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The DAG-responsive C1 domain as a drug target: structureactivity and *in vitro* pharmacology of isophthalate derivatives

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ACADEMIC DISSERTATION

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"Research is the process of going up alleys to see if they are blind."

- Marston Bates -

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ABSTRACT

Diacylglycerol (DAG) is a ubiquitous lipid second messenger that transmits signals from cell membrane receptors to intracellular effector proteins containing a specialized DAG recognition motif, the C1 domain. The protein kinase C (PKC) family of serine/threonine kinases is the bestcharacterized member of DAG effectors, but there are also six other families of proteins with a DAGresponsive C1 domain: (1) the protein kinase D (PKD) family; (2) the myotonic dystrophy kinaserelated Cdc42-binding kinases (MRCKs); (3) the DAG kinases (DGKs); (4) the Munc13 proteins; (5) the chimaerins; and (6) the Ras guanyl-releasing proteins (RasGRPs). DAG-mediated signalling regulates many cellular functions such as cell proliferation, survival, differentiation, apoptosis and motility processes that are often deregulated in cancer. As key mediators of these processes, several of the DAG effectors are regarded as promising targets for cancer drug development. Furthermore, PKC contributes to neuronal plasticity and inhibits many pathophysiological processes related to Alzheimer's disease. Activation of PKC is therefore considered a potential future therapeutic strategy for the treatment of Alzheimer's disease. The C1 domain thus represents a well-recognized drug target. However, the existing C1 domain ligands are extremely complex in their chemical structure and from the drug development point of view new C1 domain ligands with a feasible synthesis route are needed.

The purpose of these studies was to characterize the structure-activity relationships (SAR) of a novel group of C1 domain ligands, derivatives of 5-(hydroxymethyl)isophthalic acid. These compounds have a simple chemical structure and they are easy to synthesize. Furthermore, these studies aimed to investigate the *in vitro* pharmacology of the isophthalate derivatives especially focusing on their effects on cell proliferation and morphology.

The SAR studies revealed the structural elements indispensable for binding to the C1 domain of PKC: the hydroxymethyl group, both of the ester groups and sufficiently hydrophobic ester substituents. Importantly, the SAR model also held true with β 2-chimaerin, another C1-domain containing DAG effector. The active isophthalates bound to PKC with low micromolar affinities, and a selected example of these, HMI-1a3, was also shown to bind to the C1 domains of PKD1 and MRCK α at similar concentrations.

Several isophthalates had an antiproliferative effect in HeLa human cervical carcinoma cells. HMI-1a3 exhibited the most potent cytotoxic and antiproliferative effect of the derivatives tested. The isophthalates with no affinity to the C1 domain (e.g. NI-15e, the inactive derivative of HMI-1a3) had no effect on HeLa cell viability or proliferation, suggesting a C1 domain-mediated effect. HMI-1a3 also induced a morphological change characterized by cell elongation. It was accompanied with a marked reorganization of actin cytoskeleton: loss of focal adhesions and actin stress fibres. The elongation-inducing effect of HMI-1a3 was inhibited by an MRCK inhibitor, and thus seems to be at least partially mediated by MRCK. However, the mechanism of its antiproliferative effect remains unclear and may be mediated by several of the DAG effectors.

In SH-SY5Y neuroblastoma cells, which are widely used as an *in vitro* model for neuronal differentiation, HMI-1b11 inhibited cell proliferation and supported neurite growth. HMI-1a3 induced SH-SY5Y cell differentiation as well, but unlike HMI-1b11 it also induced cell death. Again, derivatives with poor binding affinity to the C1 domain had no effect. The HMI-1b11-induced response was accompanied by PKC-dependent ERK1/2 phosphorylation and up-regulation of GAP-43, which is known to mediate neuronal differentiation and to contribute to neurite outgrowth.

In conclusion, these studies identify derivatives of 5-(hydroxymethyl)isophthalic acid as a promising novel group of C1 domain ligands. The antiproliferative and cytotoxic HMI-1a3 serves as a potential lead molecule for cancer-related drug discovery. HMI-1b11 on the other hand may be useful in drug development related to neurodegenerative diseases because of its non-toxic and differentiation-inducing properties in SH-SY5Y cells. More studies using cell-based and *in vivo* models are, however, needed to fully assess the potential of isophthalates in drug development.

ABBREVIATIONS

[³H]PDBu [20-³H]phorbol -12,13-dibutyrate

Aβ Amyloid β protein
AD Alzheimer's disease
AML Acute myeloid leukaemia
ANOVA Analysis of variance
aPKC Atypical protein kinase C
APP Amyloid precursor protein
ATP Adenosine-5'-triphosphate

BAF Boc-Asp(OMe) fluoromethyl ketone

CC (domain) Coiled-coil (domain)
CNH (domain) Citron homology (domain)
CNS Central nervous system

cPKC Classical/conventional protein kinase C

DB Dulbecco's phosphate-buffered saline with 0.2% (w/v) BSA

DAG Diacylglycerol

DAPI 4',6-Diamidino-2-phenylindole

DGK Diacylglycerol kinase

DMEM Dulbecco's modified Eagle's medium

DMSO Dimethyl sulfoxide

DOG 1,2-Dioctanoyl-sn-glycerol
ECE Endothelin-converting enzyme
ECL Enhanced chemiluminescence
EDTA Ethylenediaminetetraacetic acid
EGTA Ethylene glycol tetraacetic acid
ERK Extracellular signal-regulated kinase
ERM Ezrin-radixin-moesin (a protein family)

FBS Foetal bovine serum GABA y-Aminobutyric acid

GAP-43 Growth-associated protein 43
GPCR G protein-coupled receptor
GSEA Gene set enrichment analysis
GSK3 Glycogen synthase kinase 3
GST Glutathione S-transferase
GTP Guanosine-5'-triphosphate

GTPase Guanosine-5'-triphosphate hydrolase

HDAC Histone deacetylase

HMI-1a3 Bis(3-trifluoromethylbenzyl) 5-(hydroxymethyl)isophthalate

HMI-1b10 Bis(1-ethylbutyl) 5-(hydroxymethyl)isophthalate HMI-1b11 Bis(1-ethylpentyl) 5-(hydroxymethyl)isophthalate

HSD Honestly significant difference

IC₅₀ Half maximal inhibitory concentration

ICH Immunocytochemistry
IgG Immunoglobulin G
IKK Inhibitor of NF-kB kinase
IP₃ Inositol-1,4,5-trisphosphate
JNK c-Jun N-terminal kinase

K_d Equilibrium dissociation constant
 K_i Dissociation constant of the inhibitor

KIM Kinase inhibitory motif
LDH Lactate dehydrogenase
LIMK LIM (domain) kinase

MAPK Mitogen-activated protein kinase

MARCKS Myristoylated alanine-rich C-kinase substrate

mDIA Protein diaphanous homolog MEF-2 Myocyte enhancer factor 2

MEK MAPK/ERK kinase

MI-40 Bis(1-ethylpentyl) 5-methylisophthalate

MLC Myosin light chain

MRCK Myotonic dystrophy kinase-related Cdc42-binding kinase

mRNA Messenger RNA

MTT 3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide

MUN (domain) Minimal region for Munc13 activity

nELAV Neuronal embryonic lethal abnormal vision (protein)

NFD motif Asparagine-phenylalanine-aspartate motif

NF-κB Nuclear factor kappa-B

NI-15e Bis(3-trifluoromethylbenzyl) 5-nitroisophthalate

nPKC Novel protein kinase C

p38 MAPK (mitogen-activated protein kinases 11-14)

PA Phosphatidic acid
PAK4 p21-activated kinase 4

PAP Phosphatidic acid phosphohydrolase

PB1 (domain) Phox and Bem 1 (domain)
PBD p21-binding domain
PBS Phosphate-buffered saline
PC Phosphatidylcholine
PDBu Phorbol-12,13-dibutyrate
PH (domain) Pleckstrin homology (domain)

PIP₂ Phosphatidylinositol-4,5-bisphosphate

PKB Protein kinase B (aka Akt)

PKC Protein kinase C
PKD Protein kinase D
PLC Phospholipase C
PLD Phospholipase D

PMA Phorbol-12-myristate-13-acetate

PS Phosphatidylserine

PSS Pseudosubstrate sequence
Rac-GAP Rac GTPase-activating protein
RACK Receptor for activated C kinase

RasGEF Ras guanine nucleotide exchange factor

Ras GRP Ras guanyl-releasing protein

REM Ras exchange motif
RIN1 Ras and Rab interactor 1

RNAi RNA interference

ROCK Rho-associated protein kinase

RT Room temperature
RTK Receptor tyrosine kinase
RVH (domain) recoverin homology (domain)
sAPPα Soluble amyloid precursor protein α
SAR Structure-activity relationship
SDS Sodium dodecyl sulphate

SDS-PAGE SDS polyacrylamide gel electrophoresis

SEM Standard error of mean
Sf9 Spodoptera frugiperda 9
SH2 (domain) Src homology 2 (domain)
siRNA Small interfering RNA

SNARE Soluble N-ethylmaleimide sensitive fusion protein (NSF) attachment protein receptor

STAT Signal transducer and activator of transcription

SSH Protein phosphatase Slingshot homolog

TBS Tris-buffered saline TGN Trans-Golgi network

Tris Tris(hydroxymethyl)aminomethane
TTBS 0.1% Tween 20 in Tris-buffered saline

WAVE Wiskott-Aldrich syndrome protein (WASP) family member

ORIGINAL PUBLICATIONS

This dissertation is based on the following original publications:

- Boije af Gennäs Gustav*, Talman Virpi*, Aitio Olli*, Ekokoski Elina, Finel Moshe, Tuominen Raimo K, Yli-Kauhaluoma Jari (2009) Design, synthesis and biological activity of isophthalic acid derivatives targeted to the C1 domain of PKC. *J Med Chem 52: 3969-81*.

 *equal contribution
- II Talman Virpi, Tuominen Raimo K, Boije af Gennäs Gustav, Yli-Kauhaluoma Jari, Ekokoski Elina (2011) C1 domain-targeted isophthalate derivatives induce cell elongation and cell cycle arrest in HeLa cells. PLoS ONE 6(5): e20053.
- Talman Virpi, Gateva Gergana, Ahti Marja, Ekokoski Elina, Lappalainen Pekka, Tuominen Raimo K. HeLa cell elongation induced by the C1 domain-binding isophthalate HMI-1a3 is inhibited by the MRCK inhibitor chelerythrine. *Submitted*.
- Talman Virpi*, Amadio Marialaura*, Osera Cecilia, Sorvari Salla, Boije af Gennäs Gustav, Yli-Kauhaluoma Jari, Rossi Daniela, Govoni Stefano, Collina Simona, Ekokoski Elina, Tuominen Raimo K, Pascale Alessia (2013) The C1 domain-targeted isophthalate derivative HMI-1b11 promotes neurite outgrowth and GAP-43 expression through PKCα activation in SH-SY5Y cells. *Pharmacol Res 73: 44-54*.

*equal contribution

The publications are referred to in the text by their roman numerals. The supporting information of original publications I and IV is not included in this thesis. The material is available from the author or via the internet at http://pubs.acs.org/doi/suppl/10.1021/jm900229p (46 pages) for the original publication I and at http://www.sciencedirect.com/science/article/pii/S1043661813000820 (3 pages) for the original publication IV. The original publications were reproduced with permission from the copyright holders.

1. INTRODUCTION

Protein kinases are enzymes that transfer phosphate groups from adenosine-5'-triphosphate (ATP) to their substrate proteins, generally resulting in a functional change (activation or inactivation) of the substrate. The human genome contains 518 protein kinase genes, which is 2% of all genes (Manning et al., 2002). Most eukaryotic protein kinases phosphorylate specifically serine and threonine residues in their substrates (serine/threonine kinases); some phosphorylate specifically tyrosine residues (tyrosine kinases); and a small number of kinases are able to phosphorylate all three of them (dual-specificity kinases). Protein kinases are important components of signalling cascades that regulate cell proliferation, survival, differentiation, migration and apoptosis – processes that are deregulated in for example cancer and neurodegenerative diseases.

In 1977, Yasutomi Nishizuka's group from the University of Kobe, Japan, published the first reports of a cyclic nucleotide-independent protein kinase and named it protein kinase M (M for magnesium-dependent activation) (Inoue et al., 1977; Takai et al., 1977). The enzyme was subsequently found to be activated by calcium and phospholipids and renamed protein kinase C (PKC), where C stands for calcium-dependent activation (Takai et al., 1979). Furthermore, the same group also identified diacylglycerol (DAG) as the second messenger regulating PKC activity (Kishimoto et al., 1980). Later on, it was found that PKC is not a single protein species, but actually a family of several isoforms that to some extent differ from each other both structurally and functionally.

PKC was initially shown to mediate thrombin-induced release of serotonin in human platelets (Kawahara et al., 1980). However, it was the discovery of PKC being the receptor for the tumour-promoting phorbol esters that implicated a role for PKC in controlling cell proliferation and cancer development (Castagna et al., 1982; Nishizuka, 1984). Since then, PKC has attracted enormous interest as a drug target first in cancer and later in many other diseases. Changes in PKC activity and increased or decreased expression levels of different PKC isoforms have been found in many types of cancer (Hofmann, 2004; Griner and Kazanietz, 2007). Depending on the cell type, the tissue of origin and the PKC isoform, PKCs can act as tumour promoters or tumour suppressors; thus both PKC inhibitors and activators may have potential in cancer therapy. Furthermore, vast evidence implies a role for PKC in the pathophysiology of numerous other diseases, such as Alzheimer's disease (AD), cardiac failure, autoimmune disorders and vascular complications of diabetes (Mochly-Rosen et al., 2012).

There are several possible binding sites for drugs within PKC. The conventional route of producing kinase inhibitors – by targeting the ATP binding site within the catalytic domain – has not been successful with PKC due to lack of specificity (Mochly-Rosen et al., 2012). Many PKC inhibitors have been studied in clinical trials, but none of them have yet reached the market. Problems with selectivity are not surprising, taking into account the vast number of protein kinases with relatively identical ATP-binding clefts. The regulatory region of PKC, and especially the C1 domain, may provide a possibility to develop compounds that are more selective. This approach also enables the development of PKC activators, since the C1 domain is the binding site for DAG and phorbol esters. Even though PKCs are not the only proteins containing a DAG- and phorbol ester-responsive C1 domain, the number of such proteins is considerably smaller than the number of protein kinases, and thus selectivity may be easier to achieve.

A number of C1 domain ligands have been described in the literature: some of them are derived directly from nature, and some are derivatives or analogues of naturally occurring compounds (Boije af Gennäs et al., 2011). As most of the C1 domain ligands from natural sources are highly complex in their chemical structure, their commercial production and chemical modification (e.g. for improving selectivity) is generally unfeasible. The aim of this work was to study structure-activity relationships of a novel group of C1 domain ligands, 5-(hydroxymethyl)isophthalates. The isophthalate derivatives are based on a simple C1 domain-binding template which enables easy synthesis and chemical modification. Furthermore, this work aimed at characterizing the pharmacological effects of the most promising compounds in HeLa human cervical cancer cells and in SH-SY5Y neuroblastoma cells, focusing especially on cell proliferation and morphology.

2. REVIEW OF THE LITERATURE

2.1 Diacylglycerol (DAG) signalling

Phospholipids are major components of cell membrane lipid bilayers. First clues of their role in signal transduction were brought forward in 1953, when ³²P from radiolabelled ATP was found to be incorporated into phospholipids after acetylcholine-mediated stimulation of pancreatic slices (Hokin and Hokin, 1953). Later work has shown that phospholipid hydrolysis is a common phenomenon following stimulation of cells by a variety of extracellular signals.

Diacylglycerol (DAG) is a simple lipid consisting of two fatty acids linked to a glycerol molecule through ester bonds. The combinations of fatty acid chains linked to the positions 1 and 2 of the glycerol backbone may vary, and thus DAG represents a family of heterogenic species (Carrasco and Merida, 2007). It is a constituent of biological membranes, intermediate in the synthesis of more complex lipids, and a source of free fatty acids. First and foremost, DAG plays a major role as a ubiquitous second messenger in signal transduction. It was initially found to activate PKC (Kishimoto et al., 1980; Nishizuka, 1992). Thereafter, it has been found to transmit signals from more than 100 cell surface receptors to its effector proteins inside the cell (Rhee, 2001).

Agonist-induced activation of various G protein-coupled receptors (GPCRs) and receptor tyrosine kinases (RTKs) leads to activation of phospholipase C (PLC), which hydrolyses phosphatidylinositol-4,5-bisphosphate (PIP₂) within the cell membrane (Rhee, 2001). As a result, DAG and inositol-1,4,5trisphosphate (IP₃) are formed. DAG remains at the inner layer of the phospholipid membrane and IP₃ diffuses throughout the cytosol and acts to release calcium from the endoplasmic reticulum. Alternatively, DAG can also be produced indirectly from phosphatidylcholine (PC) via phospholipase D (PLD) and phosphatidic acid phosphohydrolase (PAP) (Martin, 1988): First PLD hydrolyses PC to yield choline and phosphatidic acid (PA), and PA is then further converted to DAG by PAP. DAG production through PLD and PAP is slower and longer-lasting than direct production via PLC, thus providing a DAG synthesis route with a different temporal pattern. At Golgi membranes, DAG can also be produced by sphingomyelin synthase, which transforms ceramide and PC into sphingomyelin and DAG (Villani et al., 2008). In lipid metabolism DAG is further converted to monoacylglycerols by DAG lipases or to triacylglycerols by diacylglycerol acyltransferases (Carrasco and Merida, 2007). It can also be transformed to PC or phosphatidylethanolamine, both of which can be further metabolized to phosphatidylserine (PS). However, the main route for terminating the DAG signalling after phospholipid hydrolysis is diacylglycerol kinase (DGK)-catalysed phosphorylation of DAG to yield PA (Topham and Epand, 2009).

Increased DAG concentration within cellular membranes recruits its target proteins to the membrane, where they bind DAG by a specialized recognition module, the C1 domain. C1 domains were first characterized in PKC (Nishizuka, 1988), but since then six additional classes of proteins have been reported to contain DAG-responsive C1 domains (see chapter 2.3). While the C1 domain is regarded as the major receptor for DAG, also other protein domains, such as the catalytic domains of DAG kinases and DAG lipases, can bind DAG. With numerous routes for synthesis and degradation and various effector proteins, precise control of DAG production and clearance is crucial for appropriate cellular function. DAG-mediated signal transduction requires rapid and transient

changes in DAG pools at specific cellular compartments. Together with other intracellular responses, the spatiotemporal control of DAG production determines the nature, intensity and duration of signals initiated. Localized DAG synthesis at specific cellular compartments, such as plasma membrane, Golgi or mitochondria, also serves as a means of regulating downstream signalling. Furthermore, DAG production via PLC- or PLD-mediated pathways differ not only in temporal aspect but also in DAG species generated, and this may affect downstream signalling (Carrasco and Merida, 2007). How DAG signalling is targeted to a specific DAG effector is, however, not known.

Phorbol esters, such as phorbol-12-myristate-13-acetate (PMA) and phorbol-12,13-dibutyrate (PDBu) are natural toxins that mimic the actions of DAG and induce translocation of PKC and other DAG effectors to the membrane via binding to the C1 domain (Goel et al., 2007). They have been widely used as research tools to decipher the physiological roles of PKC and other DAG effectors. However, since phorbol esters are more potent and stabile than DAG, the responses evoked by them in the cellular environment differ greatly from those initiated by the physiological ligand DAG.

2.2 Protein kinase C (PKC), the primary DAG effector

2.2.1 PKC family members and domain structure

The family of PKC serine/threonine kinases consists of ten isoenzymes making up 2% of the human kinome, and is classified under the group of AGC kinases (named AGC after protein kinases A, G and C) (Manning et al., 2002). PKC isoforms are formed of a single polypeptide chain containing a conserved catalytic domain and a more variable regulatory region that are linked together with a so-called hinge region (Newton, 2001). They are divided into three classes based on their regulatory domain structure and activation requirements (Fig. 1). The classical/conventional PKCs (cPKCs) α , β and γ were the first individual isoforms discovered (Coussens et al., 1986). Due to alternative splicing, the gene encoding PKC β produces two protein transcripts, PKC β I and PKC β II that differ at their C terminus (Coussens et al., 1987). The calcium-independent subgroup of novel PKCs (nPKCs) comprises of isoforms δ , ϵ , η and θ (Ono et al., 1987; Osada et al., 1990; Osada et al., 1992); and the isoforms ζ and ι/λ (human/mouse homologues, respectively) belong to the subgroup of atypical PKCs (aPKCs) (Newton, 2001). The atypical PKC isoforms are more distant members of the PKC family and are not activated by DAG, like cPKCs and nPKCs. Therefore, they are not covered in this literature review.

The PKC catalytic domain resides in the C-terminal end of the polypeptide and shares substantial similarity with other serine/threonine as well as tyrosine kinases (Newton, 2001). It follows a classical bilobal kinase fold consisting of a smaller N-terminal lobe that is mainly composed of β sheets and contains the glycine-rich ATP binding site (C3 domain), and a larger predominantly α helical C-terminal lobe with binding sites for magnesium and substrates (C4 domain) (Xu et al., 2004; Grodsky et al., 2006). The C-terminal end of the catalytic domain, (V5 sequence), is more variable among PKC isoforms and participates e.g. in the regulation of the subcellular localization of the enzyme (Newton, 2001).

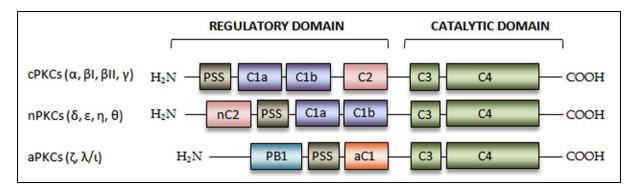


Figure 1. Schematic domain structures of protein kinase C (PKC) family members. The regulatory domains in the N-terminal part of classical and novel PKC isoforms (cPKCs and nPKCs, respectively) contain the C1a and C1b domains that are receptors for diacylglycerol (DAG), while the atypical C1 domain (aC1) of atypical PKCs (aPKCs) is unresponsive to DAG. The C2 domains bind anionic phospholipids and, in the case of cPKCs, Ca²⁺. The C2 domain of nPKCs (nC2) is insensitive to Ca²⁺. All PKC isoforms have a pseudosubstrate sequence (PSS) in the regulatory region and aPKCs also contain a Phox and Bem 1 (PB1) domain. The catalytic domain consists of two conserved subdomains: the C3 motif contains the ATP binding site, and the C4 motif binds substrates and magnesium. Reprinted with colours from IV with permission from Elsevier.

All PKC isoforms contain an autoinhibitory pseudosubstrate sequence (PSS) in their regulatory region (Newton, 2001). The sequence of the pseudosubstrate resembles that of substrate peptides, but the threonine or serine in the phosphoacceptor position is replaced by alanine. It regulates PKC enzymatic activity by binding to the substrate binding site and thus blocking the entry of substrates into the active cleft (House and Kemp, 1987). The regulatory regions of cPKCs and nPKCs also contain a tandem repeat of cysteine-rich C1-domains designated C1a and C1b (Hurley et al., 1997), which participate in the allosteric regulation and membrane targeting of PKC. Their structure and function are described in section 2.2.2.

The C2 domain found in the regulatory region of cPKCs and nPKCs, as well as in a large number of unrelated proteins, is a globular domain that is mainly composed of anti-parallel β strands (Sutton et al., 1995). It is a membrane-targeting module with affinity for anionic phospholipids and phosphatidylinositols (Rizo and Südhof, 1998). The C2 domains of cPKCs bind Ca²⁺: crystal structures of PKCα and PKCβ C2 domains revealed binding of two or three Ca²⁺ ions to conserved aspartic acid (Asp) residues and coordination of a PS directly to one of the Ca²⁺ ions (Sutton and Sprang, 1998; Verdaguer et al., 1999; Ochoa et al., 2002). The Ca²⁺-insensitive nPKC isoforms have C2 domains that lack the Asp residues critical for Ca²⁺ binding and are thus insensitive to Ca²⁺ (Ochoa et al., 2001). They possess a different topology and their Ca²⁺-independent binding to anionic lipids is mediated by loops 1 and 3 (Pappa et al., 1998; Ochoa et al., 2001). Besides serving as membrane-targeting modules, the PKC C2 domains are involved in PKC autoinhibition by intramolecular interactions with the C1 domain and in mediating protein-protein interactions (Kirwan et al., 2003; Benes et al., 2005).

2.2.2 Structure and function of PKC C1 domains

The PKC C1 domain was first identified as the conserved binding site for DAG and phorbol esters (Ono et al., 1989). It is a cysteine-rich structure of approximately 50 amino acids, with a characteristic HX₁₂CX₂CX₁₃₋₁₄CX₂CX₄HX₂CX₇C motif, where H is histidine, C is cysteine, and X is any

amino acid (Ono et al., 1989; Steinberg, 2008). The sequence resembles that of the zinc finger motif in some DNA-binding proteins (Ono et al., 1989), and correct folding of the domain requires coordinated binding of two zinc ions (Hommel et al., 1994). However, the C1 domain adopts a globular fold distinct from the DNA-binding zinc finger motifs. The crystal structure of PKCδ C1b domain with bound phorbol ester revealed that the binding site for DAG and phorbol esters is a polar groove in an otherwise hydrophobic surface of the "top" part of the C1 domain (Zhang et al., 1995). Phorbol ester binding covers the polar surface of the binding groove and completes a continuous hydrophobic surface enabling the C1 domain to penetrate partially into the lipid bilayer. The positively-charged residues in the middle part of the domain may then further stabilize the membrane insertion by interacting with negatively-charged head groups of acidic phospholipids at the membrane.

All full-length cPKC and nPKC isoforms exhibit similar affinities for DAG (dissociation constant for $[^3H]$ PDBu binding K_i =0.2-0.4 μ M) and phorbol esters (equilibrium dissociation constant K_d for PDBu <1 nM) (Kazanietz et al., 1993). Binding is fully dependent on phospholipids, particularly on PS. However, depending on the isoform, the individual C1a and C1b domains play either equivalent or non-equivalent roles in ligand binding and membrane targeting. The classical PKC γ and the novel PKC γ have C1a and C1b domains that bind both DAG and phorbol esters with high affinity and both C1 domains contribute to membrane binding of these isoforms (Irie et al., 1998; Ananthanarayanan et al., 2003; Stahelin et al., 2005). The individual C1 domains of other PKC isoforms, however, seem to play unequal roles. For example, the C1a domains of cPKC α and nPKC δ have a higher affinity for DAG, while the phorbol ester-induced activation is mediated by high affinity binding to the C1b domains (Slater et al., 1996; Ananthanarayanan et al., 2003; Stahelin et al., 2004). By contrast, the C1b domain plays a dominant role in DAG-induced membrane targeting of PKC θ (Melowic et al., 2007), which may be mediated by a differentially oriented tryptophan residue at the rim of the ligand-binding cleft (Rahman et al., 2013).

The C1 domains also play important roles in determining the subcellular destination of PKC translocation. The hydrophilicity/lipophilicity of the lipid activator can affect PKC distribution (Wang et al., 2000). Although the binding of PKC to PS and other anionic phospolipids is mediated by the C2 domain, the PS-specificity of cPKCs is mediated by their C1 domains (Bittova et al., 2001). Furthermore, additional lipid cofactors, such as ceramide and arachidonic acid can translocate PKCs to different cell membranes (Huwiler et al., 1998; Kashiwagi et al., 2002). At least for PKCδ and PKCε this has been shown to be mediated via the C1b domain (Kashiwagi et al., 2002).

An emerging role for the C1 domains is in mediating protein-protein interactions. For example, several isoforms are targeted to Golgi via a conserved methionine in the C1b domain (Schultz et al., 2004). The binding partner for C1 domains in the Golgi compartment has been identified as Golgi/endoplasmic reticulum protein p23 (Tmp21) (Wang and Kazanietz, 2010). Furthermore, PKCβII binds the centrosomal protein pericentrin via its C1a domain and thereby regulates microtubule organization (Chen et al., 2004), and PKCɛ interacts with the intermediate filament protein peripherin via its C1b domain (Sunesson et al., 2008). The C1 domain-mediated protein-protein interactions play a role in targeting PKC activity to a certain subcellular compartment, but they may also account for some of the non-catalytic functions of PKCs (see section 2.2.4). However, the extent and significance of protein-protein interactions in regulating PKC functions is not thoroughly understood.

2.2.3 Regulation of PKC activity

The activity of PKC is under strict regulation, and its phosphorylation state, conformation, and subcellular localization must be correct for its proper function. Newly synthesized PKC is catalytically incompetent and requires a series of priming phosphorylations to gain catalytic competence and appropriate intracellular localization (Newton, 2001; Steinberg, 2008). The three conserved phosphorylation sites lie within the catalytic domain: the activation loop (T497 in PKC α), the turn motif (T638 in PKC α) and the hydrophobic motif (T657 in PKC α). The mature (phosphorylated) PKC is maintained in an inactive conformation in cytosol and its activation is regulated allosterically by C1 and C2 domains. The allosteric activation mechanisms of classical and novel PKC subfamilies differ substantially from each other and are therefore presented separately.

The activity of cPKCs is predominantly regulated by intracellular levels of Ca²⁺ and DAG, and the additional lipid cofactors, such as PS, play a role in membrane targeting (Nishizuka, 1988; Nishizuka, 1992). A schematic model of cPKC activation is presented in Figure 2. Upon phospholipid hydrolysis, increased intracellular Ca²⁺ concentration first leads to binding of Ca²⁺ to the C2 domain, which increases the affinity of the C2 domain for anionic lipids and induces a rapid translocation of PKC from the cytosol to the cell membrane (Oancea and Meyer, 1998; Medkova and Cho, 1999; Bittova et al., 2001). The C2 domain-membrane interactions are mediated by PS and PIP₂ (Verdaguer et al., 1999; Corbalán-García et al., 2003a). At the membrane, cPKCs diffuse in a two-dimensional manner and the probability for encountering the rarer DAG molecules is thus increased (Nalefski and Newton, 2001). Increased DAG concentration at the membrane allows binding of DAG by the C1a domain thus inducing partial penetration of the C1a domain into the lipid bilayer and a conformational change that releases the PSS from the catalytic site (Leonard et al., 2011). The conformational change also uncovers the DAG binding site within the C1b domain, which in the inactive conformation is clamped by the C-terminal part of the catalytic domain: the so-called NFD (asparagine-phenylalanine-aspartate) motif and the amino acid residues immediately preceding it. Binding of another DAG molecule to the C1b domain releases the NFD motif thus enabling enzyme activation.

Notwithstanding the general requirement for Ca²⁺ in the activation of cPKCs, increased intracellular Ca²⁺ is dispensable for cPKC activation: a tight interaction of the C1 domain with phorbol esters or DAG can induce membrane penetration of the C1 domain and cPKC activation even in the absence of Ca²⁺ (Kazanietz et al., 1992). However, simultaneous Ca²⁺ signalling has been shown to accelerate DAG and phorbol ester binding and activation of PKCy (Oancea and Meyer, 1998), and the interplay of calcium and phospholipids thus provides a way for spatial and temporal regulation of cPKCs.

Because of the Ca²⁺-insensitivity of their C2 domains, nPKCs are mainly regulated by DAG (Nishizuka, 1988; Newton, 2001). An increase in DAG level at cellular membranes induces nPKC translocation to the membrane, where the C1 domains bind DAG and penetrate partially into the membrane releasing the PSS from the catalytic site (Lehel et al., 1995). Whether a conformational change including the NFD motif is involved also in nPKC activation is not known. Depending on the nPKC isoform, their C2 domains play diverging roles in membrane binding. The C2 domain of PKCε participates in membrane docking by binding to anionic phospholipids (Ochoa et al., 2001). In contrast to cPKCs, it shows however no selectivity for PS and actually binds PA-containing membranes with a slightly higher affinity than those containing PS (Corbalán-García et al., 2003b). The C2 domains of PKCδ and PKCθ are structurally different from those of PKCε and PKCη (see

Corbalán-García and Gomez-Fernandez, 2010), and at least the PKCδ C2 domain does not participate in membrane recruitment (Giorgione et al., 2006). The lack of C2 domain-membrane interaction is compensated by increased affinity of the C1 domain for DAG-containing membranes (Dries et al., 2007).

In addition to the general activation by Ca^{2+} and lipid cofactors, alternative ways of PKC regulation exist. The nPKC isoforms δ , ϵ and θ can be cleaved in the hinge region by caspases 3 and 7 during apoptosis, leading to the release of constitutively active catalytic fragments (Emoto et al., 1995; Datta et al., 1997; Basu et al., 2002). Furthermore, oxidative modifications can also modulate PKC activity (Gopalakrishna and Jaken, 2000).

Physiological DAG-induced PKC activation is generally transient and is terminated when DAG is metabolized. However, in the case of prolonged PKC activation e.g. after phorbol ester exposure, the activity is terminated via down-regulation at the protein level (Newton, 2001). At least two pathways for agonist-induced PKC down-regulation have been identified: ubiquitination followed by degradation by the proteasome (Lee et al., 1996b) and degradation via a proteasome-independent mechanism (Leontieva and Black, 2004). Dephosphorylation plays a major role in directing PKC for down-regulation (Lee et al., 1996a). The serine/threonine phosphatase PHLPP (pleckstrin homology (PH) domain and leucine-rich repeat protein phosphatase) is known to dephosphorylate the hydrophobic motif of cPKCs and nPKCs, thus directing them to degradation by the proteasome-dependent pathway (Gao et al., 2008).

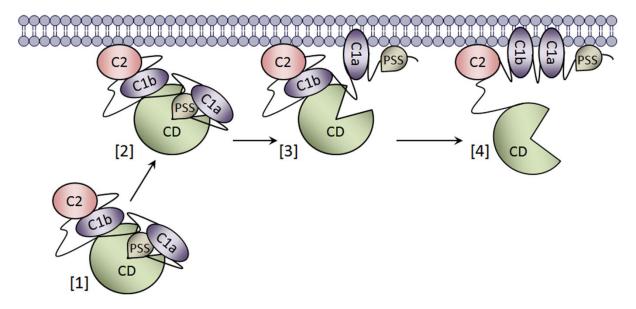


Figure 2. Schematic model for cPKC activation. Inactive PKC resides in cytosol with the pseudosubstrate sequence (PSS) and C1a domains masking the catalytic site within the catalytic domain (CD) [1]. Increased intracellular calcium concentration induces translocation of PKC to the membrane, where the C2 domain mediates binding to PS and PIP₂ [2]. Binding of DAG to the C1a domain induces a conformational change releasing the C1a domain and subsequently removing PSS from the catalytic cleft [3]. Binding of a second DAG molecule to the C1b domain results in unclamping of the C1b-kinase assembly thus activating the enzyme [4].

2.2.4 PKC-mediated signal transduction

Classical and novel PKCs are involved in an overwhelming variety of biological processes in eukaryotic organisms. Most importantly, they participate in signalling pathways controlling cell proliferation, survival, transformation, differentiation, inflammation and apoptosis (Fig. 3). Signalling routes that are controlled by PKC-mediated phosphorylation include, for instance, mitogen-activated protein kinase (MAPK) and stress-activated protein kinase (SAPK) cascades, nuclear factor κΒ (NF-κΒ) signalling, glycogen synthase kinase 3 (GSK3) signalling, protein kinase B (PKB) signalling, as well as signal transducer and activator of transcription (STAT)-regulated gene expression (Yang and Kazanietz, 2003; Mackay and Twelves, 2007). Although PKC isoforms are activated by the same second messengers and they have overlapping substrate specificities, PKC-mediated signal transduction is often specific for the isoform, for the cell type and for the stimulus. Different PKC isoforms can even have opposing effects on the same process (Chen et al., 2001; Tourkina et al., 2005). The reasons and mechanisms of such diversity are not thoroughly understood, but the unique compartmentalisation of PKC isoforms is thought to play an important role in mediating the isoformspecific effects (Yang and Kazanietz, 2003). Protein-protein interactions with a group of proteins called RACKs (receptors for activated C kinases) and other anchoring proteins participate in targeting specific PKC isoforms in close proximity to their substrates and thus control isoform-specific functions of PKCs (Mochly-Rosen, 1995). As an example, activation of c-Jun N-terminal kinase 1 (JNK1) signalling by PKC requires the presence of RACK1 (López-Bergami et al., 2005).

The Raf - MEK1/2 - ERK1/2 pathway is a good example of a signalling cascade, which can be activated by most PKC isoforms (Schönwasser et al., 1998; Mackay and Twelves, 2007). It controls cell cycle progression and cell differentiation and is implicated in induction of abnormal cell proliferation and oncogenic transformation (Roskoski, 2012). However, the outcome of PKC-induced ERK1/2 activation depends not only on the PKC isoforms, but also on the cell type and on the duration of activation. For example, PKCα activation leads to activation of ERK1/2, p38 MAPK and JNK, and subsequent cell differentiation and inhibition of proliferation in rhabdomyosarcoma cells (Mauro et al., 2002). However, in NIH3T3 mouse fibroblast cells PMA-induced PKCα activation initiates the ERK1/2 cascade and induces cell proliferation (Kolch et al., 1993). Furthermore, in cultured primary pituitary cells, a short (15 min) PMA exposure leads to PKC_E-mediated ERK1/2 activation and cell proliferation, while a longer (3 h) PMA treatment activates PKCα and attenuates the PMA-induced ERK1/2 activation and cell proliferation (Petiti et al., 2008). Moreover, the Raf-MEK-ERK1/2 cascade can be activated by PKCs in a Ras-dependent or independent manner. PKCδ activation by PMA leads to Ras-independent but Raf-dependent ERK1/2 activation in COS and NIH3T3 cells (Ueda et al., 1996), while estradiol induces PKCδ- and Ras-dependent ERK1/2 activation in MCF-7 breast cancer cells (Keshamouni et al., 2002).

An emerging role for PKC-mediated signalling lies in their non-catalytic functions, which are predominantly attributed to protein-protein interactions mediated by the regulatory domains. As an illustration, PKC ϵ induces neurite outgrowth in neuroblastoma cells via its C1b domain independently of catalytic activity (Zeidman et al., 1999a; Ling et al., 2007). Moreover, PKC α protein but not kinase activity is pivotal for glioma cell survival and proliferation (Cameron et al., 2008). The effect is mediated by the fully phosphorylated, folded form of PKC α , and it can be blocked with a C1 domain-targeted PKC inhibitor calphostin C, but not with an ATP-competitive inhibitor. However, the physiological relevance of these non-catalytic functions still remains to be clarified.

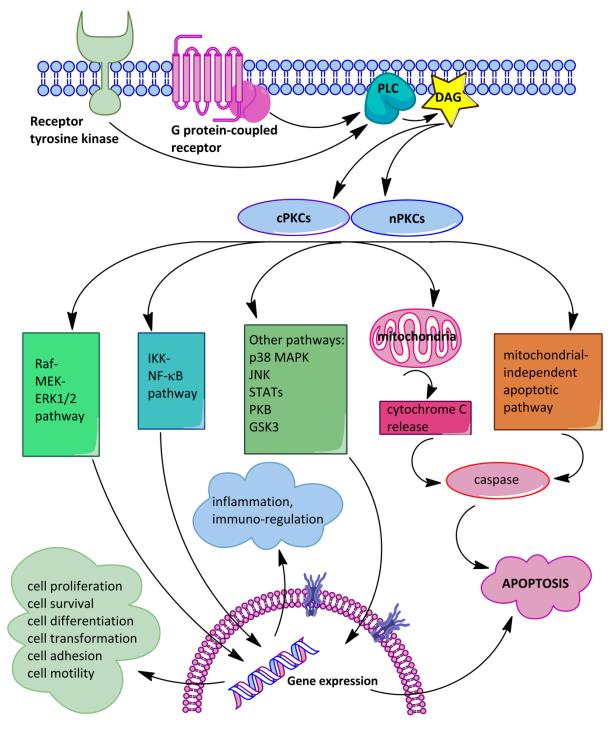


Figure 3. Signalling pathways regulated by DAG-responsive PKC isoforms. Transient diacylglycerol (DAG) generation after activation of receptor tyrosine kinases or G protein-coupled receptors activates classical and novel PKC isoforms. PKC activation modulates numerous signalling pathways that control for example cell survival, cell proliferation and apoptosis. ERK, extracellular signal-regulated protein kinase; GSK3, glycogen synthase kinase 3; IKK, inhibitor of κB kinase; JNK, c-JUN N-terminal kinase; MAPK, mitogenactivated protein kinase; MEK, MAPK kinase; NF-κB, nuclear factor κB; PKB, protein kinase B; PLC, phospholipase C; STAT, signal transducer and activator of transcription.

A vast number of knock-out animal studies have been carried out to resolve the physiological importance of each PKC isoform. However, it seems that in many cases other PKC isoforms are able to substitute for the lacking one: despite the central role for PKC in signal transduction, all PKC

knock-outs are viable and exhibit only mild phenotypic changes (reviewed in Roffey et al., 2009). Therefore, only broad and non-specific assumptions of isoform-specific physiological roles can be made based on studies with genetically modified animals. Studies with PKCα-deficient mice suggest that PKCα plays an important role in insulin signalling through the phosphoinositide 3-kinase (PI3K) cascade (Leitges et al., 2002) and in tumour formation in the two-stage skin carcinogenesis model (Hara et al., 2005). PKCy is prominently expressed in the CNS and plays a role in learning and memory: PKCy-deficient mice have altered long-term potentiation of synaptic transmission in hippocampus and exhibit deficits in spatial and contextual learning (Abeliovich et al., 1993). Also PKCs plays a role in the CNS: mice lacking PKCs exhibit altered GABAA receptor signalling and attenuated hyperalgesia (Hodge et al., 1999; Khasar et al., 1999). Deficiency of PKCn has been reported to impair wound healing and enhance tumour formation in the two-stage skin carcinogenesis model (Chida et al., 2003), whereas PKC isoforms β , δ and θ seem to be important for correct operation of the immune system. PKC β and PKC δ play indispensable but opposing roles in B cell-mediated immunity: mice deficient in PKC\$I and PKC\$II develop B cell immunodeficiency, while knocking out PKCδ induces B cell proliferation and autoimmunity (Leitges et al., 1996; Miyamoto et al., 2002). As for PKCO, mice deficient in this isoform exhibit impaired T cell receptor signalling (Sun et al., 2000).

2.3 Other DAG effectors

In addition to PKC, six other classes of proteins contain DAG- and phorbol ester-responsive C1 domains. Their schematic domain structures are presented in Figure 4. Many other proteins have atypical C1 domains that do not respond to DAG or phorbol esters. They are however not included in this literature review. Furthermore, DAG effectors that do not contain a C1 domain, such as transient receptor potential (TRP) channels, are not covered.

2.3.1 Protein kinase D (PKD)

The protein kinase D (PKD) family of serine/threonine kinases consists of three members: PKD1 (PKC μ), PKD2 and PKD3 (PKC ν) (Wang, 2006; Fu and Rubin, 2011). PKC μ and PKC ν were initially considered as members of the PKC family, but now PKD isoforms are classified as a subgroup of calcium/calmodulin-dependent protein kinase (CAMK) family based on sequence similarities of the catalytic domains (Manning et al., 2002). Similarly to PKC, PKD isoforms consist of an N-terminal regulatory region and a C-terminal catalytic domain (Fig. 4). The autoinhibitory regulatory domains include a tandem repeat of C1 domains (C1a and C1b) and a PH domain. Deletion of both C1 domains, the PH domain or the whole regulatory region leads to fully activated PKD1 (Iglesias and Rozengurt, 1998; Iglesias and Rozengurt, 1999; Vertommen et al., 2000). The individual C1 domains exhibit different ligand-binding affinities towards phorbol esters and DAG (Iglesias et al., 1998). The C1b domains of all PKD isoforms bind [3 H]PDBu with high affinity (K_d <1 nM), while their affinities for the synthetic DAG analogue 1,2-dioleoyl-sn-glycerol (DOG) are substantially lower (K_i =154-168 nM) (Chen et al., 2008a). The C1a domains of PKD1 and PKD2 have very weak affinities for PDBu or DOG, while the PKD3 C1a domain exhibits high affinity for both PDBu (K_d =1.6 nM) and DOG (K_i =44 nM). The lipid requirements for ligand binding to the PKD C1 domains do not differ significantly from

those of PKCs despite different additional membrane-targeting domains (PH domain in PKD vs. C2 domain in PKC) (Wang et al., 2003).

The activation mechanisms are best known for PKD1, but based on the similar molecular architecture PKD2 and PKD3 are likely to share common regulation with PKD1. Binding of DAG to the C1 domain results in translocation of PKD to the membrane, but generally the translocation *per se* is not sufficient for PKD activation (Wang, 2006; Fu and Rubin, 2011). PKD1 can be activated by at least two mechanisms: (I) by phosphorylation of two conserved serines (S738 and S742 in PKD1) in the activation loop (Rozengurt et al., 2005; Steinberg, 2012), and (II) by caspase-mediated cleavage resulting in the release of a constitutively active kinase domain (Endo et al., 2000).

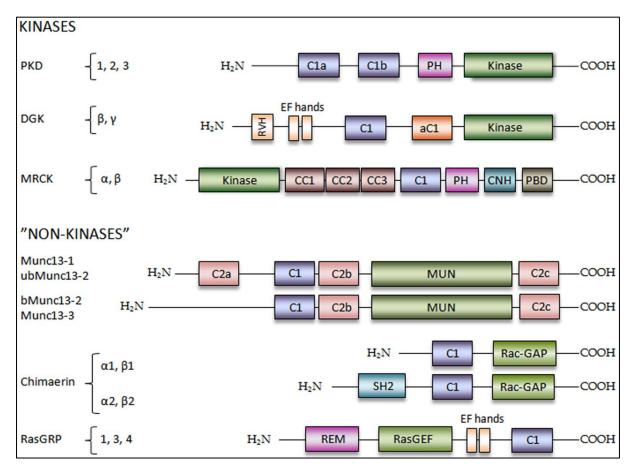


Figure 4. Schematic domain structures of "non-PKC" DAG effectors. All protein kinase D (PKD) isoforms (1-3) contain two diacylglycerol (DAG)-responsive C1 domains, whereas only diacylglycerol kinase (DGK) isoforms β and γ have C1 domains that bind DAG. The myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) isoforms α and β have been shown to bind DAG. All Munc13 isoforms (1-3) are physiological effectors of DAG. Both chimaerin genes, α- and β-chimaerin, produce two splice variants, all of which contain a DAG-responsive C1 domain. The Ras guanyl-releasing protein (RasGRP) isoforms 1, 3 and 4 are DAG-responsive, while RasGRP2 is not. aC1, atypical C1 domain; CC, coiled-coil domain; CNH, citron homology domain; C2, calcium-responsive C2 domain; MUN, MUN domain; PBD, p21-binding domain; PH, pleckstrin homology domain; Rac-GAP, Rac GTPase-activating protein (domain); RasGEF, Ras guanine nucleotide exchange factor (domain); REM, Ras exchange motif; RVH, recoverin homology domain; SH2, Src homology 2 domain.

Activation of PKD by phosphorylation is predominantly mediated by nPKCs, (Rozengurt et al., 2005), but also PKC α can phosphorylate and activate PKD (Wong and Jin, 2005). DAG production at the plasma membrane thus activates PKD by activating its upstream kinase (PKC) and by inducing its colocalization with PKC, thus enabling phosphorylation (Matthews et al., 2000; Waldron and Rozengurt, 2003). Several other phosphorylation sites and upstream kinases also regulate PKD1 activity and signalling in cells (see Steinberg, 2012). Selective activation of PKD isoforms may be mediated by colocalization of PKDs and receptor-PLC signalling modules in distinct membrane microdomains, as suggested by the Steinberg group (Guo et al., 2011). They showed that even though norepinephrine, endothelin 1 and thrombin all activate PLC β , norepinephrine selectively stimulates PKD1; thrombin selectively stimulates PKD2; and endothelin 1 stimulates both PKD1 and PKD2. However, the significance of this kind of selective regulation is unclear - especially since pathway-specific substrates are yet to be identified.

PKD isoforms promote cell survival and cell proliferation e.g. by phosphorylating heat shock protein 27 (Hsp27) and by inducing ERK1/2 phosphorylation (Wang, 2006; Guha et al., 2010). They control cytoskeleton reorganization and inhibit directed cell movement by phosphorylating and inactivating protein phosphatase SSH1L, which leads to accumulation of phosphorylated and inactive cofilin and thus inhibition of actin depolymerization (Eiseler et al., 2009). They also phosphorylate cortactin, which leads to inhibition of actin polymerization at the leading edge (Eiseler et al., 2010). PKDs can also suppress cell motility by phosphorylating the Ras and Rab interactor 1 (RIN1), E-cadherin and the transcription factor SNAI1, or by down-regulating matrix metalloproteinase (MMP) expression (Fu and Rubin, 2011; Olayioye et al., 2013). DAG-mediated recruitment of PKD to trans-Golgi network (TGN) regulates fission of protein and lipid transport vesicles that carry cargo from TGN to the cell surface (Liljedahl et al., 2001; Baron and Malhotra, 2002). PKD isoforms also participate in the control of gene expression by phosphorylating class II histone deacetylases (HDACs) 5 and 7 thereby attenuating HDAC-mediated repression of gene expression (see Fu and Rubin, 2011).

The physiological roles of individual PKD isoforms are still mostly unknown, but studies in genetically modified mice have shown that PKD1 is indispensable for embryonic development, since deficiency of catalytically active PKD1 causes embryonic lethality (Fielitz et al., 2008). Furthermore, cardiac-specific deletion of *Pkd1* revealed that PKD1 plays a key role in cardiac remodelling induced by stress stimuli (Fielitz et al., 2008). Mice deficient in PKD2 develop normally, but their T cell-dependent immunoglobulin G (IgG), immunoglobulin M and cytokine production is inhibited, implying that PKD2 plays a unique role in the regulation of mature peripheral lymphocytes (Matthews et al., 2010). No studies with PKD3 knock-out animals have been reported, but PKD3 has been suggested to play a role in pathological cardiac remodelling (Li et al., 2011) and in invasiveness of prostate cancer (Chen et al., 2008b).

2.3.2 Diacylglycerol kinases (DGKs)

DGKs are a family of lipid kinases that modulate intracellular levels of DAG and PA by phosphorylating DAG to yield PA (Shulga et al., 2011). The ten isoforms are divided into five subtypes based on their domain structure. In addition to the DAG-binding catalytic domain, all isoforms contain two or three C1 domains in their N-terminal regulatory region. However, only the C1a domains of DGK β and DGK γ respond to DAG and phorbol esters (Shindo et al., 2003), and therefore only these isoforms are covered in this literature review.

DGKs β and γ are classified into type I DGKs, and their schematic domain structure is presented in Figure 4 (Shulga et al., 2011). Interactions between the regulatory domains and the catalytic domain keep DGKs in an inactive state when no cofactors are present (Takahashi et al., 2012). Binding of Ca²⁺ to the EF hand motifs induces a conformational change that allows membrane binding and activation of the enzyme. The DGK C1 domains serve as membrane-targeting and protein-protein interaction modules. The affinities of PDBu and other C1 domain ligands for the individual DGK β and DGK γ C1a domains as well as for the whole DGK γ protein are in the same range as those observed for PKC (Shindo et al., 2003). DGK activity is also regulated by phosphorylation: for example, DGK γ can be activated via direct phosphorylation by PKC γ (Yamaguchi et al., 2006). DGK β has been reported to localize in cell periphery and to associate with actin cytoskeleton (Caricasole et al., 2002; Kobayashi et al., 2007), while DGK γ has been detected in the Golgi and nucleus (Matsubara et al., 2006; Kobayashi et al., 2007), suggesting isoform-specific physiological functions. Both isoforms, however, translocate to plasma membrane upon phorbol ester treatment (Shirai et al., 2000; Caricasole et al., 2002).

All DGK isoforms interfere with DAG signalling by ending the effects of elevated DAG levels, and thus their activity terminates DAG-initiated signalling mediated by other DAG effectors. Additionally, their influence extends to signalling cascades and proteins whose activity is regulated by PA (see Shulga et al., 2011). Although the cellular and physiological functions of DGKs have not been well characterized, several isoforms have been implicated in controlling cell proliferation and morphology and immune cell signalling (Sakane et al., 2007; Shulga et al., 2011). DGKβ is prominently expressed in neurons and plays an important role in dendritic outgrowth and neurite spine formation, thereby contributing to cognitive processes and behaviour (Hozumi et al., 2009; Kakefuda et al., 2010; Shirai et al., 2010). DGKγ, which is also predominantly expressed in the CNS, has been implicated in cytoskeletal reorganization. It binds to and activates β2-chimaerin (see section 2.3.5) thus inhibiting the formation of lamellipodia (Tsushima et al., 2004; Yasuda et al., 2007). It has also been suggested to play a role in the induction of filopodia-like protrusions independent of its catalytic activity (Tanino et al., 2012). Outside the CNS, DGKγ has been linked to macrophage differentiation (Yamada et al., 2003).

2.3.3 Myotonic dystrophy kinase-related Cdc42-binding kinases (MRCKs)

Myotonic dystrophy kinase-related Cdc42-binding kinases (MRCKs) are serine/threonine kinases that were first identified and characterized in 1998 (Leung et al., 1998). Originally two isoforms (MRCKα and MRKCβ) were identified, and MRCKγ was described in 2004 (Ng et al., 2004). MRCKs are structurally related to dystrophia myotonica protein kinases and RhoA-binding kinases (Leung et al., 1998), and their domain organization differs substantially from that of other DAG-responsive protein kinases (Fig. 4) (Leung et al., 1998; Tan et al., 2001b). The catalytic domain lies in the N-terminal end and is followed by numerous regulatory domains. The coiled-coil (CC) domains, and especially a motif termed KIM (kinase inhibitory motif) within the CC domains 2-3, have an autoinhibitory role on MRCK kinase activity, and they are suggested to keep the dimeric kinase in an inactive closed conformation (Tan et al., 2001b). The CC domains are followed by a single C1 domain (see below) and a PH domain, which participates in controlling the localization of the enzyme by interacting with lipids and cytoskeleton. The p21-binding domain (PBD) is responsible for binding to the small GTPase Cdc42. This interaction is not essential for kinase activity, and thus probably serves to target MRCK to its activators and/or substrates (Leung et al., 1998). The crystal structure of MRCKβ revealed that

in the active conformation the MRCK dimer is held together by interactions between four N-terminal helices and the C-termini of the kinase domains (Heikkilä et al., 2011).

The phorbol ester binding affinities of the isolated C1 domains of MRCK α and MRKC β are weaker (K_d values for PDBu 10 and 17 nM, respectively) as compared with those of C1b domains of PKC α or PKC δ (K_d values for PDBu 3.4 and 0.18 nM, respectively) (Choi et al., 2008). Furthermore, ligand selectivity of MRCK C1 domains resembles more that of PKC α C1b domain than that of PKC δ C1b, and the binding is fully dependent on PS. No information on the DAG/phorbol ester binding properties of MRCKy C1 domain is available. Exposure of cells to PMA increased the kinase activity of immunoprecipitated MRCKα, and therefore it was proposed that ligand binding to the C1 domain induces a conformational change that disrupts the interaction between KIM and the catalytic domain and allows activation of the kinase (Tan et al., 2001b). However, no evidence of DAGmediated activation of MRKCs in cellular context has been published. Due to the lower affinity of MRCK C1 domains for DAG it has been suggested that additional elements within the MRCK structure may be required to render the enzyme DAG-responsive (Choi et al., 2008). Alternatively, other physiological mechanisms may be more important in regulating MRCK activity. Indeed, direct interaction between KIM and leucine repeat adaptor protein 35a was shown to abrogate KIMmediated MRCK autoinhibition and activate MRCK (Tan et al., 2008). Furthermore, alternative splicing of MRCKα may affect its activity and Cdc42 binding (Tan et al., 2003).

Although not as extensively studied as many other DAG effectors, the physiological role of MRCKs in regulating cytoskeletal proteins is quite well established. Upon identification, MRCKs were already described as effectors of the small GTPase Cdc42 in promoting cytoskeletal reorganization by phosphorylating myosin light chain (MLC) 2 (Leung et al., 1998). Furthermore, MRCKs have been show to phosphorylate a number of other cytoskeleton-associated substrates, such as myosin 18 (Tan et al., 2008), myosin binding subunit of MLC phosphatase (Tan et al., 2001a), moesin (Nakamura et al., 2000) and LIM domain kinase (LIMK) (Sumi et al., 2001), which in turn phosphorylates and inactivates cofilin, an actin-depolymerizing protein. By controlling the actomyosin cytoskeleton reorganization, MRCKs have been shown to play a role in neurite outgrowth in PC12 cells (Chen et al., 1999) and in filopodia formation in NIH3T3 fibroblasts (Nakamura et al., 2000). They also control cell migration by regulating cell contractility (Groeger and Nobes, 2007) and by modulating lamellar actomyosin retrograde flow (Gomes et al., 2005). Furthermore, tumour cell invasion with rounded morphology is regulated by cooperated Cdc42/MRCK and Rho/Rho-associated protein kinase (ROCK) signalling, while invasion with elongated cell morphology depends on Cdc42/MRCK signalling (Wilkinson et al., 2005). Isoformspecific functions for MRCKs have not been reported; on the contrary, high functional redundancy seems to exist at least among isoforms α and β (Wilkinson et al., 2005; Lefort et al., 2007).

2.3.4 Munc13 proteins

Munc13s are a family of four mammalian homologues of *Caenorhabditis elegans* Unc-13 scaffolding protein that regulate synaptic vesicle exocytosis (Brose et al., 2000; Brose et al., 2004). The Munc13 isoforms 1–3 consist of two or three C2 domains depending on the isoform, a single C1 domain and a large MUN domain (Fig. 4) (Basu et al., 2005). Munc13-4 is truncated from the N-terminus so that it lacks the C1 domain and is therefore insensitive to DAG and phorbol esters (Koch et al., 2000).

The Munc13 C2 domains play a role in phospholipid recognition in a calcium-independent or calcium-dependent manner, depending on the C2 domain: only the C2b domains are sensitive to Ca²⁺ (Brose et al., 1995; Shin et al., 2010). Immediately N-terminal of the C1 domain lies a short sequence that serves as a calmodulin binding site and participates in the Ca²⁺-dependent regulation of Munc13 function (Junge et al., 2004). The large MUN domain between the central and the C-terminal C2 domains is the minimal region for Munc13 activity and it exerts its effects via protein-protein interactions (Basu et al., 2005; Li et al., 2011). However, other domains also contribute, since expression of the isolated MUN domain results in only 50% rescue of Munc13 functions in neurons from Munc13-1 and Munc13-2 double knock-out mice (Basu et al., 2005).

The C1 domains of Unc-13 and Munc13-1 bind [³H]PDBu in a phospholipid-dependent manner with low nanomolar affinity (Kazanietz et al., 1995; Betz et al., 1998). They also bind diacylglycerol and other C1 domain ligands with affinities close to that of PKCδ C1b domain, and Munc13 isoforms translocate to plasma membrane upon PMA treatment. The nuclear magnetic resonance (NMR) structure of Munc13-1 C1 domain showed an intramolecular occlusion of the DAG binding site caused by a tryptophan side chain, which was hypothesized to lead to lower affinities for the C1 domain ligands in cellular context (Shen et al., 2005). Such an effect has however not been reported in experimental conditions, and the relevance of the occlusion remains unclear.

Differential expression patterns of Munc13 isoforms implies that they may regulate cellular functions in a cell-type-specific manner. Munc13-1 is expressed in brain and in pancreatic islet cells; Munc13-2 is expressed as two splice variants (see Fig. 4): brain-specific bMunc13-2 and ubiquitous ubMunc13-2; while Munc13-3 is exclusively expressed in brain (Brose et al., 2000; Sheu et al., 2003). The physiological role of unc-13 and Munc13s is tightly bound to regulation of exocytosis, and their effects have mainly been studied in the CNS. In neurons, Munc13s participate in the regulation of calcium-triggered exocytotic fusion of synaptic vesicles by controlling the essential and rate-limiting step of exocytosis called priming (see Brose et al., 2000). It has been shown that Munc13-1 is indispensable for fusion competence of glutamatergic synaptic vesicles (Augustin et al., 1999), and that it regulates glutamatergic transmission together with Munc13-2 (Varoqueaux et al., 2002).

Genetically modified mice with deficiency in Munc13-1 or both Munc13-1 and Munc13-2, or mice that express a DAG-unresponsive Munc13-1 variant instead of the wild-type protein, die 2–3 hours after birth, even though their brains and synapses have developed normally (Augustin et al., 1999; Rhee et al., 2002; Varoqueaux et al., 2002), showing that Munc13s and their DAG-dependent regulation is essential for normal function of synapses in the CNS. Munc13s control synaptic vesicle priming by binding to syntaxin and promoting its open conformation, which then allows the formation of the SNARE (soluble NSF attachment protein receptor) complex and exocytosis (Ma et al., 2011). The Munc13-regulated pathway cooperates with DAG-mediated PKC signalling, and both pathways contribute to initiation of presynaptic potentiation (Wierda et al., 2007; Lou et al., 2008). Furthermore, by regulating vesicle fusion Munc13s also regulate neurite outgrowth prior to synaptogenesis (Broeke et al., 2010). Outside CNS, Munc13-1 has been shown to regulate insulin secretion in pancreatic beta cells (Sheu et al., 2003; Kang et al., 2006) and Munc13-2 has been reported to play a role in apoptosis (Song et al., 1999).

2.3.5 Chimaerins

The four chimaerin isoforms are Rac GTPase-activating proteins (Rac-GAPs) that are generated by alternative splicing of two genes (Yang and Kazanietz, 2007). The shorter splice variants, α 1- and β 1-chimaerins, possess a single C1 domain in the N-terminus and a C-terminal Rac-GAP domain, while the longer variants, α 2- and β 2-chimaerins, contain an additional Src homology 2 (SH2) domain in their N-terminus (Fig. 4). The C-terminal Rac-GAP domain is responsible for interactions with and selectivity for the Rac GTPase; it accelerates the hydrolysis of Rac-bound GTP thus leading to Rac inactivation (Caloca et al., 2003; Yang and Kazanietz, 2007).

The chimaerins bind phorbol esters in a C1 domain-dependent manner (Ahmed et al., 1990; Caloca et al., 1997). The binding properties of α -chimaerin C1 domain are virtually indistinguishable from PKC α in regarding their ligand-binding properties and phospholipid requirements (Areces et al., 1994), while β 2-chimaerin exhibits different ligand selectivity compared with that of PKC α (Caloca et al., 1997). Exposure to phorbol esters or DAG analogues or stimulation of cells with epidermal growth factor induce redistribution of chimaerins from cytosol to the plasma membrane and to the Golgi (Caloca et al., 1997; Caloca et al., 1999; Caloca et al., 2001; Wang et al., 2006). However, the interaction of the β 2-chimaerin C1 domain with cellular membranes requires higher concentrations of DAG or phorbol esters than for example for PKC α (Caloca et al., 2001). This difference was explained by the crystal structure: the DAG binding site of β 2-chimaerin is concealed by interactions of the C1 domain with the N-terminus, the SH2 domain, the Rac-GAP domain and the SH2-C1 linker region (Canagarajah et al., 2004). Consistently, β 1-chimaerin, the splice variant lacking the SH2 domain, translocates to membranes at 60-fold lower phorbol ester concentrations than β 2-chimaerin due to fewer intramolecular interactions constraining its C1 domain.

The role of DAG seems to be more in targeting $\alpha 2$ - and $\beta 2$ -chimaerins to the membrane than in activating them (Yang and Kazanietz, 2007). The functions of the shorter splice variants $\alpha 1$ - and $\beta 1$ -chimaerins may, however, be regulated differently due to the lack of SH2 domain-mediated autoinhibition. Indeed, protein levels of $\alpha 1$ -chimaerin in neurons are actively controlled by proteasomal degradation: DAG signalling or exposure of neurons to phorbol esters stabilizes the protein, allowing $\alpha 1$ -chimaerin accumulation and thus enhancing chimaerin-mediated Rac inhibition (Marland et al., 2011).

The target of chimaerin actions, the small GTPase Rac, is a central regulator of actin cytoskeleton organization, cell migration, transformation, cell cycle progression and gene expression (Etienne-Manneville and Hall, 2002), and chimaerins participate in regulating these phenomena by inhibiting Rac activity in response to GPCR- or RTK-initiated DAG production. The $\alpha 1$ -, $\alpha 2$ - and $\beta 2$ -chimaerins are highly expressed in the brain, while the expression of $\beta 1$ -chimaerin is largely limited to testis (Yang and Kazanietz, 2007). The high expression levels in brain suggest that chimaerins play important roles in regulating Rac-mediated responses in the CNS. Indeed, α -chimaerins were recently shown to control neuronal migration and oculomotor axon guidance (Ip et al., 2011; Ferrario et al., 2012), and $\beta 2$ -chimaerin was reported to be required for axonal pruning both *in vitro* and *in vivo* in hippocampus (Riccomagno et al., 2012). Earlier reports had already identified $\alpha 2$ - and $\alpha 1$ -chimaerin had been reported to control dendritic pruning and morphology (Buttery et al., 2006). Outside the CNS, $\alpha 2$ - and $\alpha 1$ -chimaerins are expressed in various cell lines and in T cells, where they regulate T cell receptor signalling, adhesion and chemotaxis (Yang and Kazanietz, 2007).

2.3.6 Ras guanyl-releasing proteins (RasGRPs)

Ras guanyl-releasing proteins (RasGRPs; also known as CalDAG-GEFs) are a family of four guanine nucleotide exchange factors (GEFs) that activate Ras and related small GTPases by catalysing the exchange of GDP to GTP (Stone, 2011). They are characterized by a common domain structure: The N-terminal catalytic region consists of a Ras exchange motif (REM) and a RasGEF domain, and the C-terminal regulatory region contains two EF hand motifs and a single C1 domain (Fig. 4). The EF hand motifs of RasGRPs are homologous with calcium-binding EF hand motifs of other proteins, and the original report demonstrated that the RasGRP EF hand motifs also bind Ca²⁺ (Ebinu et al., 1998). However, they have also been reported to regulate plasma membrane association of RasGRPs together with the RasGEF domain in a Ca²⁺-independent manner (Tazmini et al., 2009), and the role of Ca²⁺ in the control of RasGRP functions is thus unclear. The C1 domains of RasGRP isoforms 1, 3 and 4 are high-affinity receptors for phorbol esters and DAG, while the C1 domain of RasGRP2 is not, even though its sequence contains many of the amino acids critical for DAG/phorbol ester binding (Lorenzo et al., 2000; Johnson et al., 2007). Similarly, isoforms 1, 3 and 4 translocate to cellular membranes after DAG or PMA treatment, while RasGRP2 remains in the cytosol (Johnson et al., 2007).

The C1 domain-mediated membrane binding of RasGRPs 1, 3 and 4 seems to play a major role in their activation (Ebinu et al., 1998; Tognon et al., 1998; Reuther et al., 2002). Additionally, RasGRPs 1 and 3 are regulated by PKC-dependent phosphorylation (Teixeira et al., 2003; Roose et al., 2005). RasGRP4 contains a proline-rich region instead of the PKC phosphorylation sequence, and is therefore not phosphorylated by PKC (Zheng et al., 2005).

The functions of RasGRPs have been best characterized in the cells of the immune system. RasGRP1 is a central mediator of T cell receptor signalling (Dower et al., 2000; Ebinu et al., 2000), and indispensable for natural killer (NK) cell cytotoxicity and cytokine production (Lee et al., 2009). It also mediates B cell receptor signalling together with RasGRP3 (Coughlin et al., 2005). RasGRP4 is the only isoform expressed in mast cells, where it regulates prostaglandin D2 expression (Yang et al., 2002; Li et al., 2003). It has also been reported to mediate GPCR-mediated Ras activation in neutrophils (Suire et al., 2012). RasGRPs 1 and 3 are also expressed outside the immune system: RasGRP1 has been reported to exist in a subset of neurons (Toki et al., 2001) and RasGRP3 has been found in endothelial cells and some cancer cell lines (Yang et al., 2010; Randhawa et al., 2011; Yang et al., 2011). The exact roles of RasGRPs in these tissues and cells are however not clear.

2.4 Potential therapeutic indications for DAG effector-targeted drugs

As a consequence of the central role for DAG in mediating cellular signal transduction, PKC and other DAG effectors are important regulators of processes that contribute to pathophysiology of numerous important human diseases. PKC isoforms are implicated in cancer (Hofmann, 2004; Griner and Kazanietz, 2007), diabetes (Geraldes and King, 2010), cardiovascular diseases (Churchill et al., 2008), autoimmune diseases (Baier and Wagner, 2009), neurodegenerative diseases such as AD (Sun and Alkon, 2010) and stroke (Bright and Mochly-Rosen, 2005), among others. The other DAG effectors also mediate various pathophysiological processes. Reputed roles for DAG effectors in selected examples of such pathologies are presented below.

2.4.1 Cancer

Cancer is a large group of diseases, in which uncontrolled cell proliferation leads to formation of malignant tumours. It is one of the leading causes of death worldwide: an estimated 7.6 million cancer deaths occurred and 12.7 million new cancer cases were diagnosed in 2008 (Ferlay et al., 2010). In Finland approximately 28 000 people are diagnosed with cancer each year (Finnish Cancer Registry, 2013). Cancer arises when a single cell in a normal tissue progressively accumulates mutations that lead, first, to uncontrolled cell proliferation and inhibition of apoptosis. If the resulting malignant cells escape the immune response, they form a tumour, which is eventually becomes capable of invading to adjacent tissues and metastasizing via lymphatic or blood vessels to other sites of the body. These gained malignant properties result from disturbances in regulatory signalling pathways, which are normally under strict control. Protein kinases are examples of key regulators that are often deregulated in cancer cells (Blume-Jensen and Hunter, 2001).

The role of PKC in cancer development and progression has been extensively studied, since it was the first recognized receptor for the most potent tumour promoters known, the phorbol esters. PKC is known to co-operate with the oncogene ras during transformation and functional connections between PKC and several other oncogenes, such as fos and myc, have been identified (see Griner and Kazanietz, 2007). Mutations in PKC isoforms are rarely the cause of a cancer, but altered PKC expression has been observed in many cancers, such as breast, prostate, bladder, colon and brain cancers as well as leukaemia (reviewed in Hofmann, 2004; Griner and Kazanietz, 2007). However, the roles of individual isoforms and their relative contribution to the role of PKC in carcinogenesis seem to depend on the original tissue and the cell type. Depending on the cancer, individual PKC isoforms may be either up-regulated/down-regulated or activated/inhibited, and thus both PKC inhibitors and activators possess potential as anticancer agents. Of the DAG-responsive PKC isoforms, PKCE has a well-established role as a tumour promoter and a transforming oncogene, and it also promotes tumour invasion and metastasis (Gorin and Pan, 2009). On the other hand, PKCδ is mostly considered a tumour suppressor, although exceptions do exist (see Jackson and Foster, 2004). The roles of other DAG-responsive PKC isoforms in cancer are more conflicting and depend on the cell type and the tissue of origin. The issue is further complicated by the fact that it is not always kinase activity that mediates the PKC-dependent response. For example, in glioma cells PKCα plays an essential pro-proliferative and pro-survival role independently of its catalytic activity (Cameron et al., 2008).

Due to decades of intensive research, a vast number of PKC-targeted compounds have been developed and many of them have also been studied in clinical trials. The most popular approach has been to target the catalytic site, and several ATP-competitive PKC inhibitors (such as midostaurin and enzastaurin) have been studied for their efficacy against cancer in clinical trials. They have, however, shown no remarkable efficacy either alone or in combination with other anti-cancer agents (Mackay and Twelves, 2007; Mochly-Rosen et al., 2012). The PKCα antisense oligonucleotide aprinocarsen reached phase III clinical trials, but due to lack of efficacy and serious toxicities, its development was discontinued (Mochly-Rosen et al., 2012). Additionally, multiple classes of C1 domain-targeted PKC modulators (see chapter 2.5) and peptides inhibiting PKC protein-protein interactions have been developed (reviewed in Churchill et al., 2009).

In addition to PKC, most of the other DAG effectors also play a role in regulating processes associated with cancer development (Table 1). PKD isoforms regulate many signalling pathways

associated with cell proliferation, motility, invasion, and angiogenesis, and are thus considered potential targets for cancer therapy (reviewed in Lavalle et al., 2010; Sundram et al., 2011). However, similarly to PKC, the role of PKD in cancer seems to depend on the isoform and on the cancer type studied. PKDs have been implicated for example in breast cancer, prostate cancer, gastrointestinal cancers, lung cancer and lymphoma. Of particular interest is the proposed role for PKD in pancreatic cancer, which is a devastatingly aggressive cancer with a poor prognosis (Guha et al., 2010). PKD1 protein levels were shown to be up-regulated in pancreatic ductal adenocarcinoma tissue when compared to normal pancreatic tissue (Trauzold et al., 2003). PKD1 overexpression also increased proliferation rate and prevented apoptosis of Colo357 pancreatic adenocarcinoma cells *in vitro*. Furthermore, the PKD inhibitor CRT0066101 inhibited pancreatic cancer cell proliferation and induced apoptosis *in vitro*, and inhibited pancreatic cancer growth *in vivo* in orthotopic and subcutaneous xenograft cancer models (Harikumar et al., 2010). Inhibition of PKD may thus be a useful therapeutic strategy in pancreatic cancer.

As activators of the oncogene Ras, RasGRPs are attractive cancer drug targets. Indeed, all of the DAG-responsive RasGRP isoforms 1, 3 and 4 have been associated with cancer. The gene encoding RasGRP1 functions as an oncogene in murine lymphomas and its deregulated expression induces transformation of thymocytes and initiates lymphoma in mice (Kim et al., 2003; Klinger et al., 2005). RasGRP1 has also been shown to mediate PMA-induced Ras activation in mouse keratinocytes and thus potentially contribute to phorbol ester-induced tumour promotion in the two-stage skin carcinogenesis model (Tuthill et al., 2006). Elevated RasGRP3 levels have been demonstrated to contribute to malignant phenotype of prostate cancer and melanoma cell lines *in vitro* and in mouse xenograft tumours (Yang et al., 2010; Yang et al., 2011). Moreover, RasGRP4 was initially discovered in a screen for transforming genes in acute myeloid leukaemia (Reuther et al., 2002). Conversely, a proapoptotic signalling pathway involving RasGRPs 1 and 3 in non-Hodgkin's B cell lymphoma cells has also been described (Stang et al., 2009).

Like RasGRPs, chimaerins also mediate their signals by regulating the activity of a small GTPase. However, since the chimaerins act to inhibit Rac, they are mainly considered tumour suppressors (Griner and Kazanietz, 2007; Yang and Kazanietz, 2007). Lower β 2-chimaerin expression levels have been reported in high-grade gliomas when compared with normal brain tissue or low-grade brain tumours (Yuan et al., 1995), and β 2-chimaerin mRNA transcript levels are also lower in breast cancer tissue compared with normal breast tissue from the same patients (Yang et al., 2005). Moreover, overexpression of β 2-chimaerin in cancer cell lines inhibits cell proliferation *in vitro* and *in vivo*, and reduces invasiveness of cancer cells *in vivo* (Yang et al., 2005). Activation or up-regulation of β 2-chimaerin could thus be beneficial in the treatment of cancer.

Although not much is known about the role of DAG-responsive DGKs in regulating processes related to cancer progression, as terminators of DAG signalling they are likely to contribute to both prosurvival and pro-apoptotic signalling. DGK β was identified as a survival kinase in HeLa cells in an RNA interference (RNAi) screen on human kinases and phosphatases (MacKeigan et al., 2005). DGK γ has been reported to positively regulate cell cycle progression in several cell lines (Matsubara et al., 2006). However, it has also been shown to activate β 2-chimaerin and thus it may function as a tumour suppressor (Yasuda et al., 2007; Sakane et al., 2008).

Based on the limited number of publications, the MRCKs seem to consistently promote tumour cell survival, proliferation and invasion. MRCK α was identified as a survival kinase in HeLa cells in a

kinome-wide RNAi screen (MacKeigan et al., 2005). Combined knock-down of MRCKα and MRCKβ using RNAi inhibits invasion of colorectal cancer cells and breast cancer cells, and this combined with knock-down of ROCK further potentiates the anti-invasive effect (Wilkinson et al., 2005; Heikkilä et al., 2011). Furthermore, a combined knock-down of MRCKs and ROCK inhibits tumour development in mice injected with retrovirus-transformed keratinocytes (Lefort et al., 2007). The small GTPase Cdc42, upstream of MRCK, has also been implicated in cancer. Its effects are however complex and depend on the cell type (Stengel and Zheng, 2011).

Table 1. Roles of DAG effectors in cancer-related cellular processes.

DAG effector	Cellular respon	se	Putative role in cancer	References
РКС	proliferation survival apoptosis angiogenesis motility	↑ ↓ ↓ ↑ ↑ ↑ ↑	tumour promotion or tumour suppression	(Hofmann, 2004) ^a (Jackson and Foster, 2004) ^a (Gorin and Pan, 2009) ^a (Konopatskaya and Poole, 2010) ^a (Mochly-Rosen et al., 2012) ^a
PKD	proliferation survival apoptosis motility angiogenesis	↑ ↓ ↓ ↓ ↑ ↓ ↑ ↑	tumour promotion or tumour suppression inhibition of invasion	(Trauzold et al., 2003) (MacKeigan et al., 2005) (Eiseler et al., 2009) (Lavalle et al., 2010) ^a (Sundram et al., 2011) ^a
DGKs β and γ	survival proliferation	↑ ↑ ↓	tumour promotion or tumour suppression	(MacKeigan et al., 2005) (Matsubara et al., 2006) (Yasuda et al., 2007) (Sakane et al., 2008) ^a
MRCK	survival motility	↑	tumour promotion and invasion	(MacKeigan et al., 2005) (Wilkinson et al., 2005) (Lefort et al., 2007) (Heikkilä et al., 2011)
RasGRP	proliferation survival apoptosis	↑ ↑ ↑	tumour promotion or tumour suppression	(Kim et al., 2003) (Klinger et al., 2005) (Stang et al., 2009) (Yang et al., 2010) (Yang et al., 2011)
Chimaerins	proliferation invasiveness motility	+ + + + +	tumour suppression	(Yuan et al., 1995) (Yang et al., 2005) (Maeda et al., 2006)
Munc13			not reported	

^a and references herein

2.4.2 Alzheimer's disease (AD)

AD is a progressive neurodegenerative disease that leads to severe impairment of memory and cognitive functions, alterations in behaviour, incapacity for independent living and, finally, death. It is the leading cause of dementia (Barker et al., 2002). According to an estimate 35.6 million people lived with dementia in 2010, and the numbers are expected to almost double approximately every 20 years, reaching 115 million in 2050 (Prince et al., 2013). Currently, there is no treatment that could cure or even inhibit the progression of AD, and therefore new disease-modifying therapies are needed.

The main neuropathological change characteristic to AD is the loss of neurons and synapses, in particular in cerebral cortex, hippocampus and other subcortical structures that contribute to

memory formation (Mann et al., 1986; Roh et al., 2011). The neuronal loss is a consequence of accumulation of predominantly extracellular β amyloid (Aβ) deposits (plaques) and intracellular neurofibrillary tangles consisting of hyperphosphorylated tau protein (Selkoe, 2001). Oxidative stress, microglia activation and inflammation also contribute to neuronal damage (Kitazawa et al., 2004). The amyloid plaques result from abnormal processing of the amyloid precursor protein (APP) and consequent accumulation and aggregation of β -amyloid peptides $A\beta_{1-40}$ and $A\beta_{1-42}$ (Selkoe, 2001). APP is processed by α -, β - and γ -secretases: cleavage by α -secretase and subsequently by γ secretase produces the nontoxic soluble APP fragment (sAPPα) and the N-terminally truncated Aβ (p3), which does not aggregate. By contrast, cleavage of APP first by β-secretase and thereafter by γsecretase produces the pathogenic $A\beta_{1-40}$ and $A\beta_{1-42}$ that aggregate to form toxic oligomers and amyloid plaques. Intracellular neurofibrillary tangles result from hyperphosphorylation of tau protein, which normally functions to stabilize microtubules. Hyperphosphorylated tau aggregates and forms paired helical filaments, which build up the neurofibrillary tangles (Duff and Planel, 2005). According to the amyloid cascade hypothesis the amyloid pathology precedes tau-related pathology (Hardy and Higgins, 1992), but the issue is controversial and the initiating pathophysiological changes remain unresolved. However, strong evidence suggests that the synaptic dysfunction present prior to neuronal degeneration is caused by Aβ oligomers (see Selkoe, 2002).

PKC is involved in synaptic neurotransmission and plays major roles in learning and memory (Sun and Alkon, 2010). Several PKC substrates, including myristoylated alanine-rich C-kinase substrate (MARCKS), growth-associated protein 43 (GAP-43) and the *N*-methyl-D-aspartate (NMDA) receptor, are involved in information processing and storage. PKC protein levels are reduced in the brains of AD patients and abnormal PKC signalling in the brain has been identified as an early change in AD as well as in memory deficits related to ischemia or stroke (Alkon et al., 2007; Sun and Alkon, 2010). Such changes include PKC translocation defects, reduced levels of PKC anchoring protein RACK1, and decreased PKC activity (Wang et al., 1994; Battaini et al., 1999).

PKC isoforms regulate several pathways relevant for AD pathophysiology in vitro and in vivo (Fig. 5) (Pascale et al., 2005; Hooper et al., 2008; Amadio et al., 2009; Kim et al., 2011). For example, PKC activation has been shown to direct APP processing to the non-pathogenic α-secretase pathway, thus increasing the production of neuroprotective sAPPa and reducing the production of neurotoxic Aβ protein (Jacobsen et al., 1994; Etcheberrigaray et al., 2004). PKC activation also increases Aβ clearance and reduces tau hyperphosphorylation (Isagawa et al., 2000; Kim et al., 2011). Furthermore, PKC has been shown to protect hippocampal neurons from Aβ toxicity (Garrido et al., 2002). Additionally, PKCα phosphorylates and up-regulates nELAV (neuronal Embryonic Lethal Abnormal Vision) proteins, which regulate mRNA stability and translation (Pascale et al., 2005; Pascale et al., 2008). One of the target proteins of nELAVs is GAP-43, and both nELAVs and GAP-43 are up-regulated in vivo following PKC activation and during spatial learning (Quattrone et al., 2001; Pascale et al., 2004; Pascale et al., 2005). Neuronal ELAV proteins have also been implicated in AD pathology: nELAV levels are decreased in the brains of AD patients along with disease progression, and Aβ₁₋₄₂ causes nELAV down-regulation in SH-SY5Y neuroblastoma cells, thereby leading to downregulation of ADAM10, the best-characterized α-secretase mediating non-amyloidogenic processing of APP (Amadio et al., 2009). For these numerous reasons PKC activators are considered potential future therapeutics for the treatment of AD (Sun and Alkon, 2010).

In addition to PKC, also Munc13s play a role in APP processing: α -secretase mediated processing of APP was impaired in the brains of Munc13-1 knock-out mice, and phorbol-induced sAPP α secretion

was less pronounced in brain slices of Munc13-1 knock-out mice than in wild type mice (Rossner et al., 2004). Consistently, phorbol ester-induced sAPP α secretion was only partially inhibited by the pan-PKC inhibitor Gö6983 in neuroblastoma cells, and overexpression of Munc13-1 augmented phorbol-induced increase of sAPP α secretion. Stimulation of postsynaptic glutamate receptors rescued the defective sAPP α secretion in organotypic brain slice cultures from Munc13 knock-out mice, implying that the defective APP processing results from the lack of postsynaptic glutamatergic stimulation (Hartlage-Rübsamen et al., 2013). Treatments that activate Munc13s may thus have potential in directing APP processing to the non-amyloidogenic α -secretase route.

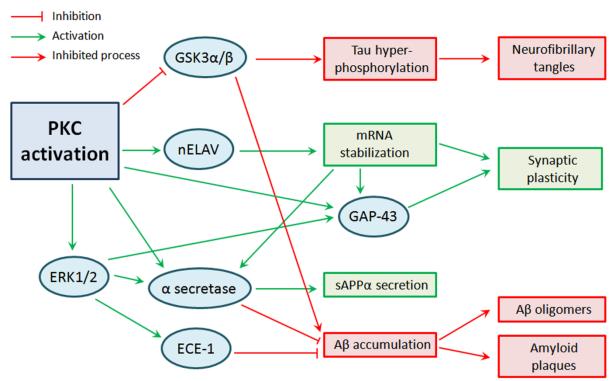


Figure 5. Postulated effects of PKC activation in Alzheimer's disease. Activation of PKC leads to: 1) inhibition of glycogen synthase kinase 3 (GSK3) activity, which in turn reduces hyperphosphorylation of tau protein and inhibits production of A θ peptides; 2) phosphorylation and activation of nELAV proteins leading to stabilization of mRNAs and thereby positively influencing expression of genes (e.g. GAP-43 and the α-secretase ADAM10) that are important in neuritogenesis, memory formation and non-amyloidogenic APP processing; 3) increased processing of amyloid precursor protein (APP) via the α-secretase route leading to increased secretion of soluble and non-toxic sAPP α and decreased accumulation of neurotoxic θ amyloid protein (A θ); 4) activation of endothelin-converting enzyme 1 (ECE-1) which degrades A θ . ERK1/2, extracellular signal-regulated kinase 1/2.

2.4.3 Other therapeutic indications

PKCs and other DAG effectors are also implicated in numerous other pathological conditions, such as cardiovascular diseases, immunological diseases and diabetes. Cardiovascular diseases are one of the leading causes of death world-wide. PKC isoforms have been implicated in numerous cardiac pathologies, such as myocardial infarction and ischaemia-reperfusion injury, cardiac arrhythmia, hypertension-induced compensatory hypertrophy and heart failure (Mochly-Rosen et al., 2012). The role of PKC however depends on the pathology and on the isoform. For example, in the ischaemic

heart activation of PKCδ mediates the acute myocardial injury, while activation of PKCε exhibits a cardioprotective effect (Chen et al., 2001). By contrast, activation of PKCs plays a pathological role during pathological compensatory cardiac hypertrophy and heart failure (Ferreira et al., 2011). Cardioprotective effects against pathological cardiac remodelling have been achieved in preclinical studies with PKC\$ and PKC\$ inhibitors. Also PKD is implicated in cardiac diseases (reviewed in Avkiran et al., 2008). Particularly, PKD isoforms 1 and 3 mediate cardiac remodelling and hypertrophy in a cooperative manner by influencing distinct hypertrophic cardiac transcription factors. PKD1 is required for pathological cardiac remodelling and it regulates cardiomyocyte hypertrophy by phosphorylating HDACs that upon phosphorylation disengage from the transcription factor MEF2 (myocyte enhancer factor-2) leading to relieved transcription repression and subsequent foetal gene activation and cardiac hypertrophy (Fielitz et al., 2008). PKD3 increases the expression of cardiac transcription factors NFATc4 (nuclear factor of activated T cells 4), Nkx2.5 (homeobox protein Nkx-2.5) and GATA-4, and thereby activates foetal gene expression and cardiac remodelling (Li et al., 2011). Since there is no treatment available that could prevent the remodelling process, inhibition of PKCs and/or PKD isoforms 1 and 3 possess potential as novel therapeutic strategies for pathological cardiac remodelling.

DAG is one of the key second messengers mediating immune cell signalling, and several families of DAG effectors, particularly PKC and RasGRPs, have been implicated in regulating immune responses (see Tan and Parker, 2003; Stone, 2011). Many PKC isoforms participate in controlling immune cell responses: PKCα plays a role in thymocyte maturation; PKCβ regulates B cell survival; PKCδ controls B cell tolerance to self-antigens; and PKCε mediates macrophage activation (Tan and Parker, 2003). In particular, PKCθ seems to be central for pathologic immune responses (e.g. autoimmunity), while being dispensable for beneficial immune responses such as protection against pathogen infection (reviewed in Zhang et al., 2013). Therefore it is considered a promising target for selective immunosuppressive therapy. RasGRPs 1 and 3 are implicated in B cell proliferation, RasGRP1 is an essential regulator of NK cell function, and RasGRP4 mediates eicosanoid production in mast cells (Stone, 2011). RasGRP4-null mice exhibit diminished inflammatory responses in experimental models of arthritis and colitis, and inhibition of RasGRP4 could thus be a potential therapeutic strategy for these diseases (Adachi et al., 2012).

Several PKC isoforms have been implicated in controlling insulin signalling and thus glucose homeostasis (Sampson and Cooper, 2006). Insulin receptor activation leads to activation of PKC, which may then regulate insulin signalling by phosphorylating e.g. the insulin receptor, insulin receptor substrate 1 (IRS-1), and GSK3. PKC may thus play a role in the development of insulin resistance (Turban and Hajduch, 2011). Furthermore, hyperglycaemia induces chronic activation of PKC isoforms, and this has been associated with development of pathological vascular complications such as atherosclerosis, nephropathy and retinopathy (Geraldes and King, 2010). The vascular complications are at least partially mediated by PKC β II, and the PKC β -selective inhibitor ruboxistaurin (LY333531) has proceeded to clinical trials against diabetic retinopathy and nephropathy (Geraldes and King, 2010). Although best known for their role in CNS, Munc13s also regulate insulin vesicle release from pancreatic β cells (Sheu et al., 2003). Insulin release from pancreatic islets of Munc13-1 null mice is severely impaired, and Munc13-1 levels are significantly reduced in pancreatic islets of type 2 diabetes patients (Kang et al., 2006; Ostenson et al., 2006). Activation of Munc13-1 may thus provide a means to restore defective insulin secretion in diabetes. Munc13s may also play a role in the development of diabetic nephropathy (Song et al., 1999).

2.5 C1 domain ligands

Since PKC and other DAG effectors participate in the pathophysiology of various severe diseases, the C1 domain is considered an attractive target for drug development. A vast amount of work has been carried out to find compounds that specifically target the DAG binding site (reviewed in Boije af Gennäs et al., 2011). The main classes of C1 domain ligands are presented in Figure 6.

Figure 6. Structures of C1 domain ligands. Functional groups that interact with the C1 domain are circled.

2.5.1 Phorbol esters and phorbol derivatives

The most widely studied C1 domain ligands and PKC activators are phorbol esters ([3] in Fig. 6), tetracyclic diterpenoids that occur naturally in many plants of the families *Euphorbiaceae* and *Thymelaeaceae* (Goel et al., 2007). The two types of phorbol esters, the active (4β) and the inactive

(4α) differ only by the orientation of the hydroxyl group at position 4. The active β -phorbol esters bind to the C1 domains with high affinity and are extremely potent tumour promoters in the 2-stage mouse skin carcinogenesis model, while the inactive α -phorbol esters exhibit no affinity for the C1 domain and are devoid of tumour-promoting activity (van Duuren et al., 1979). The 4 β -phorbol esters compete with DAG upon binding to the C1 domain (Sharkey et al., 1984) and mimic the actions of DAG albeit with 3 orders of magnitude higher affinity. In contrast to DAG, phorbol ester-induced PKC activation is persistent and leads to down-regulation (see 2.2.3). PMA (also known as 12-O-tetradecanoylphorbol-13-acetate [TPA]) and PDBu are the best characterized tumour-promoting phorbol esters, and they have been used universally as prototypes of PKC activators and as research tools in elucidating physiological and pathophysiological roles of PKCs and other DAG effectors. Furthermore, the binding affinities of other C1 domain ligands are generally measured as their ability to displace tritiated PDBu ([3 H]PDBu), which binds to cPKC and nPKC isoforms with K_d values in the range of 0.15-0.94 nM (Kazanietz et al., 1993).

Despite their tumour-promoting activity, phorbol esters have antiproliferative, differentiating and proapoptotic effects in various cancer cell lines (Rovera et al., 1979; Day et al., 1994; Trollér et al., 2001; Afrasiabi et al., 2008). The effects of PMA have even been studied in a clinical setting in patients with myelocytic leukaemia with some short-term therapeutic effects (Han et al., 1998). In addition to phorbol diesters, several other phorbol derivatives also bind to the C1 domain. Of these, prostratin (12-deoxyphorbol-13-acetate) and DPP (12-deoxyphorbol-13-phenylacetate) are non-tumour-promoting phorbol derivatives that also activate PKCs and exhibit potent *in vitro* efficacy in the activation of latent HIV reservoirs and thus represent promising adjuvants for antiretroviral therapy (Kulkosky et al., 2001; Wender et al., 2008).

2.5.2 Bryostatins and their synthetic analogues

Bryostatins ([7] in Fig. 6), natural products originally isolated from the marine bryozoan *Bugula neritina*, but actually produced by its symbiont bacteria, are a family of at least 20 macrocyclic lactones (Mutter and Wills, 2000; Davidson et al., 2001). Bryostatin 1 is the best-characterized member of the family, with nanomolar affinity for the C1 domains of PKC (K_i =1.35 nM for PKC α) (Kazanietz et al., 1994). It binds to and activates classical and novel PKC isoforms without considerable isoform selectivity. It has also been reported to activate PKD (Matthews et al., 1997), to bind to and modulate RasGRPs (Lorenzo et al., 2000; Tuthill et al., 2006), and to bind to β 2-chimaerin and induce its translocation (Caloca et al., 1997; Caloca et al., 2001).

Despite being a potent PKC activator, bryostatin 1 does not mimic all phorbol ester-induced responses in cellular models. Instead, it often antagonizes such phorbol-induced effects that it does not elicit (Kraft et al., 1986; Szállási et al., 1994a; Tuthill et al., 2006). Most importantly, bryostatin 1 is totally devoid of tumour-promoting activity and even antagonizes phorbol ester-induced tumour-promotion (Hennings et al., 1987). The opposing cellular responses to phorbol esters and bryostatins may be explained by their diverging effects on PKCs in cellular context. The patterns of down-regulation of individual PKC isoforms are different between bryostatin 1 and phorbol esters (Szállási et al., 1994b; Choi et al., 2006). Bryostatin 1-induced translocation of PKCδ is dependent on both C1a and C1b domains, while phorbol ester-induced PKCδ translocation requires only the C1b domain (Bögi et al., 1998). Moreover, typical of bryostatin 1 are its biphasic concentration-dependent effects

in many biological responses such as PKC δ down-regulation and PKD activation (Szállási et al., 1994a; Matthews et al., 1997).

Bryostatin 1 exhibits characteristic anticancer effects in many experimental *in vitro* and *in vivo* models of cancer: it inhibits tumour growth and invasion (reviewed in Clamp and Jayson, 2002), but also stimulation of proliferation and antiapoptotic effects have also been reported (Choi et al., 2006). However, the numerous phase I and phase II clinical trials against many types of cancer, both alone and as a combination therapy with other antineoplastic agents, have shown only modest responses to bryostatin 1 (Clamp and Jayson, 2002). As a non-tumour-promoting PKC activator bryostatin 1 also possesses potential in the treatment of AD: it has been reported to enhance secretion of sAPP α both *in vitro* and *in vivo*, to reduce levels of pathologic A β fragments in brains of transgenic AD mice, and to reduce premature mortality of AD mice (Etcheberrigaray et al., 2004). Furthermore, bryostatin 1 has shown promising neuroprotective and neurorestorative efficacy in a rat model of cerebral ischemia, and it may thus have potential in the treatment of e.g. ischemic stroke (Sun et al., 2009). However, no clinical trials in these indications have been reported.

Because of the complex chemical structure of bryostatins and their scarceness in the natural material, synthetic bryostatin analogues, "bryologues", with varying affinities and selectivity for PKC isoforms and individual C1 domains have been developed (Wender et al., 1999; Wender et al., 2011). Some bryologues have shown potential as anticancer agents and some show promise as activators of latent HIV reservoirs in the eradication of HIV (Stone et al., 2004; DeChristopher et al., 2012).

2.5.2 Ingenol derivatives

Ingenol derivatives ([4] in Fig. 6) are tumour-promoting macrocyclic diterpenes that are structurally closely related to phorbol esters (Nakamura et al., 1989; Boije af Gennäs et al., 2011). Ingenol-3-angelate (PEP005, ingenol mebutate) is the most studied ingenol derivative initially extracted from the sap of the plant *Euphorbia peplus*. It binds to the PKC C1 domains with subnanomolar affinity and shows no selectivity for individual PKC isoforms *in vitro* (Kedei et al., 2004). Patterns of PKC isoform translocation and down-regulation induced by ingenol-3-angelate differ from those induced by PMA, sometimes in a cell line-dependent manner (Kedei et al., 2004; Hampson et al., 2005).

Ingenol-3-angelate inhibits proliferation of various cancer cell lines and primary acute myeloid leukaemia (AML) cells (Gillespie et al., 2004; Kedei et al., 2004; Hampson et al., 2005). In leukemic cell lines and primary AML cells, it induces apoptosis by activating PKC δ and by subsequently inducing sustained activation of ERK1/2 (Hampson et al., 2005; Hampson et al., 2010). In contrast to its apoptosis-inducing effect in leukemic cells, it promotes survival of resting and activated human T cells by activating PKC θ (Lee et al., 2010).

Ingenol-3-angelate has undergone numerous clinical trials as topical treatment for actinic skin keratosis (a preliminary stage of squamous cell carcinoma) and for superficial basal cell carcinoma (Martin and Swanson, 2013), and it has recently been approved by the U.S. Food and Drug Administration (FDA) and by the European Medicines Agency (EMA) for the treatment of actinic keratosis (EMA, 2012; FDA, 2012). Its efficacy in other potential indications, such as non-melanoma skin cancers and leukaemia remains to be elucidated.

2.5.3 DAG lactones

DAG lactones ([2] in Fig. 6) are synthetic analogues of endogenous DAG with conformationally constrained backbones to surmount the entropic penalty caused by the flexible DAG structure (Marquez and Blumberg, 2003). They also contain lipophilic side chains that improve their interactions with the conserved lipophilic amino acid residues in the DAG binding cleft of the C1 domain. The most potent DAG lactones displace [3 H]PDBu from PKC C1 domains with K_i values lower than 10 nM (Nacro et al., 2000; Marquez and Blumberg, 2003; Comin et al., 2009), and the remarkable series of derivatives also includes some compounds with moderate selectivity for individual PKC isoforms (Pu et al., 2005; Comin et al., 2009). Furthermore, by carefully balancing the lipophilicity and hydrophilicity of the acyl fragments for the DAG-lactones, a 100-fold selectivity for RasGRP (K_i =0.18 nM) over PKC α (K_i =39.7 nM) was achieved (El Kazzouli et al., 2008). A DAG lactone has also been shown to bind to the C1 domains of MRCK α and β , although only at significantly higher concentrations (K_i values of 23 μ M and 26 μ M for α and β isoforms, respectively) than to PKC C1 domains (Choi et al., 2008).

Various DAG lactones have shown antiproliferative and proapoptotic effects in several cancer cell lines *in vitro* (Garcia-Bermejo et al., 2002; Duan et al., 2008; Kang et al., 2010), and at least two of them potentiated the anti-cancer effect of γ irradiation in the orthotopic prostate cancer model in mice (Duan et al., 2008; Truman et al., 2009). Some of the DAG lactones have also been demonstrated to direct APP processing into the non-pathologic α secretase route by activating PKC (Lee et al., 2006; Duan et al., 2008). Besides their potential in drug development, the DAG lactone template has been a powerful research tool, and DAG lactones have been used in extensive studies exploring ligand-C1 domain interactions and interactions of the ligand-C1 domain complex with cellular membranes, thus providing useful information for the design of novel C1 domain ligands (see, for example, Nacro et al., 2000; Pu et al., 2005; Choi et al., 2007; Comin et al., 2009).

2.5.4 Indolactams and benzolactams

The tumour-promoting indole alkaloids of the teleocidin family were first isolated from *Streptomyces mediocidicus*, and subsequently shown to bind to the same receptors as phorbol esters (see Boije af Gennäs et al., 2011). The structurally simplest member of the family, (-)-indolactam V is a weak tumour promoter, and it has been used as a starting point to synthesize new derivatives with indolactam and benzolactam structures ([5] and [6] in Fig. 6, respectively) that bind the C1 domains of PKCs with low nanomolar affinities (Endo et al., 1996; Kozikowski et al., 1997; Nakagawa et al., 1998; Irie et al., 2005; Nakagawa et al., 2006). Extensive structure-activity studies have revealed derivatives with some selectivity for certain PKC isoforms (Kozikowski et al., 1997; Nakagawa et al., 2006). However, increased selectivity has only been achieved at the cost of binding affinity. Like many PKC-activating C1 domain ligands, indolactams and benzolactams induce PKC translocation and down-regulation (Kozikowski et al., 1997; Nakagawa et al., 2006). They have also been shown to bind to the C1 domains of RasGRPs, PKD, phorbol-responsive DGKs, Munc13 and chimaerins (Caloca et al., 2001; Rong et al., 2002; Irie et al., 2004).

Indolactam and benzolactam derivatives have been reported to inhibit proliferation of several cancer cell lines (Kozikowski et al., 1997; Endo et al., 1998). Benzolactam derivatives have also shown potential efficacy in cell-based models of Alzheimer's disease as measured by APP processing and secretion of sAPP α (Ibarreta et al., 1999), as well as *in vivo* in a transgenic mouse model of AD

(Etcheberrigaray et al., 2004). However, the efficacy of a benzolactam derivative, TPPB [(2S,5S)-(E,E)-8-(5-(4-(trifluoromethyl) phenyl)-2,4-pentadienoylamino)benzolactam], and bryostatin 1 was recently compared in a SH-SY5Y neuroblastoma cell-based model, and bryostatin 1 was found to be 10–100 times more potent than TPPB in activating the α -secretase pathway of APP processing (Yi et al., 2012). The difference in potency was estimated to be due to lower potency of TPPB in activating PKC isoforms δ and ϵ . Furthermore, (–)-indolactam V has been identified as an inducer of human embryonic stem cell differentiation to the pancreatic lineage (Chen et al., 2009). The effect is at least partly mediated by PKC activation, and the discovery may provide a means to produce insulinsecreting pancreatic β cells for cell replacement therapy in diabetes mellitus with the help of small molecules.

2.5.5 Other C1 domain ligands

Calphostin C ([8] in Fig. 6) is a polycyclic aromatic perylenequinone originally isolated from the fungus *Cladosporium cladosporioides*. It inhibits PKC in a light-dependent manner (Chiarini et al., 2010) and it has been reported to bind to the active conformation of PKC and target the C1 domain (Rotenberg et al., 1995). The mechanism seems to involve an irreversible oxidative modification of PKC that leads to a conformational change that inhibits both phorbol ester binding and phosphotransferase activity (Gopalakrishna et al., 1992a). It has also been shown to inhibit DGK activity (Redman et al., 1995) and to inhibit [³H]PDBu binding to the C1 domains of RasGRP, β-chimaerin and Unc-13 (Areces et al., 1994; Kazanietz et al., 1995; Lorenzo et al., 2000). Calphostin C exhibits proapoptotic effects in several cancer cell lines and it has been proposed to be a candidate for photodynamic cancer therapy; however, growing body of evidence suggests that the mechanism of action mediating calphostin C-mediated cytotoxicity is independent of PKC (Gopalakrishna et al., 1992a; Chiarini et al., 2010). Moreover, there are few or no reports describing its effects in *in vivo* cancer models.

N-benzyladriamycin-14-valerate (AD 198; [9] in Fig. 6), a semisynthetic anthracycline derivative developed to overcome doxorubicin resistance, exhibits its cytotoxicity at least partially by modulating PKC. It binds to the phorbol ester binding groove within the C1 domain, although not as deeply as phorbol esters (Roaten et al., 2001), while the parent compound doxorubicin or the primary metabolite, AD288, exhibit no affinity for the C1 domain. It has been shown to displace [3 H]PDBu from rat brain PKC, PKCδ, the C1b domain of PKCδ as well as the from C1 domain of β2-chimaerin (Roaten et al., 2002). Although AD198 was shown to inhibit PKC activity in vitro (Roaten et al., 2002), the majority of reports suggest that in cellular context it functions as a PKC activator. It activates PKCδ and triggers the mitochondrial apoptotic cascade (He et al., 2005) thus inducing apoptosis in several treatment-resistant cancer cell lines (Harstrick et al., 1995; Lothstein et al., 2007). Furthermore, in contrast to cardiotoxic doxorubicin, it exhibits cardioprotective properties by activating PKCε (Hofmann et al., 2007).

Other nature-derived C1 domain ligands include the tumour-promoting aplysiatoxins, debromoaplysiatoxins, iridals, resveratrol and curcumin (Boije af Gennäs et al., 2011). Recently described synthetic C1 domain ligands include diacyltetrol lipids (Mamidi et al., 2012a) and curcumin derivatives alkyl cinnamates (Mamidi et al., 2012b).

3. AIMS OF THE STUDY

The mitogenic signalling mediated by DAG and the contribution of DAG effectors in the control of cell proliferation, survival, death, morphology, differentiation, and motility makes PKC and several other DAG effectors attractive cancer drug targets. Furthermore, the role of PKC isoforms in central nervous system, especially in the regulation of memory and learning, speaks for their potential as drug targets for neurological and neurodegenerative diseases. Many classes of compounds targeted to the DAG binding site, the C1 domain, have been discovered. However, the chemical structures of most C1 domain ligands are extremely complex and therefore there is a need for simple, easily synthesisable C1 domain ligands. In this context, this PhD project aimed at characterizing a group of novel C1 domain ligands, derivatives of 5-(hydroxymethyl)isophthalic acid, *in vitro* and in HeLa and SH-SY5Y cells. More specifically, the aims were:

- To resolve the structure-activity relationships of the isophthalate template and to characterize the affinity of the compounds for different PKC isoforms as well as for other DAG effectors (I, III).
- To characterize effects of the isophthalates on cell viability, proliferation and morphology using HeLa cervical cancer cells (II, III).
- To investigate the effects of isophthalate derivatives on cell differentiation and PKC signalling in SH-SY5Y neuroblastoma cells (IV).

4. MATERIALS AND METHODS

This chapter describes the materials and methods used the studies presented. More detailed descriptions are given in the respective original publications I–IV.

4.1 Drugs

Isophthalic acid derivatives were designed and synthesized at the Division of Pharmaceutical Chemistry, University of Helsinki (Helsinki, Finland). Molecular modelling was performed using the X-ray crystal structure of PKC δ C1b domain (Zhang et al., 1995) as described in I, and the compounds were synthesized as described in I and IV. Stock solutions (10–100 mM) were prepared in dimethyl sulfoxide (DMSO; esters) or in 50% DMSO in H₂O (amides) and stored at -20 °C. The structures of isophthalate derivatives discussed in this thesis are presented in Figure 7.

The pan-caspase inhibitor Boc-Asp(OMe) fluoromethyl ketone (BAF), PDBu, PMA, bryostatin 1, the MEK inhibitor U0126 and chelerythrine chloride were purchased from Sigma-Aldrich (Steinheim, Germany). The pan-PKC inhibitor Gö6983 and the cPKC inhibitor Gö6976 were acquired from Calbiochem (EMD Millipore Corporation, Billerica, MA, USA), and the PKD inhibitor CID755673 was bought from Millipore (Merck Millipore, Dundee, UK). All drugs were dissolved in DMSO, except for chelerythrine chloride, which was dissolved in 50% DMSO in H₂O, and stored at -20 °C.

$$F_3C + CF_3 +$$

Figure 7. Structures of selected isophthalate derivatives.

4.2 Production and purification of recombinant proteins

4.2.1 Production of PKCα, PKCδ and β2-chimaerin in Sf9 insect cells (I, III)

Recombinant human PKC α , PKC δ and β 2-chimaerin were produced in *Spodoptera frugiperda* Sf9 cells (Invitrogen, Carlsbad, CA, USA) using Bac-to-bac® baculovirus expression system (Invitrogen) with previously cloned expression vectors for PKC α and PKC δ (Tammela et al., 2004; Sandler et al., 2005). The plasmid for β 2-chimaerin expression was a gift from prof. Marcelo G. Kazanietz (University of Pennsylvania, Philadelphia, PA, USA) (Caloca et al., 1997). For production of recombinant PKC and chimaerin proteins, Sf9 cells were infected with an optimized amount of the recombinant baculovirus, harvested 2 days postinfection, washed with phosphate-buffered saline (PBS) and frozen at -20 °C.

4.2.2 Preparation of Sf9 cell homogenates (I, III)

Crude lysates were prepared by suspending melted Sf9 cell pellets in lysis buffer [25 mM Tris-HCl pH 7.5, 0.5 mM ethylene glycol tetraacetic acid (EGTA), 0.1% Triton-X 100] supplemented with protease inhibitors (Complete Protease Inhibitor Cocktail; Roche, Mannheim, Germany) and by incubating them on ice for 30 min. The lysates were then centrifuged (16000 g, 15 min, 4 °C) and the supernatants were collected. The protein content was determined according to Bradford (Bradford, 1976) and the supernatants were used for [3 H]PDBu binding experiments.

4.2.3 Production of the C1 domain of MRCKα in E. coli (III)

The pGEX plasmid encoding the glutathione S-transferase (GST)-fused C1 domain of MRCK α was a gift from prof. Peter M. Blumberg (Center for Cancer Research, NCI, Bethesda, MD, USA) (Choi et al., 2008). Competent *E. coli* cells (strain BL21) were transfected with the plasmid and grown overnight at 37 °C on ampicillin-containing Luria Bertani agar plates. Ampicillin-resistant colonies were picked and grown overnight at 37 °C in Luria Bertani medium supplemented with 100 μ g/ml ampicillin. Large-scale cultures were set up the next day and the expression of recombinant protein was induced when the optical density of the medium containing bacteria had reached 0.5–0.6. For induction, isopropyl-*O*-d-thiogalactopyranoside (Sigma-Aldrich) was added to a final concentration of 0.5 mM and the bacteria were grown for 4 h at 37 °C. The bacteria were then harvested, washed twice with PBS, frozen and stored at -70 °C until purification.

4.2.4 Purification the C1 domain of MRCKα (III)

The frozen pellets of E. coli were thawed and suspended into lysis buffer (Tris-HCl 20 mM pH 7.8, 50 mM NaCl, 1% Triton X-100, 0.5% Igepal, 2 mM ethylenediaminetetraacetic acid (EDTA), 2 mM EGTA, 1 mM dithiothreitol, 2 mM phenylmethanesulfonylfluoride). Cell suspensions were incubated on ice for 30 min and cells were disrupted by two passes with French press. After centrifugation (11200 g, 30 min, 4 °C) the supernatant was incubated with glutathione beads (Sigma-Aldrich) for 2 h at 4 °C. Beads were then washed and bound proteins were eluted at 4 °C with lysis buffer containing 10 mM reduced L-glutathione (from Sigma-Aldrich).

4.3 Phorbol ester displacement assays

The ability of the compounds to compete with radioactively labelled PDBu for binding to the C1 domain of PKC α and δ was determined using two modifications of the binding assay. The initial testing for all compounds was performed with a 96-well plate filtration assay (Gopalakrishna et al., 1992b) using cell homogenates from Sf9 cells overexpressing recombinant human PKC isoforms. The filtration method was also used in binding studies with β 2-chimaerin and MRCK α . Binding affinity constants were determined using commercial purified recombinant human PKC isoforms α and δ (Invitrogen, Carlsbad, CA, USA) and the centrifugation method (Lewin and Blumberg, 2003). Binding of HMI-1a3 to PKD was similarly determined using commercial purified PKC μ /PKD1 (Merck Millipore, Dundee, UK) and the centrifugation method. [20- 3 H]Phorbol-12,13-dibutyrate ([3 H]PDBu) was acquired from Amersham Radiolabeling Service (GE Healthcare, Little Chalfont, UK).

4.3.1 Filtration method for [3H]PDBu binding (I, III, IV)

Twenty micrograms of protein from homogenates of Sf9 cells overexpressing PKC α , PKC δ or β 2-chimaerin, or 40 ng of purified MRCK α C1 domain was incubated with test compounds and [3 H]PDBu for 10 min at RT in a 96-well Durapore filter plate (Millipore, Bedford, MA, USA). The final volume was 125 μ l and the concentrations in the reaction mixture were as follows: 20 mM Tris-HCl (pH 7.5), 40 μ M CaCl $_2$, 10 mM MgCl $_2$, 400 μ g/ml bovine IgG, 25 nM [3 H]PDBu, and 0.1 mg/ml phosphatidyl-Lserine. Proteins were precipitated by the addition of 125 μ L of cold 20% poly(ethylene glycol) 6000, and after a 15-min incubation on a plate shaker at RT the filters were washed and the plates were dried. Liquid scintillant was then added and radioactivity was measured using Wallac Microbeta Trilux microplate liquid scintillation counter (PerkinElmer, Waltham, MA, USA). Half maximal inhibitory concentrations (IC $_{50}$) were calculated with GraphPad Prism 4 software (GraphPad Software Inc., La Jolla, USA).

4.3.2 Centrifugation method for [3H]PDBu binding (I, III)

Purified human recombinant PKC α , PKC δ or PKC μ /PKD1 (20 ng/tube) was incubated with test compounds for 10 min at 37 °C in a reaction mixture consisting of 50 mM Tris-HCl (pH 7.4), 0.1 mg/ml phosphatidyl-L-serine, 1.8 mg/ml bovine IgG, 25 nM [3 H]PDBu, and 0.1 mM CaCl $_2$ (for PKC α) or 1 mM EGTA (for PKC δ). Samples were chilled on ice for 10 min, and 200 μ l of 35% poly(ethylene glycol) 6000 in 50 mM Tris-HCl (pH 7.4) was added. The samples were mixed, incubated on ice for 15 min, and centrifuged (15000 g, 15 min, 4 °C). Radioactivity was determined from 100 μ l aliquots of supernatants and from dried pellets. The dissociation constants (K_d) for the individual PKC isoenzymes, the IC $_{50}$ values and the inhibitory dissociation constants (K_i) for the compounds were calculated with GraphPad Prism4 software.

4.4 Cell culture (I-IV)

Cell culture solutions and reagents were from Invitrogen, unless otherwise stated. Human cervical adenocarcinoma cell line HeLa (CCL-2) was acquired from American Type Culture Collection (ATCC,

Manassas, VA, USA) and cultured in Dulbecco's modified Eagle's medium (DMEM; from Sigma-Aldrich) supplemented with 10% foetal bovine serum (FBS), 100 U/ml of penicillin, and 100 μ g/ml of streptomycin. Human neuroblastoma SH-SY5Y cells (CRL-2266; from ATCC) were cultured in DMEM/Ham's F-12 (1:1) medium supplemented with 15% FBS, 1% non-essential amino acids, 100 U/ml of penicillin, and 100 μ g/ml of streptomycin. All cell cultures were maintained at 37 °C in a humidified atmosphere of 5% CO₂ and 95% air and verified negative for mycoplasma using MycoAlert® Mycoplasma detection Kit (Lonza, Verviers, Belgium).

4.4.1 RNA interference (III)

RNAi was used to knock down PKC isoforms α and δ in order to evaluate their role in mediating isophthalate-induced effects in HeLa cells. HeLa cells were seeded onto 12-well plates (2 × 10⁵ cells/well) and transfected the next day with small interfering RNA (siRNA) constructs (ON-TARGETplus SMARTpool PRKCA for PKC α , ON-TARGETplus SMARTpool PRKCD for PKC δ , or the scrambled siRNA ON-TARGETplus siCONTROL non-targeting pool; all from Dharmacon RNA technologies, Lafayette, CO, USA) using X-tremeGENE transfection reagent (Roche). Cells were detached after 4 h, seeded onto 48-well plates (2500 cells/well) and grown for 3 days preceding drug treatments to allow for optimal silencing of target genes. Cells were then exposed to HMI-1a3 and imaged with Cell-IQ® as described in section 4.5.4. Down-regulation of PKC α and PKC δ expression was verified using Western blotting from cells harvested 1, 2, 3 and 6 days after siRNA transfection.

4.5 Cell viability and proliferation assays

For studying the effects of isophthalate derivatives on HeLa or SH-SY5Y cell viability, proliferation and morphology, several assays were used: the lactate dehydrogenase (LDH) assay was used to assess cell membrane integrity and the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay was used to study mitochondrial reduction capacity of the cells (corresponding to both cell viability and proliferation). The rate of DNA synthesis was assessed by measuring the incorporation of [methyl-³H]thymidine into the DNA of HeLa cells. Furthermore, cell proliferation and morphology of both cell lines were studied by using a continuous cell culturing platform with integrated optics and computer vision technology (Cell-IQ®, CM Technologies Ltd, Tampere, Finland) (Toimela et al., 2008). All drug exposures were conducted in normal culture medium to provide optimal growth conditions for the cells.

4.5.1 LDH assay (II)

HeLa cells were seeded onto 96-well plates (10 000 cells/well) 16–24 hours before drug treatments to allow attachment. After drug exposures, 50 μ l of medium from each well was transferred onto a new 96-well plate followed by addition of 50 μ l/well of substrate solution [1.3 mM β -nicotinamide-adenine dinucleotide, 660 μ M iodonitrotetrazolium, 54 mM L(+)-lactic acid, 280 μ M phenazine methosulfate, 0.2 M Tris-HCl (pH 8.2)]. Plates were gently shaken for 10 min and incubated for another 20 min at RT, whereafter 50 μ l of 1 M acetic acid was added to stop the reaction and absorbance was measured at 490 nm.

4.5.2 MTT assay (II, III)

HeLa cells were seeded onto 96-well plates (10 000 cells/well) 16–24 hours before drug treatments. After exposure to test compounds, MTT was added to the cells to a final concentration of 0.5 mg/ml. Plates were then incubated for 2 h at 37 °C in a humidified 5%- CO_2 atmosphere, whereafter the medium was aspirated and 200 μ l of DMSO was added to each well. Absorbance was measured at 550 nm with absorbance at 650 nm extracted as background.

4.5.3 Thymidine incorporation assay (II)

HeLa cells were seeded onto 6-well plates (4 x 10^5 cells/well) and let to attach for 16 h. Cells were then exposed to test compounds, and 0.5 μ Ci/ml [methyl- 3 H]thymidine was added to the medium for the last 6 h of the drug exposure. The cells were then washed three times with cold PBS, ice-cold 5% trichloroacetic acid was added and plates were incubated on ice for 10 min to extract residual thymidine. The trichloroacetic acid solution was discarded, cells were lysed with 0.1 M NaOH and radioactivity was measured by liquid scintillation counting.

4.5.4 Cell proliferation and morphology analysis with Cell-IQ® (II, III, IV)

HeLa cells (5000 cells/well) or SH-SY5Y cells (7500 cells/well) were seeded onto Nunc® 48-well plates (Thermo Scientific, Rockford, IL, USA) and allowed to attach overnight. The cells were then exposed to test compounds and grown in a continuous cell culturing platform with integrated optics (Cell-IQ®) in a humidified 5%-CO2 atmosphere at 37 °C for 72 h. Phase contrast microscopic images were captured automatically from 3-4 positions per well at 1 h intervals. Protocols for analysing cell numbers and cell morphology with Cell-IQ Analyzer® software were created according to manufacturer's instructions separately for both cell lines. First, segmentation parameters (maximum cell diameter, distance between cells, cell symmetry, and segmentation gradient threshold representing the sensitivity of the system for intensity changes in cell structures) were adjusted to achieve optimal cell recognition. Then a sample library of different cell morphologies was created and based on that the software learned to classify recognized cells into dead, dividing, and healthy cells. In addition, a class was added for false recognitions of background, and for HeLa cell analysis, a class for elongated cells was included. For SH-SY5Y cell analysis neurite finder was included in the protocol. The protocols were optimized several times by analysing a set of sample images and by thereafter changing the analysis parameters or adding classification samples according to the results. The protocols were also tested for accuracy by comparing classifications from a set of sample images to classifications made visually by three researchers. Finally, images captured during the experiments were analysed with the protocol. An example of HeLa cell classification is provided in Figure 8.

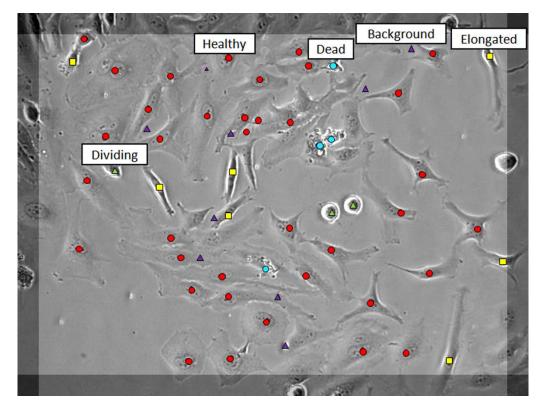


Figure 8. Classification of HeLa cells with Cell-IQ®. Cells classified as normal, "healthy", are marked with red circles, dividing with green triangles, dead with blue circles, and elongated with yellow squares. Recognitions classified as background are marked with lilac triangles.

4.6 Western blotting

4.6.1 Sample preparation (I-IV)

For immunoblotting experiments, 85–95% confluent 6-well plates of HeLa or SH-SY5Y cells were exposed to test compounds and homogenised. For the preparation of whole-cell homogenates, cells were lysed with 1% sodium dodecyl sulphate (SDS) in 10 mM Tris-HCl (pH 7.5), genomic DNA was sheared with a 25 gauge needle, lysates were centrifuged (16 000 g, 15 min, 4 °C) and protein concentrations were determined from the supernatants with bicinchoninic acid assay (Pierce BCA Protein Assay Kit, Thermo Scientific). For extracting the soluble fractions, the cells were harvested in ice-cold lysis buffer containing 20 mM Tris-HCl (pH 7.4), 0.1% Triton X-100, 2 mM EDTA, 10 mM EGTA, and protease inhibitors (Complete Protease Inhibitor Cocktail, Roche). If phosphoproteins were studied, phosphatase inhibitors (PhosSTOP Phosphatase Inhibitor Cocktail Tablets, Roche) were added to the buffer prior to use. After a 30-min incubation on ice, the lysates were centrifuged (16 000 g, 15 min, 4 °C) and the protein concentrations of the supernatants were determined using Bradford's method (Bradford, 1976).

4.6.2 Protein separation and detection (I-IV)

Equal amounts of protein were loaded onto SDS-polyacrylamide (SDS-PAGE) gels and separated under constant voltage. Proteins were then transferred onto Protran® nitrocellulose membranes

(Schleicher & Schuell, Dassel, Germany) and non-specific binding was blocked with 5% powdered non-fat milk or bovine serum albumin (BSA) in Tris-buffered saline containing 0.1% Tween 20 (TTBS) at RT. The membranes were then incubated with primary antibody (see Table 2) overnight at 4 °C and thereafter with horseradish peroxidase (HRP)-conjugated secondary antibody (see Table 2) for 1 h at RT. Immunoreactive bands were detected with enhanced chemiluminescence (ECL; SuperSignal West Pico Chemiluminescent Substrate Kit, Thermo Scientific) using GeneGnome imaging system (Syngene, Cambridge, UK). Relative densities were quantified using Scion Image or ImageJ software.

Table 2. Antibodies used in studies I-IV.

Primary antibodies, species	Dilution in ICH	Dilution in WB	Blocking in WB	Producer, product no.
β actin, r		1:1000	milk	CST, #4967
cofilin-1, r	1:50	1:1000	BSA	(Hotulainen et al., 2005)
cyclin A, m		1:2000	milk	CST, #4656
cyclin B1, m		1:2000	milk	CST, #4135
cyclin D1, m		1:2000	milk	CST, #2926
cyclin E, m		1:1000	milk	CST, #4129
ERK1, r		1:1000	milk	SCBT, sc-94
GAPDH, m		1:2500	milk	SCBT, sc-47724
p21 ^{waf1/cip1} , m		1:2000	milk	CST, #2946
p27 ^{kip1} , m		1:1000	milk	CST, #3698
phospho-Cofilin-1 (Ser3), r	1:50	1:1000	BSA	CST, #3313
phospho-ERK1/2 (Thr202/Tyr204), r		1:1000	BSA	CST, #9101
phospho-Rb (Ser795), m		1:1000	milk	CST, #9301
PKCα, m		1:1000	milk	SCBT, sc-8393
PKCβI, m		1:1000	milk	SCBT, sc-8049
ΡΚCδ, r		1:1000	milk	SCBT, sc-213
Rb, m		1:2000	milk	CST, #9309
vinculin, m	1:100			Sigma-Aldrich, V9131
Secondary antibodies	Dilution in ICH	Dilution in WB	Blocking in WB	Producer, product no.
Alexa Fluor®488 goat anti-mouse	1:200		_	Invitrogen, A-11001

Secondary antibodies	Dilution in ICH	Dilution in WB	BIOCKING IN WE	Producer, product no.
Alexa Fluor®488 goat anti-mouse	1:200			Invitrogen, A-11001
Alexa Fluor®594 goat anti-mouse	1:200		Invitrogen, A-21125	
Alexa Fluor®488 goat anti-rabbit	1:200			Invitrogen, A-11034
Alexa Fluor®647 goat anti-rabbit	1:200			Invitrogen, A-21245
HRP-linked horse anti-mouse		1:2000	milk	CST, #7076
HRP-linked goat anti-rabbit		1:2000	milk/BSA	CST, #7074

BSA, bovine serum albumin; CST, Cell Signaling Technology (Danvers, MA, USA); GAPDH, glyceraldehyde 3-phosphate dehydrogenase; ICH, immunocytochemistry; m, mouse; r, rabbit; Rb, retinoblastoma; SCBT, Santa Cruz Biotechnology (Santa Cruz, CA, USA); WB, Western blotting.

4.7 Immunocytochemistry and fluorescence microscopy (III)

HeLa cells were seeded onto 13 mm cover slips in 35 mm culture dishes, grown overnight and exposed to test compounds. After drug exposure, the coverslips were washed with PBS and fixed with 4% paraformaldehyde for 20 min at RT. Coverslips were then washed 2 times with Dulbecco's phosphate buffered saline containing 0.2% BSA (DB) and the cells were permeabilized with 0.1% Triton X-100 for 7 min. Cells were then washed, incubated with primary antibodies (see Table 2) in DB for 60 min at RT, washed again and incubated with secondary antibodies (see Table 2), phalloidin (Alexa Fluor® 488 phalloidin or Alexa Fluor® 568 phalloidin; Invitrogen) and/or 4',6-diamidino-2-phenylindole (DAPI; Sigma-Aldrich) in DB for 45 min at RT. After washing, the coverslips were

mounted onto Mowiol® (Sigma-Aldrich) containing 1,4-diazabicyclo[2.2.2]octane (DABCO; Sigma-Aldrich). Cells were imaged with a charge-coupled device camera (AxioCam HRm; Carl Zeiss Microscopy GmbH, Jena, Germany) on Axio Imager.M2 microscope (Zeiss) using PlanApo 63x/1.40 (oil) objective (Zeiss) and AxioVision Rel. 4.8 software (Zeiss).

4.8 Genome-wide gene expression analysis (III, IV)

HeLa and SH-SY5Y cells were grown to 80-90% confluence on 6-well plates and exposed to test compounds or DMSO for 12 h. The cells were then washed with PBS, detached with Trypsin-EDTA, washed again with PBS, snap-frozen in liquid nitrogen and stored at -70 °C. RNA extraction, RNA purification and genome-wide gene expression analysis were performed in the Biomedicum Functional Genomics Unit, University of Helsinki (Helsinki, Finland). Briefly, RNA was extracted and purified with RNeasy kit (Qiagen, Hilden, Germany). Total RNA was amplified and labelled with Illumina® TotalPrep RNA Labeling Kit (Life Technologies Ltd, Paisley, UK). Purified biotinylated cRNA was hybridized to HumanHT-12 v4 Expression BeadChips (Illumina®, Life Technologies) for 18 hours at 58 °C. BeadChips were then washed, blocked and stained with streptavidin-Cy3 and scanned with Illumina® iScan. The data was exported using Illumina® BeadStudio and further processed and analyzed with R/bioconductor, BeadStudion, RankProd and biomaRt. Microarray quality was evaluated using hierarchical clustering, principal component analysis and control probe analysis. The relative reliability of each array was assessed using the arrayWeights function of Limma. Gene expression levels between sample sets were compared using moderated paired t-test (package IBMT, p<0.05) with a Benjamini-Hochberg multiple test correction to minimize selection of false positives. Gene set enrichment analysis (GSEA) was performed using GOrilla (http://cblgorilla.cs.technion.ac.il) (Eden et al., 2009).

4.9 Statistical analysis (I-IV)

All statistical analyses were carried out with SPSS 16 or PASW statistics 18 software (SPSS Inc., Chicago, IL, USA). Statistical analysis for dose-response data from [3 H]PDBu binding assays (I), and cell viability and proliferation assays (II, III) as well as for immunoblotting quantification data (I - IV) was performed using one-way analysis of variance (ANOVA) followed by Tukey's honestly significant difference (HSD) post hoc test. Dunnett's multiple comparison test was used to analyse GAP-43 quantifications (IV), and PKC α protein levels after cellular fractionation (IV) was analysed with Student's t-test. Comparison of time-response curves from Cell-IQ $^{\oplus}$ (in IV) was performed with repeated measures ANOVA followed by Tukey's HSD.

5. RESULTS

5.1 Structure-activity relationship studies on isophthalate derivatives (I, III)

A starting point for the design of C1 domain ligands was the commercially available diethyl (5-hydroxymethyl)isophthalate (HMI-1b21, Fig. 7), a hit molecule from a virtual screening campaign of commercially available small molecules using the crystal structure of the PKCδ C1b domain (Zhang et al., 1995). Its structure complied with the pharmacophore model created based on phorbol (Wang et al., 1994), and it provided an easily modifiable template for the synthesis of various derivatives. Preliminary binding studies demonstrated that while HMI-1b21 did not bind to the PKC C1 domain, dipentyl (5-hydroxymethyl)isophthalate displaced [³H]PDBu from PKC (unpublished). These studies aimed to find out, which functional groups are needed and how different substituents affect binding. Furthermore, these experiments aimed at providing evidence of isophthalate binding to the PKC C1 domain in cellular context.

5.1.1 Binding to the C1 domain of PKC (I)

For studying structure-activity relationships (SAR) of the template, 42 first-generation isophthalic acid derivatives were assayed for binding to C1 domains of recombinant full-length human PKC α and PKC δ produced in Sf9 cells. A schematic presentation of the SAR studies is provided in Figure 9 (for numerical data and results of individual compounds, see Tables 1 and 2 in I). The SAR studies revealed that the 5-hydroxymethyl group and the ester groups of the template are indispensable. Additionally, sufficient hydrophobicity of the side chains is required: The dialkyl (5-hydroxymethyl)isophthalates that displaced [3 H]PDBu from PKC α and PKC δ in a concentration-dependent manner with low micromolar concentrations had *c*logP values of 5.0 or higher.

5.1.2 Binding affinity constants for PKCα and PKCδ (I)

Three isophthalate derivatives (HMI-1a3, HMI-1b10 and HMI-1b11) were selected for more detailed analysis of binding affinity. First the K_d of the radioligand [3 H]PDBu was determined for both PKC α and PKC δ (1.29 nM and 2.35 nM, respectively), and the validity and accuracy of the assay was confirmed by determining the K_i values of DOG for PKC α (40.1 \pm 6.0 nM, n=4) and of bryostatin 1 for PKC δ (0.44 \pm 0.08 nM, n=5). These values are in accordance with published data (Wender et al., 1998; Ananthanarayanan et al., 2003).

The isophthalate derivatives displaced [3 H]PDBu from PKC α and PKC δ with K_i values in the range of 205–915 nM (Fig. 10). No significant differences in affinities (potencies) between the ligands were detected. However, differences in the magnitude of maximal [3 H]PDBu displacement were observed. HMI-1a3 was the least effective isophthalate: It only displaced 55% and 37% of [3 H]PDBu from PKC α and PKC δ , respectively (Fig. 10). In comparison, HMI-1b10 was the most effective derivative displacing 84% and 88% of [3 H]PDBu from PKC α and PKC δ , respectively (Fig. 10). While HMI-1a3 was more effective in displacing [3 H]PDBu from PKC α than from PKC δ , no difference in maximal [3 H]PDBu displacement for the two PKC isoforms were observed with HMI-1b10 and HMI-1b11 (Fig. 10).

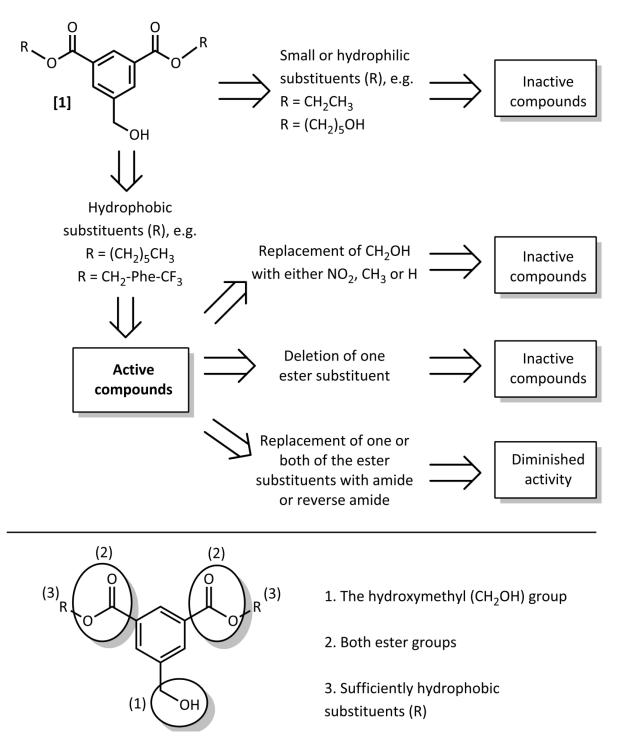


Figure 9. Schematic presentation of the structure activity relationship (SAR) studies with the isophthalate template [1]. Compounds with low micromolar binding affinity are designated as active compounds and those with no affinity for the C1 domain as inactive compounds. The lower panel presents the structural elements required for binding.

5.1.3 Binding to other DAG effectors (III)

To confirm the SAR model created based on the binding experiments with PKC, binding of 15 active and 4 inactive isophthalate derivatives to recombinant full-length β 2-chimaerin from Sf9 cell lysates was studied. The results followed the SAR model generated based on binding experiments with PKC.

The active isophthalates displaced [3 H]PDBu from β 2-chimaerin in a concentration-dependent manner with submicromolar and low micromolar concentrations, and the inactive derivatives had no affinity for the C1 domain of β 2-chimaerin (not shown, unpublished). As an example, HMI-1a3 displaced [3 H]PDBu from β 2-chimaerin with an IC $_{50}$ of 1.2 μ M (Table 3, Fig. 6 in III). To further characterize the binding properties of HMI-1a3, its affinity to the C1 domains of PKD and MRCK was studied. HMI-1a3 displaced [3 H]PDBu from PKD1 in a concentration-dependent manner in a similar concentration range as with PKCs (Table 3, Fig. 6 in III), while NI-15e exhibited no binding at concentrations up to 100 μ M (not shown, unpublished). Furthermore, HMI-1a3 bound to the C1 domain of MRCK α produced in *E. coli* in a similar low micromolar concentration range (Table 3, Fig. 6 in III).

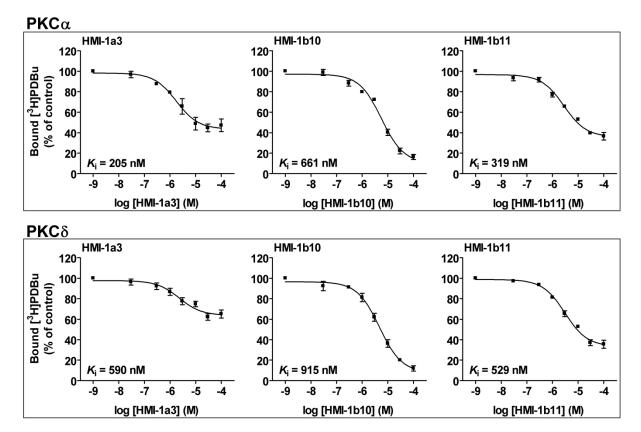


Figure 10. Binding of HMI-1a3, HMI-1b10 and HMI-1b11 to purified PKC\alpha and PKC\delta. Displacement of 10 nM [3 H]PDBu was measured with the centrifugation method in the presence of graded concentrations of isophthalates. The data was analysed with GraphPad Prism 4 using a one-site competition equation. Results are presented as mean \pm SEM from 3–5 independent experiments.

5.1.4 Effects on ERK1/2 signalling in HeLa cells (I)

To investigate whether the isophthalates regulate PKC-mediated signalling in cellular context, we studied their effects on ERK1/2 phosphorylation in HeLa cells. When added to cell culture medium, HMI-1a3 and HMI-1b10 induced PKC-dependent ERK1/2 phosphorylation, but HMI-1b11 alone had no effect (Fig. 4 in I). Instead, HMI-1b11 inhibited PMA-induced ERK1/2 phosphorylation in a concentration-dependent manner showing that it does bind to the PKC C1 domain in cellular context as well (Fig. 4 in I).

Table 3. Binding affinity of HMI-1a3 to the C1 domains of 62-chimaerin, PKD and MRCK α . The IC₅₀ value for PKC α is provided for comparison.

DAG effector IC ₅₀ (μM)		Receptor protein	Purification	Method filtration	
β2-chimaerin	2-chimaerin 1.2 recombinant fu chimaerin		crude Sf9 cell lysate (not purified)		
PKD1	6.3	recombinant 6His-tagged full length PKD1 (#14-508, Millipore)	commercially purified (72% pure)	centrifugation	
ΜRCΚα	1.3	recombinant GST-tagged C1 domain of MRCKα	affinity purified (≈80% pure)	filtration	
ΡΚCα	1.8 recombinant full length PKCα (P2232, Invitrogen)		commercially purified centrifug (95% pure)		

The data was analysed with GraphPad Prism 4 with one-site competition equation using mean and SEM values from 3-4 independent experiments.

5.2 Effects of isophthalate derivatives in HeLa cells (II, III)

5.2.1 Viability and proliferation (II)

Effects of five active and four inactive isophthalate derivatives on HeLa cell viability were studied using MTT and LDH tests after 24 and 48-hour exposures. None of the isophthalates induced necrosis as indicated by <10% cytotoxicity in the LDH assay (not shown). However, several of the active compounds induced a decrease in mitochondrial reduction capacity according to the MTT assay (Fig. 2 in II). HMI-1a3 was the most potent compound inhibiting the metabolic activity of HeLa cells with an IC₅₀ of 0.3 μ M (p<0.001) (Fig. 2 in II). HMI-1b10 and HMI-1b11, on the other hand, had only a slight effect at 20 μ M, the highest concentration tested (Fig. 2 in II), and the inactive isophthalate derivatives had no effect (Fig. 2 in II). PMA (at concentrations 0.1 nM - 1 μ M) inhibited MTT reduction only at 10 nM (p<0.01), but exhibited no cytotoxicity according to the LDH test (Fig. 2 in II). Bryostatin 1 had no influence on HeLa cell viability at concentrations 0.1-100 nM (Fig. 2 in II).

According to Cell-IQ® analysis isophthalate derivatives with low micromolar binding affinity to PKC exhibited a concentration-dependent antiproliferative effect. HMI-1a3 was the most potent derivative: It inhibited proliferation with an IC₅₀ of 2.0 μ M (Fig. 11A). The inactive isophthalates had no effect (NI-15e shown in Fig. 11A, Fig. 4 in II). PMA (at 1–1000 nM) had no significant effect on proliferation (Fig. 4 in II).

Effects of HMI-1a3 were further characterized by studying its effects on DNA synthesis. HMI-1a3 inhibited thymidine incorporation in a concentration-dependent manner after 6-hour and 24-hour exposures (IC₅₀ values 5.8 μ M and 4.5 μ M, respectively) (Fig. 3 in II). Furthermore, to investigate the influence of HMI-1a3 on cell cycle progression, its effects on various cell cycle markers was studied with Western blotting. A 24-hour exposure to 10 μ M or 20 μ M HMI-1a3 induced down-regulation of cyclins A, B1, D1 and E, and total and phosphorylated retinoblastoma protein (II, not shown). At 10 μ M (but not at 20 μ M) HMI-1a3 also down-regulated p21^{waf1/cip1} and p27^{kip1} proteins (Fig. 7 in II). In contrast, PMA and bryostatin 1 (both at 100 nM) induced prominent up-regulation of cyclin D1 and p21^{waf1/cip1}, and down-regulation of 27^{kip1} (Fig. 7 in II).

5.2.2 Morphology and cytoskeleton (II, III)

The antiproliferative isophthalate derivatives, including HMI-1a3, induced a morphological change that was characterized by cell elongation and reduced cell-to-cell contacts (Fig. 11D–F). A more detailed analysis revealed that after exposure to active isophthalates at antiproliferative concentrations the proportion of apparently healthy cells decreased and the proportion of elongated cells increased rapidly, followed by a delayed increase in the proportion of dead cells (HMI-1a3 shown in Fig. 11C). In contrast, the morphology of untreated cells and cells exposed to vehicle (DMSO) or inactive isophthalates remained unchanged (untreated cells shown in Fig. 11B). PMA induced a transient cell elongation followed by a more rounded cell morphology (Fig. 6 in II).

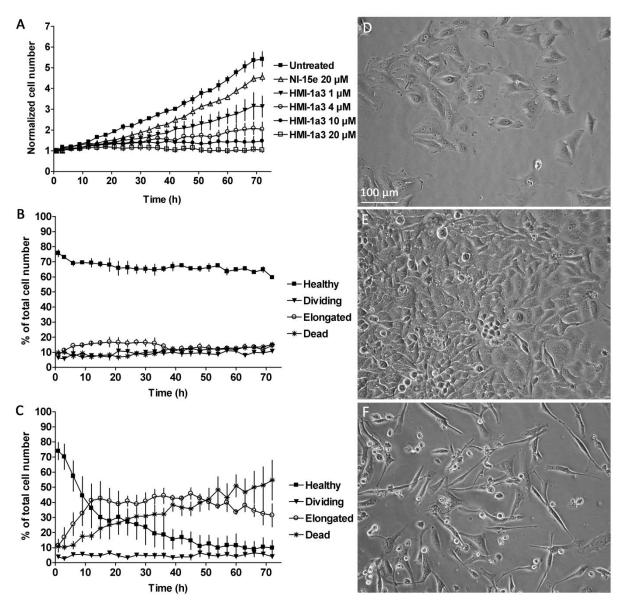


Figure 11. Effects of HMI-1a3 on HeLa cell proliferation and morphology. HeLa cells were exposed to test compounds, imaged with Cell-IQ® and analysed with Cell-IQ Analyzer® software. Quantifications from images captured with 3-hour intervals are presented in A–C (mean \pm SEM, n=3). A, normalized total cell numbers of untreated cells and cells exposed to HMI-1a3 or NI-15e; B, classification results of untreated cells; C, classification results of cells exposed to 20 μ M HMI-1a3. D–F, representative photomicrographs of untreated cells at time points 1 h (D) and 72 h (E), and of cells exposed to 20 μ M HMI-1a3 for 72 h (F).

The effects of HMI-1a3 and NI-15e on cytoskeleton were studied further using immunocytochemistry. Filamentous actin (F-actin) forms microfilaments that are a central part of the cytoskeleton and regulate cell shape and motility. The effects of HMI-1a3 and NI-15e on actin cytoskeleton were visualized using phalloidin, a toxin that binds to F-actin. Focal adhesions are protein complexes that connect the cytoskeleton to the extracellular matrix. They were visualized by staining one of their important constituents, vinculin. HMI-1a3-induced cell elongation was accompanied with loss of focal adhesions and actin stress fibres (Fig. 12), while exposure to NI-15e had no effect (not shown).

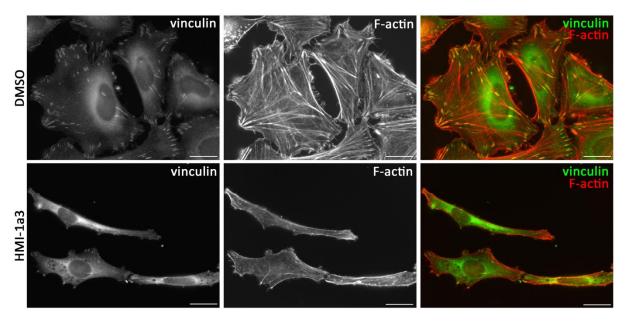


Figure 12. Effects of HMI-1a3 on HeLa cell cytoskeleton. HeLa cells were exposed to 0.2% DMSO or 20 μ M HMI-1a3 for 24, fixed and stained. Focal adhesions were visualized using an antibody against vinculin and stress fibres (F-actin) were detected with phalloidin. Representative epifluorescence microscopic images are presented (n=2 for focal adhesions, n=8 for F-actin). Scale bar, 20 μ m.

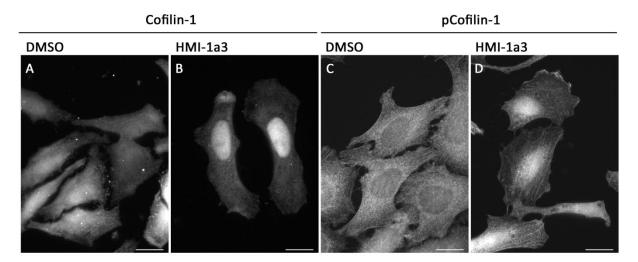


Figure 13. Effect of HMI-1a3 on the localization of cofilin-1 and phosphorylated cofilin-1 (pCofilin-1). HeLa cells were exposed to 0.1% DMSO or 10 μ M HMI-1a3 for 24 h, fixed and stained with antibodies recognizing either total cofilin-1 (A, B) or phosphorylated cofilin-1 (C, D). Representative epifluorescence microscopic images are presented (n=3). Scale bar, 20 μ m.

The prominent changes in actin cytoskeleton lead us to investigate the effects of HMI-1a3 on the phosphorylation status and intracellular localization of the actin-depolymerizing protein cofilin-1, which is the cofilin isoform present in non-muscle cells (Bernstein and Bamburg, 2010). In untreated cells or in cells treated with 0.2% DMSO or 20 μ M NI-15e cofilin-1 was localized either in the cytosol or diffusely in both cytosol and nucleus (DMSO shown in Fig. 13A, Fig. 3 and 4A in III). A 24-hour exposure to 10 μ M or 20 μ M HMI-1a3 induced a clear relocation of cofilin-1 regardless of cell morphology: Cofilin-1 was predominantly localized in the nucleus of both elongated and normal-looking cells (10 μ M HMI-1a3 shown in Fig. 13B, Fig. 3 and 4A in III). A similar pattern of localization was observed for phosphorylated cofilin-1 (Fig. 13C–D, unpublished). However, HMI-1a3 had no effect on the phosphorylation state of cofilin-1 as determined by Western blotting (Fig. 4B in III).

5.2.3 Mechanistic studies on isophthalate-induced effects in HeLa cells (II, III)

Genome-wide gene expression microarray and subsequent GSEA (Subramanian et al., 2005) were carried out to identify signalling pathways that may be responsible for mediating the effects of isophthalates in HeLa cells. Numerical comparison of genes, whose expression was statistically significantly different between the treatments, is presented in Table 4. A 12-h exposure to HMI-1a3 induced changes in a remarkably greater number of genes than HMI-1b11 or NI-15e. Based on GSEA, the biological processes that were most significantly altered in HMI-1a3-exposed cells were related to cell cycle and proliferation as well as cell motility, migration and cytoskeleton reorganization (Table 1 in III), consistent with the antiproliferative and elongation-inducing effects of HMI-1a3. Other biological processes significantly altered in HMI-1a3-exposed cells compared to NI-15e-exposed cells included for example RNA processing, cholesterol biosynthesis and small GTPase-mediated signal transduction (Table 1 in III).

Since the cell viability assays pointed to a non-necrotic mechanism of cell death, the effect of caspase inhibition on HeLa cell response to HMI-1a3 was examined. The pan-caspase inhibitor BAF (at 40 μ M) had no effect on HMI-1a3-induced changes in HeLa cell proliferation and viability when assessed with Cell-IQ® imaging (Table 5, Fig. 5 in II).

Table 4. Differential regulation of gene expression by isophthalate derivatives in HeLa cells. The table presents the numbers of genes whose mRNA level were statistically significantly different between the indicated treatments (12 h).

	DMSO (0.1%)	NI-15e (10 μM)	HMI-1b11 (10 μM)
HMI-1a3 (10 μM)	1411	1277	1396
HMI-1b11 (10 μM)	304	85	-
NI-15e (10 μM)	9	-	

To clarify the signalling pathways responsible for mediating the antiproliferative and elongation-inducing effects of HMI-1a3, the involvement of PKC and ERK1/2 signalling pathways was first investigated. Co-exposure to the pan-PKC inhibitor Gö6986 (1 μ M) or the PKC activator PMA (at 10 or 100 nM) did not modify the cytotoxic and antiproliferative effect of HMI-1a3 as determined by MTT assay (Table 5, Fig. 5 in III). Gö6983 alone had no effect on HeLa cell proliferation and it did not modify the effects of HMI-1a3 on cell proliferation, morphology or viability as assessed by Cell-IQ® imaging (Table 5, Fig. 5 in III). Furthermore, knock-down of PKC α or PKC δ with RNAi did not influence

the antiproliferative effect of HMI-1a3 (Table 5, Fig. 5 in III). The MEK inhibitor U0126 (10 μ M) was unable to inhibit HMI-1a3-induced responses as determined by the MTT assay or Cell-IQ® analysis (Table 5, Fig. 5 in III).

Based on results from gene expression microarray and GSEA indicating changes in processes linked to small GTPase-mediated signalling, PKD and MRCK were considered potential mediators of isophthalate-induced effects in HeLa cells. To investigate their role in mediating HMI-1a3-induced changes in cell morphology and proliferation, effects of the PKD inhibitor CID755673 and the MRCK inhibitor chelerythrine on HeLa cell response to HMI-1a3 were studied with Cell-IQ® imaging. CID755673 (at 1 μ M or 10 μ M) had no effect on HeLa cell proliferation or morphology, or on HMI-1a3-induced responses (Table 5, Fig. 7 in III). The MRCK inhibitor chelerythrine was toxic to HeLa cells: concentrations of 4 μ M and 10 μ M induced rapid cell death and prevented analysis with these concentrations (not shown). However, at the lower concentrations of 1 μ M and 2 μ M chelerythrine inhibited HMI-1a3-induced cell elongation: The inhibition was most prominent (38% and 42%, respectively) at the time point 24 h (table ZX, Fig. 7 in III). No significant differences were observed in the proportions of healthy, dividing or dead cells (Fig. 7 in III).

Table 5. Summary of mechanistic studies on HMI-1a3-induced effects in HeLa cells. Effects of modulation of PKC, PKD, MRCK, or ERK1/2 signalling pathways or inhibition of caspases on HMI-1a3-induced changes in HeLa cell proliferation, viability and morphology.

Target	Treatment	Response					
	Co-exposure to HMI-1a3 (at 0.1-20 μM) and	Inhibition of proliferation	Cell elongation	% of dead cells	Cytotoxicity (MTT)		
PKC	Gö6983 1 μM	-	-	-	-		
	PMA 10 nM, 100 nM	-	_	-	_		
	PKCα siRNA	-	-	-	n/a		
	PKCδ siRNA	-	_	-	n/a		
PKD	CID-755673 1 μM, 10 μM	-	-	-	n/a		
MRCK	Chelerythrine 1μM, 2 μM	-	↓	-	n/a		
MEK	U0126 10 μM	-	-	-	_		
caspases	BAF 40 μM	_	_	-	n/a		

^{-,} no effect on HMI-1a3-induced response; \downarrow , inhibition of HMI-1a3-induced response (p<0.05); n/a, not analysed

5.3 Effects of isophthalate derivatives in SH-SY5Y cells (IV)

The human neuroblastoma cell line SH-SY5Y, which is widely used as an *in vitro* model of neuronal function and differentiation (Påhlman et al., 1990; Agholme et al., 2010), was used to characterize the effects of two active isophthalates (HMI-1a3 and HMI-1b11) and their corresponding inactive derivatives (NI-15e and MI-40, respectively) on neuronal-like cells. The active isophthalates HMI-1a3 and HMI-1b11 were selected based on their divergent effects on ERK1/2 phosphorylation in HeLa cells and on HeLa cell viability and proliferation.

5.3.1 Cell proliferation, viability and morphology (IV)

Both HMI-1a3 and HMI-1b11 inhibited SH-SY5Y cell proliferation in a concentration-dependent manner, whereas MI-40 had no effect (Fig. 14A). At the end of the experiment, inhibition of proliferation was statistically significant with 20 μ M HMI-1a3 (p<0.01) and with 10–20 μ M HMI-1b11 (p<0.05). PMA was antiproliferative only at 10 nM (30% inhibition of proliferation), but not with other concentrations studied (0.1, 1, 100 and 1000 nM) (not shown and Fig. 3 in IV). HMI-1a3 induced toxicity at the highest concentration tested (20 μ M; 31% of cells were dead at 48 h), while HMI-1b11, MI-40 or PMA had no effect on cell viability (not shown, IV).

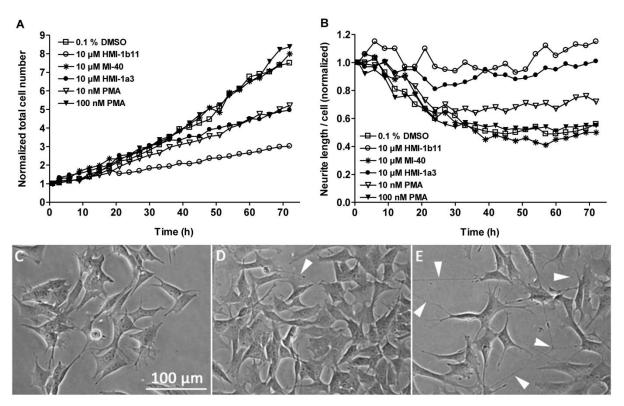


Figure 14. Effects of isophthalate derivatives on SH-SY5Y cell proliferation and morphology. Cells were exposed to vehicle (DMSO) or test compounds as indicated and imaged for 72 h with Cell-IQ $^{\circ}$. Cell numbers and neurite lengths were analysed from each image using Cell-IQ Analyzer $^{\circ}$. Quantifications of images taken at 3 hour intervals are shown as mean of 3 independent experiments (each with 4 images from different positions within the same well). A, quantification of SH-SY5Y cell proliferation; B, quantification of average neurite length; C, a representative photomicrograph of untreated cells (t=1 h); D, a representative photomicrograph of cells exposed to 0.1% DMSO (t=70 h); E, a representative photomicrograph of cells exposed to 10 μ M HMI-1b11 (t=70 h). Arrowheads indicate examples of neurites.

Based on visual observation, SH-SY5Y cells exposed to HMI-1a3 or HMI-1b11 exhibited more pronounced (longer and also branched) neurites when compared with untreated cells or cells exposed to DMSO, MI-40 or PMA (Fig. 14C–E and not shown). Quantification showed that the average neurite length of untreated cells or cells exposed to DMSO, MI-40 or PMA decreased during the first 30–40 hours of the experiment and thereafter remained constant (Fig. 14B, Fig. 3 in IV). HMI-1a3 and HMI-1b11 inhibited the decrease in neurite length in a concentration-dependent manner (Fig. 14B, Fig. 3 in IV). There was a statistically significant time-dependent change in neurite length (p<0.001, repeated measures ANOVA) and a time and treatment interaction (p<0.05), but no statistical significance for a treatment-dependent effect in post-hoc tests.

5.3.2 Genome-wide gene expression and GSEA (IV)

Because HMI-1b11 was non-toxic and supported neurite outgrowth, it was selected for gene expression microarray studies. A 12-hour exposure to 10 µM HMI-1b11 induced statistically significant changes in the expression of 1071 genes when compared with cells exposed to vehicle (not shown). GSEA suggested that the gene expression changes may be linked to nucleic acid and/or RNA processing and vesicle transport (not shown). It also revealed statistically significant enrichments in numerous biological processes linked to cell differentiation, small GTPase-mediated signalling, ERK1/2 cascade and Wnt signalling (Table 2 in IV).

5.3.3 PKC and ERK1/2 signalling and GAP-43 expression (IV)

Since the previous experiments suggested that isophthalates modulate ERK1/2 activation, and since ERK1/2 activation has been linked to differentiation of SH-SY5Y cells (Monaghan et al., 2008), the effects of isophthalates on ERK1/2 phosphorylation in SH-SY5Y cells was investigated. Exposure to either HMI-1a3 or HMI-1b11 at 10 μ M induced a rapid and strong ERK1/2 phosphorylation that was efficiently inhibited by co-exposure to the pan-PKC inhibitor Gö6983 at 1 μ M (Fig. 14A, Fig. 4 in IV). PMA (at 100 nM) also induced ERK1/2 phosphorylation, while 10 μ M NI-15e had no effect (Fig. 15A, Fig. 4 in IV). Since the cellular outcome of ERK1/2 activation may depend on the duration of the signalling, ERK1/2 phosphorylation levels were also studied after a 12-hour exposure. At this later time point, the level of phosphorylated ERK1/2 was increased in cells exposed to 10 μ M HMI-1b11 or 100 nM PMA, but not in cells exposed to 10 μ M HMI-1a3, NI-15e or MI-40 (Fig. 15A). No change in total ERK1/2 protein level was observed with isophthalate exposure times up to 24 h (not shown).

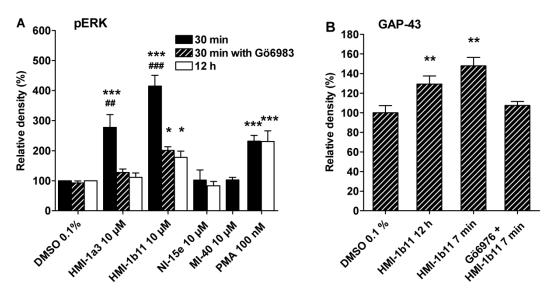


Figure 15. Effects of isophthalates on ERK1/2 phosphorylation and GAP-43 protein level in SH-SY5Y cells. A, Levels of phosphorylated ERK1/2 were determined with Western blotting from soluble fractions of cell homogenates (n=3-4; ***, p<0.001 vs. DMSO; *, p<0.05 vs. DMSO; ###, p<0.001 vs. the corresponding Gö6893-treated sample; me-way ANOVA followed by Tukey's HSD). B, SH-SY5Y cells were exposed to 10 μ M HMI-1b11 with or without the cPKC inhibitor Gö6976 (2 μ M) for indicated times, and total cell homogenates were collected 12 hours after the beginning of the exposure. Level of GAP-43 protein was determined with Western blotting (n=4-6; **, p<0.01 vs. DMSO; Dunnett's multiple comparison test).

The effect of HMI-1b11 on intracellular localization of PKC α on was studied using cell fractionation and immunoblotting. A 7-minute exposure to HMI-1b11 induced an increase of 53% (\pm 13.4%) in PKC α in the cytoskeletal fraction, and an increase of 39% (\pm 14.3%) in total PKC α protein level (Fig. 6 in IV). PKC α levels in soluble or membrane fractions remained unchanged (not shown).

PKC α activation is known to induce activation of nELAV proteins and subsequent RNA stabilization (Pascale et al., 2005). One of the target proteins of nELAVs is GAP-43, a central regulator of neuronal differentiation and plasticity (reviewed in Benowitz and Routtenberg, 1997). Based on the ERK1/2 phosphorylation studies suggesting that HMI-1b11 activates PKC and on GSEA results indicating that RNA processing may be significantly altered in HMI-1b11-treated cells, it was hypothesized that HMI-1b11 exposure could lead to up-regulation of GAP-43. Indeed, exposure to 10 μ M HMI-1b11 induced a clear increase in GAP-43 mRNA (Fig. 5 in IV), consistent with gene expression microarray data showing a 70% increase in GAP-43 mRNA (not shown). GAP-43 protein level was also increased in response to HMI-1b11 exposure, and the effect was diminished by co-exposure to the cPKC selective inhibitor Gö6976 (Fig. 15B, Fig. 5 and 7 in IV).

5.4 Effects of isophthalate derivatives on PKC protein levels (unpublished)

Most C1 domain binding PKC activators are known to induce PKC down-regulation. Since the previous data indicated that the isophthalates activate PKC in both HeLa and SH-SY5Y cells, the protein levels of selected PKC isoforms after 24-hour isophthalate exposures were investigated. In HeLa cells, HMI-1a3 and HMI-1b11 had no effect on the levels of PKC α , PKC β I or PKC δ , while PMA induced a clear down-regulation of PKC α and PKC β I, and a slight down-regulation of PKC δ (Fig. 16A, unpublished). Similarly, exposure to either HMI-1a3 or HMI-1b11 had no significant effect on PKC α , PKC β I or PKC δ protein levels in SH-SY5Y cells. However, in these cells PMA induced a strong down-regulation of PKC isoforms α and δ , but had no effect on the levels of PKC β I (Fig. 16B, unpublished).

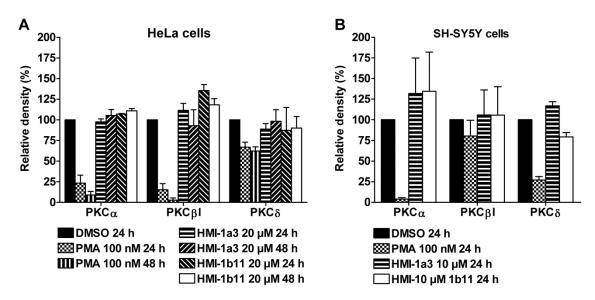


Figure 16. Effects of isophthalates on PKC protein levels in HeLa and SH-SY5Y cells. Cells were exposed to test compounds as indicated and PKC protein levels were analysed from total cell homogenates of (A) HeLa cells and (B) SH-SY5Y cells with Western blotting. Relative densities normalized to densities of θ -actin bands are presented as percentage of control (mean + SEM; n=3-6, except for HMI-1b11 in HeLa cells, where n=2).

6. DISCUSSION

6.1 Structure-activity relationships of isophthalate derivatives

Most of the existing C1 domain ligands are highly complex in their chemical structure and therefore their synthesis and chemical modification in order to achieve selectivity is difficult and laborious (Blumberg et al., 2008; Boije af Gennäs et al., 2011). Therefore, the simple isophthalate template offers an attractive possibility for the development of C1 domain ligands with an easy and effective synthesis route. The indispensable functional groups highlighted in binding experiments were consistent with results from docking experiments and the pharmacophore model. Furthermore, analogous hydroxyl and carbonyl groups are present in other well-characterized C1 domain ligands, such as phorbol esters and DAG lactones (Wang et al., 1994; Benzaria et al., 1998). The contribution of the side chains to binding affinity is difficult to assess in docking experiments, because modelling the interaction between the C1 domain and the lipid bilayer of cell membrane is unfeasible. However, it is known that hydrophobic interactions of the side chains are crucial for high affinity binding and biological effects of phorbol esters, DAG and their analogues (Zhang et al., 1995; Nacro et al., 2000; Wang et al., 2000; Blumberg et al., 2008). The present results showing that a certain level of hydrophobicity of the side chains is essential thus comply with the prevailing understanding of binding requirements. The optimal clogP values for isophthalates (>5.0) are also in line with those reported for DAG lactones (5.0–6.0) (Nacro et al., 2000).

Determination of binding affinity constants (K_i) for the selected isophthalates enables the comparison of isophthalates with other C1 domain ligands. The submicromolar K_i values of isophthalates are 100–1000 fold higher than those of phorbol esters, bryostatins or the best DAG lactones, all of which replace [3 H]PDBu with low nanomolar or subnanomolar affinities (see chapter 2.5 and Boije af Gennäs et al., 2011). The difference to the endogenous ligand DAG was smaller: approximately 10-fold. Modification of the isophthalate structure is thus needed to achieve affinities comparable to the more potent C1 domain ligands.

The finding that HMI-1a3 is somewhat less effective in displacing [³H]PDBu from PKCδ than from PKCα (although possessing similar potency for both isoforms) may suggest that it has some selectivity for cPKCs over nPKCs. Since no such difference was observed with HMI-1b10 or HMI-1b11, the most probable structural determinant for the difference is the rigidity of the aromatic side chains of HMI-1a3, which are more constrained than the flexible aliphatic side chains of HMI-1b10 and HMI-1b11. The C1 domains of classical and novel PKCs are known to differ in their ligand affinities (Pu et al., 2005; Giorgione et al., 2006; Dries et al., 2007), and the structures of their DAG binding sites may thus differ to a degree that contributes to the observed phenomenon. However, more studies are needed to clarify the mechanism behind the differences in maximal [³H]PDBu displacement.

Since PKCs are not the only proteins with a C1 domain responsive to phorbol esters and DAG, it was essential to investigate, whether isophthalates bind to other DAG/phorbol ester-responsive C1 domains as well. Based on the high similarity among DAG-responsive C1 domains, the observed binding of isophthalates to the other DAG effectors was expected. Binding studies with β2-chimaerin confirmed the SAR model created with PKC, and binding of HMI-1a3 to PKD and the C1 domain of

MRCK further indicated that isophthalates can be considered non-selective among the DAG-responsive C1 domains. Based on these studies, the affinity of HMI-1a3 to the C1 domains of PKC, PKD, β 2-chimaerin and MRCK cannot however be directly compared, since the K_i values were not determined for the "non-PKC" DAG effectors. However, the similar IC₅₀ values suggest that there are no major differences in its affinity to these proteins. Although the affinity of isophthalates to C1 domains of RasGRPs, DGKs and Munc13s was not investigated, based on high structural and sequence similarity of their C1 domains, it can be speculated that the same SAR model holds true with these DAG effectors as well.

Despite high conservation of the phorbol ester binding sites in C1 domain-containing proteins, there are some structural differences that lead to divergent ligand affinities of individual C1 domains (Dries et al., 2007; Rahman et al., 2013), suggesting that it may be possible to develop C1 domain ligands that are selective for a specific DAG effector. Although their development has proven difficult, some degree of selectivity has been achieved with e.g. DAG lactones (El Kazzouli et al., 2008; Comin et al., 2009). However, since the phospholipid composition of the cell membrane and the C1 domain-cell membrane interactions affect ligand recognition by the C1 domain in a significant manner, rational development of such selective compounds may be unfeasible. It has thus been suggested that a more practical approach would instead be semi-rational and based on assessing a desired biological response as a supplement or alternative to binding affinity (Blumberg et al., 2008).

6.2 Effects of isophthalate derivatives on PKC-mediated signalling

Although most of the known C1 domain ligands are PKC activators, some of them, such as AD198 and calphostin C, have been reported to inhibit PKC activity (Gopalakrishna et al., 1992a; Roaten et al., 2002). The binding studies discussed above do not clarify the functional outcome of isophthalate binding to PKC, and therefore it was necessary to investigate whether isophthalate binding leads to PKC inhibition or activation. Instead of determining the effects of isophthalates on PKC kinase activity *in vitro*, effects of isophthalates on PKC-mediated signalling were investigated in cellular context. The cell-based approach provides information in a more physiological environment, which is especially important with PKC because of its complex regulation including, for instance, translocation to different subcellular compartments. Moreover, as demonstrated with AD198, results from *in vitro* kinase activity assay do not necessarily illustrate the functional outcome in cellular context (see section 2.5.5) (Roaten et al., 2002; He et al., 2005).

The Raf-MEK-ERK1/2 cascade, which is widely involved in the regulation of cell proliferation and differentiation, represents one of the ubiquitous signalling cascades downstream of PKC. The finding that, in HeLa cells, HMI-1a3 and HMI-1b10 induced a rapid ERK1/2 phosphorylation that was at least partially dependent on PKC activity was the first proof of a PKC-modulating effect for the isophthalates. Furthermore, it demonstrated that the isophthalates can diffuse into the cell membrane and reach their intracellular target proteins. The observation that HMI-1b11 alone was unable to induce ERK1/2 phosphorylation, pointed to an unexpected difference between the highly similar isophthalate derivatives HMI-1b10 and HMI-1b11. The inhibition of PMA-induced ERK1/2 phosphorylation by HMI-1b11 suggested that HMI-1b11 may either function as a PKC antagonist or possess such a weak activating effect that it could not be detected with the method employed. Antagonism among the C1 domain-binding PKC activators has been previously reported at least

between bryostatin 1 and PMA (Szállási et al., 1994a; Szállási et al., 1994b). Contrastingly, both HMI-1a3 and HMI-1b11 induced a strong, PKC-dependent ERK1/2 phosphorylation in SH-SY5Y cells, showing that the signalling cascades activated by isophthalates differ depending on the cell line. PKC-mediated activation of the ERK1/2 cascade is known to be dependent on cell type, PKC isoforms and the nature of the stimulus (see section 2.2.4), offering an explanation for the divergent responses to HMI-1b11 in HeLa and SH-SY5Y cells, as well as for the difference observed in the prolonged ERK1/2 phosphorylation between the isophthalates.

In both cell lines, isophthalate-induced activation of the ERK1/2 cascade seems to be dependent on PKC activation. However, other signalling pathways may also contribute, since simultaneous exposure to the pan-PKC inhibitor Gö6983 was not always sufficient to achieve total inhibition of ERK1/2 phosphorylation. The fact that neither of the inactive isophthalates had an effect on ERK1/2 phosphorylation in SH-SY5Y cells however speaks for a C1 domain-dependent mechanism. Among DAG effectors, PKD represents a potential mediator for the "non-PKC" input, since it is ubiquitously expressed and known to regulate the Raf-MEK-ERK1/2 pathway in numerous cell types (Lavalle et al., 2010). The role of PKD in isophthalate-induced ERK1/2 phosphorylation was however not studied.

Effects of HMI-1b11 on PKC-dependent signalling were studied in more detail in SH-SY5Y cells. HMI-1b11 induced a rapid accumulation of PKC α into the cytoskeletal (Triton X-100-insoluble) fraction, where PKC α has previously been shown to associate with nELAV proteins and induce nELAV-dependent mRNA stabilization (Pascale et al., 2005). Also other C1 domain-targeting PKC activators are known to induce accumulation of PKC α in the cytoskeletal fraction (Szállási et al., 1994b; Pascale et al., 2005), although translocation to the plasma membrane is the most commonly observed phenomenon. Considering the cytoskeletal accumulation of PKC α in response to HMI-1b11, the subsequent finding of HMI-1b11-induced cPKC-dependent up-regulation of GAP-43 was logical. Although it was not demonstrated in these studies, the up-regulation probably occurs through PKC-dependent nELAV activation, as previously demonstrated in PC12 and SH-SY5Y cells (Mobarak et al., 2000; Pascale et al., 2005). It can also be further speculated that the effect may be specifically mediated by PKC α , since it has been shown to be the cPKC isoform responsible for activating the nELAV-mediated mRNA stabilization in SH-SY5Y cells (Pascale et al., 2005).

The above-discussed studies on PKC-mediated signalling demonstrate that the isophthalates induce PKC activation in both cell lines investigated. It is well known that prolonged PKC activation in response to C1 domain ligands leads to down-regulation of PKC protein levels by either a proteasome-independent mechanism or by the ubiquitin-proteasome pathway (Lee et al., 1996b; Leontieva and Black, 2004). However, isophthalates HMI-1a3 and HMI-1b11 did not induce down-regulation of PKC isoforms α , β , or δ in either of the cell lines studied. This may reflect their lower binding affinity for the C1 domain as compared with phorbol esters or bryostatin 1. The isophthalate-induced PKC activation may also be shorter-lived and thus insufficient to induce down-regulation thus resembling more DAG-induced than phorbol ester-evoked PKC activation.

6.3 Effects of isophthalate derivatives on cell viability and proliferation

As cancer is considered the best-validated therapeutic indication for C1 domain ligands, the effects of isophthalates on HeLa cervical carcinoma cell viability and proliferation were investigated. HeLa

cells are widely used in research focusing on signal transduction and cancer; however, they are generally not considered a proper cancer model. As the first-ever continuous cell line, HeLa cells have been grown *in vitro* for several decades in laboratories world-wide (Jones, 1997). Therefore, it is probable that numerous clones exist that diverge substantially from each other and from the primary tumour from which the cells were isolated in 1951. However, comprehensive spectral karyotyping of the HeLa CCL2 cell line used in these studies showed that the HeLa genome has been unexpectedly stable during years of cultivation (Macville et al., 1999). Moreover, the genomic alterations in HeLa cells correlated closely to alterations in samples from advanced stage cervical carcinoma, indicating that they may have been present already in the primary tumour and that they can be considered highly relevant to the pathology of cervical carcinoma. Additionally, the antiproliferative effects of isophthalates in SH-SY5Y neuroblastoma cells were assessed at the same time their effects on cell morphology were investigated.

In studies performed in HeLa cells various complementary methods were used in order to be able to interpret the results also from a mechanistic point of view (Kim et al., 2009). Of the cell viability tests used, the LDH assay measures cell membrane damage and can be considered a measure of necrotic cell death, while the MTT assay represents a measure of mitochondrial reduction capacity, which is attenuated in both necrosis and apoptosis, but also reflects cell proliferation. Thymidine incorporation assay that measures DNA replication is a gold standard method for assessing inhibition of cell proliferation (Griffiths and Sundaram, 2011). The Cell-IQ® analysis involves computer vision-based cell recognition from automatically acquired time-lapse series of phase contrast microscopic images of cell cultures. It also allows for classification of cells to e.g. healthy and dead according to cell morphology, thus providing information on cell proliferation, viability and morphology (Toimela et al., 2008; Pennanen et al., 2011). Quantification of cell proliferation and morphology with Cell-IQ® however requires development of a specific analysis protocol for each cell line to achieve optimal cell recognition. The present results with HMI-1a3 show close correlation between thymidine incorporation assay and cell proliferation analysis with Cell-IQ®, as reported previously (Toimela et al., 2008), confirming the accuracy of Cell-IQ® analysis.

While many of the active isophthalates were antiproliferative and cytotoxic in HeLa cells, none of the isophthalate derivatives with poor affinity to the C1 domain inhibited cell proliferation or induced cytotoxicity, suggesting a C1 domain-dependent effect. Furthermore, the finding that not all active isophthalates shared the antiproliferative and cytotoxic properties of HMI-1a3 indicates that there are differences in signalling elicited by isophthalate exposure in HeLa cells, as observed in ERK1/2 phosphorylation studies. HMI-1a3-induced cytotoxicity emerged in the MTT assay at approximately 10-fold lower concentrations than the cytotoxic or antiproliferative effects in Cell-IQ® or thymidine incorporation assays suggesting that mitochondrial function is compromised also in cells that are not yet dead. The mechanism of HMI-1a3-induced toxicity may thus involve induction of mitochondrial dysfunction. HMI-1a3 also inhibited SH-SY5Y cell proliferation, although less potently than that of HeLa cells. However, while HMI-1b11 had little effect on HeLa cell proliferation, it exhibited a clear antiproliferative effect in SHSY-5Y cells without inducing cell death. This correlates with HMI-1b11-induced ERK1/2 phosphorylation and implies that also the antiproliferative responses to isophthalates are cell line-dependent.

The mechanistic studies employing a pharmacological approach with protein kinase inhibitors and PMA as well as a genetic approach with RNA interference against specific PKC isoforms were unable to decipher the antiproliferative mechanism of HMI-1a3. Since inhibition or activation of PKC or

inhibition of PKD or MRCK had no effect on the antiproliferative response to HMI-1a3, the response seems to be independent of the activity of these kinases. Also the ERK1/2 cascade seems to be dispensable for the isophthalate-induced response even though it is a well-known mediator of mitogenic signalling. Furthermore, PKCα and PKCδ are dispensable for HMI-1a3-induced inhibition of cell proliferation, since knocking down these proteins one by one with RNAi had no effect on the antiproliferative response. The C1 domain-containing proteins targeted by the isophthalates regulate numerous interconnecting and convergent signal transduction pathways, which contribute to cell survival, proliferation and apoptosis (Fig. 16) (Brose et al., 2004). Therefore, activation or inhibition of one of the isophthalate target proteins may be compensated by alterations in other pathways. Furthermore, since at least some of these pathways are regulated by several DAG effectors at different levels, isophthalates may interfere with a certain signalling route at several points. Moreover, as the C1 domain also plays an important role in mediating protein-protein interactions (Colón-González and Kazanietz, 2006), it is possible, that the effects of isophthalates result from alterations in protein-protein interactions independently of changes in enzyme activity. It may therefore be unfeasible to decipher the exact mechanism-of-action for the isophthalates.

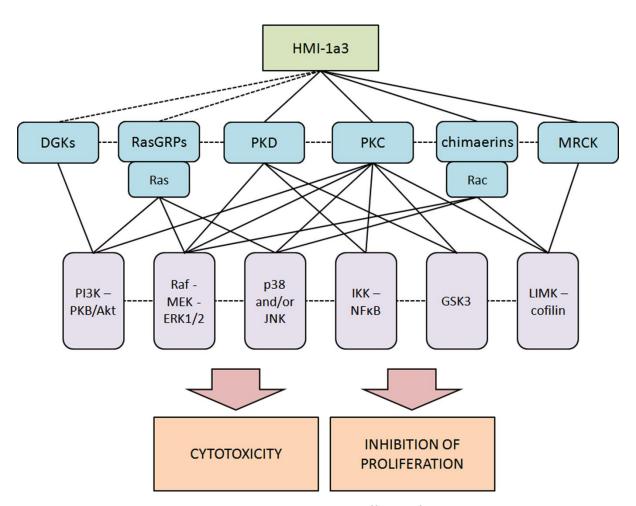


Figure 17. Potential signalling routes mediating the effects of HMI-1a3 on cell survival and proliferation. Demonstrated binding of HMI-1a3 to the targets presented is indicated with solid lines, and anticipated binding to other DAG effectors with dashed lines. The dashed lines connecting DAG effectors illustrate direct and indirect cross-talk among C1 domain-containing proteins. The following connections to signalling cascades symbolise the possible signalling routes by which the HMI-1a3-induced cytotoxic and antiproliferative effects may be mediated and are based on citations in chapters 2.2 and 2.3. The dashed lines connecting these signalling routes illustrate cross-talk among them.

Despite inconclusive results in mechanistic studies, the complete lack of cytotoxicity and antiproliferative effects in response to the inactive isophthalate derivatives strongly suggests that the effect is C1 domain-dependent and does not result from an unspecific effect related to the overall chemical structure of isophthalates. However, it seems probable that the antiproliferative and cytotoxic effects of HMI-1a3 are not mediated by a single C1 domain-containing protein, but rather that they result from modulation of several DAG effectors (Fig. 17). More studies are needed to identify the signalling routes by which HMI-1a3 induces its antiproliferative effects. Nevertheless, the results presented here suggest that HMI-1a3 exhibits potential as a lead molecule for cancer drug development, which is supported by a study reporting that it induces apoptosis in HL60 leukaemia cells but not in Swiss 3T3 fibroblasts (Galkin et al., 2008). To substantiate the potential of HMI-1a3 or other isophthalates as lead compounds for cancer drug development, further studies in other cancer cell lines and corresponding non-cancerous cell lines, as well as *in vivo* experiments with mouse xenograft models are required.

6.4 Effects of isophthalate derivatives on cell morphology and cytoskeleton

Cell morphology and motility are controlled by the organization of cytoskeletal components: the microfilaments (actin filaments), the intermediate filaments and the microtubules. Several classes of DAG effectors contribute to the regulation of cytoskeleton and may thereby influence cell shape, adhesion and motility. Moreover, phorbol esters are known to modulate cell morphology and motility through their effects on actin cytoskeleton (Larsson, 2006). Therefore, it was not a surprise that active isophthalates induced morphological changes in both cell lines studied. In HeLa cells HMI-1a3 induced prominent cell elongation, while HMI-1b11 had only a slight elongation-inducing effect at the highest concentration studied. Contrastingly, both compounds supported neurite outgrowth with similar potency in SH-SY5Y cells. Since none of the inactive isophthalate derivatives influenced cell morphology in either of the cell lines, the mechanism seems to be C1 domain-dependent. Although the effects on cell morphology correlate with the ability of isophthalates to induce ERK1/2 phosphorylation in the corresponding cell line, ERK1/2 signalling was found to be dispensable for the morphological change in HeLa cells. The role of ERK1/2 signalling in neurite outgrowth in SH-SY5Y cells was not investigated.

The morphological change was more striking in HeLa cells, where cell elongation, emergence of cellular protrusions and diminished cell spreading occurred as a result of major reorganization of actin cytoskeleton. The observed loss of focal adhesions may account for the diminished cell spreading, since focal adhesions, which connect the cytoskeleton to the extracellular matrix through integrins, are essential for cell adhesion and spreading (Wolfenson et al., 2009). The observed disruption of the contractile stress fibre network may increase the assembly of protrusive arrays of actin filaments thus inducing cellular protrusions; on the other it may decrease cell contractility resulting in cell elongation (Tojkander et al., 2012). Although not addressed in the present studies with SH-SY5Y cells, neurite outgrowth has been shown to be accompanied with loss of stress fibres in several cell lines (Ling et al., 2004; Trollér and Larsson, 2006), suggesting that similar changes in cytoskeleton may be behind the morphological responses in HeLa and SH-SY5Y cells.

The prominent nuclear translocation of cofilin-1 in response to HMI-1a3 suggests that cofilin-1 plays a role in mediating isophthalate-induced cellular effects. In addition to its well-established role in

regulating actin filament dynamics, cofilin is also implicated in nuclear import of actin, induction of apoptosis and phospholipid signalling (Paavilainen et al., 2004; Bernstein and Bamburg, 2010). Nuclear translocation of cofilin-1 is known to take place in cellular stress conditions and to regulate cofilin-actin rod formation, which is imperative for cell survival during stress (Munsie et al., 2012). Nuclear cofilin-1 also regulates transcription elongation by controlling dynamics of gene-associated actin (Obrdlik and Percipalle, 2011). The HMI-1a3-evoked nuclear accumulation of cofilin-1 may thus be connected to the prominent HMI-1a3-induced changes in gene expression and/or illustrate an unspecific response to stressful conditions.

The studies aimed to characterize the signalling pathways mediating HMI-1a3-induced cell elongation in HeLa cells pointed to a mechanism that is independent of ERK1/2 signalling, of the catalytic activity of PKC and PKD, and of the presence of PKC isoforms α and δ . However, the morphological response seems to be at least partially mediated by MRCK, since the MRCK inhibitor chelerythrine attenuated HMI-1a3-induced cell elongation. This is consistent with previous studies showing a crucial role for MRCK in cytoskeletal reorganization (Leung et al., 1998), cell spreading (Groeger and Nobes, 2007) and, particularly, in controlling elongated morphology of tumour cells (Wilkinson et al., 2005). Furthermore, Cdc42, the upstream regulator of MRCK has been reported to mediate stress fibre loss in NIH3T3 fibroblasts (Coghlan et al., 2000). The MRCK inhibitor chelerythrine has been shown not to inhibit 70 other protein kinases including PKC (Lee et al., 1998; Davies et al., 2000; Tan et al., 2011) and can thus be considered a fairly selective MRCK inhibitor. However, the role of MRCK in mediating HMI-1a3-induced cell elongation should be verified using RNAi or dominant negative MRCK constructs.

Interestingly, MRCK is one of the two DAG effectors (the other one being PKD) that regulate the phosphorylation state of cofilin-1 (see Fig. 18). MRCKα phosphorylates and activates LIM kinases, which in turn phosphorylate cofilin (Sumi et al., 2001; Bernstein and Bamburg, 2010). However, despite inducing prominent changes in cofilin-1 localization and potentially activating MRCK to induce cell elongation, HMI-1a3 had no significant effect on the level of phosphorylated cofilin-1. Spatial control of actin dynamics is crucial for appropriate function of the cytoskeleton, and cofilin phosphorylation has also been reported to occur in a highly localized manner (van Rheenen et al., 2009; Bernstein and Bamburg, 2010). Small but locally significant changes in cofilin-1 phosphorylation may not be detectable by the methods employed in this study, and the results do not rule out local changes in cofilin-1 phosphorylation. Further studies are needed to clarify the role of cofilin-1 in isophthalate-induced morphological changes.

The human neuroblastoma cell line SH-SY5Y is a well-characterized and widely used model for neuronal differentiation (Påhlman et al., 1990; Agholme et al., 2010), and PKC activation by phorbol esters is known to induce differentiation in neuroblastoma cell cultures (Söderholm et al., 2001; Trollér et al., 2001). Classical PKC isoforms have been suggested to play a role in regulating neuroblastoma cell proliferation and survival, while novel PKCs have been demonstrated to mediate neurite outgrowth (Zeidman et al., 1999a; Zeidman et al., 1999b). Furthermore, ERK1/2 signalling has been reported to contribute to SH-SY5Y cell differentiation (Monaghan et al., 2008). The isophthalate-induced responses in SH-SY5Y cells – neurite outgrowth, inhibition of cell proliferation and up-regulation of GAP-43 – are all hallmarks of neuroblastoma cell differentiation (Agholme et al., 2010).

Despite the fact that isophthalate-induced SH-SY5Y cell differentiation correlated with accumulation of PKCα in the cytoskeletal fraction, PKC-dependent activation of ERK1/2 signalling and GAP-43 upregulation, a definite role for PKC in neurite outgrowth and inhibition of cell proliferation was not demonstrated. Based on the present results with GAP-43 expression and abundant literature implying an important role for PKC in neurite outgrowth, the response can however be speculated to be PKC-dependent. PKC-induced neurite outgrowth in neuroblastoma and non-malignant cells with neuronal differentiation potential is specifically dependent on the regulatory region of PKC (Zeidman et al., 1999a; Ling et al., 2004). Furthermore, Cdc42 has been identified as an important downstream factor mediating the morphological and cytoskeletal effects of PKC (Trollér and Larsson, 2006) raising the possibility that MRCK may also play a role in neurite outgrowth, which would be logical considering its central role in the regulation of actin cytoskeleton.

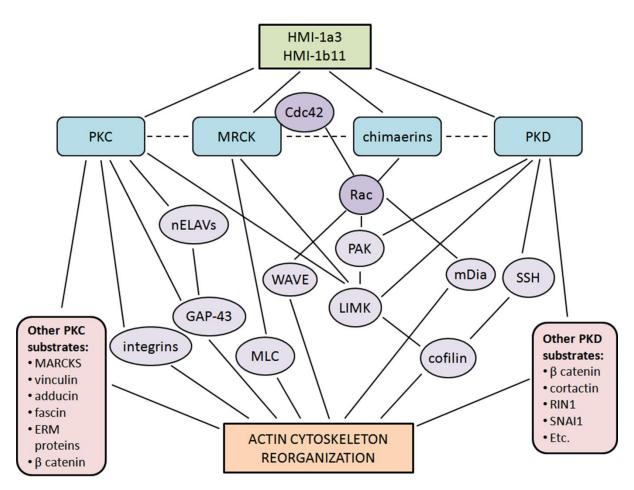


Figure 18. Potential signalling routes mediating the effects of isophthalates on actin cytoskeleton. Binding of isophthalates to the targets presented has been demonstrated in these studies. The following interactions symbolise the possible signalling routes by which the isophthalate-evoked cytoskeletal changes may be mediated. The dashed lines connecting DAG effectors illustrate direct and indirect crosstalk among the C1 domain-containing proteins. The Figure is based on citations in chapters 2.2 and 2.3. ERM, ezrin-radixin-moesin family of proteins; GAP-43, growth associated protein 43; LIMK, Lim domain kinase; MARCKS, myristoylated alanine-rich C-kinase substrate; mDIA, protein diaphanous homolog; MLC, myosin light chain; nELAVs, neuronal embryonic lethal vision proteins; PAK4, p21-activated kinase 4; RIN1, Ras and Rab interactor 1; SSH, slingshot family of phosphatases; WAVE, Wiskott-Aldrich syndrome protein family Verprolin-homologous protein.

Although probably representing different phenomena, the isophthalate-induced changes in HeLa and SH-SY5Y cell morphology include common features: HeLa cell elongation was accompanied with elongated cell processes resembling neurite outgrowth observed in SH-SY5Y cells. Furthermore, based on the present results with HeLa cells and the literature concerning neuroblastoma cells, stress fibre loss and involvement of MRCK are potential connecting factors. The mechanisms responsible for mediating the morphological changes in the two cell lines may thus be at least partially similar. The potential signalling routes by which isophthalate-induced morphological changes may be mediated are presented in Figure 18.

6.5 General discussion

Considering PKC-related drug development, the C1 domain provides several advantages over the kinase domain as a drug target. Firstly, the human genome contains more than 500 protein kinases (Manning et al., 2002) with highly conserved kinase domains, and therefore the development of specific compounds targeted to the catalytic site has proven to be extremely challenging (Karaman et al., 2008). In contrast, there are only seven families of proteins with a DAG-responsive C1 domain. Despite high conservation also among the C1 domains, the number of potential off-target interactions is considerably smaller with C1 domain-targeting compounds than with those targeting the catalytic site. Secondly, targeting the kinase domain only enables the development of inhibitors, while targeting the C1 domain provides a possibility to develop activators as well as inhibitors. By inducing a conformational change similar to that induced by DAG, C1 domain ligands can activate PKC; however, they can also inhibit its activity for example by targeting the protein to an inappropriate cellular compartment and thereby directing it away from its substrates (Blumberg et al., 2008). Furthermore, protein-protein interactions of the regulatory domains of PKCs seem to mediate biological responses independently of the catalytic activity of the enzyme (Zeidman et al., 1999a; Cameron et al., 2008; Cameron and Parker, 2009; Jacob et al., 2010), and compounds that bind to the C1 domain may be useful in modulating such interactions. Regarding PKC, the kinase domain and the C1 domain are not however the only potential drug targets. PKC isoform-specific inhibitors and activators have been developed by targeting the protein-protein interactions of e.g. PKCs and the respective RACKs (see Mochly-Rosen et al., 2012). These molecules are however peptides, which may hinder their feasibility as drugs.

Although pursuit of specificity has generally been the ultimate goal in rational drug development, it has become clear that cancer can rarely be beaten with a drug affecting only a single signalling pathway. Cancer cells usually exhibit deregulation in numerous signal transduction cascades, and drug resistance resulting from further alterations is a common cause of treatment failure. Therefore drugs that modulate several distinct molecular targets involved in the malignant pathology have been suggested to become a breakthrough in the treatment of malignancies (Daub et al., 2004; Sarkar and Li, 2009). As most of the DAG effectors participate in mediating mitogenic signalling, the possibility to modulate several of them simultaneously with compounds that bind to the C1 domain may be beneficial when targeting cancer. Furthermore, the cross-talk between DAG-mediated pathways (Brose et al., 2004; Spitaler and Cantrell, 2004; Trollér and Larsson, 2006) highlights an opportunity to intervene with a certain signalling cascade at more than one point and thereby reinforce the outcome. For example, PKC is known to phosphorylate and activate PKD (Waldron and Rozengurt, 2003), to phosphorylate and activate RasGRP3 thus enhancing Ras-ERK signalling

(Teixeira et al., 2003), and to phosphorylate and negatively regulate β 2-chimaerin facilitating Rac activation and mitogenic signalling (Griner et al., 2010). Consequently, C1 domain ligands may exhibit anti-cancer efficacy by affecting several mitogenic signalling routes and by targeting many of those at various levels. The non-selective binding profile of isophthalates among the C1 domains thus enables them to target simultaneously several proteins that play a role in cancer development.

Neurodegenerative diseases, such as AD, are a major cause of cognitive decline and mortality. Since there is no treatment that could stop the neuronal loss characteristic to these diseases, therapies that can help to preserve neurons and/or neuronal connections are urgently needed. Learning and memory are based on synaptic plasticity, and one of the key proteins mediating neuroplasticity is GAP-43 (reviewed in Benowitz and Routtenberg, 1997). PKC activity has been shown to control learning and memory by regulating GAP-43 functions at two different levels: its expression levels through nELAV-mediated mRNA stabilization and its activity through direct phosphorylation (Pascale et al., 2004; Pascale et al., 2005; Holahan and Routtenberg, 2008). PKC activation enhances cognition and improves learning also through other mechanisms, and PKC has therefore been classified as one of the "cognitive kinases" (Schwartz, 1993; Govoni et al., 2010). In addition to its beneficial effects on cognition, PKC regulates several processes linked to AD pathophysiology (Fig. 5), and the C1 domain-targeted PKC activator bryostatin 1 has been shown to reduce the Aß burden and increase the lifespan of AD transgenic mice (Etcheberrigaray et al., 2004). C1 domain ligands, such as HMI-1b11, may thus both inhibit the progression of neurodegeneration in AD and help to restore lost neuronal connections by inducing neuronal sprouting and synaptogenesis. Further studies in both in vitro and in vivo models are, however, needed to clarify the potential of HMI-1b11 as a lead molecule for AD drug development.

Isophthalate derivatives characterized in this thesis do not bind to the C1 domain as potently as many other C1 domain ligands. However, their cellular effects occur at the same concentration range as binding *in vitro* implying good cell permeability and thus availability to their target proteins. It is however noteworthy that DAG lactones and benzolactams with low nanomolar affinities for the C1 domain *in vitro* produce their cellular effects (such as PKC translocation, inhibition of cancer cell proliferation or induction of apoptosis) at micromolar concentrations (Kozikowski et al., 1997; Garcia-Bermejo et al., 2002; Truman et al., 2009). Thus, based on the evidence presented in this thesis, in the cellular context the isophthalates work at similar concentrations as other synthetic C1 domain ligands.

Despite very similar chemical structures, the isophtalates studied here exert diverging effects in cells. Some of the differences correlate closely with binding affinity to the C1 domain: the compounds that exhibit no binding *in vitro* are devoid of cytotoxic, antiproliferative and differentiation-inducing effects in the cell lines studied. Also the gene expression microarray results highlight the differences between HMI-1a3 and its inactive derivative NI-15e. Although C1 domain-independent mechanisms cannot be excluded, these results strongly suggest a C1 domain-mediated mechanism of action for the active isophthalates. However, the divergent effects of HMI-1a3 and HMI-1b11 cannot be readily explained by the binding affinity. Whether the difference observed in maximal [³H]PDBu displacement from PKC8 plays a role was not addressed. Furthermore, the differences in the responses observed in the two cell lines, exemplified by the effects of HMI-1b11 on ERK1/2 phosphorylation or gene expression (significant changes in 1071 vs. 304 genes in SH-SY5Y cells and HeLa cells, respectively), speak for cell line-specific modulation of downstream signalling typical for e.g. PKC. However, the cellular responses to isophthalates seem to differ substantially

from those induced by other C1 domain ligands, highlighting the need for further studies to elucidate the signalling pathways that mediate isophthalate-evoked responses.

When targeting the C1 domain, the potential for tumour-promotion has to be kept in mind. Although not all C1 domain ligands are tumour promoters like phorbol esters (Blumberg et al., 2008; Nelson and Alkon, 2009; Boije af Gennäs et al., 2011), such a property would hinder (although not totally preclude) the use of any therapeutic. The divergent patterns of PKC isoform translocation and down-regulation induced by C1 domain-targeting PKC activators correlate with tumour promotion (Nelson and Alkon, 2009). Particularly, there is substantial evidence that the pattern of PKCδ translocation and down-regulation is connected to tumour promotion (Lu et al., 1997; Bögi et al., 1998; Wang et al., 1999). The effects of isophthalates on PKCδ translocation were not investigated; however, since HMI-1a3 and HMI-1b11 did not induce down-regulation of PKCδ, it seems likely that they are devoid of tumour-promoting activity. On the other hand, phorbol ester-induced tumour promotion may also be regulated by other DAG effectors than PKC, such as RasGRPs (Tuthill et al., 2006).

Similarly to other xenobiotics, the use of dialkyl 5-(hydroxymethyl) isophthalates involves a risk of various other toxicities than tumour promotion discussed above. Isophthalates are chemically related to ortophthalates (commonly referred to as phthalates), which are widely used as plasticizers in polyvinyl chloride (PVC) plastics. Some, but not all, ortophthalates are suspected to disturb normal endocrine function in humans and some are known to cause reproductive and developmental toxicity in animals (Heudorf et al., 2007). Isophthalates are not used in chemical industry like ortophthalates, and their toxicological profiles have therefore not been investigated. Despite structural differences between iso- and ortophthalates, the risk of similar adverse effects cannot however be ruled out. Some of the isophthalate derivatives described in this thesis, including HMI-1a3, were shown to be devoid of mutagenic potential in a miniaturized Ames test (Galkin et al., 2008). Since the isophthalate derivatives act as allosteric modulators of various target proteins, their potential adverse effects are difficult to predict. For example, based on their PKC-activating properties, the isophthalates can be speculated to bear a risk for cardiotoxicity through activation of PKCδ (Inagaki et al., 2006). By contrast, activation of PKCε would be cardioprotective, and thus the outcome of isophthalate exposure is unpredictable. The experience of C1 domain ligand-induced adverse effects in clinical settings is limited to ingenol-3-angelate and bryostatin 1. Ingenol-3angelate is used topically and has mainly caused local skin reactions at the application site, while the dose-limiting adverse effect in the systemic use of bryostatin 1 has consistently been myalgia of an unknown aetiology (Clamp and Jayson, 2002). The studies in in vivo models will be important in deciphering the toxicological risks related to isophthalate derivatives.

7. SUMMARY AND CONCLUSIONS

The C1 domain of PKC and other DAG effectors represents an attractive drug target, especially for cancer and Alzheimer's disease. The aim of these studies was to investigate the structure-activity relationships and *in vitro* pharmacology of a novel group of C1 domain ligands, derivatives of isophthalic acid. The major findings are as follows:

- The isophthalate derivatives bind to PKC and other DAG effectors studied in a low micromolar concentration range. The following structural elements are indispensable for binding to the C1 domain: a hydroxymethyl group at position C5 of the aromatic ring, ester groups on positions C1 and C3 of the aromatic ring, and sufficient hydrophobicity of the ester substituents.
- Some of the active isophthalates, most potently HMI-1a3, inhibit proliferation of HeLa cervical cancer cells and induce non-necrotic death through a thus far unresolved mechanism.
- Some of the active isophthalates, most potently HMI-1a3, induce prominent cytoskeleton reorganization and concomitant cell elongation in HeLa cells. The effect is at least partially mediated by MRCK.
- 4) Active isophthalates, exemplified by HMI-1b11, induce differentiation of SH-SY5Y neuroblastoma cells. The cellular response is associated with activation of PKC and ERK1/2 signalling as well as up-regulation of GAP-43.

In conclusion, dialkyl 5-(hydroxymehtyl)isophthalates with a considerably simpler synthesis route compared to other C1 domain ligands represent a promising new template for PKC and C1 domain-targeted drug development. Of the first-generation isophthalates explored in this thesis, HMI-1a3 was identified as a potential lead molecule for cancer-related drug discovery because of its prominent antiproliferative activity in HeLa cells. HMI-1b11 was identified as a non-cytotoxic agent that induces differentiation and supports neurite growth in neuroblastoma cells, and it may thus have potential in drug development related to neurodegenerative diseases such as AD. However, further work is needed to improve the selectivity and potency of isophthalate derivatives, to clarify their mechanism of action in both HeLa and SH-SY5Y cells, and to assess their efficacy in cell-based and *in vivo* disease models.

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