | ioi uysicguatic | | 1 auto 2. Mediatu ujsteguatum in enuorozzi uescinstuation in vitro |
|----------------|-----------------|----------|--|
| Effect | | | References |
| TNF | protein | → | human PMΦ (Knopf et al. 1994) human monocytes (Annenkov and Baranova 1991; Cavaillon et al. 1994; Karp et al. 1998; Lepe-Zuniga and Klostergaard 1990; Matic and Simon 1991; Mengozzi et al. 1993); human PBMC (Heagy et al. 2000; Randow et al. 1997; Randow et al. 1995; Riedel and Kaufmann 2000); human dendritic cells (Karp et al. 1998); mouse RAW 264.7 cell line (Virca et al. 1989); mouse PMΦ (Ancuta et al. 1997; Kraatz et al. 1998; Kraatz et al. 1999; Kraatz et al. 1999); Li et al. 1994; Matsuura et al. 1994b; Sato et al. 2000; Takasuka et al. 1991; West et al. 1997); rabbit PMΦ (Mathison et al. 1990) |
| | mRNA | → | human MonoMac 6 cell line (Frankenberger et al. 1995; Kastenbauer and Ziegler-Heit- brock 1999; Labeta et al. 1993; Ziegler-Heitbrock et al. 1995); human PMФ (Knopf et al. 1994); mouse RAW 264.7 cell line (Virca et al. 1989); mouse PMФ (Bohuslav et al. 1998; Matsuura et al. 1994b; Takasuka et al. 1995; Takasuka et al. 1991; Tominaga et al. 1999) |
| IL-1β | protein | → | human THP-1 cell line (LaRue and McCall 1994; Yoza et al. 1998) |
| | | ll. | human monocytes (Mengozzi et al. 1993); mouse PMΦ (Takasuka et al. 1991) |
| | | † | human PBMC (Heagy et al. 2000); human PMФ (Knopf et al. 1994); mouse PMФ (Kraatz et al. 1998; Li et al. 1994) |
| | mRNA | † | human THP-1 cell line (LaRue and McCall 1994; Yoza et al. 1998; Yoza et al. 2000) |
| | | H | mouse PMФ (Takasuka et al. 1995; Takasuka et al. 1991) |
| 11-6 | protein | → | human PMФ (Knopf et al. 1994); human PBMC (Riedel and Kaufmann 2000); human monocytes (Shimauchi et al. 1999); mouse PMФ [Tominaga, 1999 #888; Nomura, 2000 #863] |
| | | 11 | human monocytes (Mengozzi et al. 1993) (Wittmann et al. 1999); mouse PMΦ [Li, 1994 #75] |

Table 3. Mediator dysregulation in endotoxin desensitization in vitro

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| Table 3 (continued) | ued) | i | |
|------------------------------|----------------|----------------|--|
| Effect | | | References |
| IL-10 | protein | → | human PBMC (Riedel and Kaufmann 2000; Randow et al. 1997; Randow et al. 1995) |
| | | ← | human MonoMac 6 cell line (Frankenberger et al. 1995); human monocytes (Shimauchi et al. 1999) |
| IL-12 | protein | → | human monocytes (Karp et al. 1998), human dendritic cells (Karp et al. 1998) |
| IL-1ra | protein | ← | human THP-1 cell line (Learn et al. 2000) |
| | | 11 | human PBMC (Randow et al. 1995) |
| CSF | protein | → | human PBMC (Riedel and Kaufmann 2000); mouse PMФ (Medvedev, 2000 #855) |
| | | ← | human PMФ (Knopf et al. 1994) |
| arachidonic acid metabolites | id metabolites | → [•] | mouse PMФ (Li et al. 1994) |
| nitric oxide derivatives | rivatives | → | mouse PMΦ (Bogdan et al. 1993; Hirohashi and Morrison 1996; Severn et al. 1993; Zhang and Morrison 1993); chicken macrophages (Chang et al. 1996) |
| | | ← | mouse PMФ (Ancuta et al. 1997; West et al. 1994; Zhang and Morrison 1993) |
| MHC II expression | sion | → | human PBMC (Wolk et al. 2000) |
| | | | |

suppressed due to sustained or even increased expression of the natural antagonist IL-1 receptor antagonist (IL-1ra) (Learn et al. 2000; Randow et al. 1995).

Suppression of TNF release was associated with decreased mRNA levels, suggesting transcriptional control of cytokine production in cell lines (Frankenberger et al. 1995; Kastenbauer and Ziegler-Heitbrock 1999; Labeta et al. 1993; Virca et al. 1989; Ziegler-Heitbrock et al. 1995), human (Knopf et al. 1994), mouse (Bohuslav et al. 1998; Matsuura et al. 1994b; Takasuka et al. 1995; Takasuka et al. 1991; Tominaga et al. 1999), and rabbit primary cells (Mathison et al. 1990). This view was challenged by Zuckerman et al. demonstrating inhibition of TNF release despite increased mRNA levels in LPSpretreated cells (Zuckerman et al. 1989).

Besides cytokine production, the regulation of nitric oxide (NO) synthesis during LPS tolerance has been studied in detail, but the results are as controversial as for regulation of IL-1. Expression of inducible NO synthase (iNOS) and NO production in response to a second LPS stimulus were suppressed (Bogdan et al. 1993; Chang et al. 1996; Hirohashi and Morrison 1996) or increased (Ancuta et al. 1997; West et al. 1994), depending on the experimental settings. In line with these data, Zhang et al. demonstrated that depending on the concentration of the primary LPS stimulus, either suppression or priming of NO production can be found (Zhang and Morrison 1993).

To sum up, *in vitro* exposure of cells to LPS results in suppression of TNF release and reprogrammed production of various other macrophage mediators in response to subsequent stimulation. Cells desensitized *in vitro* display many features of macrophages isolated from endotoxin-tolerant hosts. Despite the apparent limitations of the *in vitro* setting such as neglection of neuroendocrine regulation, glucocorticoids and the interaction of different cell types *in vivo*, much of our current knowledge concerning the mechanisms of macrophage desensitization is derived from *in vitro* experiments.

Mechanisms of Macrophage Desensitization

In the last years, our understanding of the molecular mechanisms underlying desensitization of macrophages by exposure to LPS has increased considerably. Although Larsen et al. suggested that LPS preexposure decreased the number of LPS binding sites on monocytes (Larsen and Sullivan 1984), the expression of the LPS receptor CD14 is unaffected or even increased following LPS-stimulation (Labeta et al. 1993; Matsuura et al. 1994a; Ziegler-Heitbrock et al. 1994). Thus, it is highly unlikely that tolerance is mediated via expression of this LPS receptor. However, recent results by Nomura demonstrated downregulated surface expression of the LPS signaling receptor toll like receptor 4 (TLR4) on LPS-desensitized macrophages (Nomura et al. 2000). Further downstream, refractoriness in response to LPS preexposure has been shown to be associated with altered G-protein content (Coffee et al. 1992; Makhlouf et al. 1998a), phospholipase D and phosphatidylinositol-3 kinase expression (Bowling et al. 1995). West et al. reported compromised protein kinase C (PKC) activation in LPS desensitized cells (West et al. 1997) and receptor independent stimulation of the PKC by phorbol myristate acetate could overcome the suppression of cytokine production associated with refractoriness. Others described suppressed signal transduction via both the mitogen-activated-protein (MAP) kinase cascade (Kraatz et al. 1999a; Kraatz et al. 1999b; Medvedev et al. 2000; Tominaga et al. 1999) and inhibitor of NF- κ B (I- κ B) kinases, resulting in impaired transcription of nuclear-factor-kappa B (NF-KB)- and activation protein-1 (Ap-1)-regulated genes (Medvedev et al. 2000; Yoza et al. 1998). An alternative mechanism for suppression of NF-kB-dependent gene expression was suggested by Ziegler-Heitbrock et al.. They used a human monocyte cell line (MonoMac-6) to demonstrate an upregulation of the p50 subunit of NF-KB in LPS refractory cells, leading to a predominance of transactivation-inactive p50/p50 homodimers. These homodimers bind to NF-KB motifs in several promotors and thereby inhibit the transcription of genes such as TNF (Kastenbauer and Ziegler-Heitbrock 1999; Ziegler-Heitbrock et al. 1994). Support for this hypothesis originates from experiments with p50 deficient mice that are resistant to tolerance induction by LPS (Bohuslav et al. 1998). Inhibition of gene transcription in response to a second LPS stimulus via the formation of a specific nuclear suppressor of LPS-induced gene transcription was also suggested by others (LaRue and McCall 1994; Yoza et al. 2000). LaRue et al. provided evidence that decreased LPS-induced transcription of IL-1 β in LPS-desensitized THP-1 cells was regulated by a labile repressor which required constant protein synthesis and suggested IkB-a as a potential candidate, although then a contribution of p50 had not yet been studied (LaRue and McCall 1994).

In contrast, recent data showing decreased surface expression of TLR4 on LPS-tolerized cells (Nomura et al. 2000) and suppression of IL-1 receptorassociated kinase (IRAK) activation and association with myeloid differentiation protein (MyD88) (Li et al. 2000), support the notion that already very early steps in LPS-signaling upstream of NF- κ B are altered after LPS exposure. Further evidence for this was provided by Medvedev et al. (Medvedev et al. 2000) who re-evaluated *in vitro* desensitization by IL-1 and TNF, showing induction of cross-tolerance to LPS via the IL-1 receptor but not the TNF-receptor. Intriguingly, signal transduction of the IL-1R, the LPSreceptor TLR4, and TLR2 employ similar signaling molecules (Medzhitov et

al. 1998; Yang et al. 1998; Zhang et al. 1999). Recent studies from our laboratory demonstrated that preexposure to lipoteichoic acid that induced signaling via TLR2 resulted in hyporesponsiveness to TLR4-mediated LPS signaling and vice versa (Lehner et al. 2001b). This finding adds further indirect evidence for a suppression of common signaling molecules shared by TLR2/4 and IL-1R, i.e. MyD88, IRAK, TNF receptor-activated factor 6 (TRAF6) or NF- κ B-inducing kinase (NIK) in desensitized macrophages. The view that inhibition of common signaling pathways of the IL-1R/TLR family and not diminished TLR4 surface expression is mainly responsible for macrophage hyporesponsiveness is corroborated by the finding that preexposure of macrophages to the TLR2-dependent stimulus mycoplasmal lipopeptide (MALP-2) suppressed LPS-induced TNF release without reducing the surface expression of TLR4 (Sato et al. 2000).

Despite the large number of studies dealing with macrophage hyporesponsiveness in response to LPS pretreatment, the exact mechanism of suppression of cytokine production has not been identified yet. Since there is sound evidence for a contribution of various of the aforementioned factors, it is feasible that i) macrophage desensitization is the result of the orchestrated action of multiple factors activated by the primary LPS stimulus or ii) depending on the model employed to study tolerance (species, cell type, experimental settings) varying distinct mechanisms account for refractoriness in response to inflammatory bacterial components.

Mediators of Tolerance

LPS exerts most of its effects via the activity of macrophage mediators released in response to LPS stimulation. The inflammatory response is regulated by a complex network of mediators that directly interact with each other's expression or biological activity. In this context, a number of macrophage mediators such as IL-10, TGF β or PGE₂ have potent anti-inflammatory activity by suppressing the formation of proinflammatory cytokines (Berg et al. 1995; de Waal Malefyt et al. 1991; Howard et al. 1993; Renz et al. 1988; Scales et al. 1989; Smith et al. 1996). Thus, it has been presumed that autocrine mechanisms are also involved in suppression of cytokine production during LPS tolerance.

Mediators of in vitro Desensitization

As outlined before, LPS-pretreatment of cultured macrophages results in hyporesponsiveness to cytokine release in response to a subsequent LPS stimulus. It has been shown that several cytokines could substitute for LPS as the desensitizing stimulus. Cavaillon et al. demonstrated that incubation of human PBMC with recombinant cytokines prior to restimulation with LPS partially suppressed production of TNF to a different extent. Whereas preexposure to TGFB or IL-10 reduced TNF release by nearly 60% as compared to saline pretreated cells, IL-4 and IL-1 were less effective (35% and 30% inhibition, respectively) and no inhibition at all was found after administration of TNF, IL-6, IL-8 or leukaemia inhibitory factor (Cavaillon et al. 1994). The lack of macrophage desensitization by exposure to TNF has been reported also by Li et al. (Li et al. 1994). The differential role of TNF and IL-1 β in desensitization of macrophages in vitro was confirmed by recent studies from Medvedev et al. who showed that exposure of murine macrophages to LPS or IL-1, but not to TNF, resulted in inhibition of transcription factor activation and suppressed transcription of GM-CSF and several chemokines in response to a second LPS stimulus (Medvedev et al. 2000). Unfortunately, no information on the regulation of TNF mRNA and protein was given in this study. Convincing data on the contribution of soluble mediators in desensitization of macrophages were derived from experiments with human PBMC. Randow et al. demonstrated that a combination of recombinant human IL-10 and TGFB was as effective as low-dose LPS pretreatment in terms of reduction of TNF release upon subsequent high-dose LPS stimulation, whereas preexposure to either cytokine alone only partially suppressed the release of TNF (Randow et al. 1995). In the same setting, addition of neutralizing antibodies to IL-10 and TGFB inhibited desensitization in response to the first LPS stimulus, providing direct proof for a contribution of these two anti-inflammatory cytokines in LPSinduced monocyte/macrophage refractoriness in vitro (Randow et al. 1995). The critical role of IL-10 and TGF β in downregulation of TNF production was confirmed by Karp et al., whereas inhibition of IL-12 production in LPSpretreated human monocytes was independent of these cytokines (Karp et al. 1998). In line, antibodies against IL-4 or IL-10 as well as addition of indomethacin or a iNOS inhibitor did not abrogate suppression of IL-12 p40 mRNA and protein expression in LPS-desensitized macrophages (Wittmann et al. 1999).

The production of a yet unidentified suppressor of TNF formation not identical with IL-1, IL-10 or TGF β during endotoxin tolerance was reported by Schade et al (Flach and Schade 1997; Schade et al. 1996). They showed that addition of culture supernatants of LPS-stimulated peritoneal murine macrophages from endotoxin pretreated mice suppressed TNF release by naive macrophages. Similar results on a selective inhibitor of TNF, but not of IL-1 or IL-6 synthesis in supernatants of LPS-desensitized macrophages were provided by Fahmi et al. (Fahmi and Chaby 1993). The idea of a nega-

tively acting autocrine mediator in macrophage desensitization was extended by more recent results from Baer et al. who demonstrated the production of a yet unidentified "TNF-inhibiting factor" (TIF) in supernatants of a LPS-stimulated macrophage cell line. Inhibition of TNF expression by macrophage conditioned medium was associated with selective induction of the NF- κ B p50 subunit which selectively inhibited a TNF-promoter reporter construct (Baer et al. 1998). Since a contribution of IL-4, IL-10 and TGF β was excluded, these findings provide evidence for LPS induction of a novel cytokine with selective TNF-inhibitory potential participating in endotoxin desensitization (Baer et al. 1998).

Besides cytokines, arachidonic metabolites were shown to influence the responsiveness of macrophages. It is well established that prostaglandin E_2 (PGE₂) downregulates TNF production by macrophages, probably via the elevation of cAMP (Kunkel et al. 1988; Renz et al. 1988; Scales et al. 1989). Thus it is feasible that PGE₂ produced in response to the primary desensitizing dose of LPS contributes to macrophage hyporesponsiveness. This view was supported by the finding that PGE₂ production was increased in LPSdesensitized macrophages (Li et al. 1994; Makhlouf et al. 1998b; Matic and Simon 1991; Seatter et al. 1995). However, direct addition of PGE₂ during primary culture failed to suppress TNF production upon subsequent LPS stimulation of cultured human monocytes (Matic and Simon 1991). In addition, in three different studies the addition of the cyclooxygenase inhibitor indomethacin neither prevented the development of hyporesponsiveness nor restored TNF production upon LPS restimulation (Mathison et al. 1990; Takasuka et al. 1991; Ziegler-Heitbrock et al. 1992). In contrast, by using higher concentrations of indomethacin (10-100 µM), Haas et al. could inhibit the suppression of TNF production by LPS-pretreatment (Haas et al. 1990). Thus, the contribution of arachidonic acid derivatives in desensitization of macrophages still remains to be clarified. Our recent results derived from co-culture experiments argue against a major role of soluble mediators in acquired hyporesponsiveness. Cross-desensitization induced by preexposure to LPS or LTA in wild-type macrophages was not transferred to cocultured macrophages from mice lacking functional TLR2 or TLR4 as evidenced by sustained TNF release upon re-challenge with the other stimulus (Lehner et al. 2001b). However, as we did not perform any neutralization experiments, we cannot rule out that, besides ligand-TLR interaction additional signals provided by soluble mediators were required for desensitization.

Mediators of in vivo Tolerance

As pointed out for macrophage desensitization in vitro, the involvement of soluble mediators in establishing LPS tolerance in vivo has also been discussed controversially. Attempts to induce tolerance to the pyrogenicity of subsequent endotoxin injection by repeated administration of endogenous pyrogen (EP) were not successful (Atkins 1960). In contrast, pretreatment of rabbits with IL-1 partially abolished hypotension and TNF release in response to subsequent endotoxin challenge (Kaplan et al. 1993). When mice were treated with recombinant TNF or IL-1 α , neither cytokine alone was able to mimic LPS induction of tolerance. However, the two cytokines synergized to induce features of early endotoxin tolerance, such as alterations of the monocyte/macrophage bone marrow pool and suppression of CSF release upon subsequent LPS challenge (Vogel et al. 1988). In addition, suppression of CSF release associated with LPS-tolerance was partially reversed by administration of recombinant IL-1 receptor antagonist (IL-1ra) during LPS pretreatment (Henricson et al. 1991). Administration of IL-1a or TNF but not of IL-6 to mice for four days partially inhibited the production of IL-6 and TNF in response to a subsequent LPS challenge, although to a lesser extent than LPS (Erroi et al. 1993). In line with this finding, TNF infusion in rats resulted in a reduced capacity of isolated bone marrow cells to produce TNF, IL-6 or PGE₂ upon LPS stimulation in vitro (Ogle et al. 1997). In contrast, Mathison et al. failed to suppress the production of TNF in response to LPS by pretreating rabbits with TNF infusions (Mathison et al. 1988). Pretreatment with IL-1 conferred protection to subsequent high dose LPS challenge (Alexander et al. 1991b; Leon et al. 1992) and sepsis induced by cecal ligation and puncture (CLP) (Alexander et al. 1991a) as well as E. coli induced peritonitis (Lange et al. 1992). Similar results were obtained for TNF, which induced tolerance to the lethality of subsequent LPS challenge (Alexander et al. 1991b; Fraker et al. 1988). In the model of inflammatory liver damage in galactosamine (GalN)-sensitized mice pretreatment with TNF or IL-1 was equally protective as LPS in reducing the extent of liver damage and lethality (Bohlinger et al. 1995; Libert et al. 1991; Wallach et al. 1988). Moreover, administration of IL-1, TNF or LPS induced tolerance to the toxicity of TNF injection itself, as shown for the metabolic changes, weight loss, temperature increase and lethality in response to high-dose TNF injection (only TNF pretreatment) (Fraker et al. 1988; Roth and Zeisberger 1995), as well as for low-dose TNF-induced hepatocyte apoptosis in GalNsensitized mice (TNF or IL-1 pretreatment) (Bohlinger et al. 1995; Libert et al. 1991; Wallach et al. 1988). Since enhanced clearance or neutralization of TNF in LPS- or cytokine-pretreated animals was excluded (Fraker et al. 1988;

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Roth and Zeisberger 1995) hyporesponsiveness of target cells to TNF activity itself, e.g. by downregulation of TNF receptors and by the production of acute phase proteins or anti-apoptotic factors was suggested as an additional mechanism contributing to LPS tolerance (Bohlinger et al. 1995; Hartung and Wendel 1992; Libert et al. 1991; Wallach et al. 1988). This view was corroborated by the finding that addition of acute phase proteins attenuated the GalN/TNF induced liver damage (Libert et al. 1996; Van Molle et al. 1999; Van Molle et al. 1997). Thus, the protection afforded by LPS pretreatment in the GalN/LPS model is likely to be mediated by two independent mechanisms differing in their requirement of endogenously produced cytokines. On the one hand, the reduction of TNF levels in mice pretreated with LPS suggests macrophage hyporesponsiveness similar to in vitro desensitization. As discussed before, although a role of soluble mediators in macrophage desensitization in vitro has not been fully identified, yet, evidence has been provided that soluble mediators do not suffice for downregulation of macrophage responsiveness. This view is substantiated by our unpublished results showing suppression of TNF release in TNFR1 deficient mice in response to repeated LPS injections. On the other hand, it is likely that TNF and IL-1 produced upon LPS pretreatment induce hyporesponsiveness of hepatocytes to TNF activity itself as an additional mechanism of protection.

As outlined before, several in vitro studies suggested that LPS-induced desensitization of macrophages was mediated via formation of IL-10. In line with this, administration of IL-10 protected mice against a lethal endotoxin challenge (Howard et al. 1993). However, a major role of the antiinflammatory cytokine IL-10 in mediating LPS tolerance in vivo was excluded by Berg et al. using IL-10 deficient mice. Although these mice were LPS-hyperresponsive in terms of TNF production and lethality, tolerance after an initial sublethal LPS dose developed normally as determined by decreased lethality and diminished levels of TNF and IL-6 after subsequent high dose LPS challenge. In addition, infusion of recombinant IL-10 could not substitute for the initial desensitizing dose of LPS (Berg et al. 1995). In conclusion, although evidence has been provided that cytokines such as TNF or IL-1 have the potential to mimic some of the beneficial effects of LPS pretreatment in vivo the actual role of these cytokines in LPS-induced macrophage desensitization still has to be characterized. One important point is that most investigators used recombinant cytokines produced in E. coli. Since a possible endotoxin contamination of these recombinant cytokines had not always been excluded, it is difficult to ascribe the observed effects of recombinant proteins to cytokine activity.

Besides cytokines, glucocorticoids possess a strong anti-inflammatory potential. Administration of cortisone prevented lethality after high dose LPS challenge (Geller et al. 1954) and suppressed the release of TNF, IL-1 and IL-6 (Beutler et al. 1986; Coelho et al. 1995; Goujon et al. 1996; Morrow et al. 1993; Steer et al. 2000; Waage and Bakke 1988). In line, adrenalectomy sensitized mice to the toxicity of subsequent LPS injection (Evans and Zuckerman 1991; Goujon et al. 1996; Parant and Chedid 1971). Moreover, since glucocorticoids are released in response to LPS injection, it was feasible to ascribe endotoxin tolerance to the anti-inflammatory activity of endogenous glucocorticoids (Evans and Zuckerman 1991). Studies by Evans demonstrated that LPS tolerance could not be induced in adrenalectomized mice (Evans and Zuckerman 1991). However, this view was challenged by the finding that endotoxin tolerance in terms of suppressed TNF release developed normally in adrenalectomized rats (Chautard et al. 1999). This finding confirmed earlier results from Chedid's group. In their experiments, endotoxin tolerance developed equally in the absence of glucocorticoids, as shown by adrenalectomy prior to or directly after the initial desensitizing injection of LPS, albeit on the background of overall increased susceptibility (Chedid et al. 1964). A similar status of LPS-hyperresponsiveness can be induced by repeated injections of cortisone. Also under this condition of decreased glucocorticoid responsiveness, mice were rendered endotoxintolerant by a single LPS injection (Chedid et al. 1964). Studies in the GalN/TNF model demonstrated that addition of dexamethasone did not prevent liver injury (Libert et al. 1991), indicating that at least one aspect of LPS tolerance, i.e. diminished sensitivity of hepatocytes to cytokine activity was not mediated by glucocorticoids.

These results, together with the finding that suppression of cytokine release can also be induced *in vitro* (i.e. in the absence of glucocorticoids), argue against a critical involvement of glucocorticoids in endotoxin tolerance.

Specificity of Tolerance

The question, whether early phase nonspecific tolerance is restricted to endotoxins as a class or whether it reflects a general state of altered macrophage activity resulting in diminished cytokine expression in response to non-endotoxin inflammatory stimuli as well, has not been settled. The view that tolerance is restricted to endotoxins as a class originates from experiments performed by Greisman et al. who demonstrated that rabbits rendered LPS-tolerant by infusion of endotoxin for several hours displayed a normal fever reaction in response to pyrogenic non-endotoxin challenges such as influenza virus, old tuberculin and staphylococcal enterotoxin (Greisman et al. 1966). Similarly, Roth et al. showed a lack of cross-reactivity

between LPS and muramyl-dipeptides in terms of fever induction and production of TNF and IL-6 in guinea pigs (Roth et al. 1997). However, the experimental setting used consisting of repeated injections of endotoxin over a Period of 15 days with administration of muramyl-dipeptide 3 days after the last LPS injection may have been unsuitable to study the specificity of the early phase tolerance which is most prominent within the first 48 h and then starts to wane. Lack of cross-tolerance was reported also by Mathison et al. who failed to suppress TNF-release in response to *Staphylococcus aureus* by preexposure of rabbit macrophages to LPS (Mathison et al. 1990). Similarly, LPS-tolerant Kupffer cells still produced TNF upon viral infection (Busam et al. 1991). However, differential suppression of TNF and IL-1 was reported by Wakabayashi et al. who showed that PBMC isolated from LPS-tolerant rabbits still produced TNF, but no IL-1, in response to *Staphylococcus epidermidis* (Wakabayashi et al. 1994), proposing differential regulation of these cytokines during hyporesponsiveness.

Further evidence that downregulation of monocyte/macrophage function after LPS-pretreatment is not restricted to restimulation with endotoxins was provided by Granowitz et al. (Granowitz et al. 1993). They demonstrated a reduction of cytokine release by human PBMC derived from endotoxin pretreated volunteers restimulated ex vivo with LPS, IL-1 or TSST-1. Cavaillon et al. reported suppression of TNF-release in response to zymosan, staphylococci and streptococci after exposure of human monocytes to LPS in vitro (Cavaillon et al. 1993; Cavaillon et al. 1994). Similar results were obtained more recently by Karp et al. for downregulation of IL-12 production (Karp et al. 1998). Further support for a general macrophage desensitization not restricted to LPS stemmed from Kreutz et al., who reported TNF suppression upon repeated exposure to whole S. aureus or synthetic lipopeptides (Kreutz et al. 1997). Recently, we could demonstrate macrophage cross-desensitization in terms of TNF production by LPS and lipoteichoic acids (LTA) from S. aureus via different TLR (Lehner et al. 2001b). The same held true for in vivo tolerance to liver damage by administration of galactosamine plus LPS or LTA. This extends recent findings by Sato et al., who reported cross-desensitization of macrophages by mycoplasmal lipopeptides and LPS via TLR2 and TLR4 (Sato et al. 2000). These results suggest that tolerance and macrophage desensitization could represent a general antiinflammatory mechanism induced by selected bacterial stimuli to prevent potentially harmful overshooting inflammation during sustained infection.

Restoration of Cytokine Response

To study the mechanism of cytokine suppression in LPS-desensitized macrophages, a variety of substances was tested for their ability to overcome suppression of cytokine release in response to a second LPS challenge. Several reports indicated that direct stimulation of protein kinase C by addition of PMA to desensitized macrophages had some potential to restore normal immune functions: In human monocytes pretreated with LPS, TNF release in response to PMA was even increased compared to cells preexposed only to medium (Matic and Simon 1991). Others demonstrated reversal of TNF suppression in desensitized murine macrophages by addition of PMA one hour prior to second LPS activation (West et al. 1997). The restoration of LPS responsiveness by preincubation with PMA was associated with reversed inhibition of MAPK and p38 kinase activation (Kraatz et al. 1999b). In endotoxin-tolerant mice, injection of PMA 10 min before secondary LPS challenge counteracted suppression of IL-6 and partially of CSF production, but had no effect on TNF release while IL-1ß production was even downregulated (Erroi et al. 1993; Mengozzi et al. 1991). More physiological tools to restore cytokine release include the proinflammatory cytokines interferon gamma (IFNy), granulocyte-macrophage colony stimulating factor (GM-CSF) and interleukin 12 (IL-12): It is well established that IFNy, produced by T lymphocytes or NK cells upon various inflammatory stimuli, is a potent activator of macrophage functions. These include an upregulation of MHC II expression, enhanced microbicidal activity against intracellular pathogens and release of proinflammatory cytokines (Kagaya et al. 1989; Ozmen 1994), reviewed in (Young and Hardy 1995). IFNy receptor-deficient mice display decreased sensitivity to LPS toxicity, associated with depressed TNF synthesis, diminished expression of CD14, and low plasma LPS-binding capacity (Car et al. 1994). This suggests that IFNy is an important co-stimulus for macrophage gene expression that might overcome hyporesponsiveness. Indeed, addition of IFNy to LPS-desensitized macrophages prior to or concomitant with LPS restimulation partially reversed suppression of TNF production. This was demonstrated for the MonoMac-6 cell line (Haas et al. 1990), human monocyte-derived macrophages (Matic and Simon 1992), human PBMC (Randow et al. 1997) and mouse macrophages isolated after induction of endotoxin tolerance in vivo (Bundschuh et al. 1997b). Also several features of in vivo endotoxin tolerance, such as suppression of TNF (Bundschuh et al. 1997b; Mengozzi et al. 1991) or IL-6 release (Mengozzi et al. 1991) and increased resistance to endotoxic shock (Bundschuh et al. 1997b), could be partially abolished when IFNy was injected additionally to LPS re-challenge. Administration of IFNy also reversed the suppression of

TNF, IL-6 and G-CSF release in LPS-tolerant cancer patients (Mackensen et al. 1991).

Like IFNy, GM-CSF is involved in regulation of LPS-induced cytokine production and lethality (Basu et al. 1997; Tiegs et al. 1994). Further, addition of GM-CSF partially counteracted macrophage desensitization (Bundschuh et al. 1997a; Randow et al. 1997), but the priming efficacy differed compared to IFNy, depending on the cell type used. Thus, GM-CSF was more effective than IFNy in restoring TNF production by murine monocytes and bone-marrow cells, but less effective when more differentiated macrophages such as peritoneal cells or alveolar macrophages were used (Bundschuh 1997). In contrast, suppression of TNF production in LPSpretreated human PBMC and bone marrow cells was counteracted more efficiently by IFNy (Bundschuh 1997; Randow et al. 1997). Reversal of TNF suppression in LPS-desensitized human PBMC by addition of IL-12 was also demonstrated recently. This cytokine is normally produced by monocytes/macrophages upon inflammatory stimuli and induces IFNy release by T lymphocytes and NK cells. Since IL-12 release was shown to be downregulated in desensitized macrophages, substitution with exogenous IL-12 should restore TNF release via production of IFNy. Direct proof for this hypothesis was provided by Randow et al. who showed that the effect of IL-12 was dependent on both the presence of nonmonocytic cells and production of IFNy (Randow et al. 1997). However, suppression of IFNy production by spleen cells from LPS-tolerant mice could only be partially reversed by addition of IL-12, suggesting diminished responsiveness to IL-12 as an additional mechanism of tolerance (Balkhy and Heinzel 1999).

The mechanism underlying restoration of TNF release in LPSdesensitized cells by pretreatment or coadministration of these proinflammatory cytokines is not fully clear yet. Enhancement of TNF production in response to IFN γ , GM-CSF or IL-12 is not restricted to LPS-desensitized cells, but is also found in naive monocytes/macrophages (Bundschuh et al. 1997a; Randow et al. 1997). Thus it is feasible that instead of specifically restoring signaling pathways suppressed during hyporesponsiveness, these cytokines rather act by amplifying the minimal responses that still occur in desensitized cells, using the same pathways involved in the enhancement of primary LPS responses.

Endotoxin Tolerance and Infection

Introduction

Dysbalanced production of leukocyte-derived inflammatory mediators such as cytokines, arachidonic acid metabolites, lysosomal enzymes, reactive oxygen or nitrogen intermediates is considered a major mechanism responsible for pathophysiological alterations of the microcirculation, leading to shock, multiple organ failure and eventually death in response to systemic infection or endotoxaemia (Bone 1996; Bone et al. 1997; Dinarello 1997; Dinarello 2000; Marik and Varon 1998). Experimentally induced endotoxin tolerance provides protection against lethality and morbidity in animal models of endotoxic shock and fulminant infection used to simulate the systemic inflammatory response syndrome of the septic patient. As pointed out before, LPS tolerance is associated with suppression of several cytokines, attenuation of leukocyte infiltration and consequently a reduction of organ damage. These findings suggested induction of LPS tolerance to be an interesting tool in sepsis prophylaxis (Cavaillon 1995; Gustafson et al. 1995; Salkowski et al. 1998). However, concern was raised whether suppression of inflammatory responses during LPS tolerance would interfere with normal host defense and thus predispose patients to nosocomial infection (Cavaillon 1995). Indeed, host defense against infection with small numbers of replicating pathogens requires an intact cytokine response to halt proliferation and dissemination of the pathogen (Mastroeni et al. 1999; Nakano et al. 1992). In contrast to models of acute hyperinflammation such as endotoxic shock, neutralization of proinflammatory cytokines worsens the outcome of infection with low numbers of virulent bacteria (Dai et al. 1997; Tite et al. 1991) and many cytokine-deficient mice that are resistant to inflammatory damage rapidly succumb to otherwise sublethal infections (Dai et al. 1997; Irikura et al. 1999; Mastroeni et al. 1999; O'Brien et al. 1999; Pfeffer et al. 1993; Rothe et al. 1993). Also, mice inherently hyporesponsive to LPS because of a nonfunctional mutation in the tlr4 gene (Hoshino et al. 1999; Poltorak et al. 1998; Qureshi et al. 1999; Vogel et al. 1999) display increased susceptibility to Gram-negative pathogens (Cross et al. 1995; Hagberg et al. 1984). Furthermore, experimentally induced endotoxin tolerance displays features of immunoparalysis observed frequently in post-septic or posttraumatic patients several days or weeks after systemic inflammation: Monocytes from immunoparalysed patients were impaired in their ability to produce TNF upon restimulation with LPS in vitro (Docke et al. 1997; Ertel et al. 1995; Kox et al. 1997; McCall et al. 1993; Munoz et al. 1991; Volk et al. 1996; Volk 1991; Wilson et al. 1997) and displayed diminished surface ex-

pression of MHC II (Docke et al. 1997; Kox et al. 1997; Volk et al. 1996; Volk 1991). These cellular defects were associated with an increased incidence of infectious complications and lethal outcome of disease (Hershman et al. 1990; Volk 1991). Since similar alterations of monocyte/macrophage activity were found during experimentally induced LPS tolerance, it was feasible that induction of LPS tolerance equally interfered with host defense.

In contrast, it has been known for a long time that endotoxin is a potent activator of host defense and LPS treatment is associated with protection against the lethality of irradiation, restriction of tumor growth as well as enhanced resistance to subsequent infection with various microbial pathogens (Nowotny and Behling 1982). The first reports on the curative effect of application of bacterial products on infection stemmed from treatment of patients suffering from abdominal typhus with crude extracts of bacteria at the end of the 19th century (Rumpf 1893). By this time, the widespread use of fever therapy, i.e. the injection of pyrogenic bacterial preparations, for the treatment of various diseases was initiated. An excellent review on fever therapy was written by Nowotny (Nowotny and Behling 1982).

The use of animal models to study the mechanisms underlying enhancement of host defenses by bacterial products was initiated in 1892 by Kanthack, who reported pyrogen-induced changes on leukocytes after injection of Vibrio metchnikorii filtrates into rabbits (Kanthack 1892). In 1955, Rowley was the first to describe increased resistance of mice to bacterial infection after administration of E. coli cell wall extracts 48h prior to challenge (Rowley 1955). The same protection was afforded when isolated endotoxin was injected instead of cell walls (Rowley 1956). Subsequently, this phenomenon of reduced susceptibility after endotoxin application was extended to infections with other bacterial species and even some viral pathogens (Shilo 1959). Pretreatment with endotoxin or cellular components of Gram-negative bacteria induced nonspecific protection against infection with a number of different extra- and intracellular bacteria including both Gram-negative and Gram-positive species (Boehme and Dubos 1956; Dubos and Schaedler 1956; Dubos and Schaedler 1957; Parant 1968; Parant 1980; Parant et al. 1980; Rowley 1960), reviewed in detail by Shilo (Shilo 1959) (Table 4). More recently, increased resistance of LPS-pretreated animals to lethality and organ damage associated with multi-germ sepsis, induced e.g. by CLP was reported (Neviere et al. 1999; Salkowski et al. 1998; Urbaschek et al. 1984; Urbaschek and Urbaschek 1985). Experiments performed by Rayhane et al. corroborated the notion that increased resistance is nonspecific by demonstrating improved survival and decreased fungal burden of LPS pretreated mice with disseminated Cryptococcus neoformans infection (Rayhane et al. 2000).

| I able 4. Ellect of cliqueovili oil most acterio | | | | |
|--|---|----------|--|---|
| | Challenge | Survival | Mechanism | Reference |
| Gram-negative bacteria | Escherichia coli Proteus vulgaris Pseudomonas aeruginosa Klebsiella pneumoniae Salmonella typhi | ~~~~~~ | CFU↓ (S. typhi), Properdin levels ↑ | (Landy and and Pillemer 1956) |
| | Escherichia coli | ← | serum bactericidal activity 1, RES phagocytosis 1 | (Rowley 1956) |
| | Salmonella typhi | ¢ | | (Tully et al. 1965) |
| | Salmonella dublin | ¢ | not transferred with serum, i.e. antibody independent | (Hill et al. 1974) |
| | Salmonella typhimurium Salmonella enteritidis | ←← | CFU↓, bacterial clearance↑ | (Nakano et al. 1984) |
| | Salmonella typhimurium | | serum opsonic activity f MΦ phagocytic acitivity f | (Rowley 1960) |
| | Salmonella typhimurium | ¥ | CFU 4, phagocyte accumula- tion ↑ phagocytosis/bactericidal activity of PMΦ ↑ | (Onozuka et al. 1993) |
| | Salmonella typhimurium | | CFU ↓, PMN recruitment ↑, PMN accumulation ↑, RES phagocytosis ↑ | (Lehner et al. 2001a) |
| | Klebsiella pneumoniae | | CFU ↓ , RES phagocytosis ↑ | (Galelli et al. 1977; Parant et al. 1976; Parant et al. 1980) |

Table 4. Effect of endotoxin on host defense

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| | Klebsiella pneumoniae | + | | (Kiser et al. 1956) |
|------------------------|---|-----------|--|---|
| | Pasteurella tularensis | Ļ | | (Pannell 1956a; Pannell 1956b) |
| Mycobacteria | Mycobacterium fortuitum | ţ | CFU↓, RES phagocytosis↑ | (Boehme and Dubos 1956) |
| Gram-positive bacteria | Staphylococcus aureus | ¢ | CFU ↓ | (Dubos and Schaedler 1956) |
| | Staphylococcus aureus Streptococcus pyogenes Diplococcus pneumoniae | no effect | porperdin insensitive bacteria | (Landy and and Pillemer 1956) |
| | Staphylococcus aureus | Ť | cytokine production 4 | (Astiz et al. 1994a) |
| | Streptococcus agalactiae | Ť | not transferred with serum → antibody independent | (Hill et al. 1974) |
| | Listeria monocytogenes | ÷ | CFU↓, | (Lehner et al. 2001a) |
| Mixed infection | CLP | 4 | CFU ↓, granulopoiesis ↑ | (Urbaschek et al. 1984; Urbaschek and Urbaschek 1985) |
| | CLP | ← | cytokine production 4 | (Astiz et al. 1994b) |
| Fungi | Cryptococcus neoformans | ← | CFU 4, TNF-mediated effect | (Rayhane et al. 2000) |
| Parasites | Plasmodium berghei | ← | | (MacGregor et al. 1969) |
| | | | | |

Mechanisms of Enhanced Host Defense

Humoral Factors

It has been demonstrated that enhanced resistance after LPS injection was associated with increased bactericidal activity of serum towards certain Gram-negative bacteria (Rowley 1956). Since evidence was provided that LPS administration enhanced serum bactericidal activity mainly towards properdin-sensitive organisms, increased serum properdin levels were suggested to be a major mechanism of LPS-induced resistance (Landy and Pillemer 1956). This view was questioned later by findings that LPS pretreatment afforded protection also to properdin-insensitive organisms such as Gram-positive bacteria. Moreover, alterations in host resistance against bacterial infection were not always paralleled by serum properdin levels (Howard et al. 1958). We recently provided further evidence against a major role of the complement system in LPS-induced increased resistance by demonstrating LPS-induced nonspecific resistance to S. typhimurium and L. monocytogenes in the absence of any changes in complement activity as determined in a sheep erythrocyte lysate assay (Lehner et al. 2001a). Furthermore, depletion of the central C3 protein of the complement cascade by administration of cobra venom factor did not abolish the protective effect of LPS pretreatment on S. typhimurium infection (Lehner et al. 2001a). However, increased serum opsonization activity after LPS administration was reported by several authors (Rowley 1960; Ruggiero et al. 1980). In sum, enhanced resistance to infection is associated with increased serum bactericidal or opsonization activity in some models, although direct proof for a critical contribution of the complement system is still lacking.

Macrophages

On the cellular level of host defense, LPS injection is associated with a transient depression of RES activity, followed by a longer lasting period of enhanced clearance of carbon particles, radioactive LPS, labelled chromium phosphate and viable or heat-killed bacteria by the RES (Galelli et al. 1977; Lehner et al. 2001a; Nakano et al. 1984). Detailed studies by Chedid's group demonstrated that irradiation- and cyclophosphamide-resistant cells mediated improved survival, enhanced RES phagocytic activity and reduced bacterial burden associated with LPS pretreatment of mice subsequently submitted to an otherwise lethal *Klebsiella pneumoniae* infection (Galelli et al. 1977; Parant et al. 1976; Parant et al. 1980). Although definite protection of irradiated mice by LPS injection additionally depended on a further, bone-

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marrow derived cell type not identical with T lymphocytes, their experiments strongly supported the notion that activation of RES macrophages was a major mechanism of LPS-induced host defense against *Klebsiella pneumoniae* (Galelli et al. 1977; Parant et al. 1976).

We have shown recently that enhanced hepatic phagocytosis of bacteria in LPS-pretreated mice was associated with increased numbers of Kupffer cells, the resident macrophage population of the liver (Lehner et al. 2001a). Increased Kupffer cell numbers were also reported for LPS-tolerant rats (Bautista and Spitzer 1995). Direct evidence for a contribution of Kupffer cells in LPS-stimulated clearance of bacteria was derived from experiments using chlodronate-liposomes to deplete liver macrophages prior to injection of bacteria (Lehner et al. 2001a). Ruggiero et al. used isolated perfused rat livers to demonstrate increased hepatic uptake of Escherichia coli after in vivo LPS pretreatment due to enhanced phagocytic activity of the liver and improved opsonization by the serum (Ruggiero et al. 1980). Besides an increase in Kupffer cell numbers, enhanced phagocytic activity of individual liver macrophages could account for improved hepatic clearance after LPStreatment, as demonstrated by Hafenrichter et al. for isolated Kupffer cells from LPS-pretreated rats (Hafenrichter et al. 1994). Accordingly, peritoneal macrophages exposed to LPS in vivo or in vitro showed accelerated phagocytosis of Salmonella typhimurium in vitro (Rowley 1960). In contrast to studies using murine peritoneal macrophages where an enhancement of oxidative burst activity was reported (Leon et al. 1992; Onozuka et al. 1993), Kupffer cells from LPS-pretreated rats displayed decreased generation of superoxide anions (Bautista and Spitzer 1995). However, our unpublished data indicate improved antibacterial activity of Kupffer cells from endotoxin-tolerant mice.

Neutrophilic Granulocytes

LPS induces a plethora of chemokines leading to accumulation of leukocytes, consisting mainly of neutrophilic granulocytes, at the site of LPS administration. This is of importance when bacteria are injected at the site of previous LPS administration, since the microorganisms are confronted immediately with a large number of phagocytes absent in the naive host. We recently demonstrated that intraperitoneal accumulation of leukocytes and enhanced inactivation of intraperitoneally injected *Salmonella typhimurium* during the first hours post infection was strictly dependent upon the route of LPS pretreatment. Similar results were obtained by Astiz et al. who studied the therapeutic value of administration of monophosphoryl lipid A (MPL), a detoxified LPS derivative, to mice prior to induction of peritonitis by CLP. In their setting, intraperitoneal (*i.p.*) injections of MPL were more effective in reducing mortality than intravenous (*i.v.*) MPL administration (Astiz et al. 1994b). However, activation of resident peritoneal macrophages by *i.p.* LPS injection could also account for the improved antibacterial activity.

It has long been known that endotoxin is a potent stimulator of hematopoesis. Post-endotoxin serum was shown to have potent colony-stimulating factor (CSF) activity in vitro as well as in vivo, when transferred to naive animals (Butler et al. 1978; Butler and Nowotny 1976; Chang et al. 1974). Intensive studies on radioprotection by previous administration of endotoxin suggested an important role of accelerated hematopoiesis, as reviewed by Nowotny et al. (Nowotny and Behling 1982). Administration of LPS resulted in increased white blood cell numbers (He et al. 1992; Lehner et al. 2001a), neutrophilia (Kiani et al. 1997; Lehner et al. 2001a) and augmented numbers of monocyte/macrophage precursors in the bone marrow (Madonna et al. 1986; Madonna and Vogel 1985). We demonstrated that endotoxin-pretreated mice displayed elevated numbers of circulating neutrophils throughout the course of Salmonella infection, indicating improved recruitment from the bone marrow and/or decreased rate of apoptosis of these cells after LPS treatment (Lehner et al. 2001a). A critical role of diminished neutrophil apoptosis for the survival benefit associated with endotoxin pretreatment prior to induction of multi-germ peritonitis was suggested recently (Feterowski et al. 2001). This is in line with previous findings by Yamamoto, showing a delay of neutrophil apoptosis by LPS and LPSinduced cytokines in vivo and in vitro (Yamamoto et al. 1993).

Besides an increase in overall PMN numbers, enhanced anti-microbial activity of the individual PMN could contribute to enhanced immune defense of the LPS-pretreated host. Our unpublished data indicate an increased oxidative burst response of blood PMN from LPS-tolerant mice upon stimulation *ex vivo*. The view that neutrophils play a decisive role in LPS-induced resistance to infection is substantiated by our findings that PMN depletion partially abrogated the survival benefit of LPS-pretreated mice infected with *Salmonella typhimurium* (Lehner et al. 2001a).

Lymphocytes

Activation of lymphocytes by LPS or LPS-induced mediators is well documented, and Galelli et al. demonstrated that definite protection by LPS treatment of irradiated mice required bone-marrow derived radiosensitive cells (Galelli et al. 1977). However, the adaptive immune system seems to be of minor importance for the establishment of the early phase of LPS-induced nonspecific resistance as suggested by experiments performed with athymic

or SCID-mice which showed protection in spite of lacking functional T-and B-lymphocytes (Galelli et al. 1977, our own results).

Mediators of Nonspecific Resistance

Many of the effects of endotoxin are mediated by endogenous mediators such as cytokines, arachidonic acid metabolites, reactive oxygen or nitrogen radicals. The role of autocrine mediators in the process of inducing or maintaining macrophage refractoriness is still under debate. Similarly, there is evidence that LPS-enhanced nonspecific resistance is the result of the biological activity of several cytokines produced in response to LPS injection.

Injection of IL-1 improved survival of mice infected subsequently with Listeria monocytogenes (Morikage et al. 1990), Pseudomonas aeruginosa (Morikage et al. 1990; Vogels et al. 1995; Vogels et al. 1994a; Vogels et al. 1994b; Vogels et al. 1992), Klebsiella pneumoniae (Morikage et al. 1990; Vogels et al. 1994b; Vogels et al. 1992), Escherichia coli (Lange et al. 1992) and in the sepsis model of CLP (Alexander et al. 1991b; O'Reilly et al. 1992a). Furthermore, the combination of IL-1 and TNF reduced mortality and bacterial load of mice infected with E. coli at 20-fold the LD50 (Cross et al. 1989). Pretreatment with IL-1, GM-CSF or G-CSF improved survival after aerosol pneumococcal challenge (Hebert and O'Reilly 1996; Hebert et al. 1997; Hebert et al. 1990). This effect could be due to enhanced microbicidal activity of alveolar macrophages and improved clearance of blood-borne pathogens of cytokine-pretreated mice (Hebert et al. 1994). The beneficial effect of G-CSF treatment prior to induction of bacterial peritonitis or L. monocytogenes infection was probably mediated via the recruitment or activation of PMN (Barsig et al. 1996; O'Reilly et al. 1992b; Serushago et al. 1992; Villa et al. 1998). Extensive studies on the beneficial effect of cytokine pretreatment on resolution of infection were performed in the model of Salmonella typhimurium infection of mice employed also in our studies. It has been shown that administration of TNF resulted in improved survival of otherwise lethal bacterial challenge (Nakano et al. 1990; Nauciel and Espinasse-Maes 1992). Protection against salmonella infection was also conferred by pretreatment with IFNy (Nauciel and Espinasse-Maes 1992), IL-18 (Mastroeni et al. 1999) or TGFB (Galdiero et al. 1999), IL-1 or a combination of IL-1 and TNF (Morrissey and Charrier 1994; Morrissey et al. 1995). Since LPS administration induces the formation of all of these mediators, it is feasible that nonspecific resistance is conferred via endogenous formation of these cytokines. However, direct proof for this hypothesis has not been provided yet. Studies on the role of LPS-induced cytokines in enhancing resistance to infection are hampered by the fact that normal host defense initiated by the pathogen itself also depends on an intact cytokine response. Thus, cytokine-deficient mice are unsuitable and the use of cytokine-specific antibodies requires detailed titration experiments in order to selectively neutralize only LPS-induced cytokines during the pretreatment phase but not during infection. Furthermore, because of the plethora of cytokines with similar protective effect, it is unlikely that neutralization of single mediators will abrogate the beneficial effect of LPS-pretreatment.

Outlook

The finding that LPS-pretreated animals were protected against the toxicity of endotoxin in models of septic shock and sepsis and displayed even enhanced resistance to bacterial infection, suggests the therapeutic use of endotoxin tolerance induction as a sepsis prophylaxis. However, the wellknown side-effects of endotoxin injection ranging from fever to potentially fatal systemic inflammatory responses hamper the clinical use of endotoxin administration. The use of detoxified derivatives of LPS such as synthetic lipid A could avoid this risk. Several studies have demonstrated that these substances retain the ability to protect against shock and bacterial infection despite strongly decreased toxicity (Astiz et al. 1994a; Astiz et al. 1995; Astiz et al. 1994b; Gustafson et al. 1995; Hamilton-Davies and Webb 1995; Henricson et al. 1990; Lam et al. 1991a; Lam et al. 1991b; Madonna et al. 1986; Rudbach et al. 1994; Salkowski et al. 1998; Schutze et al. 1994; Yao et al. 1994). Future experiments will evaluate the clinical value of prophylactic induction of LPS tolerance in reducing the risk of postoperative sepsis.

Abbreviations

| AP-1 | activation protein-1 |
|-------|--|
| CFU | colony forming units |
| CLP | cecal ligation and puncture |
| GalN | D-galactosamine |
| IFN | interferon |
| I-kB | inhibitor of NF-ĸB |
| IL | interleukin |
| i.p. | intraperitoneal |
| IL-1R | interleukin-1 receptor |
| IRAK | interleukin-1 receptor-associated kinase |
| i.v. | intravenous |
| LPS | lipopolysaccharide |

| LTA | lipoteichoic acid |
|------------------|-------------------------------------|
| MALP-2 | macrophage-activating lipoprotein-2 |
| MAP | mitogen-activated protein |
| MPL | monophosphoryl lipid A |
| mu | murine |
| MyD88 | myeloid differentiation protein |
| NF–ĸB | nuclear factor kappa B |
| NIK | NF-KB-inducing kinase |
| PBMC | peripheral blood mononuclear cells |
| PBS | phosphate buffered saline |
| PGE ₂ | prostaglandin E2 |
| PMN | polymorphonuclear cells |
| r | recombinant |
| RES | reticuloendothelial system |
| S. aureus | Staphylococcus aureus |
| S. typhimurium | Salmonella typhimurium |
| TLR | Toll like receptor |
| TNF | tumor necrosis factor |
| TNF-R | tumor necrosis factor receptor |
| TRAF6 | TNF receptor-activated factor 6 |
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The Structural Basis of G-Protein-Coupled Receptor Function and Dysfunction in Human Diseases

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Reviews of Physiology, Biochemistry, and Pharmacology, Vol. 144 Springer-Verlag Berlin Heidelberg 2002 The Structural Basis of G-Protein-Coupled Receptor Function

1 Introduction

Among the different families of transmembrane receptors, G-proteincoupled receptors (GPCR) form the largest superfamily being present in yeast, plants, protozoa and metazoa. Signals as multiform as light, cations, small molecules including ions, amines, amino acids, peptides, lipids, sugars, as well as large proteins enable cells of a multicellular organism to communicate with each other and with their environment. Based on the now entirely known human genome careful estimation suggests that about 3-4% of the human genes code for GPCRs. Upon interaction with extracellular ligands or light activation, GPCRs transduce the signal into the cell by activating a cascade which is initiated by catalyzing GDP-GTP exchange on heterotrimeric G proteins. Besides this main signal transduction pathway recent studies suggest that GPCRs do not only interact with G proteins but are also able to interact with novel receptor-associated proteins mediating and modifying their function.

Because of their central role in controlling almost all physiological functions, accumulating evidence highlights the involvement of GPCRs in many pathophysiological processes. Activating and inactivating mutations in GPCR genes are responsible for an increasing number of human diseases including malignancies. Functional variability resulting from GPCR polymorphisms may contribute to interindividual differences in responses to endogenous and exogenous ligands as well as drugs.

The following review will summarize current knowledge relevant to understanding the molecular basis of GPCR function and focus on the underlying mechanisms of GPCR malfunction responsible for different human diseases. This will provide the basis to discuss strategies aiming at the therapy of diseases caused by receptor dysfunction.

2 Structural Architecture of GPCRs

The diversity of receptor groups within the GPCR superfamily is the result of a long evolutionary process. It has been suggested that serotonin (5-HT) receptors have existed for more than 750 million years (Peroutka and Howell 1994). The tendency toward protein diversification depends upon gene duplications and the continuous accumulation of mutations. The maintenance of vital functions in organisms, however, strictly requires enough structural conservation to ensure the functionality of the corresponding proteins. To



ture of rhodopsin (2.8 Å resolution) shows the orientation of the TMDs relative to each other. Positions of key residues are indicated in Fig. 1A-D. Structure of family 1 GPCRs. A two-dimensional model of family 1 GPCRs and some of the highly conserved residues are shown in enlarged circles (A). The ring-like arranged seven transmembrane helices (TMDs) assemble in a counterclockwise fashion as viewed from the extracellular surface forming a compact receptor structure with a size of 75x35x48 Å (B). The models of rhodopsin (Glaxo Wellcome Experimental Research, version 3.7b2) based on the crystal structure data (Palczewski et al. 2000). The crystal strucwere generated with the softwares Cn3D (The National Center for Biotechnology Information, version 3.0) and Swiss-PdBViewer the three-dimensional rhodopsin structure viewed from extracellular (C) or laterally (D) The Structural Basis of G-Protein-Coupled Receptor Function

predict and understand the functional consequences of structural changes within a receptor molecule, detailed information about the native receptor structure in its inactive and active conformation is required. Despite the remarkable structural variety of natural GPCR agonists and a low amino acid sequence homology, hydropathy analysis and biochemical data suggest that all GPCRs share a common molecular architecture consisting of seven transmembrane domains (TMDs). Currently, a high-resolution structure is available only for bovine rhodopsin (Palczewski et al. 2000) because of the difficulties inherent in producing, purifying, and crystallizing other GPCRs. As shown in Fig. 1, the mostly α -helical TMDs are arranged in a closely packed bundle forming the transmembrane receptor core. The seven TMDs of rhodopsin vary in length from 20 to 33 residues. The N terminus of the polypeptide is located in the extracellular space whereas the C terminus shows an intracellular localization. The seven TMDs are connected by six alternating intracellular (i1-i3) and extracellular (e1-e3) loops. An extensive analysis of about 200 GPCR sequences revealed that the total length of GPCRs can vary between 311 and ~1490 amino acid residues. The largest variations in length are found in the N and C termini with sizes up to 879 and 371 amino acid residues, respectively. But also the e2 loops and i3 loops show major size differences of almost 200 residues (Otaki and Firestein 2001).

2.1 GPCR Classification

Molecular cloning studies and genome data analysis have revealed about 1200-1300 members of the GPCR superfamily in the human genome. About 40-60% out of all human GPCRs have orthologs in other species including more distantly related organisms such as Caenorhabditis elegans and Drosophila melanogaster. To date, about 190 GPCRs have been assigned to an agonist or potential ligands. More than 900 are olfactory GPCRs but the sequence of at least 63% is disrupted in man by what appears to be a random process of pseudogene formation (Glusman et al. 2001). The remaining GPCRs are pseudogenes or so called 'orphan' receptors in man. 'Orphan' GPCRs are cloned GPCRs that bind unknown ligands. More than 200 'orphan' GPCRs, not including the olfactory GPCRs, have been discovered so far. In most cases, the extent of sequence homology is insufficient to assign these 'orphan' receptors to a particular receptor subfamily. Once the sequence of a GPCR is known, understanding the function of the encoded protein becomes a task of paramount importance. Consequently, reverse molecular pharmacological and functional genomic strategies are being employed to identify the activating ligands of the cloned receptors. The reverse molecular pharmacological methodology includes expression of orphan GPCRs in mammalian cells and screening these cells for a functional response to cognate or surrogate agonists present in biological extract preparations or peptide and compound libraries (Debouck and Metcalf 2000). Many new transmitter/receptor systems have been discovered recently, and their physiological functions and potential relevance in human disease are currently being analyzed.

2.1.1 The GPCR Families

The GPCR superfamily comprises at least three major families which share little sequence homology among each other. About ninety percent out of all GPCRs are grouped into the rhodopsin-like family (family 1). Subclassifying these family 1 receptors is a difficult problem because the mean pairwise amino acid identity is 17%. Family 1 contains a large collection of receptors for autocrine, paracrine, and endocrine factors which include acetylcholine, catecholamine, peptides, glycoprotein hormones, eicosanoids, proteases, nucleotides, and lysosphingolipids. Large extracellular domains (ectodomain) are rare in GPCRs of family 1. One example comes from the glycoprotein hormone receptors in which the ectodomain is composed of leucine-rich repeats. Recent studies indicated the evolution of an expanding group of homologous leucine-rich repeat-containing GPCRs in family 1 (Hsu et al. 2000).

The GPCR family 2 (secretin receptor family), the second largest family, recruits about 60 members and is characterized not only by the lack of the structural signature sequences present in the family 1 but also by the presence of a large N-terminal ectodomain. Family 2 comprises receptors for peptides and proteins such as secretin, glucagon, calcitonin, growth hormone-releasing hormone, corticotropin-releasing factor, and pituitary adenylate cyclase-activating peptide. The long and complex disulfidebonded amino-terminal ectodomain of these receptors plays an important role in agonist binding. Six cysteine residues within the N terminus, two cysteine residues connecting the e1 and e2 loops and about a dozen residues within the TMD core are well conserved among members of this family (Ulrich et al. 1998). Recently cloned GPCRs such as the α -latrotoxin receptor and Ig-Hepta reveal sequences with similarity to family 2 GPCRs within the TMD region but are unusual in so far as they contain large and complex extracellular domains those forming a subfamily within family 2. The first reports of sequences related to family 2 GPCRs followed the isolation of

cDNA clones encoding EMR1 (EGF-module-containing mucin-like hormone receptor 1), F4/80, and CD97. The ectodomains are composed of various protein domains such as EGF domains, cadherin repeats, and thrombospondin type-1 repeats (reviewed in Stacey et al. 2000). Although the physiological functions of this subfamily are largely unknown, the acquisition of such extracellular domains leads to the possibility that members of this subfamily possess cell migration and adhesion properties. The *Drosophila* mutant *methuselah* (*mth*) was identified from a screen for single gene mutations that extended average lifespan. The protein affected by this mutation is closely related to GPCRs of the secretin receptor family. The recently resolved 2.3 Å-resolution crystal structure of the *mth* ectodomain shows a three-domain architecture (West et al. 2001).

Family 3 recruits about two dozens GPCRs such as metabotropic glutamate receptors (mGluR), taste receptors, the calcium-sensing receptor, and GABA_B receptors but also potential taste, pheromone and olfactory receptors. Like in family 2, these receptors possess large ectodomains responsible for ligand binding. Family 3 GPCRs are defined as a group of receptors comprising at least three different subfamilies that share $\geq 20\%$ amino acid identity over their seven membrane-spanning regions. Subfamily I includes the metabotropic glutamate receptors, mGluRs 1–8, which are receptors for the excitatory neurotransmitter glutamate and are widely expressed in the central nervous system. Subfamily II contains two types of receptors: the calcium-sensing receptor and a recently discovered, multigene subfamily of putative pheromone receptors, that bind and are activated by the inhibitory neurotransmitter GABA.

Finally, three additional families encompass pheromone receptors, *Dictyostelium* cAMP receptors, and proteins of the frizzled/smoothened receptor group. These receptors display a heptahelical transmembrane organization but for most of these receptors the terminology 'G-protein-coupled receptor' is controversially discussed because the relevance of G-protein coupling for receptor's signal transduction was not convincingly demonstrated.

GPCRs are not only encoded by eukaryotic genes but also by viral genes. To date, about 20 putative GPCRs have been identified within herpes, pox, and retroviruses (Bai et al. 1999, Tulman et al. 2001). Involvement of GPCRs in the pathophysiologic role of viruses has been impressively demonstrated for the Kaposi's sarcoma-associated herpes virus (KSHV) receptor and the so-called UL78 gene family found in the cytomegalovirus (Arvanitakis et al. 1997, Oliveira and Shenk 2001).

2.1.2 GPCR Diversity Due to Alternative and Tissue-Specific Splicing

Recent molecular characterization of cloned protein genes draws attention to alternative splicing as a source of structural and functional diversity. An astonishing example for gene product multiplication comes from sensoryreceptor cells in the inner ear of birds where cell-specific expression of a subset of 576 possible alternatively spliced forms of K⁺ channel mRNA occurs (Black, 1998). The amino acid sequences of many GPCRs are encoded by intronless single-copy genes. However, a number of GPCR genes show an exon/intron assembly of their coding regions, as described for rhodopsin, some amine and peptide receptors, and the glycoprotein hormone receptors. In the latter receptor subfamily, only the gene regions encoding the large N terminus are comprised of exons and introns. As a consequence, naturally occurring splice variants have been described for numerous GPCRs. Interestingly, the genomic intron/exon structure and the number of receptor subtypes are not necessarily conserved among species for a given GPCR, e.g. the angiotensin receptor subtypes in human and mouse. Extensive studies on the rhodopsin gene have shown that introns in the coding region can appear and disappear during evolution. For example, human rhodopsin is encoded by four exons, but in some fish species the coding region for rhodopsin is intronless (Venkatesh et al. 1999). The existence of introns in GPCR genes provides the potential for additional diversity by virtue of alternative splicing events which may generate distinct receptor isoforms. For example, pharmacological and molecular biological studies have resulted in the cloning of cDNAs encoding four EP prostanoid receptors. The cloning of these receptors has revealed further heterogeneity due to alternative mRNA splicing. Specifically, eight human EP₃ receptor isoforms have been identified which differ only in their C termini (Pierce and Regan, 1998). It should be noted that a tissue-specific occurrence of distinct splice variants has been described, e.g. for the PACAP receptor (Chatterjee et al. 1996) and the corticotropin releasing factor (CRF) receptor (Ardati et al. 1999).

In principle, two types of GPCR splice variants can be distinguished. First, usage of an alternative splice site can generate a functional receptor as demonstrated for a large number of GPCRs such as the EP₃ receptor (Namba et al. 1993), the thromboxane receptor (Vezza et al. 1999), the metabotropic glutamate receptor 1 (Prezeau et al. 1996), and the D₂ dopamine receptor (Guiramand et al. 1995, Seeman et al. 2000). Most variations are found in the i3 loop and the receptor C terminus which are considered to be important for G-protein coupling and interactions with other proteins (see 3.2). As shown for the EP₃ and 5-HT₄ receptor isoforms, alternative splice products

can vary in their basal activity when expressed in vitro. The extent of constitutive activity was found to be reversally correlated with the length of the Cterminal portion of the splice variants (Jin et al. 1997, Claeysen et al. 1999). In most cases, the divergence between receptor isoforms is limited to the Cterminal tail, a region involved in internalization and down-regulation. In contrast, some GPCR splice variants, when expressed in vitro, displayed similar pharmacological profiles and signaling specificity (Ito et al. 1994, Park et al. 2000). Second, an improper splicing event can produce a new protein that may display dominant negative effects on the wild-type receptor. It has been demonstrated that the expression of a truncated form of the gonadotropin-releasing hormone (GnRH) receptor can decrease the signaling efficacy of the full length receptor by reducing its cell surface expression levels (Grosse et al. 1997). This dominant negative effect was highly specific for the GnRH receptor and was probably due to heterocomplex formation between the two proteins. One may speculate that co-expression of truncated receptor isoforms may modulate the gonadotropes' responsiveness to GnRH and thus contribute to the fine tuning of gonadotropin release in vivo. Similarly, the ability of an EP_1 receptor isoform to inhibit signaling by EP_1 as well as EP4 receptors can be explained by complex formation between these different receptors (Okuda-Ashitaka et al. 1996).

2.1.3

GPCR Diversity Due to RNA Editing

RNA editing is a co- or post-transcriptional process in which selected nucleotide sequences in the mRNA are altered when compared to the genomic sequence. Double-stranded RNA-specific adenosine deaminases convert adenosine residues to inosine in messenger RNA precursors (pre-mRNA). Their main physiological substrates are pre-mRNAs. Extensive analysis of cDNAs from 5-HT_{2C} receptor reveals posttranscriptional modifications indicative of adenosine-to-inosine RNA editing (Burns et al. 1997). RNA transcripts encoding the 5-HT_{2C} receptor undergo adenosine-to-inosine RNA editing events at up to five specific sites. Interestingly, reduced G-protein-coupling efficiency for the edited isoforms is primarily due to silencing of the constitutive activity of the non-edited 5-HT_{2C} receptor (Niswender et al. 1999). No further example of modified GPCR functions by mRNA editing has been reported yet.

2.2 Arrangement and Structure of the Transmembrane Domains

The understanding of GPCR function and dysfunction requires detailed information on the receptor core structure. Like other polytopic membrane proteins, GPCRs are partially buried in the non-polar environment of the lipid bilayer by forming a compact bundle of transmembrane helices. The correct orientation and integration of the polypeptide chain is guided by a complex translocation apparatus residing in the endoplasmic reticulum (ER). Two different folding stages can be distinguished following an initial translocation of the receptor N terminus into the ER lumen. In stage I, hydrophobic α -helices are established across the lipid bilayer, and protein folding is predominantly driven by the hydrophobic effect. The TMDs adopt a secondary structure in order to minimize the polar surface area exposed to the lipid environment with the result that hydrophobic amino acids face the lipid bilayer and that the more hydrophilic amino acid residues are orientated towards the core crevice of the TMD bundle. In stage II, a functional tertiary structure is formed by establishing specific helix-helix interactions, leading to the tightly packed, ring-like structure of the TMD bundle.

In the early stage of GPCR structure/function analysis, investigators used the structure of bacteriorhodopsin, a prokaryotic ion pump with structural similarities to the GPCR superfamily, as a scaffold for topographical models of the transmembrane core of GPCRs (Baldwin, 1994). The identification of specific interhelical contact sites was required to provide information about the relative orientation of the different helices towards each other. To determine the structural determinants which actually contribute to specific helix-helix interactions, chimeric receptors were generated. Studies with chimeric muscarinic receptors provided the first experimental evidence as to how TMD1 and TMD7 are oriented relative to each other and also strongly suggested that the TMD helices in muscarinic receptors are arranged in a counterclockwise fashion as viewed from the extracellular membrane surface (Liu et al. 1995). Functional analysis of artificial metal ionbinding sites (Elling et al. 1995) and disulfide bonds (Farrens et al. 1996) as well as spectroscopic approaches (Beck et al. 1998) allowed the identification of distinct amino acid residues that are involved in helix-helix contacts and the relative orientation of single TMDs to each other. Nuclear magnetic resonance (NMR) and circular dichroism (CD) studies with peptides derived from the cytoplasmic domains of GPCRs predicted a cytosolic α -helical extension of all TMDs (Jung et al. 1995, Yeagle et al. 1997, Schulz et al. 2000a). This assumption is experimentally supported by site-directed spinlabeling studies (Farahbakhsh et al. 1995, Altenbach et al. 1996) and muta-

genesis studies (Biebermann et al. 1998). Finally, the proposed helical arrangement was confirmed by low resolution structures of the transmembrane core of rhodopsin (Unger et al. 1997) and the rhodopsin crystal structure (Palczewski et al. 2000) highlighting the feasibility of mutagenesis approaches and structural analyses of single TMD fragments. Interestingly, the overall α -helical character of TMDs is often disrupted by non- α -helical components, such as intrahelical kinks (often due to residues other than proline), 3_{10} -helices and π -helices (Riek et al. 2001).

2.3

Conserved Structural Features and their Functional Relevance

Most of the current knowledge about structure/function relationships of GPCRs is based on studies with rhodopsin and other members of the family 1 of GPCRs. Thus, this section will mainly focus on data obtained with rhodopsin-like receptors. Only a few critical amino acid residues have been preserved during evolution of the rhodopsin-like GPCR family (see Fig. 1). Despite an evolutionary conservation mutational alteration of some conserved amino acid residues does not always have the same functional consequence.

2.3.1 Disulfide Bonds in GPCRs

The majority of family 1 and also family 2 GPCRs contains a conserved pair of extracellular cysteine residues linking the first and second extracellular loops via a disulfide bond (Hausdorff et al. 1990). Numerous functional analyses of mutant GPCRs in which the cysteine residues were replaced by other amino acids have shown that this disulfide bond may be critical for receptor signaling (Kosugi et al. 1992, Savarese et al. 1992, Cook and Eidne 1997). In some receptors, however, this disulfide bond is required to maintain more distinct functions. Systematic mutagenesis studies of the conserved cysteine residues in several GPCRs showed that disruption of the disulfide bond does not influence the receptor's ability to activate G proteins but interferes with high affinity ligand binding and receptor trafficking (Le Gouill et al. 1997, Perlman et al. 1995, Schulz et al. 2000b, Zeng et al. 1999). Despite the disruption of the disulfide bond, the receptor core structure appears to remain intact, allowing receptor function. Consistent with this notion, some GPCRs, e.g. receptors for sphingosine 1-phosphate and lysophosphatidic acid, lack the conserved extracellular Cys residues. Interestingly, many GPCRs including receptors for biogenic amines, peptides and many 'orphan' GPCRs contain a second conserved pair of extracellular cysteine residues linking the N terminus and third extracellular loop. Mutational disruption of this disulfide bond results in a loss of high affinity binding of P2Y₁ receptor ligands, suggesting a pivotal role of an N terminus/e3 loopconnecting disulfide bridge for proper receptor assembly (Hoffmann et al. 1999). In chemokine receptors this disulfide bond is required for ligand binding and agonist-induced receptor function but not for constitutive activity of KSHV-GPCR (Ho et al. 1999) and CCR₅-mediated HIV entry (Blanpain et al. 1999). In the crystal structure of rhodopsin, the N-terminal segment is located just below the e3 loop. Specific non-covalent contacts maintain the proper orientation between the rhodopsin N terminus and the extracellular loops so that an additional disulfide bridge like in other GPCRs is probably not required.

2.3.2

Conserved Amino Acid Residues and Motifs in Family 1 GPCRs

Within their transmembrane core most family 1 GPCRs possess a number of highly conserved residues, such as an Asp residue in TMD2, a DRY motif at the TMD3/i2-transition, a Trp residue in TMD4, a Tyr residue in TMD5, a Pro residue in TMD6 and an N/DP(X)_nY motif in TMD7 (see Fig. 1). For example, the DRY motif located at the boundary of TMD3 and the i2 loop is a highly conserved triplet of amino acid residues known to play an essential role in GPCR function. The crystal structure of rhodopsin proposes that the residues of the DRY motif participate in several hydrogen bonds with surrounding residues of TMD6 (Palczewski et al. 2000). It was shown for rhodopsin that the corresponding Glu residue (ERY motif) is involved in proton uptake resulting in the formation of the activated metarhodopsin II intermediate (Helmreich and Hofmann, 1996). Similarly, the Asp residue in the DRY motif has been proposed to act as a proton acceptor during receptor activation, as shown for the α_{1B} adrenergic receptor (Scheer et al. 1997). Mutation of this Asp residue results in constitutive activity of many receptors (Alewijnse et al. 2000, Rasmussen et al. 1999). Kobilka and co-workers found that protonation increases basal activity by destabilizing the inactive state of the β_2 adrenergic receptor but the pH sensitivity of receptor activation was not abrogated by mutation of Asp130, which is homologous to the conserved acidic amino acid residue in the DRY motif of rhodopsin and the α_{1B} adrenergic receptor (Ghanouni et al. 2000). In the crystal structure the Glu residue forms a salt bridge with the Arg residue of the ERY motif. However, several family 1 GPCRs are known in which the acidic residue (Asp, Glu) within this motif is naturally substituted by His, Asn, Gln, Gly, Val, Thr,

Cys or Ser residues, questioning the general importance of a salt bridge and a proton uptake at this amino acid position for GPCR activation. The fully conserved Arg residue in the DRY motive is considered to be a key residue in signal transduction of GPCRs. Replacement of the conserved Arg residue by different amino acids virtually abolished G-protein coupling of many GPCRs (Franke et al. 1992, Jones et al. 1995, Scheer et al. 1996, Zhu et al. 1994). Therefore, the conserved Arg residue has been implicated as a central trigger of GDP release from the G-protein α subunit (Acharya and Karnik 1996). Recent studies with mutants of the N-formyl peptide receptor, luteinizing hormone receptor (LHR), and V2 vasopressin receptor (AVPR2) showed that G-protein coupling is only decreased but not abolished after replacement of the Arg residue in the DRY motif (Arora et al. 1997, Schöneberg et al. 1998, Seibold et al. 1998, Schulz et al. 1999) probably due to reduced receptor cell surface expression levels in response to constitutive arrestin-mediated desensitization (Barak et al. 2001). The conserved Arg residue in the human B2 adrenergic receptor, the TRH receptor, and the CB2 cannabinoid receptor could also be substituted by other amino acids without loss of G-protein coupling, indicating that the presence of the conserved Arg residue is not an absolute requirement for G-protein activation (Perlman et al. 1997, Seibold et al. 1998, Rhee et al. 2000). Taking advantage of the structurally stabilizing effect of ligands, the impaired cell surface expression and, therefore, the signal transduction of the H₂ histamine receptor mutant R116A/N was partially restored by preincubation with either an agonist or inverse agonist (Alewijnse et al. 2000). Therefore, the GPCR dysfunction caused by replacement of the Arg within the DRY motif is caused by improper receptor folding and trafficking rather than by a direct effect on receptor/G-protein coupling efficacy in many GPCRs. These results can be reconciled by assuming that the DRY motif has different functions in different GPCR classes. It has been speculated that the Arg residue directly interacts with a conserved Glu/Asp residue at the very N-terminal end of TMD6 by forming a salt bridge in the inactive conformation of the β_2 adrenergic receptor (Ballesteros et al. 2001) but refinement of the rhodopsin crystal structure (Teller et al. 2001) as well as functional studies with glycoprotein hormone receptors do not support such interaction (Schulz et al. 2000a).

The N/DP(X)_nY motif within the TMD7 near the cytoplasmic face of the plasma membrane is highly conserved (see Fig. 1). This sequence has been postulated to play important roles in receptor activation and regulation (Wang et al. 1996). It was shown that light-activation of rhodopsin rendered an epitope including residues of the N/DP(X)_nY motif accessible for an epitope-specific antibody, suggesting conformational changes of this sequence motif (Abdulaev and Ridge 1998). The Asn residue in this sequence motif is

thought to play a crucial role in receptor activation. In the cholecystokinin type B receptor, mutation of the Asn in the $N/DP(X)_nY$ motif to Ala had no effect on cell surface expression and high affinity ligand binding but completely abolished G_q-mediated signaling (Gales et al. 2000). Mutational alteration of the conserved Pro residue in the $N/DP(X)_nY$ motif resulted in a complete loss of receptor function as demonstrated *in vivo* for the AVPR2 (Tajima et al. 1996) underlining the functional importance of this motif. It is noteworthy that in a few GPCRs of family 1 the Asn/Asp residue within the $N/DP(X)_nY$ is naturally replaced by Ser, Thr, Lys, or His.

2.3.3

Posttranslational Modifications of GPCRs

The polypeptide chain of most GPCRs is posttranslationally modified including glycosylation, palmitoylation and phosphorylation. Potential Nglycosylation sites (NXS/T) and O-glycosylation sites (Sadeghi and Birnbaumer 1999, Nakagawa et al. 2001) are usually located within the extracellular N-terminal region but are also found in the extracellular loops. The number and exact positions of glycosylation sites are usually not conserved among orthologs of different species. Some GPCRs, e.g. the A2 adenosine and the human α_{2B} adrenergic receptors, completely lack consensus sites for glycosylation in their N termini but are fully active in the absence of this posttranslational modification. The functional relevance of post-translational modifications in GPCRs has been extensively studied in in vitro systems. It is well accepted that mutational disruption of potential N-glycosylation sites of most GPCRs has little effect on receptor function in vitro (Rands et al. 1990, Innamorati et al. 1996, Zeng et al. 1999). However, nonglycosylated receptors for parathyroid hormone and glycoprotein hormones in which glycosylation sites were mutated, are deficient in function (Zhang et al. 1995, Zhou et al. 2000). In the human calcium-sensing receptor, eight out of 11 potential N-linked glycosylation sites are actually utilized. Glycosylation of at least three sites is critical for cell surface expression of the receptor, but glycosylation does not appear to be critical for signal transduction (Ray et al. 1998).

Consensus acceptor phosphorylation sites for protein kinases A and C and potential receptor-specific kinase phosphorylation sites (multiple serine and threonine residues) are present in the i3 loop and the C-terminal domain. Several studies indicated that the selectivity of receptor/G-protein coupling is regulated by receptor phosphorylation (3.1.2).

Most GPCRs contain one or more conserved cysteine residues within their C-terminal tail (see Fig. 1) which are modified by covalent attachment

of palmitoyl or isoprenyl residues (Bouvier et al. 1995, Hayes et al. 1999). As known from the rhodopsin structure the palmitoyl moiety is anchored in the lipid bilayer forming a fourth intracellular (i4) loop. Depending on the specific GPCR examined, different effects on receptor phosphorylation, internalization, trafficking and G-protein-coupling profile have been described (reviewed in Bouvier et al. 1995, Wess 1998). However, several family 1 GPCRs do not have Cys residues in their C-terminal tail for posttranslational modification probably lacking the i4 loop.

2.4 GPCR Assembly and Oligomerization

2.4.1 GPCR Assembly from Independent Folding Units

Following pioneering studies with bacteriorhodopsin (Huang et al. 1981, Kahn and Engelman 1992), the successful reconstitution of adrenergic receptors (Kobilka et al. 1988) from two fragments demonstrated that the integrity of the GPCR polypeptide chain is not required for proper receptor function. Based on these findings it has been speculated that GPCRs are composed of two or more independent folding domains. To test this hypothesis rhodopsin and the m3 muscarinic receptor were split in all three intracellular and extracellular loops. It was shown that except for a construct containing only TMD1, a significant portion of all N- and C-terminal receptor fragments studied was found to be inserted into the plasma membrane in the correct orientation even when expressed alone (Ridge et al. 1995, Schöneberg et al. 1995). Co-expression of some complementary receptor polypeptide pairs, generated by splitting GPCRs in their intra- and extracellular loops, resulted in receptors which were able to bind ligands and to mediate agonist-induced signal transduction (reviewed in Gudermann et al. 1997). It is noteworthy that all attempts to assemble functional receptor proteins from solubilized receptor fragments in vitro were unsuccessful (Schöneberg et al. 1997). This indicates that molecular chaperones such as RanBP2, nina A and calnexin that are likely to assist folding of the wild-type receptor protein may also play a role in facilitating complex formation. It has been shown that chaperone-dependent mechanisms are essential for proper folding of rhodopsin (Baker et al. 1994, Ferreira et al. 1996), AVPR2 (Morello et al. 2001) and gonadotropin receptors (Rozell et al. 1998).

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2.4.2 GPCR Multimerization

The ability of functional complementation from receptor fragments is consistent with reports showing or suggesting that GPCRs can form dimers and oligomers. For several non-GPCR receptor families, such as receptor tyrosine kinases and kinase-associated cytokine receptors, agonist-induced receptor dimerization is required for initiating a signal transduction cascade. First evidence for GPCR dimerization came from crosslinking and photoaffinity labelling experiments with GnRH, LH, and muscarinic receptors (Conn et al. 1982, Avissar et al. 1983, Podesta et al. 1983). Numerous studies describing similar findings followed, but most reports of GPCR di- and oligomerization were based on co-immunoprecipitation studies. It has been argued that biochemical evidence from co-immunoprecipitation and Western blot experiments supporting the existence of GPCR oligomers is questionable, since solubilization of integral transmembrane proteins can cause artificial aggregation. However, as shown for epitope-tagged B_2 adrenergic, muscarinic and vasopressin receptors, the association is highly specific for a given receptor subtype giving rise only to homodimers (Hebert et al. 1996, Zeng and Wess 1999, Schulz et al. 2000b). In addition to investigations in transient expression systems, in vivo studies with D₂ and D₃ dopamine receptors (Nimchinsky et al. 1997, Zawarynski et al. 1998), somatostatin receptor type 5 (SSTR₅)/D₂ dopamine receptors (Rocheville et al. 2000a), and rhodopsin (Colley et al. 1995) suggest the coexistence of receptor monomers and oligomeric complexes under physiological circumstances.

One question that arises from these studies is as to whether GPCR dimers are pre-formed or are induced in the presence of the appropriate ligand. Most co-immunoprecipitation data suggest the existence of oligomeric receptor complexes under basal conditions. Examining the biological relevance of GPCR homodimerization *in vivo*, Bouvier and co-workers used a bioluminescence resonance energy transfer (BRET) technique to study receptor-receptor interactions. It was shown that β_2 adrenergic receptors and thyrotropin-releasing hormone receptors (TRHR) form constitutive homodimers that are expressed at the cell surface where they interact with agonists (Angers et al. 2000, Kroeger et al. 2001). Constitutive receptor association appears to be a general phenomenon since the yeast α -mating factor receptor forms dimers under basal conditions, as shown by a fluorescence resonance energy transfer (FRET) approach (Overton and Blumer 2000). On the other hand, there is also experimental support for an agonist driven oligomerization mechanism. Thus, the B₂ bradykinin receptor and the

CXCR₄ receptor undergo receptor dimerization after ligand binding (AbdAlla et al. 1999, Vila-Coro et al. 1999).

There is growing evidence that GPCR not only exist in homodimeric structures but also in complexes formed by different GPCRs. Expression of the recombinant GABA_{B1} receptor in COS cells resulted in a significantly lower agonist affinity when compared with native receptors. Interestingly, co-expression of the GABA_{B1} receptor and the GABA_{B2} receptor, a recently cloned novel GABA_B receptor subtype, in Xenopus oocytes and HEK-293 cells led to efficient coupling to G-protein-regulated inward rectifier K⁺ channels (GIRKs) with an agonist potency in the same range as for GABAB receptors in neurons (Jones et al. 1998, White et al. 1998, Kaupmann et al. 1998). Encouraged by these studies, an ever growing number of heterodimeric complexes has been identified. For example, there is biochemical and pharmacological evidence that the κ and δ opioid receptors as well as μ and δ opioid receptors associate with each other. The complexes exhibit ligand binding and functional properties that are distinct from those of either receptor (Jordan and Devi 1999, George et al. 2000). Heterodimer formation was also observed for other receptor subtypes such as 5-HT1R/ 5-HT_{1D} receptors and SSTR₁/SSTR₅ (Xie et al. 1999, Rocheville et al. 2000b). Hetero-oligomerization between the D2 dopamine receptor and SSTR5 was demonstrated, resulting in a novel receptor with enhanced functional activity (Rocheville et al. 2000a). In a very recent study, Zuker and colleagues showed that formation of a functional sweet taste receptor is only achieved when two taste GPCRs, T1R2 and T1R3, are coexpressed (Nelson et al. 2001). The ability of GPCRs to heterodimerize provides a new mechanism by which a cell can fine-tune its responsiveness to an agonist via co-expression of distinct GPCR subtypes.

2.4.3 The Structure of GPCR Multimers

The molecular mechanisms and structural requirements which are responsible for GPCR oligomerization are only poorly understood. There is evidence for at least three molecular mechanisms by which GPCRs can oligomerize – covalent linkage via disulfide bonds, domain interaction such as coiled-coil structure and specific interaction of the TMD regions (Fig. 2). In the case of the mGluR₅ (Romano et al. 1996) and the calcium-sensing receptor (Bai et al. 1998, Ward et al. 1998), which are members of family 3, disul-

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Fig. 2. Hypothetical structures of GPCR dimers. GPCR-dimer formation is can be mediated via covalent (disulfide bond) and non-covalent (coiled-coil structure, lateral contact) interactions (upper panel). The molecular structure of most family 1 homo- and heterodimers is currently unknown. Transmembrane domains (TMDs, numbered from 1 to 7) of GPCRs form a ring-like structure in a counter-clock wise fashion as viewed from extracellular (lower panel). GPCRs are composed of at least two independent folding domains (TMDs1-5 and TMDs6-7) which are connected by the i3 loop. Accumulating evidence suggests that wild-type GPCRs can exist in dimeric complexes, and two structural models of dimer formation have been suggested (Gouldson et al. 1998). The contact interface of so-called 'swapped dimers' is recruited from the rearrangement of two independent folding domains of the individual receptor monomers. The ring-like TMD arrangement is still retained by the complementary exchange of the two folding domains. In lateral contact dimers, a site-to-site interaction of the individual receptor molecules is assumed

fide bonds between the extracellular portions are of critical importance for receptor dimerization. Recently, crystal structures of the extracellular ligand-binding region of mGluR1 - in a complex with glutamate and in two non-liganded forms - have been resolved showing disulfide-linked homodimers (Kunishima et al. 2000). In contrast, it was demonstrated that mutant calcium-sensing receptors without extracellular cysteines form dimers on the cell surface to a similar extent as observed for wild-type recep-

tors (Zhang et al. 2000). Interestingly, the GABA_{B2} receptor was initially discovered by a yeast two hybrid approach using the C terminus of the GABA_{B1} receptor for screening a human brain cDNA library. Heterodimer formation was assumed to be mediated via a coiled-coil structure of the C terminal of the two receptors (White et al. 1998). It was found later that a C-terminal retention motif RXR(R) is masked by GABA_B receptor dimerization allowing the plasma membrane expression of the assembled complexes (Margeta-Mitrovic et al. 2000). However, association of both GABA_B receptors was demonstrated even in the absence of their cytoplasmic C termini (Pagano et al. 2001).

Most studies agree that homo- and heterodimers found for rhodopsinlike GPCRs represent non-covalent complexes. Thus, two structural models of dimer formation have been proposed for family 1 GPCRs (Gouldson et al. 1998). In one dimeric structure, referred to as 'contact dimer', two tightly packed bundles of seven TMDs are positioned next to each other. The contact interface between the two monomeric receptors is assumed to be located between the lipid-orientated transmembrane receptor portions (see Fig. 2). The so-called 'domain-swapped dimer' has been proposed to explain the reconstitution phenomenon observed with truncated and chimeric GPCRs (Maggio et al. 1993, Schulz et al. 2000b). In this dimer structure, the two receptor molecules fold around a hydrophilic interface by exchanging their N-terminal (TMDs1-5) and C-terminal (TMDs6-7) folding domains (see Fig. 2). Attempting both hypothetical dimer structures data with the AVPR2 and D₂ dopamine receptor strongly support an oligomeric structure in which family 1 GPCRs form contact oligomers by lateral interaction rather than by a domain-swapping mechanism (Schulz et al. 2000b, Lee et al. 2000). High resolution X-ray structure determinations of three heptahelical membrane proteins, the bacteriorhodopsin, the halorhodopsin and the sensory rhodopsin II, clearly show that both proteins assemble to multimers (Luecke et al. 1999, Kolbe et al. 2000, Royant et al. 2001). The proton pump bacteriorhodopsin shares structural similarities with the GPCR family including the assembly from multiple independent folding units. In the trimeric structure found in bacteriorhodopsin and halorhodopsin crystals, TMDs2-4 of the three molecules face each other forming an inner circle of TMDs. In the dimeric sensory rhodopsin II TMDI and TMD7 contact each other. Structural data did not provide any support for a domain-swapping mechanism of oligomerization. Similarly, other polytopic membranespanning proteins which homo-oligomerize in order to build a functional complex, such as aquaporins, assemble via lateral interaction (Walz et al. 1997).

Taken together, recent data strongly support oligomeric GPCR structures. Functional studies with mutant GPCRs provided strong evidence that oligomerization occurs by lateral interaction rather than by a domainswapped mechanism (Lee et al. 2000, Schulz et al. 2000b). There is growing evidence that GPCR dimerization has consequences for physiologic receptor functions such as formation of receptor 'subtypes' with new ligand binding or signaling abilities (Jordan and Devi 1999, AbdAlla et al. 2000).

3 Diversity of Physiological GPCR Function

In the post-genome era long established views of receptor pharmacology are changing since modifications of GPCR structure and function can contribute to the pharmacological diversity found for products of a single GPCR gene. The changes in GPCR structure and function can occur at different levels. For example, gene duplication events that have led to multiple receptor subtypes are the cause for a considerable functional diversity found in one transmitter system. Moreover, tissue-specific splicing, RNA editing, and variations in posttranslational modifications can multiply the products derived from one GPCR gene. In addition, tissue- or cell-specific expression of effectors can modify the ligand preference and signal transduction capabilities of GPCRs, so that specificity and function of a given GPCR can vary when expressed in a different cellular environment.

3.1

Current Models of Receptor Activation

It is truly one of the most exciting issues within the GPCR field to unravel structural changes in the receptor protein while transducing extracellular signals. The classical 'ternary complex model' postulates that receptor activation leads to the agonist-promoted formation of an active "ternary" complex of agonist, receptor, and G protein (De Lean et al. 1980). This model had to be extended in order to account for the fact that many receptors can activate G proteins in the absence of agonist (Lefkowitz et al. 1993). Based on these seminal observations, receptors are assumed to exist in an equilibrium between the inactive state R and the active state R* (Fig. 3). The model predicts that, even in the absence of agonist, a certain fraction of receptors will spontaneously adopt an active conformation, permitting agonist-independent G-protein activation. In keeping with this current concept, some wild-type receptors like the D_{1B} dopamine receptor, the H₃ histamine receptor, the melanocortin type 4 (MC4) receptor and the thyrotropin receptors.



Fig. 3. Ligand- and mutation-induced effects on the functional equilibrium of GPCRs (A) and the functional conformations in GPCRs with multiple coupling abilities (B). (A) According to allosteric ternary complex models of receptor activation (Lefkowitz et al. 1993), GPCRs exist in an equilibrium between the inactive (R) and active (R*) conformation responsible for spontaneous activity. R* has high affinity for G proteins. Agonist (A) binding to the free receptor (uncoupled from G proteins) leads to stabilization of a partly activated form of the receptor (R*) that is able to couple to the G protein. Inverse agonists decrease the spontaneous activity of receptors by shifting the equilibrium towards R. Like agonists or inverse agonists, activating or inactivating mutations are capable of shifting the equilibrium toward R* and R, respectively. Neutral antagonists bind to the receptor but have no influence on the R/R* equilibrium and compete for both agonists and inverse agonists. (B) Agonists also stabilize the activated, coupled form of the receptor (AR* + G*). Most GPCRs couple to more than one G protein (G* and G**). There is evidence that distinct conformational states (R* and R**) favor the interaction with one or the other Gprotein family

tor (TSHR) display significantly elevated basal activity even in the unliganded state (Tiberi and Caron 1994, Cetani et al. 1996, Biebermann et al. 1998, Nijenhuis et al. 2001). To describe mutant receptors characterized by a shift of the isomerization equilibrium towards the active conformation, the term 'constitutive activity' has been coined. By definition, such receptors can activate G proteins in the absence of agonist.

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3.1.1 Structural Aspects of GPCR Activation

Conformational changes accompanying receptor activation have been initially studied in the photoreceptor rhodopsin. Here, the ligand, 11-cisretinal, is already positioned in the transmembrane bundle and isomerizes upon illumination to function as agonist. Using a variety of biophysical methods, conformational differences between the inactive rhodopsin and the activated metarhodopsin II were characterized (reviewed in Helmreich and Hofmann 1996, Okada et al. 2001). Site-directed spin-labeling studies and studies with artificially created zinc binding sites indicate that movements of TMD3 and TMD6 relative to one another are required for Gprotein activation (Farrens et al. 1996, Sheikh et al. 1996). Available evidence indicates that light-induced helix movements in rhodopsin occur only after termination of the early photochemical events. In the subsequent so-called 'Meta'- states, the photoreceptor remains in a G-protein dependent equilibrium between active and inactive conformations and the photolyzed chromophore all-trans-retinal or its analogs act as full or partial agonists (Okada et al. 2001). This has provided the evidence that the metarhodopsin states fit into the general ternary complex scheme for GPCRs. Additional evidence for a relative movement between TMD3 and TMD6 in other GPCRs was provided by direct fluorescence labeling of the B2 adrenergic receptor (Gether et al. 1995, Gether et al. 1997, Ghanouni et al. 2001) or by monitoring the accessibility of Cys residues to a hydrophilic sulfhydryl-specific reagent during receptor activation (Javitch et al. 1997).

Site-directed mutagenesis approaches have been used successfully to examine several aspects of receptor structure-function relationships including ligand binding, G-protein coupling, receptor folding, and mechanisms of activation. In vitro mutagenesis studies with several GPCRs provided compelling evidence for the existence of intramolecular constraining determinants which stabilize the inactive receptor conformation. Mutational alteration of such intramolecular contact sites can lead to constitutive receptor activation. Most of the mutations found to be responsible for constitutive receptor activity are located in the C-terminal portion of the i3 loop and within different TMDs. Interhelical salt bridges, as specific structural determinants stabilizing the inactive state, have been identified in rhodopsin (Robinson et al. 1992) and the α_{1B} adrenergic receptor (Porter et al. 1996). The identification of such specific contact sites provides valuable information about the orientation of the different helices relative towards each other.

The largest number of different activating mutations has been identified in the TSHR and LHR, providing important insights into the structural requirements of receptor quiescence. In the LHR, a tightly packed hydrophobic cluster and a specific H-bonding network formed between the cytoplasmic portions of TMD5 and TMD6 and the central regions of TMD6 and TMD7 is thought to maintain the inactive receptor conformation. Mutagenesis data suggested that LHR activation is associated with the disruption of key interhelical side-chain interactions (Lin et al. 1997). Recent data with constitutive active LHR and TSHR mutants implicate that in addition to interhelical interactions the inactive conformation of GPCRs is also stabilized by specific intrahelical structures (Schulz et al. 2000a).

3.1.2

Determinants of G-Protein/Receptor Interaction and Coupling Specificity

Since more than one thousand GPCRs interact with a limited repertoire of G proteins, the issue of coupling specificity needs to be addressed. Based on primary amino acid similarity of the α subunits, G proteins are grouped into four major families, G_s, G_{i/0}, G_{q/11}, and G_{12/13}. Nearly two decades after the cloning of the first GPCRs, there are still many open questions relating to the mechanisms of GPCR/G-protein interaction and the molecular elements determining G-protein coupling specificity. Over the past few years, an increasing number of GPCRs with a broad G-protein coupling profile has been identified (Gudermann et al. 1997).

Structural elements determining signaling specificity are located in both the G protein and the receptor. Numerous *in vitro* mutagenesis studies have been performed with G-protein α subunits to understand how coupling selectivity is achieved. The C terminus as well as the N terminus of the α subunit make important contributions to appropriate receptor/G-protein recognition (Wess, 1998).

The exact nature of G-protein interaction sites within the receptor is currently unknown and may vary between the different GPCRs and G proteins. It is assumed that not only the intracellular loops but also the cytoplasmic sides of the TMDs participate in GPCR/G-protein coupling. Indeed, peptides derived from the i3 loop/TMD6 junction can activate G proteins (Abell and Segaloff 1997, Varrault et al. 1994). Likewise, site-directed mutagenesis studies with GPCRs examined the structural elements that participate in Gprotein interactions and that determine the coupling profile of a given receptor. For example, the il loop of the formyl peptide receptor (Amatruda et al. 1995) and the cholecystokinin CCK_A receptor (Wu et al. 1997), the i2 loop of the V_{1A} vasopressin receptor (Liu and Wess 1996), and the i3 loop of the endothelin ET_B receptor (Takagi et al. 1995) have been demonstrated to participate in G-protein activation. Taking advantage of chimeric GPCRs designed between structurally related receptor subtypes that are clearly distinguishable with regard to their signaling abilities, studies on muscarinic (Blüml et al. 1994, Blin et al. 1995) and vasopressin receptors (Erlenbach and Wess, 1998) disclosed the importance of several distinct residues for selective G-protein recognition.

The established view of the importance of the intracellular loops in Gprotein interaction and specificity is challenged by recent studies with the TSHR and LHR. Large deletions or alanine replacement of most amino acid residues in the i3 loops did not abolish signal transduction, excluding a substantial participation of the i3 loop in G-protein recognition at least in glycoprotein hormone receptors (Wonerow et al. 1998, Schulz et al. 1999, Schulz et al. 2000a). In the m3 muscarinic receptor, a segment of 112 amino acids (central portion of the i3 loop) can be deleted without loss of receptor function (Schöneberg et al. 1995). Similarly, systematic reduction of the length of the i3 loop in the tachykinin NK-1 receptor revealed that most of the loop sequence can be substituted or even deleted without affecting ligand affinity or signal transduction (Nielsen et al. 1998). Further support for the notion that most of the i3 loop sequences are dispensable for G-protein coupling comes from structural comparison of GPCR loop sequences showing that especially the i3 loop varies extremely in length and that there is no obvious sequence homology between GPCRs of similar coupling profiles. Studies with receptor peptides that are able to activate G proteins directly indicate that the cytoplasmic extensions of the TMDs probably provide the surface for G-protein interaction rather than the loops themselves (Abell and Segaloff 1997).

The ability of a GPCR to couple to more than one G-protein subfamily can be conceived as a loss of specificity due to the absence of inhibitory determinants or as a gain of specific contact sites within the receptor molecule. Two general mechanisms explaining multiple coupling events have been suggested – a 'parallel' and a 'sequential' G-protein activation model. In the 'parallel' model the receptor can adopt two or more active conformations (R*, R**) in an equilibrium. In the 'sequential' G-protein activation model one active conformation (R*) initiates the signal transduction cascade which modifies the receptor protein (e.g. phosphorylation). The modified receptor can now adopt the second active conformation (R**). Functional and mutational analyses of GPCRs interacting with more than one G-protein family provide evidence for both concepts. Lefkowitz and colleagues offered experimental evidence for a sequential G-protein activation mechanism (Daaka et al. 1997). Agonist-induced activation of the β_2 adrenergic receptor results in cAMP formation via the G_s/adenylyl cyclase pathway followed by cAMP-dependent protein kinase-mediated receptor phosphorylation. Receptor phosphorylation represents a crucial molecular switch mechanism to allow for G_i-mediated ERK activation. These finding are of interest since several primarily G_s-coupled receptors are also capable of activating G_i. Similar results were obtained with the prostacyclin receptor which is primarily coupled to G_s. Following cAMP-dependent protein kinase A activation and receptor phosphorylation at position Ser357 the prostacyclin receptor couples additionally to G_i and G_q (Lawler et al. 2001).

In support of a parallel model of G-protein activation it has been demonstrated that point mutations can selectively abolish receptor coupling to one G-protein subfamily (Surprenant et al. 1992, Gilchrist et al. 1996, Biebermann et al. 1998, Fuchs et al. 2001). On the other hand, the coupling profile of a GPCR can be extended by mutational changes. Concomitantly with G_s activation, the LHR mediates fairly modest agonist-induced phosphoinositide breakdown via G_i recruitment. It was observed that several LHR mutations at the very N-terminal end of TMD6 profoundly enhanced agonist-induced IP accumulation, most likely via G_{q/11} activation (Schulz et al. 1999). These findings are consistent with the concept that GPCRs can exist in at least two distinct active conformations, R* and R**, which differ in their G-protein coupling pattern. Based on this notion, it is also conceivable that different agonists can stabilize distinct ternary complexes. One may speculate that such pathway-selective agonists may represent the protagonists of a new class of therapeutic agents.

3.2

Receptor Domains Interacting with Additional Targets of GPCR Signalling

The four major classes of G-protein α subunits act on well known cellular targets mainly defining the cellular response like changes in the levels of cAMP, IPs, or cations. Upon receptor-mediated GDP release and GTP binding to the α subunit, the α subunit and $\beta\gamma$ subunits dissociate. In addition to the α subunit, free $\beta\gamma$ subunits are modulators of an increasing variety of cellular proteins such as phospholipases, adenylyl cyclases, channels, and kinases (Hamm 1998). More recently, co-precipitation studies, expression cloning strategies and yeast two-hybrid screening approaches have uncovered an ever growing number of targets and co-factors for GPCR signaling (Hall et al. 1999). Most contact sites for co-factor interaction are located in the receptor C termini. For example, the endocytotic sorting of the β_2 adrenergic receptor is regulated by postsynaptic density/disc-large/ZO1 (PDZ)- domain-mediated protein interaction. Phosphorylation of a serine by GPCR kinase-5 (GRK-5) within the receptor C terminus enables binding of the phosphoprotein EBP50, thus linking the receptor to the actin cytoskeleton (Cao et al. 1999). Several other PDZ-domain-containing proteins like the Na⁺/H⁺ exchanger regulatory factor (NHERF) (Hall et al. 1998), MUPP1 (Ullmer et al. 1998), a subunit of the eukaryotic initiation factor 2B (Klein et al. 1997), and cortactin-binding protein 1 (Zitzer et al. 1999) which interact with a PDZ (S/TXV) motif of GPCRs have been identified. A NHERF-binding site (DS/TxL) in the carboxy-terminal tail of β_2 adrenoceptor becomes available after ligand binding. The carboxy-terminal PDZ domain on NHERF directs its association with the receptor, thereby releasing NHE from the negative regulatory effect of NHERF. It was recently shown that the recruitment of nitric-oxide synthases following stimulation of the serotonin 5-HT_{2B} receptor is mediated via the PDZ motif at the receptor C terminus (Manivet et al. 2000). In contrast, the B_2 bradykinin receptor appears to inhibit the endothelial nitric-oxide synthase by direct interaction (Ju et al. 1998).

A mechanism whereby different cells and tissues can regulate cell membrane expression and functional characteristics of GPCRs has recently been disclosed by the discovery of receptor-activity-modifying proteins (RAMPs) (McLatchie et al. 1998). Calcitonin-gene-related peptide (CGRP) and adrenomedullin are related peptides which interact with the same GPCR, the calcitonin-receptor-like receptor (CRLR). Depending on which RAMP ise expressed in a given cell, the CRLR will generate the CGRP and adrenomedullin receptors when associated with RAMP1 and RAMP2, respectively (McLatchie et al. 1998). RAMPs also control glycosylation of the CRLR and transport of the receptor protein to the cell membrane. There are no further examples for an involvement of RAMPs in modifying the function of other GPCR.

A recently identified ER-membrane-associated protein, DRiP78, binds to a conserved motif (FxxxFxxxF) within the D₁ dopamine receptor C terminus which functions as an ER-export signal (Bermak et al. 2001). The metabotropic glutamate receptors mGluR_{1A} and mGluR₅ contain a Homer ligand binding sequence in their cytoplasmic C terminus which directs the association with the EVH-like domain of Homer proteins. Subsequently, selfmultimerization of Homer protein links the mGluRs to IP₃ receptors regulating the agonist-independent activity of mGluRs (Tu et al. 1998, Xiao et al. 1998, Ango et al. 2001). Association between the C-terminal portion of the D₅ dopamine receptor and the i2 loop of the GABA_A receptor γ_2 subunit is likely to be responsible for the functional interaction of these two functionally and structurally divergent receptors (Liu et al. 2000). Using a yeast two-hybrid approach, p38JAB1, a protein initially identified as cJun co-factor, binds to the C terminus of premature LHR and promotes its degradation (Li et al. 2000). A functional interaction with the human homolog of the Shk1 kinase-binding protein from yeast has been demonstrated for the somatostatin type 1 receptor (Schwarzler et al. 2000). Several catecholamine receptors contain Src homology (SH) 2 and 3 domain binding motifs within the i3 loop enabling the receptor to interact with a variety of SH3 domain-containing proteins (Oldenhof et al. 1998). For example, the SH3 domain of the SH3p4 protein associates with the polyproline motif in the B_1 adrenergic receptor (Tang et al. 1999). The physiological relevance of these many identified interactions remains to be determined.

4 General Aspects of GPCR Dysfunction

The direct and indirect control of an extraordinary variety of physiological functions by GPCRs increase the likelihood that GPCRs are also of pathophysiological relevance. In principle, three different scenarios are conceivable. First, the receptor is functionally altered by mutations of the receptor gene or genes necessary for secondary structural features, e.g. posttranslational modification or receptor folding. Mutationally induced GPCR dysfunction can cause gain or loss of physiological function. Generally, such disorders are subdivided into acquired and hereditary malfunctions. Gainof-function mutations are frequently found in adenomas, but germ-line transmission is rare because of the disease-limited life-time or reproductive ability. Currently, this situation is changing because of progress made in diagnosis and therapy, for example in congenital hyperthyroidism (Grüters et al. 1999). Loss-of-function mutations are associated almost exclusively with hereditary transmission. With a few exceptions which are discussed later, the pathological consequence of loss-of-function mutations become apparent only when both alleles are affected by homozygous or compound heterozygous alterations. Genomic analysis of mutant mice and genetargeting disruption techniques guided many studies to disease-causing GPCR mutations in man (Lin et al. 1993, Stein et al. 1994, Hosoda et al. 1994). Second, a given GPCR is required for the effect of a pathogenic agent (e.g. co-receptors for HIV entry). For example, certain chemokine receptors play a role in HIV pathogenesis, as demonstrated by the occurrence of a CCR5 deletion mutant, which is frequently found in the Caucasian population and confers a strong, although incomplete protection to homozygotes (Samson et al. 1996, Liu et al. 1996). In contrast, disease-modifying mutations were described for CX3CR₁, resulting in a more rapidly progressing

form of AIDS (Faure et al. 2000). Which of the 15 known HIV co-receptors are important *in vivo* is poorly defined. And *third*, the pathogenic agent induces the expression of an endogenous GPCR or carries a GPCR in its own genome to cause pathologic effects. The pathophysiologic role of a viral GPCR has been demonstrated for the herpes virus type 8 participating in Kaposi's sarcoma development. It should also be noted that ectopic GPCR expression and permanent receptor stimulation has been implicated in tumor induction and growth (Dhanasekaran et al. 1995, Ferris et al. 1997). In many endocrine tumors, an inappropriate receptor cell surface expression is the cause of significant hormone liberation causing secondary pathological effects (de Herder et al. 1994).

4.1 Diseases Caused by Mutations in GPCRs

Naturally occurring gain-of-function mutations are responsible for only a few human diseases (Table 1). Most mutations are described for the glycoprotein hormone receptors, LHR and TSHR. It is assumed that more than 80% of all toxic or autonomous adenomas of the thyroid are caused by activating mutations in the TSHR (Parma et al. 1997, Tonacchera et al. 1998). Constitutive activation of the G_s/adenylyl cyclase pathway is mainly responsible for the phenotypes found in Jansens's metaphyseal chondrodysplasia, familiar and acquired hyperthyroidism, male-limited precocious puberty, and hypoparathyroidism.

Permanent activation of pathways involving phospholipase C has the potential to promote carcinogenesis as shown for chronic agonist stimulation of G_q -coupling receptors (Allen et al. 1991, Gutkind et al. 1991). Distinct mutations in the TSHR and the LHR can constitutively activate phospholipase C, in addition to the G_s /adenylyl cyclase system, and promote the development of thyroid carcinoma and Leydig-cell tumors, respectively (Russo et al. 1995, Liu et al. 1999). Pathogenicity of viral GPCRs is also associated with constitutive receptor activity. The KSHV-GPCR, closely related to chemokine and interleukin receptors, was found to agonist-independently activate the $G_{q/11}$ /PLC signal transduction pathway (Arvanitakis et al. 1997). The KSHV-GPCR contains a VRY sequence instead of the highly conserved DRY motif in the i2 loop (see 2.3). The chemokine receptor CXCR₂ is closely related to KSHV-GPCR. The mutant D138V in which the Asp of the DRY motif was replaced by Val exhibited transforming potential similar to the KSHV-GPCR (Burger et al. 1999). Smoothened, a GPCR of the frizzled fam-

| GPCR | Gain-of-function disease | Reference |
|--|--|--|
| PTH/PTH-related peptide receptor TSHR | Jansens's metaphyseal chondrodysplasia Hyperthyroidism, thyroid carcinoma | Schipani et al. 1995 Parma et al. 1993, Russo et al. 1995 |
| LHR | male-limited precocious puberty, seminoma, Leydig-cell tumor | Shenker et al. 1993, Martin et al. 1998, Liu et al. 1999 |
| Ca ²⁺ -sensing receptor | dominant and sporadic hypoparathyroidism | Baron et al. 1996 |
| rhodopsin | night blindness, retinitis pigmentosa | Rao et al. 1994, Robinson et al. 1992 |
| smoothened K SHV-GPCR | sporadic basal-cell carcinoma Kaposi's sarcoma | Xie et al. 1998 Arvanitakis et al. 1997 |
| GPCR | Loss-of-function disease | Reference |
| endothelin B receptor | Hirschsprung's disease | Puffenberger et al. 1994 |
| melanocortin type 1 receptor | UV-induced skin damage | Valverde et al. 1995 |
| melanocortin type 2 receptor | ACTH resistance syndrome | Clark et al. 1993 |
| melanocortin type 4 receptor | dominant and recessive obesity | Yeo et al. 1998, Vaisse et al. 1998, |
| | | Farooqi et al. 2000 |
| FSHR | ovarian dysplasia, amenorrhea, secondary amenorrhea | Aittomäki et al. 1995, Beau et al. 1998 |
| GnRH receptor | hypogonadotropic hypogonadism | de Roux et al. 1997, Layman et al. 1998 |
| Ca ²⁴ -sensing receptor | hyperparathyroidism | Pollak et al. 1993 |
| PTH/PTH-related peptide receptor | Blomstrand chondrodysplasia | Zhang et al. 1998, Jobert et al. 1998 |
| LHR | pseudohermaphrodidism, hypospadias | Kremer et al. 1995, Misrahi et al. 1997 |
| TSHR | hypothyroidsm, thyroid hypoplasia | Biebermann et al. 1997 |
| thromboxane A2 receptor | bleeding disorder | Hirata et al. 1994 |
| P2Y ₁₂ receptor | bleeding disorder | Hollopeter et al. 2001 |
| hypocretin (orexin) receptor type 2 | narcolepsy | Lin et al. 1999 |
| AVPR2 | nephrogenic diabetes insipidus (NDI), partial NDI | Rosenthal et al. 1992, |
| | | Sadeghi et al. 1997a |
| rhodopsin | retinitis pigmentosa | Dryja et al. 1990 |
| opsin | color blindness | Weitz et al. 1992 |
| retinal GPCR (RGR) | retinitis pigmentosa | Morimura et al. 1999 |
| glucagon receptor | non-insulin-dependent diabetes mellitus | Hager et al. 1995 |
| TRH receptor | isolated central hypothyroidism | Collu et al. 1997 |
| GHRH recentor | Durarfiere | 11 |

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ily, utilizes hedgehog and probably also G-protein-dependent signaling pathways (DeCamp et al. 2000, Liu et al. 2001), and activating mutations in this receptor can lead to basal-cell carcinoma (Xie et al. 1998).

The chance of mutational inactivation of receptor proteins is naturally higher than the mutational generation of a constitutively active GPCR. A large number of structural alterations has been described including amino acid substitutions, truncations by nonsense or frameshift mutations, insertions, rearrangement as well as small and large deletions. This diversity of structural modifications, all leading to the same result characterized by impairment or total loss of receptor function, is reflected by more than twenty human diseases known to be caused by inactivating mutations (Table 1). Most diseases display a recessive inheritance, but in some cases, such as dominant obesity (Yeo et al. 1998), the phenotype becomes apparent if only one allele is altered. Besides complete phenotypes, partial loss-of-function or heterozygosity can cause variations in the phenotypical appearance as found for secondary amenorrhea (Beau et al. 1998), hypospadias (Misrahi et al. 1997), partial NDI (Sadeghi et al. 1997), fertile eunuch variant of idiopathic hypogonadotropic hypogonadism (Pitteloud et al. 2001), and hyperthyrotropinemia (Sunthornthepvarakui et al. 1995).

To date, a large number of variants (polymorphisms) in GPCR genes has been identified (for review see Rana et al. 2001). At a polymorphic locus the rarer allele must occur with a frequency greater than 1% in the population. The availability of a reference sequence of the human genome provides the basis for studying the nature of sequence variation, particularly single nucleotide polymorphisms (SNPs), in human populations. SNPs occur at a frequency of approximately 0.5–1 SNP/kb throughout the genome when the sequence of individuals is compared (Mullikin et al. 2000, The genome international sequencing consortium 2001, Venter et al. 2001). SNP typing is a powerful tool for genetic analysis because sequence variants are responsible for the genetic component of individuality, disease susceptibility, and drug response. The latter point will have an important impact on drug design, therapeutic regimes and side effects.

Some SNPs in GPCRs were associated with distinct phenotypes or diseases and functionally characterized *in vitro* (Table 2). Most interesting, a common variant of the β_1 adrenergic receptor (G389R) displays increased constitutive activity, however, no prominent phenotype was observed (Mason et al. 1999). No clearly related phenotype was found for the naturally occurring D₄ dopamine receptor deficiency (Nothen et al. 1994). This is in agreement with D₄ dopamine receptor-lacking mice displaying locomotor supersensitivity to ethanol, cocaine, and methamphetamine but no obvious phenotype under normal conditions (Rubinstein et al. 1997).

| Table 2. Selected mutations/ | 'polymorphisms found in GP | Table 2. Selected mutations/polymorphisms found in GPCRs that were associated with/without distinct human phenotypes | Sec |
|-------------------------------------|----------------------------|--|-------------------------|
| GPCR | Mutation/Polymorphism | Functional consequence / association with | Reference |
| glucagon receptor | G40S | n.d. / essential hypertension | Brand et al. 1999 |
| calcitonin receptor | silent mutation | n.d. / reduced fracture risk in post-menopausal woman | Taboulet et al. 1998 |
| α _{1A} adrenergic receptor | R492C | no major functional consequences / no obvious phenotype | Shibata et al. 1996 |
| α _{2A} adrenergic receptor | N251K | gain of agonist function <i>in vitro</i> / no phenotype | Small et al. 2000 |
| α _{2B} adrenergic receptor | in-frame deletion | decreased receptor desensitization / reduced metabolic rate | Heinonen et al. 1999 |
| α_{2C} adrenergic receptor | in-frame deletion | n.d. / no obvious phenotype | Feng et al. 2001 |
| ß1 adrenergic receptor | G389R | constitutive activity / no obvious phenotype | Mason et al. 1999 |
| ß2 adrenergic receptor | R16G | enhanced agonist-induced down-regulation / nocturnal asthma | Turki et al. 1995 |
| • | Q27E | decreased agonist-induced down-regulation / no obvious phenotype | Green et al. 1994 |
| | T164I | decreased agonist-induced efficacy / no obvious phenotype | Brodde et al. 2001 |
| ß3 adrenergic receptor | W64R | n.d. / glucose intolerance, fatty liver, obesity | Shima et al. 1998 |
| 5-HT _{1A} receptor | G22S | attenuated agonist-induced down-regulation / no obvious phenotype | Rotondo et al. 1997 |
| 5-HT _{1B} receptor | F124C | increased drug potency / no obvious phenotype | Kiel et al. 2000 |
| 5-HT _{2A} receptor | H452Y | no major functional consequences / no obvious phenotype | Arranz et al. 1998 |
| | silent mutation | n.d. / schizophrenia | Williams et al. 1996 |
| 5-HT _{2C} receptor | C23S | decreased agonist affinity / no obvious phenotype | Lappalainen et al. 1995 |
| 5-HT _{sA} receptor | PI5S | n.d. / schizophrenia | Iwata et al. 2001 |
| AT _{1A} receptor | silent mutation | n.d. / hypertension | Van Geel et al. 2000 |
| D2 dopamine receptor | V I 54I (heterozygous) | n.d. / myoclonus dystonia | Klein et al. 1999 |
| | P310S, S311C | decreased Gi-coupling efficacy / no obvious phenotype | Cravchik et al. 1996 |
| D4 dopamine receptor | V194G | decreased agonist affinity / low weight, no axilly or pubic hair | Liu et al. 1996 |
| I | deletion (homozygous) | n.d. / acousticus neurinoma, obesity, autonomic nervous system | Nothen et al. 1994 |
| | | disturbances | |
| D5 dopamine receptor | C335X (heterozygous) | n.d. / no obvious phenotype | Sobell et al. 1995 |
| melatonin 1b receptor | G24E, R54W, L66F, | n.d. / no obvious phenotype | Ebisawa et al. 1999 |
| | A157V (heterozygous) | n.d. / no obvious phenotype | Ebisawa et al. 2000 |
| CCR2 | V64I | no major functional consequences / delay in the progression to AIDS | Smith et al. 1997 |
| CX3CR | V 2491, T280M | n.d. / progressed to AIDS more rapidly | Faure et al. 2000 |
| CCK _B receptor | E288K | increased drug efficacy / no obvious phenotype | Kopin et al. 1997 |
| μ-opioid receptor | N40D | increased agonist affinity / no obvious phenotype | Bond et al. 1998 |
| P2Y2 | R334C | no major functional consequences / no obvious phenotype | Janssens et al. 1999 |
| melanocortin type 2 receptor | K6T, V811 | n.d. / no obvious phenotype | Hani et al. 2001 |
| melanocortin type 5 receptor | F209L | no major functional consequences / no obvious phenotype | Hatta et al. 2001 |
| n.d. not determined | | | |

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Fig. 4. Molecular mechanisms influencing proper GPCR function. Mutations within GPCR genes can affect receptor function at different levels. At the genomic level, partial or complete gene deletion can interfere with gene transcription. Small genomic alterations can lead to nonsense-mediated mRNA decay, splicing errors and changes in RNA editing (mRNA level). Mutation-induced structural changes in the receptor protein can interfere with proper receptor folding and trafficking (posttranslational level), thus promoting protein degradation in endosomes. Finally, mutations can also abolish receptor signal-ing by disturbance of the ligand binding domain or G-protein interaction sites (functional level) Normally, most of the functionally relevant GPCR mutations which do not cause pathologic changes in man are apparently compensated by other mechanisms. However, GPCR mutations can become clinically relevant when challenged (diseases, intoxication). It was shown for a naturally occurring human CCK_B receptor variant (E288K) that the maximal level of receptor-mediated second messenger signaling achieved by synthetic compounds (drug efficacy) is markedly increased compared with values obtained with the wild-type receptor (Kopin et al. 1997). It is likely that completion of the human genome project will lead to a rapid progress in the detection of polymorphisms within distinct GPCR genes.

4.2

Mechanisms of GPCR Alteration

Improper receptor function due to structural alterations can manifest itself at different stages of the GPCR 'life cycle' (Fig. 4). The following section will focus on the molecular mechanisms affecting proper receptor function. Since naturally occurring mutations in the rhodopsin, AVPR2 and the glycoprotein hormone receptors have been studied in great detail, these receptors will serve as model systems to delineate more general principles.

4.2.1 Genomic Level

Like in other hereditary disorders, most diseases caused by GPCR dysfunction are based on genomic alterations with functional effects at different supragenomic levels. Distinct types of genomic alterations can be differentiated - missense mutations, nonsense mutations, small deletions or insertions (in-frame, frameshift) and large or complex deletions. However, the presence of an apparent phenotype depends on the structural impact of the mutation on receptor function. In X-linked myotubular myopathy (Laporte et al. 2000) and retinoblastoma (Lohmann 1999), most point mutations lead to truncations of the myotubularin and RB1 gene product, respectively. In contrast, over 850 different mutations were identified in the cystic fibrosis transmembrane conductance regulator (CFTR) gene coding for a chloride conductance protein, but 70% of all autosomal recessive cystic fibrosis cases are caused by a single triplet deletion (Δ F508) (Zielenski 2000). To date, more than 170 different mutations have been identified within the AVPR2 gene responsible for NDI (Table 3). Out of all clinically relevant mutations detected in GPCRs about 75% are missense mutations. In about 25% of all

| Except for the AVPR2 and the endothelin B receptor mutation count include inactivating and activating mutations. The following Except for the AVPR2 and the endothelin B receptor mutation count include inactivating and activating mutations. The following sources were used: The Human Gene Mutation Database (http://archive.uwcm.ac.uk/uwcm/mg/hgmd/), CASRdb database (http://data.mch.mcgill.ca/casrdb/), TSH-receptor database (http://www.uni-leipzig.de/-innere/TSH/), Diabetes insipidus database (http://www.nedcon.mcgill.ca/nephros/) and the available literature (http://www.ncbi.nlm.nih.gov/entrez/) | nations round ind the endo he Human a/casrdb/), ' gill.ca/nephr | the in second of of the in B receptor Gene Mutation (SH-receptor data os() and the availation | mutation count inc Database (http://www.u ble literature (http:// | lude inactivating and urchive uwcm.ac.uk/uv uni-leipzig.de/~innere /www.ncbi.nlm.nih.go | activating mut vcm/mg/hgmd/) /TSH/), Diabete v/entrez/) | ations. The following , CASRdb database s insipidus database |
|---|---|---|---|--|---|--|
| Mutation | AVPR2 | Ca ²⁺ -sensing receptor | endothelin B receptor | MC-4 receptor rhodopsin | rhodopsin | TSH receptor |
| Total mutations | 172 % of total | 59 % of total | 18 % of total | 23 % of total | 106 % of total | 49 % of total |
| Missense Nonsense Small insertion (ins.) Small deletion (del.) Small del./ins. Large/complex ins./del. Splice site | 51.2 (88) 10.5 (18) 7.6 (13) 23.2 (40) - 5.8 (10) 1.7 (3) | 86.4 (51) 3.4 (2) 5.1 (3) - 1.7 (1) 1.7 (1) 1.7 (1) | 66.7 (12) 11.1 (2) 5.6 (1) 5.6 (1) - 5.6 (1) 5.6 (1) | 78.3 (18) 4.3 (1) 13.0 (3) 4.3 (1) - | 82.1 (87) 4.7 (5) 0.9 (1) 7.5 (8) - 0.9 (1) 3.8 (4) | 85.7 (42) 4.1 (2) 6.1 (3) 2.0 (1) 2.0 (1) |

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cases, the mutation resulted in a complete loss or a truncation of the receptor protein due to nonsense mutation, small deletions or insertions and large deletions. Figure 5 depicts all AVPR2 missense mutations and the genomic localization of two large AVPR2 gene deletions. As a consequence of loss-of-function mutations in the AVPR2, the renal response to arginine vasopressin (AVP) is impaired resulting in clinical characteristics of NDI which include hypernatremic dehydration, polyuria, polydipsia, fever, and constipation.

Inactivating mutations in the TSHR have been shown to cause congenital hypothyroidism with variable degree of severity. Besides euthyroid TSH resistance (Sunthornthepvarakui et al. 1995), moderate and severe congenital hypothyroidism caused by compound heterozygosity for inactivating mutations were described in patients with thyroid hypoplasia (Clifton-Bligh et al. 1997, Biebermann et al. 1997).

This large variety of mutations in a member of the GPCR family described above is restricted only to a loss-of-function phenotype. In contrast, gain-of-receptor function is only induced when residues important for receptor quiescence are substituted by distinct amino acids. Therefore, the frequency of activating mutations is lower when compared with inactivating mutations. However, the pathologic consequences caused by constitutive receptor activity are often clinically more apparent, and the underlying genetic defects can usually be identified more easily due to dominant heredity. Additionally, the ability to compensate for somatic mutations leading to constitutive receptor activity appears to be limited.

In the TSHR, both inactivating and activating mutations have been identified (Grüters et al. 1999). Somatic gain-of-function mutations of the TSHR were found in autonomous thyroid adenomas (Parma et al. 1993) and more recently in thyroid insular carcinoma (Russo et al. 1996). Several studies estimated the number of thyroid adenomas caused by activating mutations in the TSHR up to 80% (Parma et al. 1997). However, congenital hyperthyroidism is a rare disease which is mostly caused by transplacental passage of maternal TSHR-stimulating autoantibodies in Graves' disease. Sporadic cases of congenital non-autoimmune hyperthyroidism (Kopp et al. 1995, De Roux et al. 1996) and a few familiar cases of non-autoimmune hyperthyroidism with childhood or later onset (Duprez et al. 1994, Tonacchera et al. 1996, Grüters et al. 1998) were found to be caused by TSHR mutations leading to constitutive activation of the receptor. Activating mutations are mostly located in the TMDs, preferentially in TMD6 and the juxtamembrane portion of the i3 loop and TMD6. Only one amino acid position located within the large extracellular domain (S281) was identified in the TSHR vulnerable for


- o conserved residue within mammalian vasopressin/oxytocin receptors
- missense mutation and conserved residue within mammalian
 - vasopressin/oxytocin receptors
- missense mutation



activating mutations (Grüters et al. 1998). Most mutations found resulted in amino acid substitutions, but in two cases in-frame deletions were identified as a cause for hyperthyroidism (Parma et al. 1997, Wonerow et al. 1998).

Such site-specific preferences for gain-of-function mutations are determined functionally. This holds partially true also for inactivating mutations (no inactivating substitution mutations have been reported in the very C terminus of any GPCR), but mutation hotspots are probably based on the presence of vulnerable elements (e.g. CpG sites) within GPCR genes. The mutational mechanisms are multiform. Methylation of DNA is an epigenetic modification that can play an important role in the control of gene expression in mammalian cells. The enzyme involved in this process is DNA methyltransferase, which catalyzes the transfer of a methyl group from Sadenosyl-methionine to cytosine residues to form 5-methylcytosine (5MeC), a modified base that is found mostly at CpG sites in the genome. Many types of DNA damage (oxidative lesions, alkylation of bases, abasic sites, photodimers, etc.) interfere with the ability of mammalian cell DNA to be methylated at CpG dinucleotides by DNA-methyltransferases (DNA-MTases). This can result in altered distribution patterns of 5-methylcytosine (5MeC) residues at CpG sites. CpG sites in DNA represent mutational hotspots, with both the presence of 5MeC in DNA and the catalytic activity of DNA-MTases being intrinsically mutagenic. Many recurrent mutations within the AVPR2

Fig. 5A-E. Model of the AVPR2 and location of missense mutations and large deletions found in patients with X-linked nephrogenic diabetes insipidus. About 22% of all amino acid residues are fully conserved among mammalian vasopressin/oxytocin receptors (green and blue; upper panel). Over 170 different mutations have been identified in the AVPR2 gene of NDI patients. About 50% out of all missense were found at positions which are conserved (blue). Other positions of missense found in NDI patients are shown in red. PCR screening of the Xq28 region of two NDI patients revealed submicroscopic deletions (detailed Xq28 map: lower panels A-C). In one case, the breakpoints were located within the first intron of the AVPR2 gene and the 3'-breakpoint in the last intron (intron 21) of the C1 gene (D). In a second NDI patient (E), the 5'-breakpoint was located within the 5'-untranslated region of the AVPR2 gene and the 3'-breakpoint within the first intron sequence of the C1 gene (panels C, E). To identify the exact positions of the deletion breakpoints, suitable primers pairs were used to amplify interstitial genomic sequence (Schöneberg et al. 1999, Schulz and Schöneberg 2000c). The bars in panel C, D, and E mark the exons of the AVPR2 gene (blue) and the C1 gene (red). Locus abbreviations: L1CAM, neuronal cell adhesion molecule 1, AVPR2, arginine-vasopressin V2 receptor, C1, rhoGAP C1, TE, N-acetyl transferase related protein, RbP, renin-binding protein, HCF1, host cell factor 1, IRAK, interleukin-1 receptor-associated kinase. The nucleotide positions refer to the numbering of the original sequence submission of the Xq28-L1CAM locus (GenBank accession number: U52112)

gene such as D85N, V88M, R106C, R113W, R137H, R181C, R202C, and R337X are probably caused by the hypermutability at such CpG dinucleotides.

Large deletions or rearrangements of chromosomes usually results in fetal abortion and complex syndromes (Tharapel et al. 1993, Ferrero et al. 1997). Submicroscopic alterations have been made responsible for more distinct phenotypes such as mental retardation (Fries et al. 1993), Emery-Dreifuss muscular dystrophy (Small et al. 1997), monoamine oxidase deficiency (Sims et al. 1989), developmental disorders (Gedeon et al. 1995) and myotubular myopathy (Hu et al. 1996). There are only a few reports in which genes encoding for GPCRs are included in microdeletions (Restagno et al. 1993, Laue et al. 1996, Gromoll et al. 2000). To date, only eight submicroscopic deletions or rearrangements have been found in patients with NDI (Bichet et al. 1994, van Lieburget et al. 1995, Jinnouchi et al. 1996, Schöneberg et al. 1999, Arthus et al. 2000, Schulz and Schöneberg 2000c). However, an exact identification of the breakpoints is lacking in most studies but is of considerable interest since the microdeletion can include other functionally important genes. Analysis of the AVPR2 gene of a boy with classical symptoms of NDI revealed a 21.5-kb deletion within Xq28 (Schöneberg et al. 1999). The upstream breakpoint was found within the 5'-untranslated region of the AVPR2 gene and the 3'-breakpoint was localized within the first intron sequence of the C1 gene (Fig. 5). Based on amino acid sequence similarity and functional data, the C1 gene encodes a protein (ARHGAP4) which is thought to function as a Rho GTPase-activating protein (rhoGAP) (Nagase et al. 1995, Tribioli et al. 1996). In a second NDI patient, the 5'-breakpoint is located within the first intron of the AVPR2 gene, and the 3'-breakpoint includes almost half of intron 21, the coding sequence of the C-terminal 77 amino acid residues and the complete 3'-untranslated region (3'-UTR) of the C1 gene (see Fig. 5). Repetitive genomic sequences are often found in close proximity to deletion breakpoints, and identification can help to clarify the mechanism by which the deletion was produced. Since repetitive DNA is abundant in the human genome, it is commonly suggested that microdeletions arise through mispairing of large duplicated sequences (Chen et al. 1997). For example, Alu repeats were found to be involved in homologous and non-homologous recombination events in α° -thalassaemia (Harteveld et al. 1997). Analyses of the breakpoint regions for homologous sequences in both NDI patients (see above) revealed a lack of sequence similarities suggesting a non-homologous recombination event or chromosomal breaks and re-junction as cause for these interstitial deletions. In the absence of any information about the physiological relevance and specific functions of this specific rhoGAP, a thorough clinical and laboratory investigation was initiated. However, both patients did not reveal any major abnormalities besides clearly defined NDI symptoms caused by deletion of the AVPR2 gene.

Phenotype diversity as found in diseases caused by activating and inactivating mutations in GPCRs mainly depends on the location of the alteration and the structural changes made by the mutation. However, other mechanisms such as mosaicism, skewed X-chromosome inactivation and genomic imprinting have to be considered when phenotype diversity is caused by the same mutation. Very early mutation in the patient's genome can result a mosaicism. Only a few cases of mutational mosaicisms have been reported in GPCR-related diseases (Pasel at al. 2000, Biebermann et al. 2001). The occurrence of an inactivating mutation on one allele is usually compensated by the non-mutated second allele (recessive heredity). X-chromosomally located single-copy genes often do not follow this paradigm. In some cases heterozygous occurrence of inactivating mutations in an X-chromosomally located single-copy gene can cause the same disorder as found in hemizygous males (Moses et al. 1995, Nomura et al. 1997). In female embryogenesis, X-chromosome inactivation occurs early at about the 32 to 64 cell stage, and the number of progenitor cells for individual tissues is presumed to be small (Heard et al. 1997). Once an X chromosome has been selected for inactivation, it is irreversible, and the same X chromosome is inactivated in all descendants of that cell. The random process of X-chromosome inactivation results in a normal distribution of skewing among females. The incidence of extreme skewing (90:10) in peripheral blood of 162 normal neonates was 2% (Busque et al. 1996). Skewed X-chromosome inactivation with a partial phenotype of NDI has been observed in female carries of inactivating AVPR2 mutations (Nomura et al. 1997, Arthus et al. 2000, Schulz und Schöneberg 2000c).

An epigenetic imprinting mechanism that is based on a gamete-specific methylation imprint restricts expression of a subset of mammalian genes to one parental chromosome. The most impressive example of genomic imprinting in GPCR signal transduction was described for the $G_s \alpha$ -subunit (Weinstein and Yu 1999). Albright hereditary osteodystrophy is caused by heterozygous inactivating mutations of the gene encoding the $G_s \alpha$ -subunit. When the mutation is inherited from the mother, the offspring will develop pseudohypoparathyroidism type Ia including both hormone resistance and somatic abnormalities. When the mutation is derived from the father, children will have normal parathyroid hormone responses while exhibiting the somatic features of so-called pseudopseudohypoparathyroidism. The mas protooncogene encodes a mitogenic GPCR and provides another example for an imprinting phenomenon. It was demonstrated in mice that the maternally inherited allele is transcriptionally repressed in a developmental and tissue-specific manner (Villar and Pedersen 1994).

Heterozygote mutations in the melanocortin-4 receptor gene (MC4-R) were detected which were assumed to lead to the dominant phenotype of extreme obesity. It has been hypothesized that the mutation found in these subjects resulted in a loss of gene function which causes obesity due to haploinsufficiency of the MC4-R gene. However, in contrast to the initial observations (Vaisse et al. 1998, Yeo et al. 1998), moderate obesity mainly applied to males can also be associated with these mutations (Sina et al. 1999). These examples demonstrate that skewed X-chromosome inactivation and genomic imprinting phenomena should be considered if a distinct phenotype caused by inactivating mutations in GPCRs occurs in heterozygote individuals.

4.2.2

Transcriptional Level

Regulation of GPCR transcription and post-transcriptional processes such as splicing and mRNA degradation involves complex cellular mechanisms all fine tuning the receptor resonsiveness (for review see Danner and Lohse 1999). Thus, numerous polymorphisms have been identified within the putative promoter regions, 5' and 3' untranslated (UTR) regions, and introns of GPCR genes (for review see Rana et al. 2001). Many of these polymorphisms in the non-coding regions were associated with human diseases and altered drug responses. However, most studies lack clear experimental evidence for the suggested mechanisms by which the mutation should affect receptor function.

There are only a few reports describing functionally relevant mutations in the donor or acceptor splice sites of GPCRs. In the AVPR2 gene, three NDI-causing mutations in the splice sites of the second intron were identified (Wildin et al. 1994, Wildin et al. 1998, Arthus et al. 2000). Mutations in endothelin B receptor (ET_BR) gene are responsible for congenital aganglionosis (Hirschsprung's disease). In one patient a heterozygous point mutation at the splice donor site of intron 3 was identified leading to premature termination of translation of ET_BR mRNA (Inoue et al. 1998). Besides lossof-function mutations within the exons of the TSHR, rhodopsin, and the retinal G-protein-coupled receptor (RGR), disease-causing mutations were also found in the intron/exon boundaries of these genes (Macke et al. 1993, Reig et al. 1996, Gagne et al. 1998, Morimura et al. 1999). The impact of mutations affecting receptor mRNA maturation at the posttranscriptional stage is probably underestimated. For example, even 'silent' exon or intron mutations may influence proper mRNA splicing by introducing a new consensus acceptor/donor splice site which, if used, would encode a nonsense or truncated protein. Additionally, it should be taken in consideration (at least theoretically) that functional alteration of the endogenous splicing machinery can indirectly influence normal GPCR function.

All eukaryotes possess the ability to detect and degrade mRNA harboring premature signals for the termination of translation. This ensures that truncated proteins are seldom made, reducing the accumulation of rogue proteins that might be deleterious. Despite the ubiquitous nature of nonsensemediated mRNA decay and its demonstrated role in the modulation of phenotypes resulting from selected nonsense alleles, very little is known regarding its basic mechanism or the selective pressure for complete evolutionary conservation of this function (Culbertson 1999). For example, 89% of mutations in the ATM gene that cause ataxia-telangiectasia (Gilad et al. 1996) lead to premature chain termination, and many of these mutations can trigger nonsense-mediated mRNA decay. As estimated for the AVPR2, about 40% of all mutations will result in a premature stop of receptor protein translation (see 4.2.1). The impact of nonsense-mediated mRNA decay in the pathomechanism of GPCR dysfunction has not been studied yet. Chain-terminating mutations that decrease mRNA abundance by reducing the half-life of mRNA typically behave like loss-of-function alleles. However, nonsensemediated mRNA decay appears to be not always complete, and some chaintermination mutations confer a dominant phenotype when the RNAsurveillance system is bypassed. Escape from nonsense-mediated mRNA decay can occur by exon skipping due to a nonsense mutation located at a position that affects splice-site selection through changes in RNA structure or a long open reading frame resulting from a mutationally induced frame shift.

The expression of truncated GPCRs has been demonstrated by immunologic and functional methods *in vivo* and *in vitro* (Ridge et al. 1995, Schöneberg et al. 1995, Schöneberg et al. 1996, Heymann and Subramaniam 1997, Grosse et al. 1997, Schöneberg et al. 1998). As demonstrated in stably transfected CHO cells expressing low amounts of truncated AVPR2, the existence of such truncated receptor proteins was not due to saturation of the machinery degrading mutant mRNA (Schöneberg et al. 1997). *In vivo* studies showed that a truncated D₃ dopamine receptor variant (D_{3nf}) is endogenously expressed in monkey and rat cortical neurons (Nimchinsky et al. 1997). Screening of cDNA libraries, expressed sequence tag (EST) databases and genomic analyses revealed that some GPCR genes encode truncated receptors (pseudogenes) as found for a human neuropeptide Y receptor (Rose et al. 1997), a human 5-HT₄-like receptor (Liu et al. 1998), psiGPR32, and psiGPR33 (Marchese et al. 1998).

Dominant-negative effects of truncated GPCRs on wild-type receptor function have been demonstrated for the CCR₅ (Benkirane et al. 1997), the AVPR2 (Zhu and Wess 1998), and the GnRH receptor (Grosse et al. 1997). Therefore, it is reasonable to assume that dominant effects caused by prematurely terminated receptor proteins which escaped nonsense-mediated mRNA decay may contribute to the pathomechanism of loss-of-function mutations (see 4.2.3).

4.2.3

Translational and Posttranslational Level

Once a GPCR has been synthesized, the receptor polypeptide adopts a structure which enables the receptor to pass through the ER quality control machinery. Inherited mutations leading to incompletely folded proteins that are retained intracellularly by the ER quality control system are a recurring observation (Cheng et al. 1990, Singh et al. 1997). The basic mechanisms in the process of GPCR folding and trafficking are poorly understood. Despite the lack of detailed information, the folding and trafficking process is recognized as an important part in realizing proper GPCR function. To clearly differentiate between trafficking defects and abolished agonist binding and/or functional coupling, immunologic methods should be applied, in addition to second messenger and radioligand binding assays (Schöneberg et al. 1998).

Numerous investigations have focused on the identification of structural elements within GPCRs necessary to maintain proper receptor folding. The receptor C terminus appears to contain structural information relevant for GPCR folding. Systematic studies with C-terminally truncated or mutated AVPR2s underscored the importance of the C-terminal tail for receptor trafficking (Wenkert et al. 1996, Sadeghi et al. 1997a, Schülein et al. 1998). However, naturally occurring and artificial truncations after TMD7 do virtually not affect the function of other GPCRs, e.g. the gonadotropin-releasing hormone receptor, neurokinin-2 receptor (Alblas et al. 1995), glucagon receptor (Unson et al. 1995), follitropin receptor (Hipkin et al. 1995), LHR (Zhu et al. 1993, Wang et al. 1996), and parathyroid hormone (PTH)/PTHrelated peptide receptor (Iida-Klein et al. 1995).

In some cases, it was found that the retention of the mutant protein, but not alteration of its functional properties, is responsible for the disease. For example, it was shown that a mutant CFTR (Δ F508) can form functional cAMP-activated chloride channels when it can escape the ER and be expressed at the cell surface (Zeitlin 2000). Because temperature is known to affect protein folding, Jaquette and Segaloff (1997) examined the effects of reduced temperature on cell surface expression of intracellularly retained mutant LHRs. It was demonstrated that preincubation of the cells for 48 h at 26 °C markedly increased both hCG binding ability and cAMP production, suggesting that decreased temperatures can allow partially misfolded LHRs to fold properly and to be transported to the cell surface.

Impaired insertion of the wild-type receptor into the plasma membrane is a common mechanism underlying the dominant negative effects of coexpressed mutant or truncated receptors. For example, some functionally inactive mutants (N285I, K298X) of the PAF receptor display dominant negative effects on the wild-type receptor due to intracellular retention (Le Gouill et al. 1999). Interestingly, a dominant positive effect, as reflected by constitutive receptor activation, was observed after co-expression of the wild-type and a mutant (D63N) PAF receptor (Le Gouill et al. 1999). It should be noted that dominant negative effects of mutant GPCRs on wildtype receptor function can also be caused by other mechanisms such as titrating G proteins away from the wild-type receptor (Leavitt et al. 1999). Thus, expression of truncated or modified receptor proteins may highlight a novel principle of specific modulation of GPCR function with physiological and pathophysiological relevance. It was demonstrated that a naturally occurring allele coding for a truncated CCR₅ chemokine receptor which functions as a co-receptor for infection by primary M-tropic HIV-1 strains exerts a dominant negative effect on the viral env protein-mediated cell fusion (Samson et al. 1996). It was later shown that the truncated receptor complexes with the wild-type CCR5 and that this interaction retains CCR5 in the ER resulting in reduced cell surface expression (Benkirane et al. 1997). In addition, defective intracellular transport due to the formation of misfolded complexes between wild-type and mutant rhodopsin in the ER is held responsible for the dominant effect of one mutant allele in case of retinal degeneration in Drosophila (Colley et al. 1995). To understand the pathophysiology of retinitis pigmentosa caused by mutations in the human rhodopsin gene leading to truncated receptor proteins, heterozygote individuals carrying nonsense mutations (Q64X, Q344X) or an intron 4 splice site mutation were studied. Although the three mutations interfered with normal rod cell function, there was allele specificity for the pattern of retinal dysfunction (Jacobson et al. 1994). One may speculate that the observed differences in the phenotype are due to variations in nonsense-mediated mRNA decay. Interestingly, there is one reported case of autosomal dominant retinitis pigmentosa in which the normal termination codon is replaced by a Glu codon. Examination of the genomic sequence revealed that the next termination codon lies 153 bp downstream of the natural stop codon. Termination of translation at this point would add additional 51 amino acid residues to the C terminus of rhodopsin (Bessant et al. 1999).

An other example comes from mutant MC4 receptors that has been found in patients with familiar obesity (see Table 1). The heterozygous occurrence of missense mutations as well as truncating mutations in the MC4 receptor are the cause of the clinical phenotype (Vaisse et al. 1998, Yeo et al. 1998). One may speculate that dominant negative effects of the wild type receptor function contributes to the molecular pathomechanism.

Posttranslational formation of one or more extracellular disulfide bonds is essential for receptor trafficking and high affinity ligand binding (see 1.2.1). Disease-causing mutations of the highly conserved disulfide bond connecting the e1 and the e2 loops have been identified in the AVPR2 (Bichet et al. 1994), rhodopsin (al-Maghtheh et al. 1993, Fuchs et al. 1994) and the ACTH receptor (Naville et al. 1996).

Many of the mutations in the e1 and e2 loops found in patients with NDI and retinitis pigmentosa are characterized by substitutions of various amino acid residues to Cys residues (Sung et al. 1991, Fujiwara et al. 1995, Schöneberg et al. 1998). For example, five such missense mutations, R106C, R181C, G185C, R202C, and Y205C, were identified in the AVPR2 gene (Bichet 1998). These findings together with a phylogenetic sequence comparison (see Fig. 5) suggest that the mutational introduction of only one new Cys residue in the extracellular loops causes altered receptor function. One Cys residue in the e1 loop (Cys 112) and two Cys residues in the e2 loop (Cys192 and Cys195) are available to form a disulfide bond in the wild-type AVPR2. The presence of an additional Cys residue in the extracellular domain caused by mutations may offer alternatives in disulfide bond formation. A recent study by Schülein et al. (2000) offered an additional explanation for the mechanism of AVPR2 dysfunction caused by Cys substitutions. It was shown that an additional C195A mutation results in a functional rescue of the mutant AVPR2s (Schülein et al. 2000). Since C195 is not conserved in mammalians AVPR2s and is not required for wild-type receptor function (Schulz et al. 2000b), these data suggest a mechanism in which C195 forms a new disulfide bond with a mutationally introduced Cys residue, interfering with high affinity binding. Such a mechanism may also account for Cys mutations in rhodopsin leading to an uneven number of Cys residues in the extracellular loops (Schülein et al. 2000).

The polypeptide chain of most GPCRs is posttranslationally modified by N-glycosylation, palmitoylation, and phosphorylation. Clinically relevant mutations of such potential posttranslational modification sites are rare, and only a few examples were published. Substitution mutations altering potential glycosylation sites in rhodopsin were described in families with retinitis pigmentosa (Bunge et al. 1993, Sullivan et al. 1993). A polymorphismus leading to an alteration of a potential N-glycosylation site of the μ -opioid receptor (N40D) is present in almost 10% of the population. This receptor variant displays a higher affinity for β -endorphin as compared with the wild type receptor (Bond et al. 1998). These findings underline the functional importance of GPCR glycosylation *in vivo*.

Most rhodopsin-like GPCRs display consensus sites for lipid modifications at Cys residues conserved within the C-terminal receptor tail. There are no reports highlighting the importance of this specific post-translational modification *in vivo*. Similarly, no clinical phenotype as a functional consequence of mutations affecting potential phosphorylation consensus sites has been reported yet. Increased receptor phosphorylation has been demonstrated for constitutively active GPCR (Ren et al. 1993, Westphal et al. 1995). Since cross-desensitization of other GPCRs within a given cell is a common phenomenon, one can speculate that the functions of other receptors are also influenced by constitutive receptor activation.

4.2.4

Ligand Binding and Signal Transduction

Once a mutated GPCR has passed through the ER folding control machinery and reached the cell surface, the mutation can still interfere with ligand binding and/or G-protein coupling. There are numerous clinically relevant examples for GPCR mutations showing that loss of receptor function is mainly caused by reduced affinity for the natural ligand (Biebermann et al. 1997, Schöneberg et al. 1998, de Roux et al. 1999, Albertazzi et al. 2000, Morello et al. 2001). For example, an NDI-causing AVPR2 mutation (F105V) which is located in the e1 loop is properly delivered to the cell surface and displays an unchanged maximum cAMP response. Impaired ligand binding was reflected by a concentration-response curve that was shifted towards higher vasopressin concentrations (Pasel et al. 2000). In principle, alteration of the agonist binding pocket can occur either through direct or indirect mechanisms. The first case involves positions that directly participate in ligand interaction. Indirect disturbance of the ligand binding site can occur if residues are mutated that are involved in stabilizing the ligand binding pocket. A clear separation of direct from indirect effects is often difficult.

Isolated defects of receptor/G-protein signaling without effects on receptor trafficking and/or ligand binding are extremely rare. One example comes from Hirschsprung's disease caused by mutations in the ET_BR gene. A mutant ET_BR (W276C) exhibits wild-type binding affinity but interferes with

efficient coupling to G_q without affecting $G_{i/o}$ -coupling (Imamura et al. 2000). These data suggest that Hirschsprung's disease is mainly caused by defects in the G_q signaling pathway. Controversially, two other ET_BR mutants (G57S and R319W) bound endothelin-1 normally and induced calcium transients in the same way as wild type, but did not inhibit adenylyl cyclase (Fuchs et al. 2001). This may indicate that an additional non-G-protein-mediated signaling pathway is involved in the pathophysiology of ET_BR dysfunction.

Analysis of the biochemical properties of mutant AVPR2s causing a partial NDI phenotype revealed that cell surface expression of D85N (see Fig. 5) is not altered (Sadeghi et al. 1997b). A 50-fold increase in the EC_{50} value and a decreased maximum cAMP response, but almost unchanged affinity, indicate a substantial decrease in the coupling efficiency of D85N to G_s. However, mutation-induced impairment of receptor signaling is usually accompanied by additional defects in receptor trafficking and ligand binding.

Changes in signal transduction are more prominent when the mutation induces agonist-independent receptor activation. Some activating mutations were naturally found (see Table 1), but most constitutively active GPCRs were artificially generated and tested in in vitro systems. The i3 loop and TMD6 of GPCRs have been identified as regions that are crucial for receptor/G-protein interactions. Assuming an equal frequency of germline mutations in all GPCR genes, it is astonishing that only a few activating mutations have been identified in vivo. Many constitutively active GPCRs may often result in an early letal phenotype. An other reason for the low natural occurrence is that constitutively active receptors are less stable in vivo, and, therefore, a clinically relevant phenotype may not always become apparent as shown for a constitutively active β_2 adrenergic receptor in transgenic mice. However, treatment of the transgenic mice with various adrenergic receptor ligands resulted in receptor overexpression and an increase in cardiac functions by stabilizing the mutant receptor protein (Samama et al. 1997).

As stated above, most GPCRs have the capability of coupling to more than one G protein. Distinct receptor/G-protein pathways can be differentially influenced by activating mutations. Selective constitutive activation of only one signal transduction pathway was shown for adrenergic receptors (Perez et al. 1996, Zuscik et al. 1998). Mutational activation of the LHR is the cause of male-limited precocious puberty due constitutive activation of the G_s/adenylyl cyclase pathway (Shenker et al. 1993). In addition to the G_s/adenylyl cyclase system, the activated LHR is known to stimulate G_i and phospholipase C. Depending on the precise nature of the mutation, constitutive LHR activation is observed in the latter signaling pathway which probably accounts for the malign transformation of Leydig cells (Liu et al. 1999). These findings further support the idea of multiple and distinct activation states in GPCRs (see 3.1).

In principle, naturally occurring GPCR mutations may also result in an increase in ligand affinity and/or signal transduction efficiency. As a consequence, lower concentrations (or even basal levels) of the endogenous ligand are sufficient to mediate a maximal physiological response. Such mutant receptors should cause similar pathophysiological effects as found for activating mutations if the dysfunction is not compensated by other mechanisms such as a decrease in agonist concentration or receptor cell surface expression. A pathophysiologically relevant example for this scenario remains to be identified.

5 Therapeutic Strategies to Restore Altered GPCR Function

5.1

General Considerations

To date, the therapy of diseases caused by GPCR dysfunction focuses mainly on treating clinical symptoms. It is beyond the scope of this review to address all therapeutic strategies used to alleviate the symptoms caused by GPCR dysfunction. This section focuses primarily on new strategies which may become therapeutically useful in the future. The most desirable strategy to treat inherited disorders in man is the site-specific reversion of the mutation by restoring the normal nucleotide sequence. However, a major obstacle to successful gene therapy is the relative inefficiency of current targeting strategies in mammalian cells. Gene targeting may be accomplished by homologous recombination and mismatch correction of DNA heteroduplexes. Homologous recombination, initially considered to be of limited use for gene therapy because of its low frequency in mammalian cells, has recently emerged as a potential strategy. Different approaches have been used including small or large homologous DNA fragments, adenovirus-associated viral vectors, and RNA/DNA chimeric oligonucleotides. One promising approach is based on recent observations of recombinogenic activity of specifically designed chimeric RNA/DNA oligonucleotides (Cole-Strauss et al. 1996, Rando et al. 2000, Alexeev et al. 2000). However, the gene repair efficiency remains low and has not been tested in clinically relevant settings.

Treatment of diseases caused by GPCR dysfunction may not always require genetic approaches. For example, loss-of-function mutations in the TSHR have been demonstrated to cause some familial forms of athyreosis with an absolute thyroxine (T_4) deficiency resulting in developmental and mental retardation (Biebermann et al. 1997). Early discovery of the genetic defect by neonatal screening and rapid clinical management are important for patients, as these patients will have normal fertility. The goals of treatment are to raise the serum T_4 as rapidly as possible into the normal range to maintain normal growth and development (Grüters et al. 1999). Simple hormone substitution is also the treatment of choice in hypogonadotropic hypogonadism (Zitzmann and Nieschlag 2000)

5.2 Ligand Binding-Directed Strategies

It has been shown for a large number of inactivating mutations in GPCRs that alteration of the agonist binding site reduces ligand affinity but leaves maximal coupling efficacy unchanged. Therefore, patients with such inactivating mutations may benefit from high agonist doses or from administration of an agonist displaying a higher affinity to the mutant receptor than the natural ligand. The usefulness of this principle has been demonstrated in dogs suffering from NDI because of a low affinity AVPR2. Prolonged treatment with high doses of an AVPR2 specific agonist, 1-deamino [D-Arg8] vasopressin (dDAVP), rendered the NDI-affected dogs near normal in terms of water intake and urine osmolality (Luzius et al. 1992). Recombinant TSH 'superagonists' with increased receptor affinity and efficacy were designed for the TSHR by combining evolutionary considerations, sequence comparisons and homology modeling (Grossmann et al. 1998). Success in treatment of TSHR and any other GPCR dysfunction with high affinity agonists in man is still lacking.

In the traditional model, the unliganded receptor was assumed to be quiescent, but differences in basal second messenger levels depending on the receptor type and expression levels have questioned this theory. The simplest model addressing the latter phenomenon suggests that receptors exist in an equilibrium between two conformations, an inactive stage R and an active stage R* (see 3.1). Agonists are thought to alter the position of the equilibrium by stabilizing R* (see Fig. 3). Antagonists do not preferentially stabilize either state of the receptor but compete for agonist or inverse agonist binding. Inverse agonists stabilize the R state, thus leading to decreased basal receptor activity. In many cases high levels of (ectopically) expressed GPCRs can produce substantial constitutive activity, and an inverse agonist would be preferable for eliminating GPCR-induced cellular responses rather than an antagonist (Milligan et al. 1995, Milligan and Bond 1997). Because GPCRs are thought to exist in an equilibrium between R and R*, an increase in the total receptor number will also increase the total number with the R^{*} conformation which may become pathophysiologically relevant (Bond et al. 1995). In thyreotoxicosis, the number of cardiac β adrenergic receptors is increased causing an increase in heart-beat frequency. A combination of thyreostatic drugs and β adrenergic blockers with negative intrinsic activity are used in the treatment of this life-threatening condition.

One may speculate that inverse agonists would become the number one choice in the treatment of diseases caused by activating mutations. To date, positive results in the treatment of patients suffering form diseases caused by activating GPCR mutations with an inverse agonist have not been reported. There are, however, a few experimental examples suggesting a benefit of this strategy. For instance, mutations of Lys at position 296 (K296E and K296M) found in certain patients with autosomal dominant retinitis pigmentosa leads to constitutive activity of rhodopsin. It was shown that the 11-cis C19 retinylamine is an effective inhibitor of the naturally occurring constitutively active mutant rhodopsins (Yang et al. 1997). Constitutive activity of the viral receptor KSHV-GPCR is an important factor in Kaposi's sarcoma pathogenesis. It has been demonstrated recently that the human interferon (IFN)-y-inducible protein 10 (HuIP-10), a CXC chemokine, and the stromal cell-derived factor-1 α specifically inhibit signaling of KSHV-GPCR and KSHV-GPCR-induced proliferation of NIH 3T3 cells (Geras-Raaka et al. 1998a, Rosenkilde et al. 1999). These data may promote the development of non-peptide inverse agonist drugs for the treatment of Kaposi's sarcoma.

Unfortunately, the use of an inverse agonist may not always represent a suitable therapeutic strategy. Although a compound may behave as an inverse agonist of the wild-type receptor, it may become a potent and efficient agonist of a constitutively active receptor mutant. Several examples of mutation-induced changes in GPCR pharmacological properties have been reported, these include cholecystokinin (Beinborn et al. 1998) and bradykinin (Marie et al. 1999) mutant receptors.

5.3 GPCR Expression- and Downregulation-Directed Strategies

Suppression of receptor mRNA transcription as well as induction of receptor downregulation and degradation may also represent a suitable concept for silencing constitutively active GPCRs. As already mentioned above, Kaposi's sarcoma-associated herpes virus, which is consistently present in tissues of patients with Kaposi's sarcoma and primary effusion lymphomas, contains a gene that encodes a constitutively active GPCR (KSHV-GPCR). It was shown that co-expression of GPCR-specific kinases and activation of protein kinase C inhibit constitutive KSHV-GPCR signaling (Geras-Raaka et al. 1998b).

In heart failure, compensatory mechanisms involve an increased activity of the sympathetic nervous system mainly due to elevated norepinephrine plasma levels ('quasi' constitutive activation). This increase in agonism can lead to β adrenergic receptor desensitization and, therefore, in loss of receptor function. β Adrenergic receptor desensitization is mediated through enhanced activity of the β adrenergic receptor kinase (β ARK1) in ischemic and failing myocardium. Adenoviral-mediated gene delivery of an inhibitor of β ARK1, β ARKct, preserves normal β adrenergic receptor function presumably by inhibiting desensitization through endogenous β_1 adrenergic receptors (White et al. 2000).

On the other hand, constitutively elevated levels of GPCR agonists can be useful in the treatment of diseases. In congestive heart failure, high systemic levels of AVP result in vasoconstriction and reduced cardiac contractility mediated by the V_1 vasopressin receptor. The AVPR2 is physiologically expressed in the kidney but not in the myocardium. Ectopic expression of a recombinant AVPR2 in the myocardium which promotes activation of the G_s/adenylyl cyclase system (like the β_1 adrenergic receptor) results in a positive inotropic effect in heart failure, mediated by the high endogenous AVP levels (Laugwitz et al. 1999). In contrast to the findings with adrenergic receptors, AVPR2 expression does not undergo significant downregulation.

Another promising novel approach takes advantage of specifically engineered GPCRs referred to as RASSLs (receptor activated solely by a synthetic ligand). Specifically, the κ opioid receptor, which couples to $G_{i/o}$, was modified to respond exclusively to synthetic small molecule agonists and not to their natural agonists (Coward et al. 1998). RASSL-transgenic mice were used to control physiologic events depending on activation of the $G_{i/o}$ signal transduction pathway in a tissue specific manner (Redfern et al. 1999). Recently, Liggett and co-workers generated a β_2 adrenergic receptor which was activated only by a non-biogenic amine agonist which itself failed to activate the wild-type receptor (Small et al. 2001). RASSL may have an implication in specific targeting of cells or tissues for diagnostic and therapeutic purposes.

5.4

Receptor Folding-Directed Strategies

To date, methods aimed at correcting genetic defects at the genomic level are of limited effectiveness. This requires a search for therapeutic alternatives. Based on findings that GPCRs are composed of multiple folding units (see 2.4), it was demonstrated that mutant AVPR2s containing clinically relevant mutations in the C-terminal third of the receptor protein can be functionally rescued by co-expression with a non-mutated C-terminal AVPR2 fragment (Schöneberg et al. 1996). Since such polypeptides are expected to interact only with those mutant receptors from which they are derived, this approach would offer the great advantage that the fragments exert their pharmacological effects only in tissues or cells in which the mutant receptors are physiologically expressed. Therefore, embedding of a tissue-specific promoter in the expression cassette of the therapeutic delivery system is not essentially required. To test the potential therapeutic usefulness of this co-expression strategy, cell lines stably expressing low levels of functionally inactive mutant AVPR2s were infected with a recombinant adenovirus carrying a AVPR2 gene fragment encoding the C-terminal third of the receptor protein. Adenovirus-mediated expression of receptor fragments resulted in cell-specific molecular correction of functional receptor defects, indicating that this approach may lead to novel strategies in the treatment of diseases caused by inactivating GPCR mutations (Schöneberg et al. 1997). These findings are probably relevant not only for GPCRs but also for polytopic integral membrane proteins in general. For example, it has been demonstrated that many proteins containing multiple membranespanning domains can be assembled from two or more protein fragments. These proteins include sodium channels (Stühmer et al. 1989), the a-factor transporter in yeast (Berkower and Michaelis 1991), adenylyl cyclases (Tang et al. 1995), GLUT1 glucose transporter (Cope et al. 1994), and lactose permease (Bibi and Kaback 1990, Zen et al. 1994).

Therapeutic approaches aiming at the modulation of chaperone function were pioneered by studies with CFTR. Mutations in the CFTR gene reduce the probability of the mutant protein to dissociate from molecular chaperones and largely prevent protein maturation through the secretory pathway to the plasma membrane. These mutant CFTR molecules are rapidly degraded by cytoplasmic proteasomes (Kopito 1999). Treatment of cells expressing the Δ F508 mutant with a number of low molecular weight compounds such as glycerol, dimethylsulfoxide and trimethylamine oxide, all known to stabilize proteins in their native conformation ('chemical chaperones'), results in the correct processing of the mutant CFTR protein and its delivery to the plasma membrane, thus restoring CFTR function (Brown et al. 1996, Sato et al. 1996). Trafficking-deficient aquaporin-2 proteins, as found in patients with recessive NDI, were also redistributed normally after treatment with 'chemical chaperones' (Tamarappoo and Verkman 1998).

Treatment of cells expressing the H_2 histamine receptor with the inverse agonists cimetidine and ranitidine led to an increase of receptor number probably by stabilizing the receptor structure (Smit et al. 1996). Stabilizing

effects and receptor up-regulation by inverse agonist treatment were also observed with a constitutively active TRH receptor (Heinflink et al. 1995) and the α_{1B} -adrenergic receptor (Lee et al. 1997). Recently, this approach has been successfully used to functionally rescue clinically relevant AVPR2 mutants by pretreatment of transfected cells with the nonpeptidic AVPR2 antagonists, SR121463A and VPA-985 (Morello et al. 2000). Therefore, the effects of temperature (see 4.2.3), chemical chaperones and structurestabilizing ligands on the intracellular processing of mutant GPCRs suggest that strategies designed to promote protein folding/stability *in vivo* may eventually lead to the development of novel therapies for diseases caused by GPCR dysfunction.

5.5 Modulation of Receptor Function by Receptor-Derived Polypeptides

The exact nature of GPCR/G-protein interaction sites is currently unknown and may vary between different GPCRs and G proteins. It is assumed that not only the intracellular loops but also the cytoplasmic sides of the TMDs participate in GPCR/G-protein coupling. Indeed, peptides derived from the i3 loop/TMD6 junction can activate the G_s/adenylyl cyclase system (Abell and Segaloff 1997, Abell et al. 1998) or inhibit adenylyl cyclase via G_i proteins (Varrault et al. 1994). Several other studies using expression plasmids coding for cytoplasmic receptor fragments demonstrated impaired receptor/G-protein coupling (Ulloa-Aguirre et al. 1998, Thompson et al. 1998). Recently, the usefulness of dominant negative mutations introduced into the G_s α -subunit was demonstrated as a specific tool for dissection of G_smediated signals in cultured cells (Iiri et al. 1999). Since these approaches appear to be specific for a single signaling cascade but lack receptor specificity, such methods will probably have a limited therapeutic relevance.

In accord with the multiple folding unit model of GPCRs, specific inhibition of GPCR function can be achieved by co-expression or administration of single TMDs. It was shown for the β_2 adrenergic receptor, the D₁ dopamine receptor, and the CCK_A receptor that TMD6-derived peptides were able to concentration-dependently inhibit receptor signaling (Hebert et al. 1996, George et al. 1998, Tarasova et al. 1999). A potential therapeutic usefulness of this approach was shown for CXCR₄ and CCR₅ chemokine receptors which serve as co-receptors for HIV-1 entry. Peptides derived from chemokine receptor TMDs can serve as potent and specific receptor antagonists and can block HIV-1 replication *in vitro* (Tarasova et al. 1999).

5.6 Animal Models Suitable for Testing New Therapeutic Strategies

Genomic analysis of mutant mice and gene-targeting disruption techniques guided many studies to disease-causing GPCR mutations in man (Lin et al. 1993, Stein et al. 1994, Hosoda et al. 1994). A large number of GPCRs has been targeted in mice to study the phenotype induced by gene disruption (reviewed in Offermanns 2000). About 50% of GPCR-defective mouse strains show a defined phenotype, about 40% have an obvious phenotype after challenging. This data indicate that the number of uncovered phenotypes caused by mutated GPCR genes in man will increase in the near future.

Only a limited number of mouse strains are available carrying phenotype-causing point mutations in GPCR genes opening the possibility to test therapeutic strategies to restore altered GPCR function. Several examples are discussed in the following. The hyt/hyt hypothyroid mouse displays an autosomal recessive, fetal-onset, severe hypothyroidism. The mutants are characterized by retarded growth, infertility, mild anemia, elevated serum cholesterol, very low to undetectable serum thyroxine, and elevated serum thyroid-stimulating hormone. Thyroid glands are in the normal location but are reduced in size and hypoplastic. Mutant mice respond to thyroid hormone therapy by improved growth and fertility (Beamer et al. 1981). Genetic analysis of the hyt/hyt locus at chromosome 12 revealed a single base exchange in the TSHR gene which leads to the replacement of a highly conserved Pro at amino acid position 556 (TMD4) with Leu (Stein et al. 1994). Mutant mice respond to thyroid hormone therapy by improved growth and fertility but alternative approaches besides hormone substitution to rescue thyroid function have not been tested.

The little mouse is a dwarf strain characterized by low levels of growth hormone, pituitary hypoplasia, and an unresponsiveness to treatment with exogenous growth hormone-releasing hormone (GRHR). Genetic mapping and cloning studies have localized this defect to a point mutation in the Nterminal extracellular domain of the GRHR receptor, a member of family 2 GPCRs, where an Asp residue at position 60 is mutated to Gly (Godfrey et al. 1993). Consistent with the dwarf phenotype, the mutant receptor is inactive, and cells expressing the mutant receptor do not accumulate cAMP in response to GHRH.

Mouse coat color genes have long been studied as a paradigm for genetic interactions in development. Piebald-lethal mice exhibit a recessive phenotype identical to that of the ET_BR knockout mice (Hirschsprung's disease). Southern blotting revealed a deletion encompassing the entire ET_BR gene in

Piebald-lethal mice (Hosoda et al. 1994). However, reconstitution of the ET_BR gene by genetic or other approaches has not been attempted so far.

In X-linked NDI more than hundred inactivating mutations have been reported within the AVPR2 gene (Bichet 1998). Current pharmacological treatment strategies of X-linked NDI include the administration of thiazide diuretics along with a reduction in salt intake, frequently in combination with prostaglandin synthesis inhibitors. However, these drugs only lead to a partial reduction in urine production, and their use is often associated with severe side effects including disturbances in electrolyte balance as well as renal and gastrointestinal complications. An animal model of X-linked NDI should allow detailed studies of the pathophysiology of this disease and should greatly facilitate the development of new therapeutic strategies including rescue attempts with receptor fragments. Premature chaintermination mutations have been successfully used in mice to induce lossof-function of the D₃ dopamine receptor (Accili et al. 1996) and the 5-HT_{1A} receptor (Heisler et al. 1998). Therefore, a nonsense mutation known to cause X-linked NDI in humans (E242X) was introduced into the mouse genome (Yun et al. 2000). AVPR2-deficient male (-/y) mice die within the first week after birth, apparently due to hypernatremia and dehydration caused by the inability of these animals to concentrate urine. The body weight and the urine osmolality levels of the (-/y) mice are significantly reduced. Interestingly, adult female AVPR2 (+/-) mice show clear symptoms of NDI, including reduced urine-concentrating ability, polyuria, and polydipsia. The AVPR2-deficient mice will assist in the development of novel therapeutic strategies including functional reconstitution attempts at the genomic and protein levels.

There are only a few examples in the literature reporting animal phenotypes caused by activating mutations. Activating receptor mutations were found in the mouse melanocortin-1 receptor (E92K, L98P) resulting in dark coat color (Lu et al. 1998). Mice expressing constitutive active receptors in a tissue-specific manner were generated for the PTH/PTHrP receptor (Schipani et al. 1997) and the β_2 adrenergic receptor (Samama et al. 1997) and may serve as model systems for therapeutic approaches in the future.

6

Summary and Future Perspectives in GPCR Research

Sequencing of entire genomes of many higher organisms will be completed in the next few years. This information will allow the identification of new GPCRs which are more distantly related to known receptors and will help to understand the function of human GPCRs as well. Hundreds of 'orphan' GPCRs have been discovered so far. Defining the role of each GPCR under physiological and pathophysiological circumstances and using this information to control GPCR activity therapeutically represents one of the major challenges for molecular medicine in the coming post-genome era. Recent molecular characterization of cloned protein genes draws attention to alternative splicing and mRNA editing as a source of structural and functional diversity. Tissue-specific splicing has also been reported for several GPCRs and is likely to further increase the number of known GPCR isoforms. GPCR diversity is primarily based on the existence of multiple receptor subtypes due to gene duplication events. The existence of introns in GPCR genes provides the potential for additional diversity by virtue of alternative splicing events which may generate distinct receptor isoforms (Kilpatrick et al. 1999).

A more detailed understanding of the function of GPCRs will be achieved as we identify sequences that control receptor expression. Numerous studies have been undertaken aimed at the identification and functional characterization of GPCR promoter sequences. The major questions that still need to be addressed dealing with the molecular basis of time- and tissue-specific expression as well as cellular inputs necessary for GPCR expression. By comparing corresponding genomic sequences in different species, e.g. man, mouse, chicken, and zebrafish, regions that have been highly conserved during evolution can be identified, many of which reflect conserved functions such as gene regulation. These approaches, in combination with mouse genetics, promise to greatly accelerate our understanding of regulation and expression of GPCR genes.

Undoubtedly, resolving the crystal structure of rhodopsin was a milestone in the history of GPCR research (Palczewski et al. 2000). This structural information provides a solid basis for further experimental structure/function relationship studies and for computer models of other GPCRs. Clearly, the success in crystallizing an integral membrane receptor will encourage projects to increase the resolution of the rhodopsin model and to analyze other GPCRs. Future attempts will aim at resolving the fine structure of different functional states in GPCR activation and the co-crystallization of a GPCR in complex with the G protein or other GPCR-associated proteins. These studies should eventually provide detailed structural information about the molecular architecture of the receptor/transducer interface. It should be noted that direct physical methods such as X-ray crystallography can only provide information of a static structure. There are numerous examples showing distinct differences in the fine structure when NMR derived structures in solution are compared with those obtained with X-ray crystallography (Barbato et al. 1999, Erbel et al. 1999, Yuan et al. 1999). Structural

information about the receptor protein in its natural environment obtained from biophysical methods as well as mutagenesis and biochemical approaches is still needed to supplement current GPCR models. The correctness of GPCR models will be measured by the success of computer-aided drug design and the correct prediction of the functional consequences of specific mutations.

Identification of a growing number of receptor-binding proteins suggests alternative signaling mechanisms. Structural determinants within the C terminus and the intracellular loops provide potential interaction sites with other cellular proteins. Such partners may serve as direct signaling target or adapter proteins in the down-stream signaling pathway. Yeast two-hybrid and co-immunoprecipitation experiments are powerful methods for identifying novel proteins that bind to GPCRs. These same techniques, coupled with mutagenesis experiments, have been used to define the regions of interaction between pairs of proteins. Thus, an increasing number of non-Gprotein interaction partners has been identified during the past few years (see 3.2, for review see Heuss and Gerber 2000). Detailed analyses of the interface for protein interaction revealed a large set of modules, such as SH domains and PDZ domains mediating the GPCR/protein association. The diversity of relevant interactions is likely to grow steadily, particularly since homologous and heterologous GPCR oligomerization has begun to emerge as a rather general phenomenon. Functional characterization of these alternative signaling pathways and the elucidation of the molecular basis of their interactions will advance our understanding of GPCR function in the future.

Human genome research has made it possible to identify the presence of gene mutations in persons with inherited disorders, who may be carriers of genetic disorders, or who are at risk for future development of inherited diseases. Molecular analysis of inherited disorders, population screening of genetic diseases, as well as studies of the genetic basis of variable drug response involve efficient screening for mutations in multiple DNA samples. Thus, high throughput mutation screening methods are of great importance. Traditional methods for mutation screening like SSCP and heteroduplex analysis lack sensitivity and are difficult to automate. However, recent developments in DNA fragment analysis by capillary electrophoresis and microchip-based technologies have made fully automated mutation screening possible and have dramatically increased the possible sample throughput. This offers the possibility to include promoter and intron sequences into the screening routine at a financially acceptable level. The concept that variations in non-coding regions may affect GPCR function is derived from extensive studies with a non-G-protein-coupled membrane receptor. Familial hypercholesterolemia is not only caused by mutations in the coding sequence of the low density lipoprotein (LDL) receptor gene but also by mutations in the promoter region (Koivisto et al. 1994). Such direct linkage of promoter polymorphisms/ mutations with a human disease phenotype has not yet been demonstrated for GPCRs. Numerous studies have been undertaken to link polymorphisms found in the 5'-untranslated region of adrenergic, serotonin and dopamine receptors to psychiatric disorders, but clear proof is still missing. A recent study provides evidence for linkage between CCR5 promoter polymorphisms and long-term asymptomatic HIV-1 infection (Clegg et al. 2000). Genetic variability of GPCR genes influencing cardiovascular phenotypes in normal persons is likely to be relevant to cardiovascular disease. The potential clinical relevance of polymorphisms found in the 3'-untranslated region of the angiotensin receptor type 1 gene associated with arterial hypertension, aortic stiffness and coronary artery disease is currently under investigation (Castellano et al. 1996). Improved understanding of the complex regulation of GPCR expression will probably uncover clinically relevant alterations in the non-coding regions of GPCR genes.

The prospects for the development of gene therapy treatments for certain diseases have been fuelled by advances in the understanding of the molecular basis of these disorders. Certainly, the number of diseases caused by GPCR malfunction will increase in the future. As for other genetic defects, the primary goal of a therapeutic intervention will be the reversal of the disease-causing mutation at the genomic level. Since this approach is limited by low recombination efficiency, most genetic strategies aim at the supragenomic level such as transfer of complete expression cassettes. The ability to transfer and appropriately express the genes encoding molecules of interest is dependent on the availability of effective gene transfer vectors.

After more than one century since the term 'receptor' has been introduced by Paul Ehrlich and after almost two decades since the first GPCR, rhodopsin, was cloned by Nathans and Hogness (1983), this field of research is still exponentially expanding. Long established views are changing since GPCR dimerization, alternative pathways in GPCRs signaling and their pathomechanistic contributions in human diseases have been discovered. Defining the role of each GPCR and using this information to control GPCR activity therapeutically represents one of the major challenges for molecular medicine in the coming post-genome era.

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Abbreviations

| AVP | arginine vasopressin |
|-------------|---|
| AVPR2 | V2 vasopressin receptor |
| BARK1 | ß adrenergic receptor kinase |
| BRET | bioluminescence resonance energy transfer |
| CCK-R | cholecystokinin receptor |
| CD | circular dichroism |
| CFTR | cystic fibrosis transmembrane conductance regulator |
| CGRP | calcitonin-gene-related peptide |
| CRLR | calcitonin-receptor-like receptor |
| DNA-Mtases | DNA-methyltransferases |
| e1-e3 loops | extracellular loops 1-3 |
| ET-R | endothelin receptor |
| FRET | fluorescence resonance energy transfer |
| FSHR | follitropin receptor |
| GIRK | G-protein-regulated inward rectifier K ⁺ channel |
| GnRH | gonadotropin-releasing hormone |
| GPCR | G-protein-coupled receptor |
| GRK | G-protein-coupled receptor kinase |
| hCG | human choriogonadotropin |
| i1-i3 loops | intracellular loops 1-3 |
| IP | inositol phosphate |
| KSHV-GPCR | Kaposi's sarcoma-associated herpes virus receptor |
| LHR | lutropin receptor |
| NDI | X-linked nephrogenic diabetes insipidus |
| NMR | nuclear magnetic resonance |
| PAF | platelet-activating factor |
| PDZ | postsynaptic density/disc-large/ZO1 |
| RAMP | receptor-activity-modifying protein |
| rhoGAP | Rho GTPase-activating protein |
| SNP | single nucleotide polymorphism |
| SSCP | single-strand conformational polymorphism |
| SSTR | somatostatin receptor |
| TMD | transmembrane domain |
| TRH | thyrotropin-releasing hormone |
| TSHR | thyrotropin receptor |
| | |

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