Mammalian cells stably overexpressing N-acylphosphatidylethanolaminehydrolysing phospholipase D exhibit significantly decreased levels of N-acylphosphatidylethanolamines

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In animal tissues, NAEs (*N*-acylethanolamines), including *N*arachidonoylethanolamine (anandamide), are primarily formed from their corresponding NAPEs (*N*-acylphosphatidylethanolamines) by a phosphodiesterase of the PLD (phospholipase D) type (NAPE-PLD). Recently, we cloned cDNAs of NAPE-PLD from mouse, rat and human [Okamoto, Morishita, Tsuboi, Tonai and Ueda (2004) J. Biol. Chem. **279**, 5298–5305]. However, it remained unclear whether NAPE-PLD acts on endogenous NAPEs contained in the membrane of living cells. To address this question, we stably transfected two mammalian cell lines (HEK-293 and CHO-K1) with mouse NAPE-PLD cDNA, and investigated the endogenous levels and compositions of NAPEs and NAEs in these cells, compared with mock-transfected cells, with the aid of GC-MS. The overexpression of NAPE-PLD caused

INTRODUCTION

Ethanolamides of long-chain fatty acids, collectively referred to as NAEs (*N*-acylethanolamines), are ubiquitous trace constituents of mammalian cells and tissues (reviewed in [1,2]). In most animal tissues, major NAEs are saturated and mono-unsaturated, whereas polyunsaturated NAEs, including *N*-arachidonoylethanolamine (anandamide), are minor components [3–9]. NAEs often accumulate in large amounts under pathological conditions, such as irreversible myocardial or cerebral ischaemia [10,11], brain trauma [12] and cytotoxicity [7,13]. They can also increase reversibly under nutritional and other stress [9] and they are of additional interest since a variety of biological activities such as anti-inflammatory, analgesic and neuroprotective actions have been ascribed to them (reviewed in [1,14,15] and *N-*oleoylethanolamine appears to have anorexic effects [16]). In addition, anandamide was found to be an endogenous agonist of cannabinoid [17] and vanilloid receptors [18], and was reported to exhibit a variety of cannabimimetic activities (reviewed in [19]).

In animal tissues, NAEs are generated from PE (phosphatidylethanolamine) through the 'transacylation–phosphodiesterase pathway', which is composed of two consecutive enzyme-catalysed reactions (reviewed in [20–23]). The first reaction is the transfer of a fatty acyl chain from the *sn*-1 position of a glycerophospholipid to the amino group of PE by a calcium-dependent, energy-independent *N*-acyltransferase, leading to the formation a decrease in the total amount of NAPEs by 50–90% with a 1.5-fold increase in the total amount of NAEs, suggesting that the recombinant NAPE-PLD utilizes endogenous NAPE as a substrate in the cell. Since the compositions of NAEs and NAPEs of NAPE-PLD-overexpressing cells and mock-transfected cells were very similar, the enzyme did not appear to discriminate among the N-acyl groups of endogenous NAPEs. These results confirm that overexpressed NAPE-PLD is capable of forming NAEs, including anandamide, in living cells.

Key words: anandamide, fatty acid amide hydrolase, *N*-acylethanolamine, *N*-acylphosphatidylethanolamine, mammalian cell, phospholipase D.

of NAPE (*N*-acylphosphatidylethanolamine) [24,25]. The second reaction is the hydrolysis of NAPE to NAE and phosphatidic acid by a phosphodiesterase of the PLD (phospholipase D) type (NAPE-PLD) [26–28]. All NAEs, including anandamide, are synthesized by the same pathway [29]. NAEs are hydrolysed to fatty acid and ethanolamine [30] by FAAH (fatty acid amide hydrolase) [30–32] or an acid amidase [33,34].

Recently, we purified NAPE-PLD from the particulate fraction of rat heart and cloned its cDNA from mouse, rat and human [35]. The deduced primary structure showed no homology with other known PLDs, but was suggested to belong to the β -lactamase fold family. The recombinant NAPE-PLD expressed in COS-7 cells produced various long-chain NAEs including anandamide from their corresponding NAPEs with similar Michaelis constant (K_m) and maximal velocity (V_{max}) values [35]. NAPE-PLD is a membrane-bound protein, and the substrate NAPE also exists as a membrane constituent of the cell [25,28,36]. However, it remained unclear whether NAPE-PLD acts towards endogenous NAPEs integrated into the membrane of living cells.

In the present study, we stably transfected two mammalian cell lines, HEK-293 (human embryonic kidney 293) and CHO-K1 (Chinese-hamster ovary-K1), with mouse NAPE-PLD cDNA, and investigated the effect of the overexpressed NAPE-PLD on the levels and compositions of endogenous NAPEs and NAEs with the aid of GC-MS. We found that overexpression of NAPE-PLD caused a decrease in the total amount of NAPEs and an increase

Abbreviations used: CHO cell, Chinese-hamster ovary cell; FAAH, fatty acid amide hydrolase; FCS, fetal calf serum; HEK-293 cell, human embryonic kidney 293 cell; MAFP, methyl arachidonyl fluorophosphonate; NAE, N-acylethanolamine; NAPE, N-acylphosphatidylethanolamine; PE, phosphatidylethanolamine; PLD, phospholipase D.

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in the total amount of NAEs without showing obvious selectivity for N-acyl species of the endogenous NAPEs and NAEs.

MATERIALS AND METHODS

Materials

[1-14C]Palmitic acid was purchased from PerkinElmer Life Sciences (Boston, MA, U.S.A.), [1-14C]arachidonic acid, horseradish peroxidase-linked anti-rabbit IgG, Hybond P and enhanced chemiluminescence (ECL®) kit from Amersham Biosciences (Piscataway, NJ, U.S.A.), anandamide, MAFP (methyl arachidonyl fluorophosphonate) and URB597 from Cayman Chemical (Ann Arbor, MI, U.S.A.), palmitic acid, 1,2-dioleoyl-PE and PLD (*Streptomyces chromofuscus*) from Sigma (St. Louis, MO, U.S.A.) and ethanolamine and Triton X-100 from Nakalai Tesque (Kyoto, Japan). HEK-293 cells and CHO-K1 cells were obtained from Health Science Research Resources (Osaka, Japan), Dulbecco's modified Eagle's medium, RPMI 1640 medium, Lipofectamine[™] and hygromycin B from Invitrogen (Carlsbad, CA, U.S.A.), pIREShyg2 from BD Biosciences (Franklin Lakes, NJ, U.S.A.), FCS (fetal calf serum) from PAA Laboratories (Linz, Austria), protein assay dye reagent concentrate from Bio-Rad (Hercules, CA, U.S.A.) and precoated silica gel 60 F254 aluminium sheets for TLC (20 cm \times 20 cm, 0.2 mm thickness) from Merck (Darmstadt, Germany). Both *t-*butyldimethylchlorosilane/imidazole reagent and solid-phase extraction cartridges were from Alltech Associates (Deerfield, IL, U.S.A.). $N-[$ ¹⁴C]palmitoyl-PE was prepared from $[1-$ ¹⁴C]palmitic acid and 1,2-dioleoyl-PE as described previously [26]. [Arachidonoyl-1- 14 C]Anandamide was prepared from [1- 14 C]arachidonic acid and ethanolamine [37]. The products were purified by TLC with a mixture of chloroform/methanol/28% ammonium hydroxide (40:10:1, by vol.). A full-length mouse NAPE-PLD cDNA (GenBank® accession no. AB112350) was prepared as described previously [35].

Stable expression of NAPE-PLD in HEK-293 and CHO-K1 cells

HEK-293 and CHO-K1 cells were maintained in Dulbecco's modified Eagle's medium or RPMI 1640 medium respectively, with 10% (v/v) FCS at 37 °C in humidified air containing 5 % $CO₂$. The full-length mouse NAPE-PLD cDNA was inserted into a pIREShyg2 mammalian expression vector by the use of NaeI and BamHI sites of the multicloning sites. HEK-293 and CHO-K1 cells were transfected with the plasmid by LipofectamineTM. Hygromycin B-resistant cell populations were selected in the medium containing 150 μ g/ml hygromycin B. From the selected cell populations, 12 clonal cell lines were isolated by colony lifting and maintained in the hygromycin B-containing medium. The NAPE-PLD activity in each clone was examined with *N*palmitoyl-PE as substrate. Several clones with a high NAPE-PLD activity were then established, and the clones showing the highest enzyme activity were used in the present study. Control HEK-293 or CHO-K1 cells were prepared by the same method, except that the insert-free pIREShyg2 vector was used for transfection. To prepare cell homogenates, the harvested cells were suspended in 20 mM Tris/HCl (pH 7.4) and sonicated three times each for 3 s. Protein concentrations were determined by the method of Bradford [38] with BSA as the standard.

Enzyme assay

For the NAPE-PLD assay, the cell homogenate was incubated with 100 μ M *N*-[¹⁴C]palmitoyl-PE (10000 c.p.m. in 5 μ l of ethanol) in 100 μ l of 50 mM Tris/HCl (pH 7.5) containing 0.1% Triton

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X-100 and 1 µM MAFP at 37 *◦*C for 10 min. A mixture of chloroform/methanol $(2:1, v/v, 0.3 \text{ ml})$ was added to the reaction mixture to terminate the reaction. After centrifugation, $100 \mu l$ of the lower layer was spotted on to a silica gel thin-layer plate (height 10 cm). The sample was then developed in chloroform/methanol/28% ammonium hydroxide (40:10:1, by vol.) at 4 *◦* C for 20 min. Distribution of radioactivity on the plate was quantified by a BAS1500 bioimaging analyser (Fujix, Tokyo, Japan).

For the FAAH assay, the cell homogenate was incubated with 100 μ M [¹⁴C]anandamide (10000 c.p.m. in 5 μ l of DMSO) in 100 µl of 50 mM Tris/HCl (pH 9.0) at 37 *◦*C for 10 min. A mixture of diethyl ether/methanol/1 M citric acid (30:4:1, by vol., 0.3 ml) was added to the reaction mixture to terminate the reaction. After centrifugation, 100 μ l of the upper layer was spotted on to a silica gel thin-layer plate (height 10 cm). TLC and quantification of radioactivity were performed as described for the NAPE-PLD assay.

Western blotting

Western blotting was performed using rabbit anti-NAPE-PLD antiserum [35]. The cell homogenates were subjected to SDS/ PAGE (10% polyacrylamide) and electrotransferred on to a hydrophobic PVDF membrane (Hybond P). The membrane was blocked with PBS containing 0.1% Tween 20 and 5% (w/v) dried milk (buffer A) and then incubated with anti-NAPE-PLD antiserum (1:5000 dilution) in buffer A at 4 *◦* C for 1 h, followed by incubation with the horseradish peroxidase-labelled secondary antibody (1:2000 dilution) in buffer A at 4 *◦*C for 1 h. The membrane was finally treated with ECL® reagents and visualized by a LAS1000plus lumino imaging analyser (Fujix).

Lipid extraction, sample preparation and GC-MS analysis

Total lipids were extracted from the cell pellets by the Folch procedure [39] after removing the media. At the beginning of each extraction procedure, the internal standards $(20 \text{ ng of each } [{}^{2}H_{4}]$ -NAE and 19 pmol of C_{17} NAPE) were added to the samples. Aliquots of the final extract were taken to assay for lipid phosphorus [40]. NAEs and NAPEs were isolated with silica solidphase extraction cartridges using chloroform/methanol mixtures of 49:1 and 4:1 (v/v) respectively. NAPE samples were digested with *S. chromofuscus* PLD [41] and the resulting NAEs were separated by solid-phase extraction chromatography. NAE samples were converted into *t*-butyldimethysilyl derivatives and analysed by GC-MS with a Hewlett–Packard 5890 gas chromatograph equipped with a 5972 mass selective detector and a 7673 autosampler as described in [42]. The HP5MS column, 30 m \times 0.25 mm inner diameter (Hewlett–Packard, Palo Alto, CA, U.S.A.) was programmed from 230 to 280 *◦*C at 2.5 *◦* C/min. The M-57 ions were monitored in selected ion monitoring mode.

As a separate experiment, the mock cells and NAPE-PLDexpressing CHO-K1 cells were incubated with RPMI 1640 medium containing 0.1% FCS at 37 *◦*C for 48 h in the presence of 3μ M URB597 or vehicle (0.1 % DMSO) with one change of medium at 24 h. Total lipids were then extracted from the cell pellets.

RESULTS

To examine whether or not NAPE-PLD utilizes endogenous membrane-bound NAPE as substrate, we stably transfected two mammalian cell lines (HEK-293 and CHO-K1) with mouse NAPE-PLD cDNA. By transfecting the cells with a pIREShyg2 vector harbouring the NAPE-PLD cDNA, followed by selecting for resistance against hygromycin B, we established clonal cell lines

Figure 1 Stable expression of recombinant NAPE-PLD in HEK-293 and CHO-K1 cells

Western blotting was performed with anti-NAPE-PLD antiserum as described in the Materials and methods section. Lane 1, HEK-293 cell homogenates (20 μ g of protein) transfected with the insert-free vector; lane 2, HEK-293 cell homogenates (20 μ g of protein) transfected with mouse NAPE-PLD cDNA; lane 3, CHO-K1 cell homogenates (20 μ g of protein) transfected with the insert-free vector; lane 4, CHO-K1 cell homogenates (20 μ g of protein) transfected with mouse NAPE-PLD cDNA; lane 5, COS-7 cell homogenates (5 μ g of protein) transiently expressing mouse NAPE-PLD prepared as described previously [35].

Table 1 The NAPE-PLD and FAAH activities of mock cells and NAPE-PLDexpressing cells

	Vector	Specific enzyme activity $[nmol \cdot min^{-1} \cdot (mq \text{ of protein})^{-1}]$		
Host cell		NAPE-PLD*	FAAH ⁺	
HEK-293 CHO-K1	Insert-free vector NAPE-PLD cDNA Insert-free vector NAPE-PLD cDNA	$0.011 + 0.010$ $2.07 + 0.08$ $0.023 + 0.004$ $0.95 + 0.08$	$0.11 + 0.03$ $0.13 + 0.04$ $1.60 + 0.28$ $1.65 + 0.23$	

 $*$ The cell homogenate was allowed to react with 100 μ M N-[¹⁴C]palmitoyl-PE in the presence of 0.1 % Triton X-100 and 1 μ M MAFP (an FAAH inhibitor). Means + S.D. are shown ($n = 3$). † The cell homogenate was allowed to react with 100 μ M [¹⁴C]anandamide. Means + S.D. are shown $(n = 3)$.

that stably expressed NAPE-PLD. As analysed by Western blotting with anti-NAPE-PLD antibody [35], the homogenates of HEK-293 and CHO-K1 cells stably transfected with the NAPE-PLD cDNA revealed an immunoreactive protein band of approx. 46 kDa (Figure 1, lanes 2 and 4). The recombinant NAPE-PLD transiently expressed in COS-7 cells used as a positive control gave a band at the same position (lane 5). In contrast, the immunoreactive band was hardly detectable with the homogenates of the cells transfected with the insert-free vector (mock cells) (lanes 1 and 3). Reverse transcriptase–PCR, however, revealed mRNA of endogenous NAPE-PLD in control HEK-293 cells (results not shown), suggesting expression of endogenous NAPE-PLD in the cells.

The homogenates of the mock and NAPE-PLD-expressing cells were then allowed to react with $N-[$ ¹⁴C]palmitoyl-PE, and the product, *N*-[¹⁴C]palmitoylethanolamine, was separated by TLC. The results indicated that the NAPE-PLD-expressing HEK-293 and CHO-K1 cells had a NAPE-PLD specific activity of 2.07 \pm 0.08 or 0.95 \pm 0.08 nmol · min^{−1} · (mg of protein)^{−1} at 37 [°]C re-
constituely (Table 1). Although these values were lower than spectively (Table 1). Although these values were lower than the specific enzyme activity of COS-7 cells transiently expressing NAPE-PLD [25 nmol · min⁻¹ · (mg of protein)⁻¹], they were 50– 200-fold higher than those of the endogenous NAPE-PLD in mock HEK-293 and CHO-K1 cells $[0.011–0.023 \text{ nmol} \cdot \text{min}^{-1} \cdot (\text{mg})$ of protein)−¹]. Moreover, we examined the endogenous activity of FAAH in these cells, which should contribute to the degradation of NAEs produced by NAPE-PLD. The FAAH activity was assayed by allowing the homogenates of the mock and NAPE-PLD-expressing cells to react with [¹⁴C]anandamide, followed by separation of the produced [¹⁴C]arachidonic acid by TLC. The results clarified that the endogenous FAAH activity was much higher than the endogenous NAPE-PLD activity in both the cells

Table 2 NAPE content and composition in NAPE-PLD-expressing cells and the mock cells of HEK-293

† The values are the means for duplicate experiments.

(Table 1). In addition, the specific FAAH activity of CHO-K1 cells was 16-fold higher than that of HEK-293 cells. We also found that the overexpression of NAPE-PLD did not affect the endogenous FAAH activity in these cell lines.

We then examined the contents of NAPE and NAE in the NAPE-PLD-expressing cells and mock cells. Total lipids were extracted from the cells [39], and the NAPE and NAE fractions were separated with a silica cartridge. NAPEs were hydrolysed to their corresponding NAEs with *S. chromofuscus* PLD. NAEs isolated as such or prepared from NAPEs were then subjected to GC-MS analysis as described previously [9,42]. The contents of NAPEs (Tables 2 and 4) and NAEs (Tables 3 and 5) in HEK-293 cells (Tables 2 and 3) or CHO-K1 cells (Tables 4 and 5) are presented. In these analyses, six types of NAPEs with a different N-acyl species and their corresponding NAEs were separately quantified. The amide-linked fatty acids were palmitic acid (shown as 16:0), stearic acid (18:0), oleic acid (18:1, *n* − 9), vaccenic acid (18:1, $n - 7$), linoleic acid (18:2, $n - 6$) and arachidonic acid (20:4, $n - 6$). We performed the same experiments twice at different times, and the results are presented separately as 'first experiment' and 'second experiment' in each Table. We chose to list the data separately, because they were obtained with different cell populations and therefore exhibited differences in absolute amounts. However, within the second experiment, we performed two separate analyses, which yielded very similar results that were averaged.

When total amounts of NAPEs were compared between the NAPE-PLD-expressing cells and mock HEK-293 cells (Table 2), the total level in the NAPE-PLD cells was only approx. 9% of that in the mock cells. Moreover, with CHO-K1 cells (Table 4), the total NAPE level in the NAPE-PLD cells was 50– 58% of that in the mock cells. In contrast, the total level of NAEs in the NAPE-PLD cells was 1.4–1.5-fold (HEK-293 cells; Table 3) or 1.2–1.6-fold (CHO-K1 cells; Table 5) higher than that in the corresponding mock cells. Thus the overexpression of NAPE-PLD in both the cell lines caused a remarkable decrease in the endogenous NAPE levels with a concomitant increase in the NAE levels. These results suggest that recombinant NAPE-PLD

Table 3 NAE content and composition in NAPE-PLD-expressing cells and the mock HEK-293 cells

The values were obtained from a single sample.

† The values are the means for duplicate experiments.

Table 4 NAPE content and composition in NAPE-PLD-expressing cells and the mock CHO-K1 cells

	NAPE content					
	First experiment*		Second experiment+			
	$pmol/\mu$ mol phosphorus	$\%$	$pmol/\mu$ mol phosphorus	$\%$		
Mock cells						
16:0	62.20	33.89	18.38	37.83		
18:0	30.11	16.41	5.66	11.65		
18:1, $n - 9$	40.55	22.10	9.22	18.98		
18:1, $n - 7$	44.29	24.13	13.57	27.93		
18:2, $n-6$	3.96	2.16	1.47	3.03		
20:4. $n-6$	2.41	1.31	0.28	0.58		
Total	183.52	100	48.58	100		
NAPE-PLD-expressing cells						
16:0	31.35	34.17	11.17	39.37		
18:0	12.89	14.05	4.54	16.00		
18:1, $n - 9$	29.01	31.62	6.43	22.66		
18:1, $n - 7$	14.51	15.82	4.57	16.11		
18:2, $n-6$	2.95	3.22	1.40	4.93		
20:4, $n - 6$	1.03	1.12	0.26	0.92		
Total	91.74	100	28.37	100		
	* The values were obtained from a single sample.					

† The values are the means for duplicate experiments.

is active in the intact cells and utilizes endogenous membranebound NAPE as substrate.

We next examined whether or not the overexpression of NAPE-PLD affected the composition of the N-acyl species of NAPEs and NAEs. In the mock cells of HEK-293, the most predominant Nfatty acyl moiety of NAPE was palmitic acid, accounting for 40–41% of the total NAPE amount, followed by oleic acid, stearic acid and vaccenic acid (Table 2). *N*-arachidonoyl-PE (an anandamide precursor) amounted to only 0.7–0.8%. The mock CHO-K1 cells also revealed a similar composition: the most abundant N-acyl moiety was palmitic acid, accounting for 34– 38%, followed by vaccenic acid, oleic acid and stearic acid (Table 4). Although the total levels of NAPE in the NAPE-PLD-

Table 5 NAE content and composition in NAPE-PLD-expressing cells and the mock CHO-K1 cells

† The values are shown as the means for duplicate experiments.

expressing cells were lower than those of the mock cells as indicated above, the overexpression of NAPE-PLD in HEK-293 (Table 2) and CHO-K1 cells (Table 4) did not bring about a remarkable change in the composition of the N-acyl moiety of NAPEs. There was no obvious change in the percentage of *N*arachidonoyl-PE, whereas the proportion of *N*-vaccenoyl-PE was decreased.

We also compared the NAE composition between the NAPE-PLD cells and mock cells. The most predominant NAE in the mock cells was *N*-palmitoylethanolamine, accounting for 47– 60% (HEK-293 cells; Table 3) or 34–46% (CHO-K1 cells; Table 5) of the total NAE amounts. Anandamide was a minor component, accounting only for 1–3% (HEK-293 cells; Table 3) or 3–12% (CHO-K1 cells; Table 5). When NAPE-PLD was overexpressed in both cells, no obvious change in the composition of NAEs was observed. These results reveal that the N-acyl moieties of NAPE and NAE in HEK-293 and CHO-K1 cells consist primarily of saturated and mono-unsaturated acyl groups, and the expressed NAPE-PLD did not appear to show any substrate selectivity for N-acyl species of the endogenous NAPEs in cells.

DISCUSSION

NAPE-PLD was described as a phosphodiesterase hydrolysing NAPE to NAE and phosphatidic acid more than 20 years ago [43], and has been characterized with crude enzyme preparations [26,27,44]. A series of enzymological studies strongly suggested that NAPE-PLD is distinct from PLDs of the HKD/phosphatidyltransferase family that are involved in signal transduction [3,27,44]. Our recent cDNA cloning clarified that NAPE-PLD is a novel type of PLD belonging to the β -lactamase fold family and is not structurally or functionally related to the known PLDs [35]. We also demonstrated that the recombinant enzyme does not have selectivity for N-acyl groups of NAPEs, as was also shown with rat brain microsomes [3]. Furthermore, we showed that the mRNA and protein of NAPE-PLD are widely expressed in various mouse tissues, strongly suggesting an important role for NAPE-PLD in the formation of NAEs, including anandamide, in animal tissues.

However, since NAPE represents only a very minor component of cellular membrane phospholipids, it was necessary to examine whether NAPE-PLD utilizes the endogenous membrane-bound NAPE of living cells. In the present study, we successfully established clones stably overexpressing NAPE-PLD from HEK-293 cells and CHO-K1 cells, which showed a high *N*-palmitoyl-PE-hydrolysing activity $[1-2 \text{ nmol} \cdot \text{min}^{-1} \cdot (\text{mg of protein})^{-1}]$. When the NAPE-PLD-expressing cells were compared with the mock cells, we found that overexpression of NAPE-PLD caused a decrease in the total amount of NAPEs by 50–90% and a 1.5-fold increase in the total amount of NAEs, without major changes in the N-acyl compositions of these lipids. These results confirm that overexpressed NAPE-PLD is capable of forming NAEs, including anandamide, in living cells.

As shown in Tables 2–5, total levels of NAPE and NAE on a phospholipid basis in the mock HEK-293 and CHO-K1 cells were $48.6-200.4$ pmol/ μ mol phosphorus and $4.62-9.93$ pmol/ μ mol phosphorus respectively. This means that the NAPE levels were 9.8–39.7 times higher than the NAE levels. In a variety of normal human tissues, NAPE ranged from 21.26 to 221.1 pmol/ μ mol phosphorus, whereas NAE ranged from 6.60 to 27.68 pmol/ μ mol phosphorus [6,45]. These NAPE levels were 3–17 times higher than the NAE levels. In addition, mouse peritoneal macrophages and mouse epidermal JB6 P+ cells showed 127.0–187.4 pmol/ μ mol phosphorus of NAPE and 16.84–57.92 pmol/ μ mol phosphorus of NAE [8,9,42]. The ratios of NAPE to NAE ranged from 3 to 11. Thus the endogenous levels of NAPE and NAE in HEK-293 and CHO-K1 cells in the present study were within the range of values reported previously, and the considerably higher NAPE levels compared with NAE levels in the two cell lines were also consistent with data from other animal tissues or cells.

As expected, the NAPE-PLD-overexpressing cells showed lower levels of NAPE and higher levels of NAE when compared with the mock cells. However, the decrease in NAPE was much greater than the increase in NAE. This difference might be explained by the rather fast metabolic turnover of these lipids [8]. NAE is hydrolysed to fatty acid and ethanolamine by either FAAH [31,32] or an acid amidase [33,34] and we actually detected an endogenous FAAH activity in HEK-293 and CHO-K1 cells (Table 1). Furthermore, we examined the contribution of FAAH to the regulation of NAE levels by incubating CHO-K1 cells for 48 h in the presence of the FAAH inhibitor URB597 [46]. This treatment resulted in an approx. 5-fold increase in total NAE in both the mock cells and NAPE-PLD cells (results not shown). However, the inhibitor did not cause a remarkable difference in NAE levels between the mock cells and NAPE-PLD cells. This result suggests that FAAH prevents NAE accumulation in cells, but its role in regulating NAE levels appeared to be limited in our system. Also, while NAPEs remain in the membrane, NAEs can be released outside the cell [9,13,29] and may bind to proteins in the aqueous environment [47,48]. The mechanisms for the moderate increase in NAE levels, in spite of a significant decrease of its immediate precursor, remained unclarified, but this finding supported the concept that NAEs may be messenger molecules of potential physiological significance [21,23,49], whose levels must be controlled.

Due to their precursor–product relationship, the N-acyl compositions of NAPE and NAE of most mammalian cells and tissues investigated so far are very similar, with saturated and monounsaturated moieties predominating over polyunsaturated ones [3–9], and the same was observed with the HEK-293 and CHO-K1 cells in the present study. Since saturated and mono-unsaturated NAEs do not act as cannabinoid receptor agonists, it has been a matter of debate whether the transacylation–phosphodiesterase pathway can contribute to the selective formation of anandamide [20,23]. Sugiura et al. [3] previously reported that NAPE-PLD of rat brain microsomes is actually somewhat less active with *N*-arachidonoyl-PE than other NAPEs. Recently, we confirmed that the recombinant NAPE-PLD does not discriminate between various NAPEs including *N*-arachidonoyl-PE as substrates [35]. However, we could not rule out the possibility that intact cells possess mechanisms to influence substrate specificity of NAPE-PLD, resulting in the selective generation of anandamide. We were therefore interested in finding whether the overexpression of NAPE-PLD causes a selective decrease in *N*-arachidonoyl-PE or a selective generation of anandamide in intact cells. Because, in the present study, we observed no remarkable change in the relative amounts of *N-*arachidonoyl-PE or anandamide with the NAPE-PLD-overexpressing cells, it appears that the NAPE-PLD in these cells acts almost equally on all NAPEs, as previously observed with cell-free preparations [35].

It is believed that the transacylation–phosphodiesterase pathway is primarily regulated by the activation of a Ca^{2+} -dependent *N*-acyltransferase that generates NAPE [2,20]. Hansen et al. previously reported that, in cortical neurons in primary culture, the formation of NAE increased in parallel with NAPE formation on exposure to glutamate, calcium ionophore and sodium azide [13,50]. Taken together, it was suggested that NAPE-PLD is constitutively active and that the availability of the substrate NAPE determines the rate of NAE formation. However, our present results suggest that the expression level of NAPE-PLD could be another regulatory mechanism. Thus the cellular stimuli inducing NAPE-PLD at the transcriptional level may lead to an increase in NAE production. In fact it was reported recently that lipopolysaccharide enhances the NAPE-PLD activity in RAW264.7 macrophages, and the involvement of a transcriptional mechanism was suggested [51].

Alternatively, Di Marzo et al. [52] reported that the treatment of J774 macrophages with ionomycin resulted in the production of a peak corresponding to anandamide as well as a decrease in the levels of NAPE-like metabolites, suggesting that NAPE-PLD is activated by Ca^{2+} in cells; however, other macrophages did not respond to ionophore treatment with any change in NAE/ NAPE turnover [8]. Also, we previously showed that NAPE-PLD, partially purified from rat heart, could be stimulated with Ca^{2+} [53,54]. However, since millimolar concentrations of Ca^{2+} were required for a significant activation of the enzyme and several other bivalent cations could fully substitute for Ca^{2+} , the physiological importance of Ca^{2+} as an NAPE-PLD activator remains uncertain and further studies are required to identify the possible mechanism that activates NAPE-PLD. A purified recombinant enzyme will help us to answer this question at the molecular level. Moreover, for the comprehensive understanding of regulatory mechanism in the transacylase–phosphodiesterase pathway, cDNA cloning and functional expression of *N*-acyltransferase will be needed.

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