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Long-term adaptation to high doses of morphine causes desensitization of μ-OR- and δ-OR-stimulated G-protein response in forebrain cortex but does not decrease the amount of G-protein alpha subunits

Authors' Contribution:
A Study Design
B Data Collection
C Statistical Analysis
D Data Interpretation
E Manuscript Preparation
F Literature Search
G Funds Collection

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Summary

Background: The functional activity of trimeric guanine-nucleotide-binding proteins (G-proteins) represents an essential step in linking and regulation of the opioid receptor (μ-, δ- and κ-OR)-initiated signaling pathways. Theoretical basis and/or molecular mechanism(s) of opioid tolerance and addiction proceeding in the central nervous system were not studied in the forebrain cortex of mammals with respect to quantitative analysis of opioid-stimulated trimeric G-protein activity.

Material/Methods: G-protein activity was measured in Percoll^{R}-purified plasma membranes (PM) isolated from the frontal brain cortex of control and morphine-treated rats by both high-affinity [^{32}P]GTPase and [^{35}S]GTPγS binding assays. Exposition to morphine was performed by intra-muscular application of this drug. Control animals were injected with sterile PBS.

Results: Both μ-OR (DAMGO)- and δ-OR (DADLE)-responses were clearly *desensitized* in PM isolated from morphine-treated rats; κ-OR (U-69593)- and baclofen ($GABA_B$-R)-stimulated [^{35}S]GTPγS binding was unchanged, indicating the specificity of the morphine effect. Under such conditions, the amount of G-protein alpha subunits was unchanged. The *order of efficacy* DADLE>DAMGO>U-69593 was the same in control and morphine-treated PM. Behavioral tests indicated that morphine-treated animals were fully drug-dependent and developed tolerance to subsequent drug addition.

Conclusions: Prolonged exposure of rats to high doses of morphine results in decrease of the over-all output of OR-stimulated G-protein activity in the forebrain cortex but does not decrease the amount of these regulatory proteins. These data support the view that the mechanism of the long-term adaptation to high doses of morphine is primarily based on desensitization of OR-response preferentially oriented to μ-OR and δ-OR.

key words: morphine • G-protein • forebrain cortex • plasma membranes • opioid receptors

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Background

Physiological action of opioid drugs requires an initial interaction with opioid receptors [1]. These receptors were classified as members of the rhodopsin family of G-protein coupled receptors, GPCR. Cloning of these receptors indicated that there are 3 distinct genes that code for 3 subtypes of opioid receptors, μ-OR, δ-OR and κ-OR [2–7]. Results from μ-OR knock-out mouse indicated that most if not all of the physiological effects of morphine are mediated via μ-OR [8].

All of these receptors are known to inhibit adenylyl cyclase activity in pertussis toxin-dependent manner by activation of G_i/G_o class of trimeric G-proteins [9]. These proteins (G_i1, G_i2, G_i3, G_o1, G_o2, G_o*) are present in the brain in large quantities, and inhibit adenylyl cyclase activity or regulate ionic channels in pertussis toxin-dependent manner [10–14]. More recent data have suggested the role of G_z protein, the only pertussis toxin-insensitive member of G_i/G_o family. The role of this G-protein, however, was demonstrated in the acute, *short-term* inhibitory effect of opioid drugs on AC activity, but not in generation of the state arising by long-term adaptation to morphine known as opioid tolerance [15].

Adenylyl cyclase (AC) is regulated by trimeric G-proteins, thus any significant change in AC activity should be preceded by alternation of trimeric G-protein activity. Several *in vitro* studies have indicated that the relationship between receptor occupancy and G-protein activation depends on the receptor density [16–18]; the magnitude of agonist-stimulated G-protein activity was proportional to the corresponding receptor densities in crude membrane preparations of monkey cortex and thalamus [19]. In our work, polytron homogenization resulted in degradation of abundant brain mitochondria and contamination of resulting PM fragments. To avoid this contamination, brain homogenization had to be performed mildly in a *loosely-fitting* teflon-glass Elvehjm-Potter homogenizer; furthermore, to preserve the full functional activity of G-proteins, membrane preparations should be snap frozen in liquid nitrogen and used only once [20]. Therefore, in this work, the purified PM preparation from brain cortex was used and DAMGO (μ-OR)-, DADLE (δ-OR)-, and U-69596 (κ-OR)-stimulated G-protein activity was compared in control and morphine-treated rats. Baclofen ($GABA_B$ agonist)-stimulated [^{35}S]GTPγS binding was used as a reference standard covering the activity of this highly expressed/abundant but unrelated brain GPCR as far as OR-induced signaling cascades are involved.

Material and Methods

Chemicals

DAMGO (2-D-alanine^2-4-methylphenylalanine-5-glycine-ol)-enkefalin = Tyr-D-Ala-Gly-N-methyl-Phe-Gly-ol (E7384), DADLE (2-D-alanine-5-D-leucine)-enkefalin = Tyr-D-Ala-Gly-Phe-D-Leu (Sigma E7384) and U-69593 (Sigma U-103) [(5α, 7α, 8β)-(–)-N-methyl-N-(7-(1-pyrrodinyl)-1-oxaspiro(4,5)dec-8-yl) benzeneacetamide were purchased from Sigma. [^{35}S] GTPγS (1115 Ci/mmol, SJ1320) and [21,22-^{3}H]ouabain (32 mCi/mmol; TRK 429) were from Amersham. [γ-^{32}P]GTP (1050 Ci/mmol, NEG 004) were purchased from Perkin-Elmer, NEN Life Sciences. Complete protease inhibitor cocktail was from Roche Diagnostic, Mannheim, Germany (cat. no. 1697498).

Antisera oriented against the brain $G_i\alpha1$, $G_i\alpha2$, $G_i\alpha3$ and Gβ subunit proteins were prepared as described previously [10–12,14]. Production of the rabbit primary polyclonal antipeptide sera anti-$G_s\alpha$, anti-$G_i\alpha$ 1, 2, anti-$G_i\alpha3$, anti-$G_q\alpha/G_{11}\alpha$ and anti-Gβ (B1) was performed according to [21–23] and [24–26]. We have also used $G_s\alpha$-(G-5040)-oriented antibodies from Sigma. The antisera prepared in our laboratory were previously characterized by Novotny et al. [27] and Ihnatovych et al. [28]. Caveolin-oriented antisera C13630 and C37120 were purchased from Transduction Laboratories (Nottingham, U.K.).

Animals

Male Wistar rats were killed by decapitation under ether narcosis (90-day-old, 160–180g), the frontal brain was rapidly removed and the cerebral cortex was quickly separated from white matter, snap frozen in liquid nitrogen and stored at –70° C until use.

Morphine treatment of experimental animals

Rats were exposed to morphine by intra-muscular application according to the following protocol: 10 mg/kg (day 1 and 2), 15 mg/kg (day 3 and 4), 20 mg/kg (day 5 and 6), 30 mg/kg (day 7 and 8), 40 mg/kg (day 9) and 50 mg/kg (day 10). Control animals were injected with sterile normal saline (0.9%NaCl). Control and morphine-treated animals were killed by decapitation under ether narcosis. The animals were sacrificed 24 hours after the last doses of morphine or normal saline. Brain cortex was removed, frozen in liquid nitrogen and stored in a –80° C freezer.

Isolation of plasma membrane fraction from rat brain cortex

Rat brain cortex was minced with a razor blade on a pre-cooled plate and diluted in STEM medium containing 250 mM sucrose, 20 mM Tris-HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.6, fresh 1 mM PMSF plus complete protease inhibitor cocktail. It was then homogenized mildly in a loosely-fitting Teflon-glass homogenizer for 5 min (2 g w.w. per 10 ml) and centrifuged for 5 min at 3500 rpm. The resulting post-nuclear supernatant (PNS) was filtered through nylon nets of decreasing size (330, 110 and 75 mesh, Nitex) and applied on top of Percoll^R in Beckman Ti70 tubes (30 ml of 27.4% Percoll in STE medium). Centrifugation for 30 min at 30000 rpm (65000×g) resulted in the separation of 2 clearly visible layers [29].The upper layer represented plasma membrane fraction (PM), while the lower layer contained mitochondria (MITO). The upper layer was removed, diluted 1:3 in STEM medium and centrifuged in a Beckman Ti70 rotor for 90 min at 50000 rpm (175000×g). Membrane sediment was removed from the compact, gel-like sediment of Percoll and rehomogenized by hand in a small volume of 50 mM Tris-HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.4 (TME medium).

Agonist-stimulated high-affinity GTPase

GTPase activity was measured in 3 assay incubation buffers containing i) [^{32}P]GTP plus 100 μM GTP (non-specific,

low-affinity GTPase), ii) [^{32}P]GTP + 0.5 μM GTP and iii) [^{32}P]GTP + 0.5 μM GTP + agonist as described previously [20,30]. Basal, high-affinity GTPase was calculated as the difference between GTPase activity measured at [^{32}P]GTP + 0.5 μM GTP and the low-affinity GTPase measured at 100 μM GTP; net increment of agonist-stimulation was calculated as the difference between [^{32}P]GTP + 0.5 μM GTP + agonist-stimulated GTPase (baclofen, DADLE, DAMGO, somatostatin, carbachol) and the basal, high-affinity GTPase measured at 0.5 μM GTP.

Agonist-stimulated [^{35}S]GTPγS binding

Membranes were incubated with (total) or without (basal) 1 mM baclofen ($GABA_B$-R agonist) in a final volume of 100 μl of reaction mix containing 20 mM HEPES, pH 7.4, 3 mM $MgCl_2$, 100 mM NaCl, 2 μM GDP, 0.2 mM ascorbate and 1 nM [^{35}S]GTPγS (about 100,000 dpm per assay) for 30 min at 30°C. The binding reaction was terminated by dilution with 3 ml of ice-cold 20 mM HEPES, pH 7.4, 3 mM $MgCl_2$ and filtration through Whatman GF/C filters on a Brandel cell harvester. Radioactivity remaining on the filters was determined by liquid scintillation using BioScint cocktail. Non-specific GTPγS binding was determined in parallel assays containing 10 μM unlabelled GTPγS.

[^{35}S]GTPγS binding was also measured in the absence (basal) or presence of a constant concentration of 1 mM baclofen ($GABA_B$-R) or 100 μM DAMGO (μ-OR agonist) plus increasing concentrations of GDP (2, 10, 20, 30, 50 and 100 μM). Assays were carried out as before (30 min at 30°C). The non-specific binding, defined as that remaining at 10 μM GTPγS, was subtracted from the basal ± agonist-stimulated level at each point.

Finally, the dose-response curves of agonist stimulation of [^{35}S]GTPγS binding [baclofen ($GABA_B$-R), DADLE (δ-OR agonist), DAMGO (μ-OR agonist) and U-69593 (κ-OR agonist)] were measured at a single [^{35}S]GTPγS concentration (1 nM) and 20 μM GDP in all binding assay media. The quantitative parameters of [^{35}S]GTPγS binding (EC_{50}) were analyzed by GraphPad Prism 4. The net increment (Δ) of agonist stimulation was calculated as the difference between agonist-stimulated and the basal level of binding.

SDS-PAGE and immunoblotting

The aliquots of membrane fractions (20 μg of proteins per sample) were mixed 1:1 with 2× concentrated Laemmli buffer (SLB) and heated for 3 min at 95°C. Standard SDS-PAGE (10% w/v acrylamide/0.26% w/v bis-acrylamide) was carried out as described before in detail [31–33]. Molecular mass determinations were based on pre-stained molecular mass markers (Sigma, SDS 7B). After SDS-PAGE, proteins were transferred to nitrocellulose and blocked for 1 h at room temperature in 3% (w/v) low-fat milk in TBS-Tween buffer [10 mM Tris-HCl, pH 8.0, 150 mM NaCl, 0.1% (v/v) Tween 20]. Antibodies were added in TBS-Tween containing 1% (w/v) low-fat milk and incubated for at least 2 h. The primary antibody was then removed and the blot washed extensively (3×10 min) in TBS-Tween. Secondary antibodies (donkey anti-rabbit IgG or sheep anti-mouse IgG conjugated with horse-radish peroxidase) were diluted in TBS-Tween containing 1% (w/v) low-fat milk, applied for 1 h and after 3 10-min washes the blots were developed by ECL technique using Super Signal West Dura (Pierce) as substrate. The developed blots were scanned with an imaging densitometer ScanJett 5370C (HP) and quantified by Aida Image Analyzer v. 3.28.

Behavioral tests

Morphine dependence was checked by evaluating the physical signs of *opiate abstinence syndrome* [34]. Morphine-induced *analgesic tolerance* was assessed by a modified *hot-plate* test [35] and *hind paw withdrawal* test [36]. All these tests were performed 24 h after the final dose of morphine or saline (control).

Analgesic tolerance (hot-plate test)

Rats were divided into 4 groups (3 animals each). Whereas control C_S and morphine-treated M_S rats were injected with saline (0.9% NaCl, i.p.), morphine (10 mg/kg, i.p.) was administered to control C_M and morphine-treated M_M animals 1 hour before commencement of the test. Rats were placed on an elevated 3 mm thick, clear glass plate, covered with a non-binding, clear Plexiglas cage, and were left to adapt to the testing environment for at least 10 min. A focused light source with a halogen bulb (50 W) delivering the heat stimuli was then located below the glass plate just under the plantar surface of 1 of the rat's hind paws and triggered together with a timer. The time for the first movement of the foot was noted. A test cut-off time of 30 s was chosen to avoid possible tissue damage. Each measurement was repeated 3 times, with at least a 5 min interval.

Analgesic tolerance (hind paw withdrawal test)

Rats were divided into 4 groups and injected with saline or morphine as described above. The hind paw withdrawal test in response to mechanical stimulation was performed in a standard way using *Frey filaments*. The rats were placed on an elevated plastic mesh (4×4 mm perforations) in a transparent cage that allowed full access to the paws from underneath. A series of 8 calibrated von Frey filaments (no. 1–8) with increasing bending force (equivalent to 10, 20, 35, 59, 80, 140, 290, and 370 mN) was used to determine mechanical sensitivity. Starting with the thinnest filament (no. 1), the filaments were successively applied from below perpendicularly to poke the plantar surface of each hind foot with sufficient force to cause slight bending. Each stimulus was repeated 6 times for each hind paw, with intervals of approximately 8–10 s. The number of positive responses (*paw withdrawal*) in each group of tested rats was recorded for each Frey filament.

Behavioral assessment of morphine withdrawal

The withdrawal syndrome was precipitated by naloxone added 24 h after the final dose of morphine. In this way, the physical dependence of experimental animals on morphine was indicated. Naloxone (2 mg/kg, i.p.) was administered to control and morphine-treated rats (3 animals in each group). Immediately after the injection of naloxone, control and morphine-treated rats were placed separately in clear Plexiglass cages with clean bedding and the following

Table 1. Agonist-stimulated GTPase in Percoll^R-purified PM isolated from brain cortex of control rats.

	pmol·min^{-1}·mg^{-1}	%
Basal	25.4±3.1	100±12
Baclofen	35.6±4.2	140±17*
Somatostatine	28.5±2.2	112±9 NS
Carbachol	29.0±3.0	114±12 NS
Isoprenaline	27.4±2.8	110±8 NS
DADLE	30.2±4.5	119±18 NS
DAMGO	29.3±3.1	115±12 NS

The difference between agonist-stimulated and basal level of high-affinity GTPase was measured in PM isolated from control rats and expressed as pmol per min per mg protein. Concentration of baclofen ($GAGA_B$-R), somatostatin, carbachol (mACh-R), isoprenaline (β-AR), DADLE (δ-OR) and DAMGO (μ-OR) was 100 μM. Data represent the mean ± SEM of three experiments; * – indicates significant difference between agonist-stimulated and basal level of enzyme activity, $p<0.05$; NS – non-significant.

selected behavioral parameters were observed continuously for 30 min: body shakes, teeth chatter and vacuous chewing. The number of these episodic types of behavior was recorded and an additional score was calculated based on multiplicities of 5 incidents: **0**, no incidents; **1**, 1–5 incidents; **2**, 6–10 incidents; and **3**, >11 incidents. Additionally, ptosis, irritability to touch and diarrhea were also observed. Because these withdrawal signs could not be defined in discrete episodes, these types of behavior were assessed using predefined anchor points on a 4-point scale: **0**, absent; **1**, mild; **2**, moderate; and **3**, marked.

Protein determination

The method of Lowry was used for determination of protein. Bovine serum albumin (Sigma, Fraction V) was used as standard. Data were calculated by fitting the data with calibration curve as quadratic equation.

Results

Agonist-stimulated GTPase in PM isolated from brain cortex of control, morphine-unexposed rats

Plasma membrane fraction (PM) was separated from the brain mitochondria in Percoll^R gradient according to Bourova et al. [29]. Comparison of the efficacy of different GPCR agonists when increasing high-affinity GTPase indicated that baclofen ($GABA_B$-R agonist) was the only ligand significantly increasing the basal level of enzyme activity: at 10 μg PM protein per assay, baclofen-stimulated GTPase represented 140% of the basal level (Table 1). The effect of other GPCR agonists was not significantly different from the basal level. This held for carbachol (mACh-R), somatostatin, and isoprenaline (β-AR), as well as OR agonists DADLE and DAMGO. Thus, under standard conditions of GTPase assay, OR-stimulated G-protein activity was undetectable.

Table 2. Increase of agonist-stimulated component of [^{35}S]GTPγS binding by increasing GDP concentrations.

A	Baclofen-stimulated [^{35}S]GTPγS binding		
GDP (μM)	%	Δ (pmol·mg^{-1})	p
2	102±5	0.038	NS
10	119±6	0.372	<0.05
20	143±12	0.631	<0.01
30	181±11	0.825	<0.01
50	179±16	0.635	<0.01
B	**DAMGO-stimulated [^{35}S]GTPγS binding**		
GDP (μM)	%	Δ (pmol·mg^{-1})	p
2	104±9	0.094	NS
10	95±8	–0.118	NS
20	115±12	0.265	<0.05
30	135±11	0.475	<0.01
50	141±16	0.387	<0.01

[^{35}S]GTPγS binding to PM isolated from control rats was measured as "*one-point*" assay at 1 nM [^{35}S]GTPγS in the presence of increasing concentration of GDP. Binding was measured in the absence (basal) or presence of 1 mM baclofen or 100 μM DAMGO. Agonist-stimulated level was expressed as % of the basal level (100%). Net increment of agonist stimulation was calculated as the difference between agonist-stimulated and basal level of binding and expressed as pmol·mg^{-1}. Data represent the mean ± SEM of binding assays performed in triplicates.

Baclofen-($GABA_B$-R) and DAMGO (μ-OR)-stimulated [^{35}S]GTPγS binding in brain cortex PM isolated from control rats

In the second part of our work, we tried to distinguish among different GTPγS binding sites with the aim to detect the agonist-responsive component of G-protein activity more clearly. [^{35}S]GTPγS binding was measured at 1 nM [^{35}S]GTPγS in the presence of increasing concentrations of GDP (Table 2). The constant, supra-maximal, 1 mM concentration of baclofen or 100 μM DAMGO (μ-OR agonist) were used for detection of the total level of binding (B_{total}); the basal level of binding (B_{basal}) was determined in parallel assays in the absence of these agonists.

Increase of GDP concentration in the binding mix was associated with the decrease of both agonist-stimulated (B_{total}) and the basal levels of [^{35}S]GTPγS binding (B_{basal}); however, the inhibitory effect of GDP on the basal level was more pronounced than on the total binding. In the absence of GDP, there was no significant difference between total and basal level of binding (NS). The same held for the data collected at 2 μM GDP (NS). The first significant stimulation was measured at 10 μM GDP for baclofen ($p<0.05$); the effect of DAMGO, being much smaller than of baclofen, was under these conditions not yet significant (NS). The data collected at 20, 30 and 50 μM GDP indicated a highly significant difference between B_{total} and B_{basal}

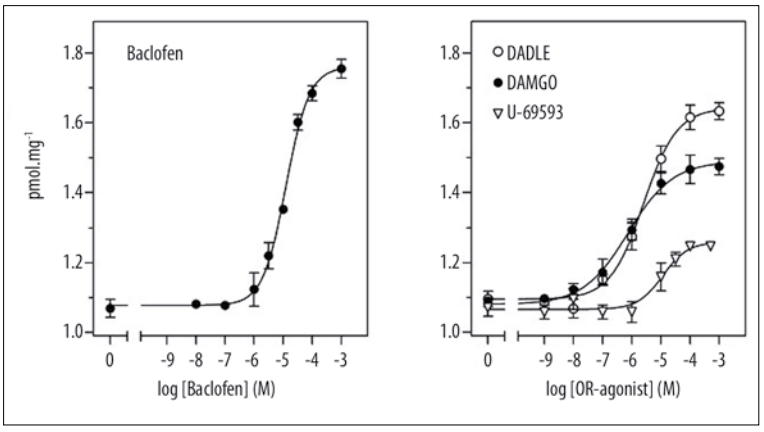

Figure 1. Dose-response curves of agonist-stimulation of [^{35}S]GTPγS binding in Percoll^{R}-purified PM isolated from brain cortex of control, morphine-untreated rats. [^{35}S]GTPγS binding reaction was performed at a single radioligand concentration (1 nM) in the absence (basal) or presence of increasing concentrations of baclofen ($GABA_B$-R), DADLE (δ-OR), DAMGO (μ-OR) or U-69593 (κ-OR). All assays were performed in the presence of 20 μM GDP and 10 μg of protein per tube. The binding reaction was started by transfer from 0°C to 30°C and continued for 30 min at 30°C. Non-specific binding was measured at 10 μM GTPγS and subtracted from the basal ± agonist-stimulated level at each point. Data represent the mean ±SEM of the single PM preparation analyzed in triplicates.

values ($p<0.01$) what indicated significant stimulation by both agonists (Table 2).

Further increase of GDP concentration to 100 μM was reflected in decrease of [^{35}S]GTPγS binding to the very low levels; the difference between B_{total} and B_{basal} (for both baclofen and DAMGO) became under such conditions smaller than at 20–50 μM GDP (data not shown). Thus, the optimum range of GDP concentrations for detection of agonist-stimulated [^{35}S]GTPγS binding in brain cortex PM was between 20 μM and 50 μM GDP. Under these conditions, agonist-stimulated component of total binding was clearly detectable as the positive difference between B_{total} and B_{basal} and could be expressed either as the net-increment of stimulation ($\Delta=B_{total}-B_{basal}$) or the ratio between baclofen-stimulated and basal level of binding (B_{total}/B_{basal}).

In this way (Table 2), the new methodology for detection of agonist-stimulated trimeric G protein activity was introduced in isolated plasma membranes from brain tissue. The very high basal level of G protein activity (GTPγS binding) had to be suppressed by excess of GDP. Under such conditions, i.e. in the presence of 20–30 μM GDP, the increase of the basal level of binding by agonist was high and nice dose-response curves could have been measured (Figures 1, 2). However, sensitivity of response was shifted by 2 orders of magnitude to the right because the active conformation of GPCR had to compete (when effecting the nucleotide binding site of G proteins in reaction mix), with this high concentration of GDP. GDP acts under such conditions as a "competitive inhibitory agent". Therefore, the high concentrations of agonists such as baclofen and DAMGO had to be used.

OR-stimulated [^{35}S]GTPγS binding in brain cortex PM isolated from control rats; ***dose-response curves***

Based on methodological improvements described in the previous section (Table 2), the next part of our work was aimed at analysis of the dose-response curves of OR agonists in PM isolated from control animals. The dose-response curves were measured at a single concentration of [^{35}S]GTPγS (1 nM) and 20 μM GDP in *all* binding assay media. Baclofen ($GABA_B$-agonist) was used as reference standard having significant effect when increasing high-affinity GTPase activity (Table 1) or [^{35}S]GTPγS binding (Table 2). The *efficacy* of agonist effect was judged as the difference between the maximum-stimulated and the basal level of binding (maximum net-increment, Δ_{max}).

Data presented in Figure 1 indicated highly significant stimulation of the basal level by all agonists ($p<0.01$); the maximum net increment (Δ_{max}) of stimulation decreased in the order: baclofen ($GABA_B$-R)>DADLE (δ-OR-DAMGO (μ-OR)>U-69593 (κ-OR) [0.69>0.54>0.38>0.18 pmol·mg^{-1}]; the ratio between agonist-stimulated and basal level of binding decreased in the same order: baclofen >DADLE>DAMGO>U-69593 [165>149>135>117%].

Comparison of OR-stimulated [^{35}S]GTPγS binding in brain cortex PM isolated from control and morphine-treated rats; *dose-response curves*

The dose-response curves of baclofen-, DADLE-, DAMGO- and U-69593-stimulated [^{35}S]GTPγS binding were subsequently measured and compared in PM isolated in parallel from both control and morphine-treated rats. As before, the 20 μM GDP was included in all binding assay media, and baclofen ($GABA_B$-R agonist) was used as a negative standard having significant effect on basal G-protein activity, whose action should not be affected by morphine-treatment of experimental animals.

PM isolated from morphine-treated rats exhibited significantly lower level of DADLE- and DAMGO-stimulated [^{35}S]GTPγS binding than membranes isolated from control, morphine-unexposed rats (Figure 2, middle panels). This difference was highly significant ($p<0.01$) and manifested in the whole range of DADLE or DAMGO concentrations; maximum net-increment Δ_{max} of OR stimulation was 0.35 and 0.26 pmol·mg^{-1} for DADLE and DAMGO, respectively. Morphine treatment caused the decrease of these values to 0.15 and 0.11 pmol·mg^{-1}. Baclofen-stimulated binding was unchanged; the stimulatory effect of κ-OR agonist U-69593 was also unchanged. Therefore, the data collected in all types of G-protein activity assays performed in this work could have been summarized as follows:

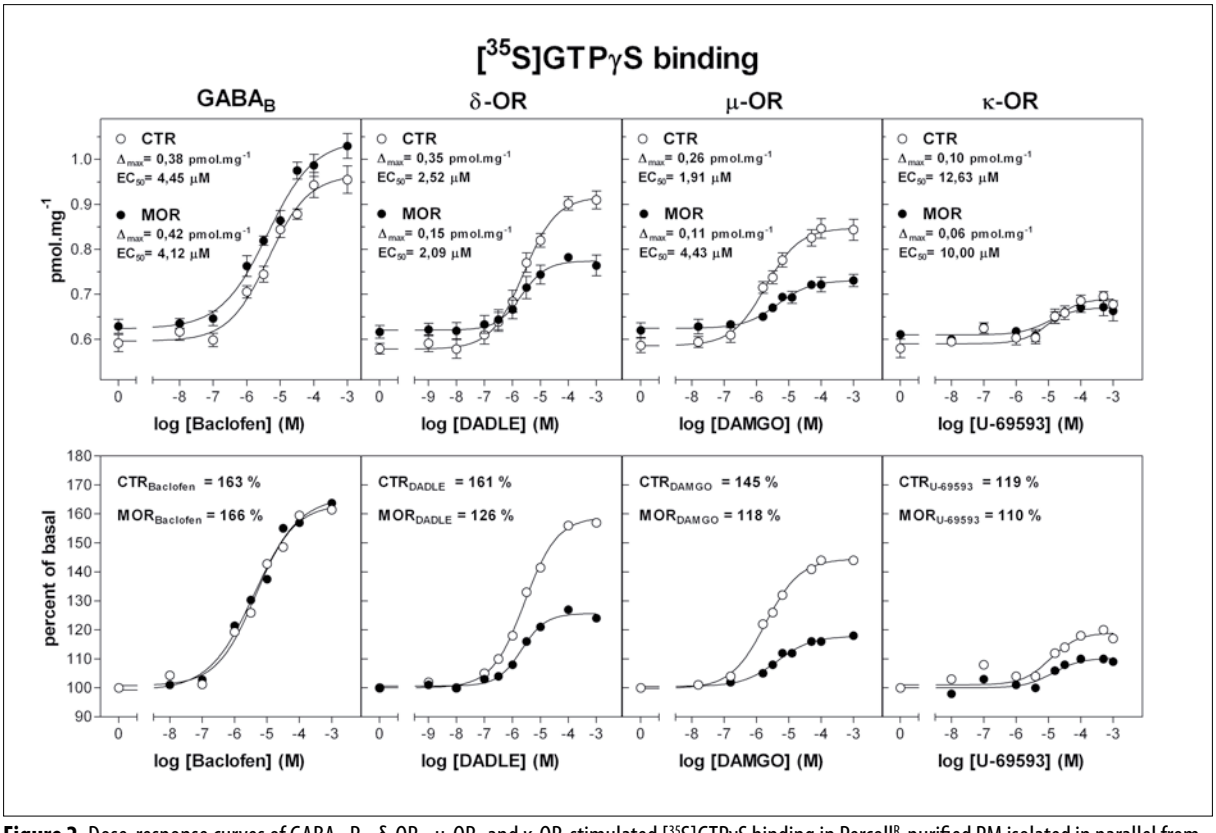

Figure 2. Dose-response curves of $GABA_B$-R-, δ-OR-, μ-OR- and κ-OR-stimulated [^{35}S]GTPγS binding in Percoll^R-purified PM isolated in parallel from control and morphine-treated rats. [^{35}S]GTPγS binding was performed at a single radioligand concentration (1 nM) in the absence (basal) or presence of increasing concentrations of agonists of $GABA_B$-R (baclofen), δ-OR (DADLE), μ-OR (DAMGO) or κ-OR (U-69593). All assays were performed in the presence of 20 μM GDP and 10 μg of protein per tube. The binding reaction was started by transfer from 0°C to 30°C and continued for 30 min at 30°C. Non-specific binding was measured at 10 μM GTPγS and subtracted from the basal ± agonist-stimulated level at each point. Δ_{max}, net increment of agonist stimulation was calculated as the difference between maximum agonist-stimulated and basal level of binding (pmol·mg^{-1} protein);% of stimulation was expressed as the ratio between agonist-stimulated and the basal level. Data represent the mean ±SEM of three PM preparations (± morphine), each analyzed in triplicates.

– OR-stimulated, high-affinity GTPase activity was undetectable in purified PM isolated from rat brain cortex PM (Table 1); the only GPCR agonist significantly increasing the basal level of GTPase activity was baclofen ($GABA_B$-R);
– analysis of [^{35}S]GTPγS binding in the presence of increasing concentrations of GDP indicated that the optimum range for detection of agonist effect was between 20 μM and 50 μμM GDP (Table 2);
– dose-response curves of agonist stimulation of [^{35}S]GTPγS binding in PM isolated from control animals indicated the order of efficacy: baclofen ($GABA_B$-R) >DADLE (δ-OR)>DAMGO (μ-OR) >U-69593 (κ-OR), Figure 1);
– comparison of the dose-response curves of different OR agonists in PM isolated in parallel from control and morphine-treated rats indicated the *highly significant decrease* of δ- and μ-opioid responses in PM isolated from morphine-treated rats (Figure 2);
– morphine treatment did not influence the dose-response curves of baclofen ($GABA_B$-R)-stimulated and U-69593 (κ-OR)-stimulated [^{35}S]GTPγS binding (Figure 2);
– the order of efficacy baclofen >DAMGO>DADLE>U69593 was the same in PM isolated from control and morphine-treated animals and thus unchanged by long-term adaptation to high-doses of morphine.

Comparison of G-protein density in PM isolated from control and morphine-treated rats

Determination G-protein activity presented in the previous paragraphs was accompanied by analysis of G-protein content in parallel PM samples. Data shown in Figure 3 indicated the unchanged level of the major class of OR-related trimeric G-proteins, $G_i1/G_i2\alpha$. A small increase of $G_i3\alpha$ protein was noticed (<120% of the control level). The pertussis toxin-insensitive member of G_i/G_o family, $G_z\alpha$ protein, was decreased, but no more than to 77% when compared with the control level, 100%. The OR-unrelated and ubiquitously expressed $G_q/G_{11}\alpha$ and $G_s\alpha$ proteins were unchanged. Thus, the decrease in activity of trimeric G-proteins was **not** accompanied by any significant change in membrane density of all the major classes of trimeric G-protein α subunits. This type of evidence may be regarded as additional support for a desensitization mechanism of morphine action, as the more drastic adaptation should be reflected in the decrease of the cognate G-protein alpha subunits in PM isolated from morphine-treated rats, *down-regulation* [37–40].

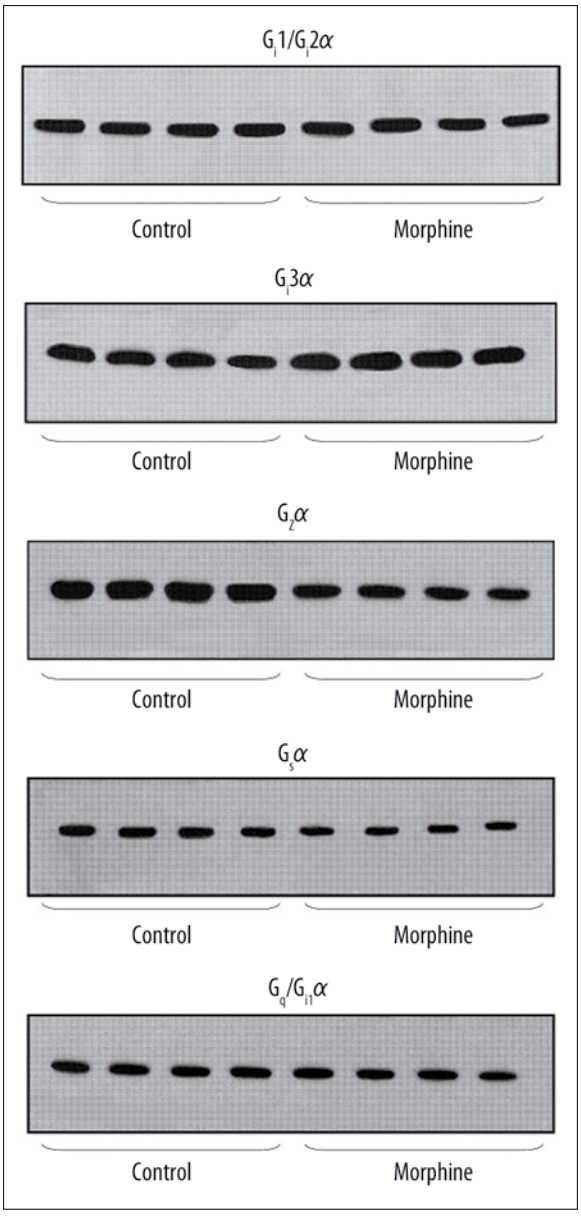

Figure 3. Comparison of G-protein content in PM isolated from control and morphine-treated rats; $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_z\alpha$, $G_s\alpha$, $G_q/G_{11}\alpha$. The 20 µg of PM protein was resolved by SDS-PAGE and G-protein α subunits were identified by immunoblotting with specific antibodies, see Methods. **A**, $G_i1/G_i2\alpha$; **B**, $G_i3\alpha$; **C**, $G_z\alpha$; **D**, $G_s\alpha$; **E**, $G_q/G_{11}\alpha$. Left lanes, control samples; right lanes, morphine-treated samples. The difference between control and morphine-treated samples was analyzed by Student's t-test and expressed as% of control level (100%): $G_i1/G_i2\alpha$ (99±2%; NS), $G_i3\alpha$ (119±4%; $p<0.05$), $G_z\alpha$ (77±5%; $p<0.01$), $G_s\alpha$ (98±4%; NS), $G_q/G_{11}\alpha$ (96±4%; NS); NS, non-significant.

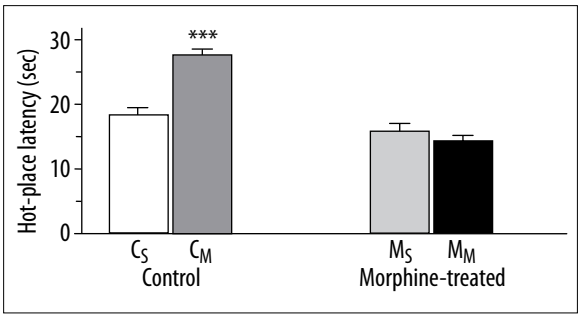

Figure 4. Hot-plate test. Rats were treated for 10 days with saline (C) or morphine (M) and 24 h after the final dose, anti-nociceptive effects of acute morphine administration were tested as described in Methods. One hour before testing their sensitivity to heat stimulation, control and morphine-treated rats were injected either with saline (C_S and M_S) or morphine (C_M and M_M). Data are expressed as means ±SEM (n=3 in each group). One-way ANOVA revealed a clear difference between C_M rats and all the other three tested groups (***, $p<0.001$).

Drug tolerance and dependence in rats treated with morphine under *in vivo* conditions. *Behavioral studies*

The biochemical studies of agonist-stimulated G-protein activity in isolated PM were extended by analysis of behavioral effects of morphine under *in vivo* conditions. These effects were analyzed by 2 tests of *tolerance* and a test of *dependence*. The day after administration of the last dose of morphine (see the Methods for detailed protocol of morphine additions), the tolerance to additional drug exposure was detected clearly *by hot-plate* and *hind paw withdrawal* tests (Figures 4, 5). The state of *dependence* of experimental animals, precipitated by intra-peritoneal administration of naloxone, was manifested by ptosis, chewing, diarrhea, increased sensitivity to touch and teeth chattering (Table 3).

There was no significant difference between control C_S and morphine-treated M_S rats in sensitivity to heat stimulation (*hot-plate test*), which was determined as delay in hind paw withdrawal (Figure 4). Acute administration of morphine did not change the sensitivity of morphine-treated rats (M_M), but it caused a highly significant analgesic effect in control C_M animals (Figure 4). These data indicated that the rats treated for 10 days with morphine developed a clear tolerance to this drug. This conclusion was also supported by the results of *hind paw withdrawal* test: there was no significant difference in sensitivity to mechanical stimulation between morphine-treated rats after acute injection of saline (M_S) or morphine (M_M) (Figure 5). In contrast, an acute dose of morphine totally blocked the response to stimulation by Frey filaments in control animals (Figure 5). Interestingly, morphine-treated rats were much more sensitive to mechanical stimulation as compared to control animals. Because the increased sensitivity to touch is considered as one of the main signs of opiate dependence (withdrawal state), the observed phenomenon can be ascribed to the development of **morphine dependence** in the tested morphine-treated animals.

Precipitation of morphine **withdrawal state** by naloxone resulted in a rapid and dramatic opiate abstinence syndrome in all tested morphine-treated rats. There were no such detectable signs of abstinence syndrome in the corresponding control animals. Characteristics of some morphine withdrawal behaviors are displayed in Table 3. All these observations confirmed that rats treated for 10 days with morphine developed a clear dependence on the drug.

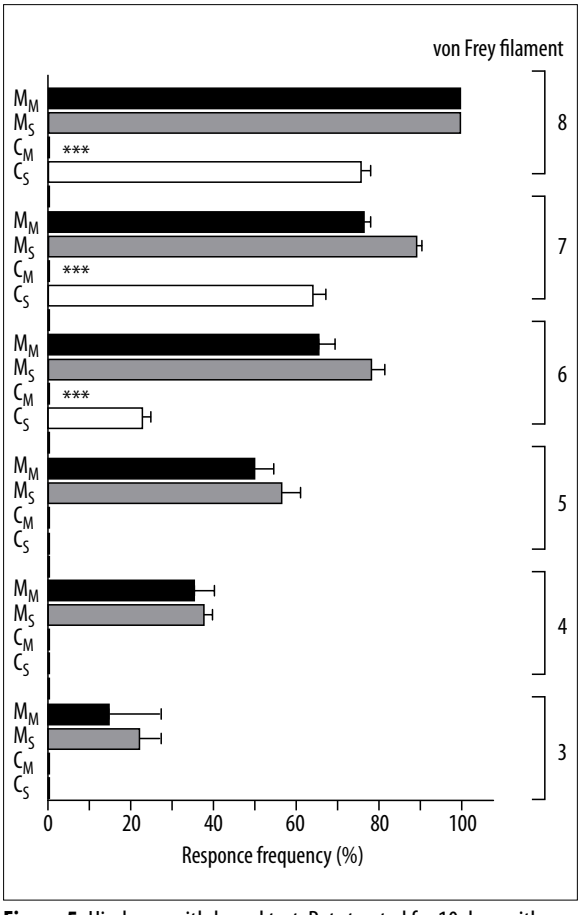

Figure 5. Hind paw withdrawal test. Rats treated for 10 days with saline (C) or morphine (M) were tested for their sensitivity to mechanical stimulation as described in Methods. Twenty-four hours after the final dose the rats were injected either with saline (C_S and M_S) or morphine (C_M and M_M) and one hour later they were poked with different von Frey filaments in their hind paws. Since there was a barely noticeable response to stimulation with very thin filaments (no. 1 and 2), only responses to filaments no. 3–8 are shown here. The occurrence of paw withdrawal was expressed as response frequency (i.e., number of trials accompanied by paw withdrawal/12×100). Values are plotted as means ±SEM (n=3 in each group). There was a clear and pronounced difference in sensitivity to mechanical stimulation between saline- and morphine-treated rats. The effect of acute administration of morphine to control animals was highly significant (***, $p<0.001$) when using von Frey filaments no. 6–8.

Discussion

Opioid *addiction* is a neurological disease symptomatically characterized by drug tolerance, dependence and craving. Data collected over the years aiming at characterization of this disease at cellular or molecular levels may be divided into 2 main hypotheses (for review see [1,41]). According to the *homeostatic* theory, the drug disturbs the cellular homeostasis and the effects are compensated by activation of **new** synthetic pathways that produce the opposite effects and thus restore homeostasis. The second theory considers the primary role of *drug-receptor interaction*, more specifically the

Table 3. Opiate withdrawal behavior in rats treated chronically with morphine

Behavior	Withdrawal score
Body shakes	0.7±0.3
Teeth clatter	2.7±0.3
Vacuous chewing	1.3±0.3
Ptosis	2.7±0.3
Irritability to touch	3.0±0.2
Diarrhoea	2.7±0.3

The values shown were calculated from scores of 0–3 for each behavior observed in morphine-treated rats during 30 min following administration of naloxone and represent the mean ±SEM. No withdrawal signs were observed in these animals before administration of naloxone except for a rather increased sensitivity to handling.

phenomenon of *desensitization* of hormone action proceeding at receptor level. The ability of the receptor to transmit the signal further down-stream becomes inactivated; the receptor becomes less sensitive to the drug. These 2 hypotheses are not mutually exclusive, as prolonged or repeated stimulation of target cells or tissues by a given GPCR agonist induces *desensitization* (decrease) of hormone responsiveness, which is compensated by re-sensitization (increase) proceeding on a longer-time basis. In a short-term scale, the OR induced increase in activity of inhibitory G-proteins (G_i/G_o) and inhibition of AC activity may be followed by increase of these activities proceeding in a long-term scale. The unequivocal difference between the 2 hypotheses/models is **not** in the sequence of counter-acting responses but in the simple fact that the *homeostatic* model involves an alteration in the amount of macromolecules, i.e., it implicitly involves synthesis of new protein molecules *de novo*, while the *change in drug-receptor* interaction model does not. It may be easily explained by a change in the activity of already existing signaling molecules such as receptors, G-proteins or adenylyl cyclases [1].

In this work we compared the opioid-stimulated G-protein activity in purified brain cortex PM isolated from control and morphine-treated rats. In the first part of our work we tried to analyze the high-affinity GTPase activity [42–47]. The ability of different GPCR agonists to stimulate the high-affinity GTPase was relatively low, and OR-agonists were unable to increase this activity in a statistically significant manner (Table 1). Baclofen, $GABA_B$-receptor agonist, was the only GPCR ligand significantly increasing GTPase activity by about 120–140% in different PM preparations. This result is in agreement with earlier data of Odagaki et al. [48] indicating that stimulation of high-affinity GTPase in frontal cortical membranes by several agonists other than $GABA_B$ receptor agonists was too low to quantify and was insufficient for comparing stimulation among different GPCR.

Therefore, in the second part of our work we tried to distinguish among different [^{35}S]GTPγS binding sites and improve methodological conditions for detection of agonist-stimulated component of G-protein activity. [^{35}S]GTPγS

binding was measured in the presence of increasing concentrations of GDP (2–100 μM) ± $GABA_B$-agonist baclofen or μ-OR agonist DAMGO. The results indicated that the optimum range for detection of agonist-stimulated component of [^{35}S]GTPγS binding was at 20–50 μM GDP (Table 2).

Subsequently, the dose-response curves of agonist-stimulation of [^{35}S]GTPγS binding were measured at a single concentration of [^{35}S]GTPγS (1 nM) plus 20 μM GDP in all binding assay media (Figure 1). Comparison of dose-response curves of baclofen ($GABA_B$-R)-, DADLE (δ-OR)-, DAMGO (μ-OR)- and U-69593 (κ-OR)-stimulated binding in PM isolated from control rats indicated that the highest *net increment* of agonist stimulation was detected with the order of efficacy: baclofen ($GABA_B$-R)>DADLE (δ-OR)>DAMGO (μ-OR)>U-69593 (κ-OR) [0.69>0.54>0.38>0.18 pmol·mg^{-1}]; the ratio between agonist-stimulated and basal level of binding decreased with the same order: baclofen >DADLE>DAMGO>U-69593 [165>149>135>117%].

Comparison of PM isolated from control and morphine-treated animals was performed in another, independent set of experiments (Figure 2). The data indicated the same order of efficacy in control and morphine-treated PM [baclofen ($GABA_B$-R)>DADLE (δ-OR)>DAMGO (μ-OR)>U-69593 (κ-OR)] and a *highly significant decrease* ($p<0.01$) of DADLE- and DAMGO-stimulated binding in morphine-treated rats (Figure 2, middle panels). The desensitization of G-protein response was manifested in the whole range of DADLE and DAMGO concentrations. Baclofen ($GABA_B$-R)- and U-69593 (κ-OR)-stimulated binding was **unchanged,** indicating the specificity of morphine-induced change.

The functional studies of G-protein activity indicating the desensitization of δ-OR and μ-OR responses were extended by analysis of the G-protein content (Figure 3). The unchanged level of the OR-related trimeric G-proteins $G_i1/G_i2\alpha$ was detected; the same result was found for the other 2 most widely expressed G-proteins $G_s\alpha$ and $G_q/G_{11}\alpha$. The decrease of $G_z\alpha$ protein, which has been reported to participate directly in the short-term mechanism of morphine action [15], and small increase of $G_i3\alpha$ were the only significant changes we were able to notice.

Behavioral studies performed under *in vivo* conditions in the last part of our work (Figures 4, 5, Table 3) indicated that the experimental animals were fully *drug dependent*, i.e., they developed tolerance to additional morphine exposure and much lower sensitivity to pain, as expected in an addicted state.

Desensitization of μ- and δ-opioid receptor response in frontal brain cortex of rats adapted to high doses of morphine for a prolonged period of time (10 days) is surprising, as the previous work using brain slices and quantitative [^{35}S]GTPγS autoradiography in this part of the brain did not indicate any difference [49]. DAMGO was highly effective when increasing the basal level of binding (191%), but the basal as well as DAMGO-stimulated binding was not different when compared in control and morphine-treated rats (exposed to increasing doses of morphine for 12 days, 10–320 mg/kg). Similar data has been published for heroine [50,51].

Decrease of both μ- and δ-OR-initiated signaling described in our present work is unlikely to arise from non-specific phenomena, because $GABA_B$-R- and κ-OR-stimulated [^{35}S]GTPγS binding was unchanged. Difference between results of Sim et al. [49], Sim-Selley et al. [50] and our data may be explained either by widely different GDP concentrations used in the binding assays (mM range in the case of autoradiographic studies), or by preparation of brain slices at high temperature (–35°C). The full preservation of agonist-stimulated G-protein activity is achieved only when the biological material is snap frozen in liquid nitrogen and used only once (after melting and storage at 0–4°C in the course of membrane isolation or G-protein activity assays). We have repeatedly experienced this fact in measurements of isoprenaline-sensitive adenylylcyclase in S49 lymphoma cells [52,53], DADLE-stimulated [^{35}S]GTPγS binding in HEK293 cells expressing DOR-G_i1 protein [20]or baclofen-stimulated high-affinity GTPase and [^{35}S]GTPγS binding in membranes from frontal brain cortex [30,54].

Previous extensive analysis of distribution of μ-, δ- and κ-OR and G-protein activity in rodent brain, together with the results indicating that morphine's analgesic and addictive properties, were abolished in mice lacking the μ-opioid receptor, has unambiguously demonstrated that μ-receptors mediate both the therapeutic and the adverse activities of this compound [8,55,56]. Therefore, our results demonstrating the order of efficacy DADLE (δ-OR)>DAMGO (μ-OR)>U-69593 (κ-OR) and desensitization of δ-OR mediated response at the level of G-protein activity bring new evidence which has so far not been noticed in the literature to date. Our results are compatible with findings indicating the relatively high density of δ-OR in adult rat forebrain [19,57] together with minor functional significance of κ-OR mediated cascade in this part of CNS [58].

It might be argued that G-protein activity measured in our biochemical work does not necessarily reflect the *in vivo* situation, however, behavioral studies performed under *in vivo* conditions (Figures 4, 5, Table 3) indicated that rats exposed to morphine according to our experimental protocol [increasing doses of morphine for 10 days: 10 mg/kg (day 1 and 2), 15 mg/kg (day 3 and 4), 20 mg/kg (day 5 and 6), 30 mg/kg (day 7 and 8), 40 mg/kg (day 9), 50 mg/kg (day 10)] developed tolerance and much lower sensitivity to pain in comparison with control animals.

Please note that determination of G-protein activity in our work was carried out under the *most simple assay conditions*, i.e., we did **not** use more sophisticated immuno-precipitation protocols, which might increase OR-stimulation of G-protein activity, but might also introduce artificial changes caused by differences in reactivity of G_i1-, G_i2- or G_i3-oriented antibodies. Alternation of antibody reactivity in the course of 10 days of morphine exposure cannot be excluded a priori. Therefore, the simple strategy based on isolation of subcellular membrane fraction enriched in and containing the major part of GPCR and G-proteins, i.e., of plasma membranes [29], together with the definition of the optimum range of GDP concentrations for detection of agonist-stimulated [^{35}S]GTPγS binding, appeared to be the better choice.

Desensitization of *both* μ-OR and δ-OR -stimulated G-protein responses in the *crucial* brain structure, frontal cortex, which has been unequivocally demonstrated in this work, supports the idea of the primary role of receptor-G-protein interaction

in genesis of addictive state [41,1]. Demonstration that desensitization of μ-OR and δ-OR-initiated G-protein pathways proceeds in the cerebral cortex, which has thus far been regarded as a less important brain area in drug addiction when compared with the brain stem, hippocampus and hypothalamus, suggests a more complex picture of integrative interactions among all parts of the brain in this severe phase of the addicted state. This conclusion seems logical, as dramatic changes in behavior of drug addicted animals (Figures 3, 4, Table 3) *should be* accompanied by detectable biochemical changes in the frontal brain cortex, representing the functionally uppermost part of the CNS.

Conclusions

Desensitization of μ-OR- and δ-OR-stimulated G-protein activity was measured in purified plasma membranes isolated from forebrain cortex of rats adapted to high doses of morphine for 10 days. Responsiveness to baclofen ($GABA_B$-R agonist) and U-69593 (κ-OR agonist) was unchanged, indicating the specificity of the morphine effect. Under these conditions the amount of G-protein alpha subunits was unchanged. Behavioral tests performed under *in vivo* conditions indicated that morphine-treated animals were fully drug-dependent and developed tolerance to subsequent drug addition. *These results support the view that the mechanism of addiction to morphine is primarily based on desensitization of OR response, which proceeds primarily at the level of G-protein functional activity.*

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Plasma Membrane Density of $GABA_B$-R1a, $GABA_B$-R1b, GABA-R2 and Trimeric G-proteins in the Course of Postnatal Development of Rat Brain Cortex

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Summary

With the aim to understand the onset of expression and developmental profile of plasma membrane (PM) content /density of crucial components of $GABA_B$-R signaling cascade, $GABA_B$-R1a, $GABA_B$-R1b, $GABA_B$-R2, $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$ and Gβ subunit proteins were determined by quantitative immunoblotting and compared in PM isolated from brain cortex of rats of different ages: between postnatal-day-1 (PD1) and 90 (PD90). PM density of $GABA_B$-R1a, $GABA_B$-R2, $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$ and Gβ was high already at birth and further development was reflected in parallel decrease of both $GABA_B$-R1a and $GABA_B$-R2 subunits. The major decrease of $GABA_B$-R1a and $GABA_B$-R2 occurred between the birth and PD15: to 55 % (R1a, **) and 51 % (R2, **), respectively. Contrarily, PM level of the cognate G-proteins $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$ and Gβ was unchanged in the course of the whole postnatal period of brain cortex development. Maturation of $GABA_B$-R cascade was substantially different from ontogenetic profile of prototypical plasma membrane marker, Na, K-ATPase, which was low at birth and further development was reflected in continuous increase of PM density of this enzyme. Major change occurred between the birth and PD25. In adult rats, membrane content of Na, K-ATPase was 3-times higher than around the birth.

Key words

$GABA_B$-R • Postnatal development • Rat brain cortex • G-proteins • Na, K-ATPase

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Introduction

$GABA_B$-receptors were defined as a class of bicuculline-insensitive GABA receptors for which (-)-baclofen is a specific agonist and phaclofen and 2-hydroxy-saclofen represent specific antagonists (Hill and Bowery 1981, Bowery *et al.* 1985, 1987, Kerr and Ong 1995). These receptors are not physically bound to ionic channels and belong to the family of G-protein coupled receptors, GPCR (Kerr and Ong 1995). Thus, the primary signal initiated by binding of GABA to $GABA_B$-R is transmitted further downstream by trimeric G-proteins.

The central nervous system is known to contain high levels of all trimeric Gα subunits. The three species of inhibitory G-proteins, $G_i\alpha1$, $G_i\alpha2$ and $G_i\alpha3$ (Mumby *et al.* 1988), the long ($G_s\alpha L$) and short ($G_s\alpha S$) variants of the stimulatory $G_s\alpha$ protein (Bray *et al.* 1986), phosphoinositidase C-linked $G_q\alpha$ and $G_{11}\alpha$ proteins (Milligan 1993) as well as representatives of $G_{12}\alpha/G_{13}\alpha$ family of G-proteins (Harhammer *et al.* 1994, 1996) were identified in brain tissue in high amounts. The major G-proteins of brain, however, are members of $G_o\alpha$ family. The two isoforms of $G_o\alpha$ subunits, $G_o\alpha1$ and $G_o\alpha2$, represent up to 1 % of the total membrane protein in the brain tissue (Giershick *et al.* 1986, Goldsmith *et al.* 1987, 1988, Milligan 1988, 1990). Accordingly, the content of Gβ subunits is very high in brain (Asano *et al.* 1988). It should be also mentioned that the complexity of biochemical composition of the brain tissue is not limited to G-proteins, but it is equally high for adenylylcyclase (AC) molecules because all the isoforms (ACI-X) of this

key regulatory enzyme of GPCR-initiated cascades were identified in CNS and their PM content was found to respond readily to physiological state of experimental animals (Ujcikova *et al*. 2011).

Regulation of the specificity and efficiency of coupling between GPCRs and trimeric G-proteins in natural tissue such as brain is therefore highly complex. GPCRs usually exert their action through activation of preferential G-proteins (in a given cell type), however, a single type of receptor can be also coupled to several G-proteins (Boege *et al.* 1991, Gerhardt and Neubig 1991, Raymond 1995, Dascal 1997, Gudermann *et al.* 1997, Hildebrandt 1997). Furthermore, the given type of G-protein may be activated by different receptors. Under such conditions, it is reasonable to assume that a complicated functional arrangement denominated as cross talk among individual members of G-protein-mediated cascades exists and provides an effective regulatory mechanism for the convergence or divergence of actions of a single neurotransmitter in nervous tissue.

Receptor-initiated activation of G-proteins results in the release of free Gα and Gβγ subunits from the non-active Gαβγ trimer; subsequently, both free Gα and Gβγ subunits mediate the signal transmission further downstream. Thus, besides the functional networks of Gi1α-, Gi2α-, Gi3α-, Go1α- and Go2α-mediated signaling, Gβγ-mediated cascades represent no less complicated regulatory circuits. The main Gβγ-regulated effectors of presynaptic $GABA_B$-receptors are P/Q-and N-type voltage-dependent Ca^{2+} channels (Chen and van den Pol 1998, Bussieres and El Manira 1999, Barral *et al.* 2000). $GABA_B$-receptors inhibit these Ca^{2+} channels at both excitatory and inhibitory terminals, thereby restricting neurotransmitter release. Depending on whether the terminal releases an inhibitory or excitatory neurotransmitter, the presynaptic $GABA_B$ receptors increase or decrease the excitability of the postsynaptic neuron (Pinard *et al.* 2010).

Presynaptic $GABA_B$ receptors restrict neurotransmitter release not only by inhibiting Ca^{2+} channels but also by retarding the recruitment of synaptic vesicles (Sakaba and Neher 2003). More recent evidence suggests that presynaptic $GABA_B$-receptors may couple to inwardly rectifying Kir3-type K^+ channels (also designated GIRK channels) to inhibit glutamate release (Ladera *et al.* 2008, Fernandez-Alacid *et al.* 2009); however, Kir3 channels are generally considered as the main effectors of postsynaptic $GABA_B$-receptors (Pinard *et al.* 2010).

Binding of GABA to postsynaptic $GABA_B$-R results in activation of Kir3 channels, induction of K^+ efflux and hyperpolarization of postsynaptic membrane. This change of membrane potential shunts excitatory currents in a non-specific way. Finally, under such conditions, the so-called slow inhibitory postsynaptic potentials (IPSPs) are generated. Activation of postsynaptic $GABA_B$-receptors was also found to decrease the activity of Ca^{2+} channels, which inhibit dendritic Ca^{2+}-spike propagation (Perez-Garci *et al.* 2006).

The present state of knowledge about the plasma membrane part of $GABA_B$-receptor signaling cascade in the brain may thus be described as a mutually interrelated regulatory network of $GABA_B$-R, PTX-sensitive G-proteins of $G_i/G_o\alpha$ family, various AC isoforms and ionic channels such as $GABA_A$-R (Xu and Wojcik 1986, Simonds 1999, Sunahara and Taussig 2002, Padgett and Schlesinger 2010, Pinard *et al.* 2010). Functionally, in this network, primary inhibitory signals proceeding at receptor level are followed by both positive and negative feedback regulatory loops tuning the whole regulatory circuit to an optimum output (Padgett and Schlesinger 2010, Pinard *et al.* 2010). These circuits are therefore highly complex and important for brain function as GABA represents the main inhibitory neurotransmitter of mammalian brain.

Our previous results indicated that the plasma membrane density of $GABA_B$-R, determined by a saturation binding assay with antagonist [^{3}H]CGP54626, was highest in 1-day-old animals and then it was dramatically decreased in 15- and 90-day-old rats (Kagan *et al.* 2012). Intrinsic efficacy of $GABA_B$-receptors, measured as agonist-stimulated, high-affinity [^{35}S]GTPγS binding, was also high at birth (PD1, PD2), however, it increased further during the first two weeks of postnatal life and reached the maximum between PD9 and PD15. In older rats, both baclofen- and SKF97541-stimulated [^{35}S]GTPγS binding was decreased so that the level in adult rats (PD90) was not different from that in newborn animals.

The aim of our present work was to establish the structural correlate to these functional studies of $GABA_B$-R ontogenesis by determination of PM density of $GABA_B$-R1a, $GABA_B$-R1b, $GABA_B$-R2, $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$ and Gβ subunit proteins by quantitative immunoblottig with specific antibodies. We have also determined PTX-insensitive $G_{12}\alpha$ protein as a test of maturation of intracellular "membrane traffic", as

vesicular transport within the neuron is an important part of optimum functioning of CNS. The general trend of brain cortex maturation was screened by analysis of prototypical plasma membrane marker, ouabain-dependent Na, K-ATPase (EC 3.6.1.3).

Material and Methods

The experiments were approved by Animal Care and Use Committee of the Institute of Physiology, Academy of Sciences of the Czech Republic to be in agreement with Animal Protection Law of the Czech Republic as well as European Comunity Council directives 86/609/EEC.

Chemicals and radiochemicals

$GABA_B$-receptor agonists baclofen (β-p-chlorophenyl-GABA), SKF 97541 [3-aminopropyl (methyl) phosphinic acid] and antagonist [^{3}H]CGP 54626 (41.5 Ci/mmol, cat. no. R1088) were purchased from Tocris. [21, 22-^{3}H]ouabain (30 mCi/mmol; NET211001) was from Perkin Elmer. The complete protease inhibitor cocktail was from Roche Diagnostic (cat. no. 1697498). All other chemicals were of highest quality available.

Primary antisera and antibodies

$G_i1/G_i2\alpha$, $G_i3\alpha$ and $G_o1/G_o2\alpha$ subunit proteins were identified by antipeptide antibodies prepared as described originally by Gierschik *et al.* (1986), Goldsmith *et al.* (1987), Backlund *et al.* (1988) and Milligan (1988, 1990). These antisera were previously characterized in our laboratory (Ihnatovych *et al.* 2002a). Polyclonal antibodies oriented against $GABA_B$-R1 (R-300, sc-14006), $GABA_B$-R2 (H-300, sc-28792), Gβ (T-20, sc-378) $G_z\alpha$ (I-20, sc-388), $G_{12}\alpha$ (S-20, sc-409) and α subunit of Na, K-ATPase (H-300, sc-28800) were from Santa Cruz.

Isolation of plasma membrane-enriched fraction from rat brain cortex

Rat brain cortex was minced with a razor blade on a pre-cooled plate and diluted in STEM medium containing 250 mM sucrose, 20 mM Tris-HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.6, fresh 1 mM PMSF plus protease inhibitor cocktail. It was then homogenized mildly in loosely-fitting Teflon-glass homogenizer for 5 min (2 g w. w. per 10 ml) and centrifuged for 5 min at 3500 rpm. Resulting post-nuclear supernatant (PNS) was filtered through Nylon nets of decreasing size (330, 110 and 75 mesh, Nitex) and applied on top of Percoll in Beckman Ti70 tubes (30 ml of 27.4 % Percoll in STE medium). Centrifugation for 60 min at 30000 rpm (65000 x g) resulted in the separation of two clearly visible layers (Bourova *et al.* 2009). The upper layer represented plasma membrane fraction (PM); the lower layer contained mitochondria (MITO). The upper layer was removed, diluted 1:3 in STEM medium and centrifuged in Beckman Ti70 rotor for 90 min at 50000 rpm (175000 x g). Membrane sediment was removed from the compact, gel-like sediment of Percoll, re-homogenized by hand in a small volume of 50 mM Tris-HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.4 (TME medium), snap frozen in liquid nitrogen and stored at –80 °C.

SDS-PAGE and immunoblotting

Aliquots of PM were solubilised in NuPAGE SDS Sample Buffer (4x) with an addition of NuPAGE Sample Reducing Agent (10x) according to manufacturer's instructions. Samples were heated at 70 °C for 10 min, loaded at 10 μg/well and resolved by NuPAGE 4-12 % or 10 % Bis-Tris polyacrylamide gels (10 wells, 1 mm thick) using 3-(N-morpholino) propane sulfonic acid (MOPS), sodium dodecyl sulfate (SDS) running buffer with NuPAGE Antioxidant prior to blotting on nitrocellulose membranes (Protran, Schleicher & Schuell). Molecular mass determinations were based on pre-stained molecular mass markers (Sigma, SDS 7B).

After SDS-PAGE, the proteins were transferred to nitrocellulose and blocked for 1 h at room temperature in 5 % (w/v) low-fat milk in TBS-Tween buffer [10 mM Tris-HCl, pH 8.0, 150 mM NaCl, 0.1 % (v/v) Tween 20]. Antibodies were added in TBS-Tween containing 1 % (w/v) low-fat milk and incubated for at least 2 h. The primary antibody was then removed and the blot washed extensively (3 x 10 min) in TBS-Tween. Secondary antibodies (donkey anti-rabbit IgG conjugated with horseradish peroxidase) were diluted in TBS-Tween containing 1 % (w/v) low-fat milk applied for 1 h, and after three 10-min washes the blots were developed by ECL technique using Super Signal West Dura (Pierce) as substrate. The developed blots were scanned with an imaging densitometer ScanJett 5370C (HP) and quantified by Aida Image Analyzer v. 3.28 (Ray test).

[^{3}H]CGP54626 binding; one-point assay

Membranes (100 μg protein per assay) were incubated with 12 nM [^{3}H]CGP54626 in a final volume

of 100 µl of binding mix containing (A) 50 mM Tris-HCl (pH 7.4) alone, (B) 50 mM Tris-HCl (pH 7.4) plus 2.5 mM $CaCl_2$ or (C) 50 mM Tris-HCl (pH 7.4) plus 5 mM $MgCl_2$ for 60 min at 30 °C. The bound and free radioactivity was separated by filtration and determined by liquid scintillation as described. Non-specific binding was determined in the presence of 1 mM GABA.

Na, K-ATPase; [^{3}H]ouabain binding

Sodium plus potassium-activated, oubain-dependent Na, K-ATPase (E.C. 3.6.1.3) was determined by "one-point" [^{3}H]ouabain binding assay according to Svoboda *et al.* (1988). Membranes (50 µg of protein) were incubated with 20 nM [^{3}H]ouabain in a total volume of 0.45 ml of 5 mM $NaHPO_4$, 5 mM $MgCl_2$, 50 mM Tris-HCl, pH 7.6 (Mg-Pi buffer) for 90 min at 30 °C. The bound and free radioactivity was separated by filtration through Whatman GF/B filters in Brandel cell harvester. Filters were washed 3× with 3 ml of ice-cold incubation buffer and placed in 4 ml of scintillation cocktail (CytoScint, ICN). Radioactivity remaining on filters was determined after 10 h at room temperature by liquid scintillation. Non-specific binding was determined in the presence of 1 µM unlabelled ouabain.

Statistical analysis

The significance of difference between the immunoblot signal determined in fetuses 1-day before the birth (100 %) and signals determined at different age intervals (PD1, PD2, PD5, PD9, PD10, PD15, PD25, PD35, PD42, PD47, PD90) was analyzed by one-way test of variance ANOVA followed by Bonferroni's *post-hoc* comparison test using GraphPad*Prism4*.

One-way ANOVA followed by Bonferroni's *post-hoc* comparison test was also used for statistical analysis of the difference of [^{3}H]CGP54626 and [^{3}H]ouabain binding to PM isolated from 1-, 15- and 90-day-old rats.

Protein determination

Lowry method was used for determination of membrane protein using bovine serum albumin (Sigma, Fraction V) as a standard. Data were calculated by fitting the calibration curve as a quadratic equation.

Results

Our previous results indicated an early functional maturation of $GABA_B$-R signaling cascade in rat brain cortex (Kagan *at al.* 2012). Agonists baclofen and SKF97541 exhibited significant efficiency (both potency and efficacy) already at PD2 and the highest number of $GABA_B$-R, determined as maximum binding capacity (B_{max}) for specific antagonist [^{3}H]CGP54626, was determined in 1-day-old animals (PD1). In older rats, the number of [^{3}H]CGP54626 binding sites was decreased, in contrast to agonist-stimulated G-protein activity, which was increased during the first two weeks of postnatal life. The maximum of agonist-stimulated G-protein activity, measured as baclofen- or SKF97541-stimulated [^{35}S]GTPγS binding, was observed on PD14-15. Maximum of [^{35}S]GTPγS binding was followed by continuous decrease of G-protein activity till the adulthood (90-day-old rats).

Immunoblot analysis of plasma membrane density of $GABA_B$-R1a, $GABA_B$-R1b, $GABA_B$-R2 and of the cognate, PTX-sensitive G-proteins performed in this work (Fig. 1 and 2) indicated that expression level of $GABA_B$-R1a, $GABA_B$-R1b, $GABA_B$-R2 and of all individual members of G_i/G_o family ($G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$[1] and Gβ subunit proteins) was high already around the birth, i.e. in fetuses 1 day before the birth (D-1) and in 1- and 2-day-old rats (PD1 and PD2). Subsequently, membrane density of $GABA_B$-R1a, $GABA_B$-R1b and $GABA_B$-R2 was decreased more or less in parallel till PD15 (Fig. 1). At this age interval, the $GABA_B$-R subunits represented 55±15 % ($GABA_B$-R1a), 70±17 % ($GABA_B$-R1b) and 51±5 % ($GABA_B$-R2) of the level detected in newborn rats, 100 %. In early postnatal period (up to PD15), PM expression level of $GABA_B$-R1b was lower than of $GABA_B$-R1a.

By contrast, the membrane density of all G-proteins ($G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$, $G_{12}\alpha$[1] and Gβ) was unchanged in the course of the whole postnatal period, i.e. between PD2 and PD90 (Fig. 2). Expressed in more detail, the immunoblot signals of all G-proteins in PM samples containing the same amount of protein (10 µg) and prepared from fetuses 1 day before the birth and 1-, 2-, 5-, 9-, 10-, 15-, 25-, 35-, 42-, 47- and 90-day-old rats, were the same, i.e. not statistically different when compared with the control signal in fetuses 1 day before

[1] Though being insensitive to PTX and thus unrelated to $GABA_B$-R, the ontogenetic profile of $G_{12}\alpha$ protein was also measured with the aim to obtain information about the important group of G-proteins regulating membrane traffic (Harhammer *et al.* 1994, 1996, Hildebrant *et al.* 1997). The developmental change of these proteins was similar to that of other G-proteins. The prenatal level was high and afterwards, it decreased slowly and continuously till the adulthood.

the birth, 100 %. Thus, there was a clear disparity between development of receptor and G-proteins functionally participating in $GABA_B$-R signaling cascade: membrane density of $GABA_B$-R subunit proteins was substantially decreased between the birth and "opening of eyes" period, while the cognate, trimeric G-proteins of Gi/Go family were unchanged.

In the second part of our work, we have extended our recent results (Kagan *et al.* 2012) and compared antagonist [^{3}H]CGP54626 binding in ion-free, 2.5 mM $CaCl_2$ and 5 mM $MgCl_2$ containing incubation media (Fig. 3) in PM isolated from 1-, 13- and 90-days old rats. The use of ion-free incubation medium was introduced by Ko *et al*. (2003) for determination of the number of μ-, δ- and κ-opioid receptors in monkey brain cortex and hypothalamus. Comparison of the level of [^{3}H]CGP54626 binding in these media was performed by a "one-point assay" at the constant concentration of 15 nM of this radioligand.

The decrease of [^{3}H]CGP54626 binding was noticed in all incubation media, however, due the low level of binding, this decrease was not significant in ion-free medium (Fig. 3). The highly significant decrease was measured in 2.5 mM $CaCl_2$ ($p<0.001$) and 5 mM $MgCl_2$ ($p<0.01$) containing media. Please note that the level of binding in 2.5 mM $CaCl_2$ was much higher that in 5 mM $MgCl_2$. This result reflects and may be interpreted as a natural consequence of the presence of 2.5 mM calcium in extracellular medium surrounding $GABA_B$-R ligand binding site located on $GABA_B$-R1 (Padgett and Slesinger 2010, Pinard *et al.* 2010) and is in agreement with the previous agonist binding studies of $GABA_B$-R in rat brain cortex synaptosomes (Bowery *et al.* 1983). The decrease of $GABA_B$-R1a, $GABA_B$-R1b and $GABA_B$-R2 subunits (Fig. 1) proceeded in parallel with the decrease of antagonist binding (Fig. 3). However, it was terminated at PD15, while antagonist binding was decreased further till the adulthood (PD90).

Postnatal development of $GABA_B$-R1, $GABA_B$-R2, G-proteins and ligand binding to $GABA_B$-R was substantially different from maturation of the prototypical plasma membrane marker, Na, K-ATPase (Fig. 4A,B). Membrane density of α-subunit of Na, K-ATPase was low at birth (PD1, PD2) and further development was reflected in a marked increase of this protein. The major increase occurred between the birth and PD25. Since this age interval, PM content of Na, K-ATPase was not significantly altered in PM isolated from 35-, 42- and

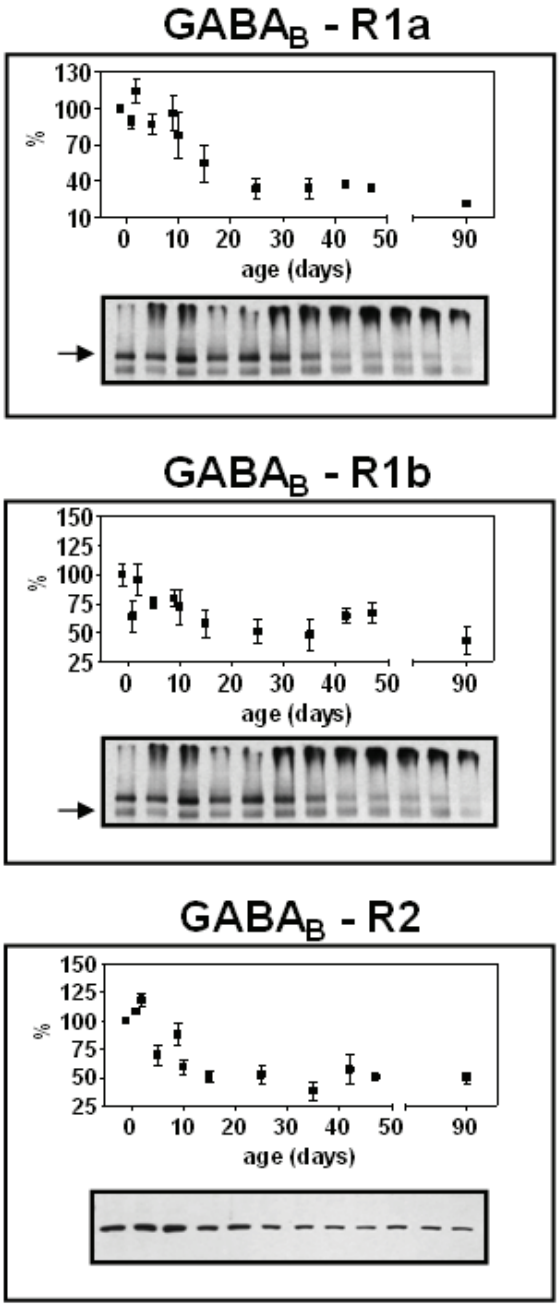

Fig. 1. Plasma membrane density of $GABA_B$-R1a, $GABA_B$-R1b, $GABA_B$-R2 subunit proteins; immunoblot analysis. PM proteins (10 μg per well) were resolved by Invitrogen NuPAGE system in 4-12 % gradient gel and identified by immunoblotting with specific antibodies as described in Methods. Data represent the average of five immunoblots ± SEM. Significance of the difference between the immunoblot signal determined in fetuses 1 day before the birth (D-1, 100 %) and signals determined at different ages (PD1, PD2, PD5, PD9, PD10, PD15, PD25, PD35, PD42, PD47, PD90) was analyzed by one-way ANOVA followed by Bonferroni's *post-hoc* comparison test using GraphPad*Prism4*. **$GABA_B$-R1a:** D-1 vs 15 (**, $P<0.01$), PD2 vs PD15 (**, $P<0.01$), PD2 vs PD90 (**, $P<0.01$), PD15 vs PD90 (NS, $P>0.05$). **$GABA_B$-R1b:** D-1 vs PD15 (NS, $P>0.05$), PD2 vs PD15 (NS, $P>0.05$), PD15 vs PD90 (NS, $P>0.05$), D-1 vs PD90 (**, $P<0.01$), PD2 vs PD90 (*, $P<0.05$). **$GABA_B$-R2:** D-1 vs PD15 (*, $P<0.05$), PD2 vs PD15 (**, $P< 0.01$), PD2 vs PD90 (**, $P< 0.01$), PD15 vs PD90 (NS, $P>0.05$).

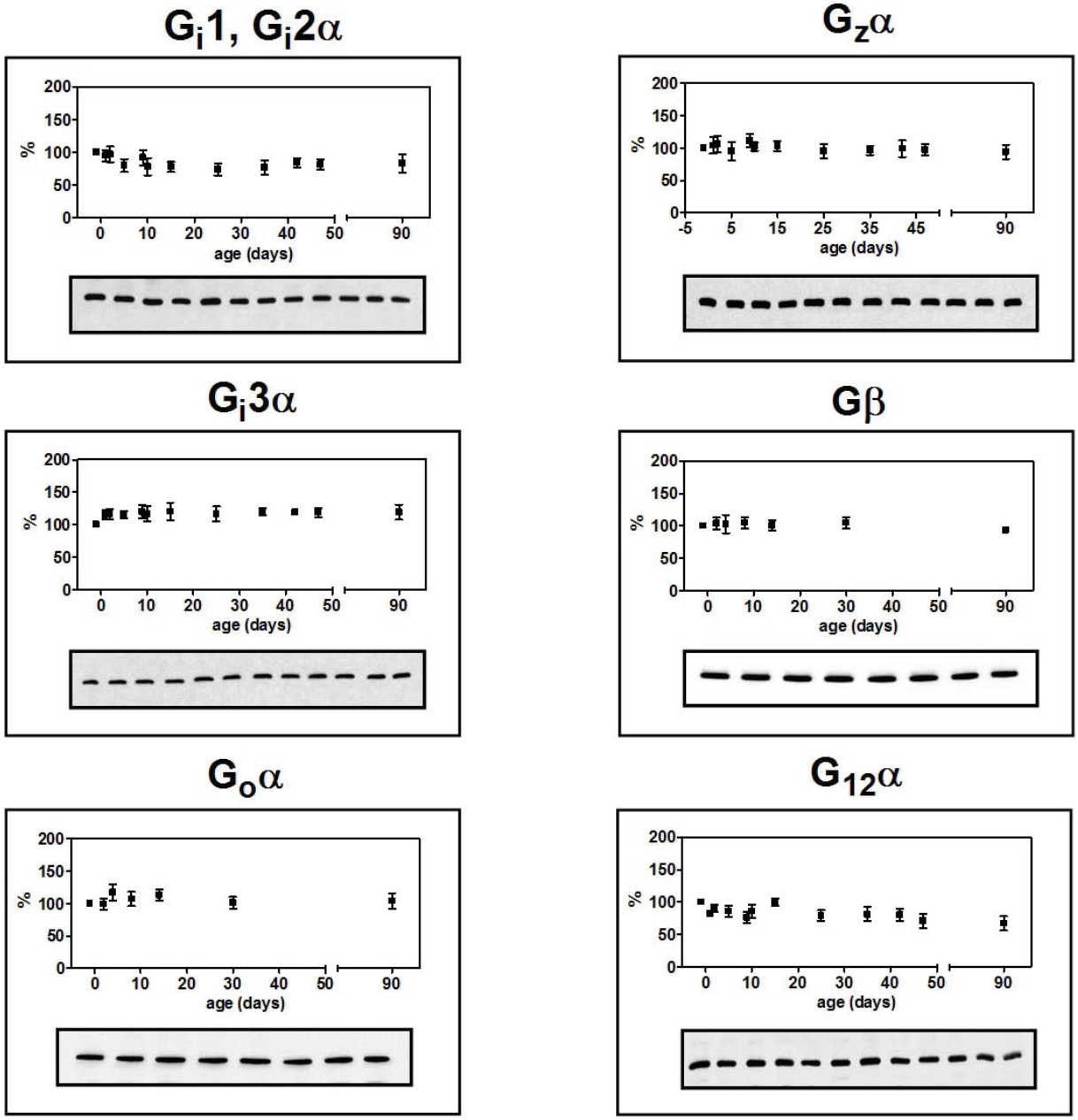

Fig. 2. Plasma membrane density of $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$, $G\beta$ and $G_{12}\alpha$ subunit proteins; immunoblot analysis. The expression of G-proteins was analyzed in the same plasma membrane samples as those used for detection of $GABA_B$-R subunits. G-proteins were unchanged in the course of the whole postnatal period as there was no significant difference between immunoblot signals detected around the birth (D-1, PD1, PD2) and at all other ages: $G_i1/G_i2\alpha$ ($p>0.05$); $G_i3\alpha$ ($p>0.05$), $G_o\alpha$ ($p>0.05$), $G_z\alpha$ ($p>0.05$) and $G\beta$ ($p>0.05$) at all ages. $G_{12}\alpha$ was decreased between PD1 and PD90 (*, $p<0.05$).

90-day-old rats. The intensity of average immunoblot signal in adult rats (PD90) was 3.5-times higher than around the birth (day -1, PD1 and PD2).

Virtually the same results were obtained when selective inhibitor [^{3}H]ouabain was used for determination of Na, K-ATPase (Fig. 4C). The major increase of [^{3}H]ouabain binding in PM was noticed between the birth and PD25. Since PD25, the binding of this radioligand was not significantly different from the adult animals. [^{3}H]ouabain binding in 90-day-old rats (13.89 pmol.mg^{-1}) was 1.6x higher than in 15-day-old rats (8.64 pmol.mg^{-1}) and 2.6x higher than in fetuses 1 day before the birth (5.44 pmol.mg^{-1}). Thus, the overall maturation of brain cortex PM composition monitored by a developmental study of Na, K-ATPase molecules proceeds after the birth, while the level of $GABA_B$-signaling proteins is high at birth and further decreased ($GABA_B$-R) or unchanged (G-proteins).

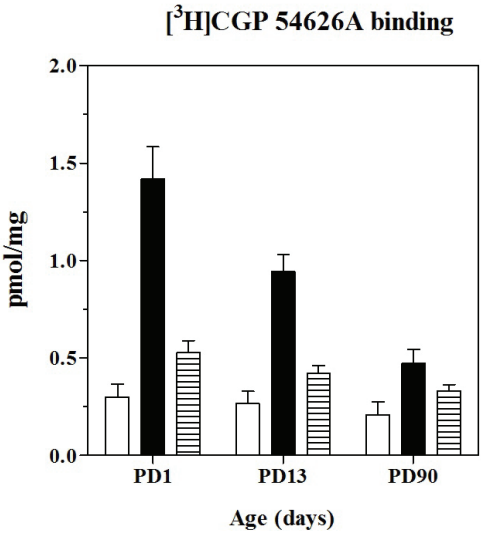

Fig. 3. Decrease of [^{3}H]CGP54626A binding in the course of postnatal ontogenesis. PM (100 μg protein per assay) isolated from 1-(PD1), 13-(PD13) and 90-(PD90)-day- old rats were incubated with 12 nM [^{3}H]CGP54626A in 50 mM Tris-HCl with no additions (□, open columns), in 50 mM Tris plus 2.5 mM $CaCl_2$ (■, full columns) or in 50 mM Tris-HCl plus 5 mM $MgCl_2$ (≡, hatched columns). Non-specific binding was determined in the presence of 1 mM GABA. Data represent the average of 3 binding assays performed in quadruplicates ± SEM. Comparison of binding data in PM isolated from PD1, PD13 and PD90 was performed by one-way ANOVA followed by Bonferroni's *post-hoc* comparison test. Open columns (□): PD1 versus PD13, NS, p>0.05; PD1 versus PD90, NS, p>0.05; PD13 versus PD90, NS, p>0.05. Full columns (■): PD1 versus PD13, **, p<0.01; PD1 versus PD90, ***, p<0.001; PD13 versus PD90, ***, p<0.001. Hatched columns (≡): PD1 versus PD13, NS, p>0.05; PD1 versus PD90, **, p<0.01; PD13 versus PD90, NS, p>0.05.

Discussion

In the brain, $GABA_B$-R-initiated signal transfer to G-proteins and from G-proteins to adenylyl cyclase (AC) represents a rather intricate trans-membrane process (Bormann 1988, Boege *et al.* 1991, Padgett and Slesinger 2010) because all its pivotal components occur in multiple isoforms with distinct functional properties, and the cognate G-proteins of G_i/G_o family exert both stimulatory and inhibitory effects on the overall AC activity, which represents the final outcome of the ten different isoenzymes, ACI-X (Backlund *et al.* 1988, Tang *et al.* 1992, Taussig *et al.* 1994, Simonds 1999, Sunahara and Taussig 2002). Our previous analysis of postnatal development of adenylyl cyclase in various brain areas indicated a marked activation of this enzyme in membranes prepared from 12-15-day-old rats (Ihnatovych *et al.* 2002b). The activity of the basal-, manganese-, fluoride-, GTP- and forskolin-stimulated AC was low at birth (PD1), increased sharply during the first two weeks of postnatal life, reached a maximum between

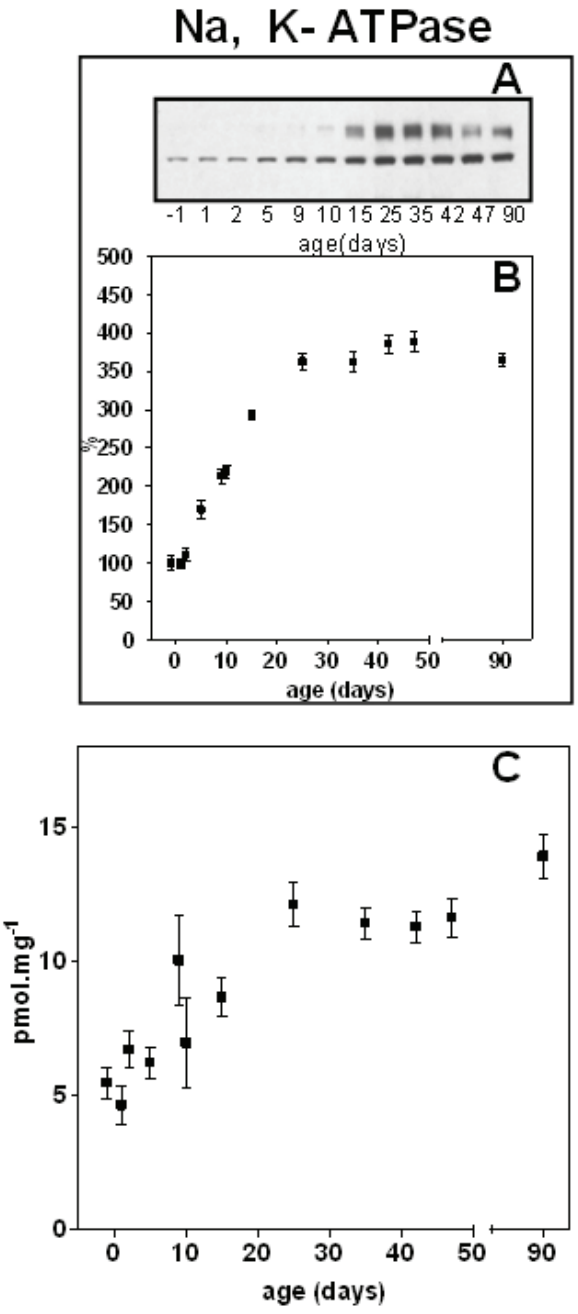

Fig. 4. Plasma membrane density of Na, K-ATPase; immunoblot analysis and [^{3}H]ouabain binding. Immunoblot detection of α-subunit of Na, K-ATPase was performed by polyclonal Ab (Santa Cruz, sc-28800). **(A)** Typical immunoblot. **(B)** Average of 5 immunoblots. The significance of the difference between the immunoblot signal determined in fetuses 1 day before the birth (100 %) and signals determined at different ages (PD1, PD2, PD5, PD9, PD10, PD15, PD25, PD35, PD42, PD47, PD90) was analyzed by one-way ANOVA followed by Bonferroni's test using GraphPad*Prism 4*. Since PD5, the increase of Na,K-ATPase was highly significant (**, p<0.01). **(C)** [^{3}H]ouabain binding was measured as described in Methods. Data represent the average ± SEM of three experiments performed in triplicates. Significance of the difference between the binding at different age intervals was analyzed by one-way ANOVA followed by Bonferroni's test: fetuses D-1 versus PD15 (*, p<0.05), D-1 versus PD25 (**, p<0.01), D-1 versus PD90 (**, p<0.01), PD15 versus PD25 (*, p<0.05), PD15 versus PD90 (**, p<0.01), PD25 versus PD90 (NS, p>0.05).

P12 and PD15 and then decreased to the level in 18-day-old rats. The maximum AC activities were roughly 4-times higher than those at birth. In older rats, AC activities were decreased further so that the level in adult animals (PD90) was about the same as that at birth (PD1). These results had also shown that there was a marked difference between the development of AC enzyme activity and protein content of individual AC isoforms. The immunoblot analysis indicated no significant change of ACI, but a continuous increase of ACII, IV and VI from PD1 to PD18. Since this age, membrane density of ACI, II, IV and VI was unchanged until the adulthood.

When considering other effectors of $GABA_B$-R but AC, presynaptic inhibition of voltage-gated Ca^{2+} channels (Ca_v) by $GABA_B$-R agonists has to be primarily considered (Dunlap and Fishbach 1981, Robertson and Taylor 1986, Dolphin 1990, 1991, Santos *et al.* 1995). Presynaptic inhibition of Ca_v by $GABA_B$-R agonists was demonstrated at early stages of postnatal development in rat somatosensory cortex at PD7 (Fukuda *et al.* 1993) and in hippocampus at PD6 (DiScenna *et al.* 1994). Postsynaptic $GABA_B$-receptors were found to be functioning in the cerebral cortex of rats only at postnatal day 17, i.e. 10 days later than presynaptic ones (Fukuda *et al.* 1993). It may be therefore suggested that the significant efficacy of baclofen and SKF97541 when activating G-proteins in newborn rat brain cortex (Kagan *et al.* 2012) is physiologically related to presynaptic inhibition of Ca_v channels mediated by G_o family of G-proteins. In accordance with this suggestion, PM density of $G_o\alpha$ and Gβ proteins was high already at PD1 and PD2 (Fig. 2).

G-protein regulated, inwardly rectifying potassium channels (GIRKs) represent another plausible candidate for interpretation of our data besides AC and voltage-gated Ca^{2+} channels (Ca_v). Activation of the $GABA_B$-R increases membrane conductance for potassium and reduces neuronal excitability by direct activation of the GIRK channels *via* free Gβγ subunits released from trimeric G-protein complex (Misgeld *et al.* 1995, Watts *et al.* 1996). The $GABA_B$-receptor was shown to be primarily K^+-linked in the hippocampus (Gahwiler and Brown 1985). GIRK channel activation by $G_{i/o}$-coupled GPCR results in hyperpolarization of the neuron and inhibition of neuronal activity (Dascal 1997). In this way, similarly to the $GABA_B$-Ca_V currents, the $GABA_B$-GIRK currents are considered as inhibitory ones. In similarity with $GABA_B$-R expression patterns, the $GABA_B$-GIRK currents have been identified in many brain regions including hippocampus, thalamus and cerebellum (Gahwiler and Brown 1985, Watts *et al.* 1996).

Functional characterization of individual $GABA_B$-R subunits in heterologous expression systems revealed a remarkable property of $GABA_B$-receptors: $GABA_B$-R1/$GABA_B$-R2 subunits must be co-expressed to form a functional $GABA_B$-receptor dimmer; when expressed individually, the subunits failed to form physiologically normal receptors (Jones *et al.* 1998, Couve *et al.* 1998, Kaupmann *et al.* 1998, Kuner *et al.* 1999, Galvez *et al.* 2001, Padgett and Slesinger 2010). It has been also discovered that the $GABA_B$-R1 subunit contains an endoplasmic reticulum (ER) retention signal, which prevents forward trafficking of this receptor subunit (Margeta-Mitrovic *et al.* 2000). Dimerization of $GABA_B$-R1 with the $GABA_B$-R2 shields ER retention signal and permits surface expression of both $GABA_B$-R1 and $GABA_B$-R2. Yeast two-hybrid analysis revealed that the C-terminus of $GABA_B$-R1 and $GABA_B$-R2 was an important pre-requisite for heterodimerization of these subunits (White *et al.* 1998). CD spectroscopic analysis of a 30 amino acid sequence in C-termini of these proteins revealed a coiled-coil domain between the $GABA_B$-R1 and $GABA_B$-R2, which was required for the subunit-specific formation of the functional receptor dimmer (Kammerer *et al.* 1999). Interestingly, the C-terminus of $GABA_B$-R2 subunit also regulates lateral diffusion of the receptor in hippocampal neurons suggesting that it helps to control receptor expression levels at the plasma membrane (Pooler and McIlhinney 2007).

In this work, the postnatal development of $GABA_B$-R1a, $GABA_B$-R1b and $GABA_B$-R2 was studied in plasma membranes isolated from brain cortex of rats of different ages by Western blotting. PM density of $GABA_B$-R1a, $GABA_B$-R1b and $GABA_B$-R2 was determined in parallel with trimeric Gα- and Gβ-subunits. Antagonist [^{3}H]CGP54626 binding was measured in the same membrane samples. Subsequently, data collected on $GABA_B$-R were compared with the ontogenetic profile of prototypical plasma membrane marker Na, K-ATPase, which was used as an indicator of general brain development.

The detailed immunoblot analysis clearly showed that PM density of all $GABA_B$-R subunits was high at the birth (in fetuses D-1, PD1 and PD2) and subsequently it was largely decreased till PD15 (Fig. 1).

The $GABA_B$-R subunits in PM isolated from 15-days-old rats represented 55 % ($GABA_B$-R1a), 70 % ($GABA_B$-R1b) and 51 % ($GABA_B$-R2) of the level in newborn rats (100 %), respectively. The postnatal decrease of $GABA_B$-R1b subunit was relatively smaller when compared with $GABA_B$-R1a and $GABA_B$-R2. The decrease of $GABA_B$-R1a, $GABA_B$-R1b and $GABA_B$-R2 was accompanied by a decrease in the number of antagonist [^{3}H]CGP54626 binding sites, which was demonstrated in the presence of both calcium (2.5 mM $CaCl_2$) and magnesium (5 mM $MgCl_2$) ions. The ion-free buffer, which has been successfully used in μ-, δ- and κ-opioid receptor binding assays (Ko *et al.* 2003), was impropriate for radioligad binding assays of $GABA_B$-R.

In accordance with our data, the high levels of $GABA_B$-R1a in synaptic membranes isolated from brain cortex were also detected in the first postnatal days by Malitschek *et al.* (1998) and Fritschy *et al.* (1999) and these high levels of $GABA_B$-R1a were subsequently decreased till the adulthood. Both authors also described the different expression pattern for $GABA_B$-R1a and $GABA_B$-R1b isoforms. $GABA_B$-R1b was less abundant at birth than $GABA_B$-R1a, slightly increasing at postnatal days 10-14 and then decreasing till adulthood. Marked increase (3x) of PM density of Na, K-ATPase molecules was fully consistent with developmental study of Na, K-ATPase activity indicating manifold increase (5x) in membranes prepared by sucrose-density gradient centrifugation from the whole rat brain (Samson and Quinn 1967).

Our data thus indicated that the functional maturation of $GABA_B$-R signaling pathway is not finished at birth, in spite of the fact that these receptors are expressed in high amount (Fig. 1) and exhibit considerable ability to activate G-proteins with maximum of baclofen-stimulated [^{35}S]GTPγS binding at PD14-15 (Kagan *et al.* 2012). Increase of [^{35}S]GTPγS binding between the birth and PD14-15 was followed by a decrease in 18-day-old rats and further decrease till the adulthood (PD90). Accordingly, the peak value of [^{3}H]GABA binding was detected at PD14 in rat brain cortical slices by quantitative autoradiography and this high level of [^{3}H]GABA binding subsequently declined to the adult level (Turgeon and Albin 1994).

Contrarily, membrane density of all members of Gi/Go family of G-proteins was unchanged in the course of the whole postnatal development. The explanation why the "average" G-protein level in PM is unchanged in spite of the major change of G-protein function characterized by the peak level of baclofen- or SKF97541-stimulated [^{35}S]GTPγS binding at PD14-15 (Kagan *et al.* 2011), is unknown at present. It may be related to signaling *via* other effectors than AC (Ca_v and GIRKs); it may also reflect the fact that the data collected in mixture of all PM fragments do not reveal heterogeneities of protein composition in different PM compartments denominated as membrane domains/rafts (Moffett *et al.* 2000, Becher *et al.* 2001, 2004).

Conclusions

Our data indicate that the full complement of $GABA_B$-receptor protein molecules and cognate G-proteins exists in rat brain cortex already at birth. Functional maturation of $GABA_B$-R cascade in the course of the first two weeks of postnatal life was associated with a parallel decrease of plasma membrane density of $GABA_B$-R1a (55±15 %) and $GABA_B$-R2 (51±5 %) subunits; $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$, $G_{12}\alpha$ and Gβ, $GABA_B$-R1b proteins were unchanged. Decrease of $GABA_B$-R subunits proceeded together with the decrease of antagonist [^{3}H]CGP54626 binding measured in ion-free, 2.5 mM $CaCl_2$ or 5 mM $MgCl_2$. The age interval between PD1 and PD14-15 represents the critical period for structural as well as functional maturation of $GABA_B$-R signaling cascade in rat brain cortex plasma membranes.

Conflict of Interest

There is no conflict of interest.

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Abbreviations

Baclofen, β-p-chlorophenyl-GABA; Ca_v, voltage-dependent calcium channels; GABA, γ-aminobutyric acid; $GABA_B$-R, metabotropic receptor for GABA; GIRKs, inwardly rectifying potassium channels; GPCR, G-protein-coupled receptor; G-proteins, heterotrimeric guanine nucleotide-binding regulatory proteins; $G_s\alpha$, G-protein stimulating adenylyl cyclase activity; $G_i/G_o\alpha$, G-proteins inhibiting adenylyl cyclase activity in pertussis-toxin sensitive manner; $G_q/G_{11}\alpha$, G-proteins stimulating phoshoplipase C in pertussis-toxin independent manner; [^{35}S]GTPγS, guanosine-5′-[γ-^{35}S]

triphosphate; PD, postnatal day; P_i, inorganic phosphate; PMSF, phenylmethylsulfonyl fluoride; PTX, pertussis toxin; SKF 97541, aminopropyl (methyl) phosphinic acid; w.w., wet weight.

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Ontogenetic Development of $GABA_B$-Receptor Signaling Cascade in Plasma Membranes Isolated From Rat Brain Cortex; the Number of $GABA_B$-Receptors Is High Already Shortly After the Birth

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Summary

Our data indicate the significant intrinsic efficacy of $GABA_B$-receptors in rat brain cortex already at birth (PD1, PD2). Subsequently, baclofen- and SKF97541-stimulated G-protein activity, measured by agonist-stimulated, high-affinity [^{35}S]GTPγS binding assay, was increased; the highest level of both baclofen and SKF97541-stimulated [^{35}S]GTPγS binding was detected between PD10 and PD15. In older rats, baclofen- and SKF97541-stimulated [^{35}S]GTPγS binding was continuously decreased so, that the level in adult, 90-days old animals, was not different from that in newborn animals. The potency of G-protein response to baclofen (characterized by EC_{50} values) was also high at birth but unchanged by further postnatal development. An individual variance among different agonists was observed in this respect as the potency of SKF97541 response was decreased between the birth and adulthood. Accordingly, the highest plasma membrane density of $GABA_B$-R, determined by saturation binding assay with antagonist [^{3}H]CGP54626, was measured in 1-day old animals (2.27±0.08 pmol · mg^{-1}). The further development was reflected in a decrease of [^{3}H]CGP54626 binding as the B_{max} values of 1.38±0.05 and 0.93±0.04 pmol · mg^{-1} were determined in PM isolated from 13- and 90-days old rats, respectively.

Key words

Postnatal development • $GABA_B$-receptor • G-protein coupling/ activation • Baclofen • SKF97541

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Introduction

Historically, $GABA_B$ receptors were pharmacologically distinguished from $GABA_A$ receptors as bicuculline-insensitive GABA binding sites for which agonist is (-)-baclofen (Hill and Bowery 1981, Bowery *et al.* 1983, 1985, 1989, 1993, Hill *et al.* 1984, Hill 1985). After discovery of specific antagonists, $GABA_B$ receptors were defined as a class of bicuculline-insensitive GABA receptors for which (-)-baclofen is a specific agonist and phaclofen and 2-hydroxy-saclofen are specific antagonists (Kerr and Ong 1995). Later, more potent agonist SKF97541 was introduced and electrophysiologically characterized at pre- and postsynaptic binding sites on neurons in rat brain slices (Seabrook *et al.* 1990). $GABA_B$-receptors are not physically bound to an ionic channel and belong to the family of G-protein-coupled receptors, GPCRs (Bowery *et al.* 1983, 1985, 1989, 1993, Kerr and Ong 1995). Thus, the signal initiated by binding of GABA to these receptors is transmitted further downstream by trimeric G-proteins.

$GABA_B$-R agonist stimulation of G-protein activity (measured as high-affinity [^{35}S]GTPγS binding or [^{32}P-γ]GTPase assays) was important experimental evidence indicating that the effect of $GABA_B$-R agonists is mediated *via* trimeric G-proteins (Bowery *et al.* 1983, 1985, 1989, 1993). Close correlation between distribution of baclofen-stimulated GTPase activity and regional distribution of $GABA_B$-receptors in rat brain supported this idea. Furthermore, baclofen-stimulated GTPase *in vitro* was significantly inhibited by pertussis toxin (PTX) and specific antipeptide antisera oriented against $G_i\alpha$

subunit proteins (Sweeney and Dolphin 1992). Electrophysiological studies using specific antisera indicated that both PTX-sensitive $G_i\alpha$ and $G_o\alpha$ subunit proteins were activated by $GABA_B$-R agonists (Dolphin 1990, 1991).

With the aim to understand the maturation of $GABA_B$-R signaling cascade more fully, the early postnatal development of functional coupling between $GABA_B$-R and the cognate G-proteins was studied in plasma membranes isolated from rat brain cortex. The dose-response curves of the two potent agonists baclofen and SKF97541 were determined by high-affinity [^{35}S]GTPγS binding assay and compared in rats of different ages; the number of $GABA_B$-R was determined by saturation binding assay with specific antagonist [^{3}H]CGP54626.

Methods

Materials

$GABA_B$-receptor agonists baclofen (β-p-chlorophenyl-GABA), SKF97541 [3-aminopropyl (methyl) phosphinic acid] and antagonist [^{3}H]CGP54626 (41.5 Ci/mmol, cat. no. R1088) were purchased from Tocris. [^{35}S]GTPγS (1250 Ci/mmol) was from Perkin-Elmer (NEG030H). Complete protease inhibitor cocktail was from Roche Diagnostic (cat. no. 1697498). All other chemicals were of highest quality available.

Isolation of plasma membrane-enriched fraction from rat brain cortex

The experiments were approved by Animal Care and Use Committee of the Institute of Physiology, Academy of Sciences of the Czech Republic to be in agreement with Animal Protection Law of the Czech Republic as well as European Community Council directives 86/609/EEC.

Rat brain cortex was minced with razor blade on pre-cooled plate and diluted in STEM medium containing 250 mM sucrose, 20 mM Tris-HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.6, fresh 1 mM PMSF plus protease inhibitor cocktail. It was then homogenized mildly in loosely-fitting Teflon-glass homogenizer for 5 min (2 g w.w. per 10 ml) and centrifuged for 5 min at 3500 rpm. Resulting post-nuclear supernatant (PNS) was filtered through Nylon nets of decreasing size (330, 110 and 75 mesh, Nitex) and applied on top of Percoll in Beckman Ti70 tubes (30 ml of 27.4 % Percoll in STE medium). Centrifugation for 60 min at 30000 rpm (65000 x g) resulted in the separation of two clearly visible layers (Bourova *et al.* 2009). The upper layer represented plasma membrane fraction (PM); the lower layer contained mitochondria (MITO). The upper layer was removed, diluted 1:3 in STEM medium and centrifuged in Beckman Ti70 rotor for 90 min at 50000 rpm (175000 x g). Membrane sediment was removed from the compact, gel-like sediment of Percoll, re-homogenized by hand in a small volume of 50 mM Tris-HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.4 (TME medium), snap frozen in liquid nitrogen and stored at –80 °C.

Agonist-stimulated [^{35}S]GTPγS binding
Dose-response curves

Membranes prepared from 2-, 14- and 90-day-old rats of selected ages were incubated with (total binding, B_{total}) or without (basal binding, B_{basal}) increasing concentrations of $GABA_B$-R agonists baclofen and SKF97541 (10^{-10}-10^{-3} M) in final volume of 100 µl of reaction mix containing 20 mM HEPES, pH 7.4, 3 mM $MgCl_2$, 100 mM NaCl, 20 µM GDP, 0.2 mM ascorbate and [^{35}S]GTPγS (about 100-200,000 dpm per assay) for 30 min at 30 °C. The binding reaction was terminated by dilution with 3 ml of ice-cold 20 mM HEPES, pH 7.4, 3 mM $MgCl_2$ and filtration through Whatman GF/C filters on Brandel cell harvester. Radioactivity remaining on the filters was determined by liquid scintillation using Rotiszcint Eco Plus cocktail. Non-specific binding was determined in parallel assays containing 10 µM unlabelled GTPγS. Data were analyzed by GraphPad Prism 4 (GraphPad Software, San Diego, CA, USA) and B_{basal}, B_{max} and EC_{50}, values calculated according to the method of least-squares by fitting the data with sigmoidal dose-response curve.

"One-point assay"

With the aim to screen PM prepared from all age intervals under the same assay conditions, membranes (20 µg protein per assay) were incubated with ($B_{agonist}$) or without (B_{basal}) 1 mM baclofen or 100 µM SKF97541 in final volume of 100 µl of reaction mix containing 20 mM HEPES, pH 7.4, 3 mM $MgCl_2$, 20 µM GDP, 0.2 mM ascorbate and [^{35}S]GTPγS (1-2 nM) for 30 min at 30 °C. The binding reaction was discontinued by dilution with 3 ml of ice-cold 2 mM HEPES, pH 7.4, 0.15 mM $MgCl_2$ and immediate filtration through Whatman GF/C filters on Brandel cell harvester. Radioactivity remaining on the filters was determined by liquid scintillation using Rotiszcint Eco Plus cocktail. Non-specific GTPγS binding was determined in parallel assays containing

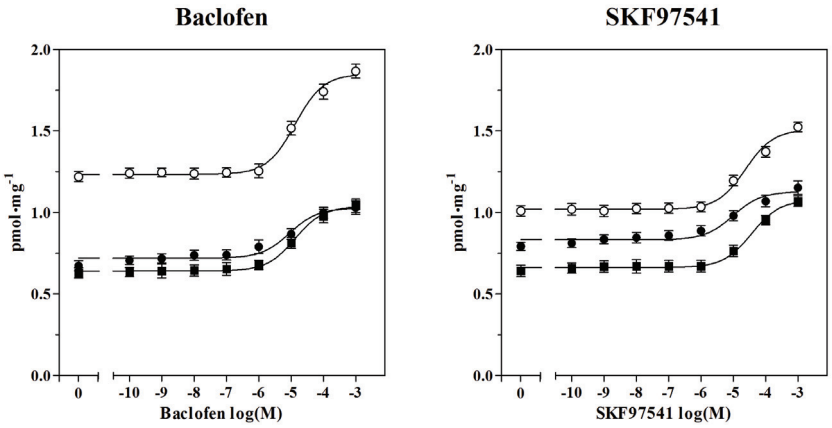

Fig. 1. Dose-response curves of baclofen and SKF97541-stimulated [^{35}S]GTPγS binding in PM isolated from 2-, 14- and 90-day-old rats. PM were isolated in parallel from brain cortex of 2 (●)-, 14 (○)- and 90 (■)-day-old rats and the high-affinity [^{35}S]GTPγS binding was measured in the presence of increasing concentrations of GABA$_B$-R agonists (-)-baclofen (left) or (-)-SKF97541 (right panel) in different age groups as described in Methods. The binding data were fitted by sigmoidal dose-response curves using GraphPad Prism 4 and represent the average of three experiments ± S.E.M. Differences between the averaged dose-response curves corresponding to PM prepared from 2-(PD2), 14-(PD14) and 90-days (PD90) old rats were statistically analyzed by one-way ANOVA followed by Bonferroni's *post-hoc* comparison test. **Left** (baclofen): PD2 (●) versus PD14 (○), p<0.0001, ****; PD14 (○) versus PD90 (■), p<0.0001, ****; PD2 (○) versus PD90 (■), NS, p>0.05. **Right** (SKF97541): PD2 (●) versus PD14 (○), p<0.05, *; PD14 (○) versus PD90 (■), p>0.05, NS; PD2 (○) versus PD90 (■), p<0.0001, ****.

10 μM GTPγS. The binding data were analyzed by GraphPad Prism 4 and represent an average ± S.E.M. of 3 experiments.

[^{3}H]CGP54626 binding; saturation binding study

Membranes (100 μg protein per assay) were incubated with increasing concentrations of GABA$_B$-antagonist [^{3}H]CGP54626 (0.06-36.8 nM) in final volume of 100 μl of binding mix containing 50 mM Tris-HCl (pH 7.4) plus 2.5 mM $CaCl_2$ for 60 min at 30 °C. The bound and free radioactivity was separated by filtration through Whatman GF/B filters in Brandel cell harvestor. Filters were washed 3x with 3 ml of ice-cold incubation buffer and radioactivity remaining and placed in 5 ml of scintillation cocktail (Rotiszint Eco Plus). The non-specific binding was determined in the presence of 1 mM GABA in binding mix. Data were analyzed by GraphPad Prism 4 and K_d and B_{max} values calculated according to the method of the least-squares by fitting the data with rectangular hyperbola.

Protein determination

The method of Lowry was used for determination of membrane protein. Bovine serum albumin (Sigma, Fraction V) was used as standard. Data were calculated by fitting the data with calibration curve as quadratic equation.

Results

The efficacy and potency of GABA$_B$-receptors in plasma membranes isolated from brain cortex of 2-, 14- and 90-days old rats was determined as baclofen- and SKF97541-stimulated, high-affinity [^{35}S]GTPγS binding in the presence of 20 μM GDP in reaction mix to suppress the low-affinity binding of this non-hydrolysable analog of GTP (Bourova *et al.* 2009). Dose-response curves were measured in 0.1 nM-1 mM range of baclofen or SKF97541 concentrations and the significance of differences among PM prepared from 2- (PD2), 14- (PD14) and 90-days (PD90) old rats was analyzed by one-way ANOVA followed by Bonferroni's *post-hoc* comparison test using GraphPad Prism 4 software (Fig. 1).

Both agonists exhibited the significant ability to increase the basal level of binding measured in the absence of agonist (B_{basal}) already in 2-day-old animals (PD2). This ability was further increased in the course of the first two weeks of postnatal life (compare PD2 and PD14, Fig. 1), but virtually unchanged when viewed over the whole period of brain development as the averaged dose-response curve corresponding to PD2 was not significantly different from that measured in adult rats (PD90). The same applied to the net-increment of agonist stimulation (Δ) and % stimulation of the basal level of [^{35}S]GTPγS binding (Table 1). The highest baclofen- and SKF97541-stimulated [^{35}S]GTPγS binding was measured between postnatal day 10 and 15 and than it steeply and continuously decreased towards the adult level (Fig. 2).

The potency (EC_{50} estimates) of G-protein response to baclofen was not significantly different in membranes prepared from 2-, 14- and 90-day-old rats, but decreased from the birth to adulthood in the case of SKF97541 (Table 1). This finding is compatible with electrophysiological studies of brain maturation indicating an altered sensitivity to different GABA$_B$-R agonists or antagonists and similar trends of postnatal changes of GABA$_B$-R efficacy (Bernasconi *et al.* 1992, Hosford *et al.* 1992, Marescaux *et al*. 1992, Lin *et al.* 1993, Kubová *et al*. 1996, Mareš 2008).

Table 1. Maximum response (B_{max}) and affinity (EC_{50}) of baclofen- and SKF97541-stimulated [^{35}S]GTPγS binding in PM isolated from 2-, 14- and 90-days old rats**.**

A(-)-baclofen	**2-days**	**14-days**	**90-days**
B_{basal}	0.72 ± 0.01	1.23 ± 0.02	0.64 ± 0.01
B_{max}	1.03 ± 0.02	1.85 ± 0.03	1.04 ± 0.01
$\Delta = B_{max} - B_{basal}$	0.31	0.62	0.40
$100 \times B_{max} / B_{basal}$	152 %	152 %	166 %
EC_{50} (μM)	9.00 (4.46-18.15)	13.34 (7.81-22.88)	13.26 (9.96-17.65)
B(-)-SKF97541			
B_{basal}	0.83 ± 0.01	1.02 ± 0.01	0.66 ± 0.01
B_{max}	1.13 ± 0.02	1.51 ± 0.02	1.08 ± 0.02
$\Delta = B_{max} - B_{basal}$	0.30	0.49	0.42
$100 \times B_{max} / B_{basal}$	142 %	152 %	168 %
EC_{50} (μM)	9.79 (5.30-18.10)	23.45 (14.34-38.35)	36.51 (21.87-60.95)

B_{basal} (pmol · mg^{-1}), binding in the absence of agonist; B_{max} (pmol · mg^{-1}), binding at saturating agonist concentration; $\Delta = B_{max} - B_{basal}$, net-increment of agonist stimulation; $100 \times B_{max} / B_{basal}$, % stimulation of the basal level by agonist. EC_{50} (μM), agonist concentration inducing half-maximum stimulation (95 % confidence limit). B_{max}, B_{basal} and EC_{50} values were determined by analysis of the sigmoidal dose-response curves of baclofen- (**A**) and SKF97541- (**B**) stimulated [^{35}S]GTPγS binding presented in Figure 1 by GraphPad Prism 4 and represent the average of three experiments ± S.E.M. The significance of difference between B_{basal}, B_{max} and EC_{50} values in PM prepared from 2 (PD2)-, 14 (PD14)- and 90 (PD90)-days-old rats was determined by one-way ANOVA followed by Bonferroni's *post-hoc* comparison test. **A (baclofen)**. B_{basal} (PD2 versus PD14, p<0.0001, ****; PD14 versus PD90, p<0.0001, ****; PD2 versus PD90, p>0.05, not significant. B_{max} (PD2 versus PD14, p<0.0001, ****; PD14 versus PD90, p<0.0001, ****; PD2 versus PD90, p>0.05, not significant. EC_{50} (PD2 versus PD14, p>0.05, NS; PD14 versus PD90, p>0.05, NS; PD2 versus PD90, p>0.05, NS. **B (SKF97541)**. B_{basal} (PD2 versus PD14, p<0.001, ***; PD14 versus PD90, p<0.0001, ****; PD2 versus PD90, p<0.001, ***. B_{max} (PD2 versus PD14, p<0.001, ***; PD14 versus PD90, p<0.0001, ****; PD2 versus PD90, p>0.05, NS. EC_{50} (PD2 versus PD14, p>0.05, NS; PD14 versus PD90, p>0.05, NS; PD2 versus PD90, p<0.01, **).

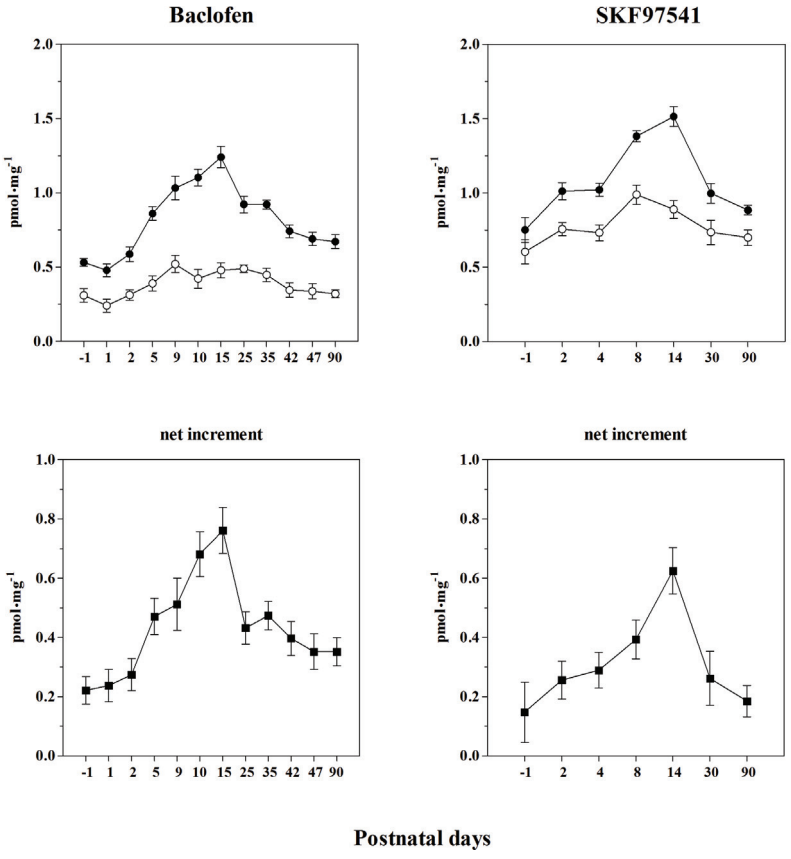

Fig. 2. Baclofen- and SKF97541-stimulated [^{35}S]GTPγS binding; one-point assay. **Upper panels.** PM were isolated from fetuses (-1) and from 1-, 2-, 4-, 5-, 9-, 10-, 14-, 15-, 25-, 30-, 35-, 42-, 47- and 90-days old rats, frozen in liquid nitrogen and used only once. Baclofen- and SKF97541-stimulated [^{35}S]GTPγS binding was determined in different age groups as described in Methods in the presence (●, $B_{agonist}$) or absence (○, B_{basal}) of 1 mM baclofen (**left panel**) or 100 μM SKF97541 (**right panel**). The significance of difference between the two sets of data ($B_{agonist}$ versus B_{basal}) at all age intervals was analyzed by Student s t-test using GraphPad Prism 4: baclofen, p<0.0001, ****; SKF97541, p<0.0022, **. The same type of comparison ($B_{agonist}$ versus B_{basal}) was also performed at individual age intervals: **baclofen** [day -1 (*), PD2 (**), PD5(****), PD9(***), PD10(****), PD15(**), PD25(***), PD35(****), PD42(***), PD47(**), PD90(***)]. **SKF97541** [day -1 (NS), PD2 (NS), PD4(*), PD8(*), PD14(**), PD30(NS), PD90(NS)]. **Lower panels.** Difference between agonist-stimulated ($B_{agonist}$) and basal (B_{basal}) level of binding was expressed as the net-increment of agonist stimulation $\Delta = B_{agonist} - B_{basal}$. Data represent the average ± S.E.M. of three experiments.

The existence of the maximum of GABA$_B$-R agonist-stimulated [^{35}S]GTPγS binding between PD10 and PD15 (Fig. 2) has to be considered together with our previous data indicating the striking maximum of basal, manganese-, fluoride- and forskoline-stimulated AC activity in 12-day-old rats (Ihnatovych *et al.* 2002; see discussion for further details). Thus, the increase of baclofen- and SKF97541-stimulated G-protein activity during the first two weeks of postnatal life, its maximum in 10-15-day-old rats and the subsequent decrease is related in time to the maximum and subsequent decrease of AC activity.

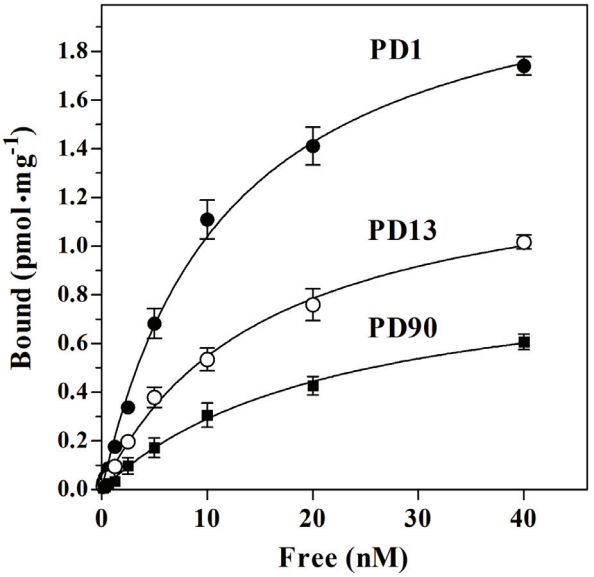

Fig. 3. Saturation of [^{3}H]CGP54626 binding sites in PM isolated from 1-, 13- and 90-day-old rats. Maximum number (B_{max}) and affinity (K_d) of specific [^{3}H]CGP54626 binding sites was determined in PM isolated in parallel from brain cortex of 1 (●)-, 13 (○)- and 90 (■)-days old rats by direct saturation binding assay as described in Methods. B_{max} (maximum binding capacity) and K_d (dissociation constant) of specific [^{3}H]CGP54626 binding sites were calculated by fitting the data by 1-site hyperbola by GraphPad Prism 4 and represent the average ± S.E.M. of 3 experiments. One-way ANOVA followed by Bonferroni's *post-hoc* comparison test was used for statistical analysis of the difference between B_{max} or K_d values in PM prepared from rats of different ages. B_{max} : PD1 versus PD13, $p<0.01$, **; PD13 versus PD90, $p<0.001$, ***; PD13 versus PD90, $p<0.05$, *. K_d: PD1 versus PD13, $p>0.05$, NS; PD13 versus PD90, $p<0.01$, **; PD13 versus PD90, $p<0.05$, *.

Plasma membrane density of GABA$_B$-R at different age intervals was measured by saturation binding study with specific antagonist [^{3}H]CGP54626. Data presented in Figure 3 indicated clearly that the highest PM density of GABA$_B$-R, estimated as the maximum binding capacity (B_{max}) of [^{3}H]CGP54626 binding sites, was detected in PM samples prepared from 1-day-old rats (2.27±0.08 pmol · mg^{-1}). The further development was reflected in a marked decrease of [^{3}H]CGP54626 binding as the B_{max} values of 1.38±0.05 and 0.93±0.04 pmol · mg^{-1} were determined in PM isolated from 13- and 90-days old rats, respectively. The dissociation constant (K_d) was increased from 11.8 nM (PD1) to 15.3 nM (PD13) and 22.1 nM (PD90), indicating the decreased affinity and qualitative change of GABA$_B$-R binding sites towards this antagonist in the course of rat brain cortex maturation.

Discussion

Data presented in this work (Figs 1 and 2) indicate a noticeable extent of compatibility of our present results with experimental data obtained by functional assays of adenylyl cyclase (AC) activity in the presence or absence of GABA$_B$-R agonists, which were previously reported by us (Ihnatovych *et al*. 2002). Maximum activation of baclofen- and SKF97541-stimulated [^{35}S]GTPγS binding coincided with the developmental profile of AC activity. The maximum of agonist-stimulated G-protein activity (Fig. 2) as well as basal, fluoride-, GTP- and forskoline-stimulated AC (Ihnatovych *et al*. 2002) was found in the same period of brain development, between PD10 and PD15. However, marked difference between the two sets of data was noticed as well. Maturation of functional coupling of GABA$_B$-R with G-proteins preceded maturation of AC system because AC activity was low at birth while both baclofen and SKF97541 exhibited significant efficacy already at PD2 (Fig. 1).

Plasma membrane density of GABA$_B$-R determined by saturation binding study with specific antagonist [^{3}H]CGP54626 was also high, virtually the highest, when compared with 13- and 90-day-old rats (Fig. 3). It may be therefore suggested that the physiological significance of the high receptor number and significant efficacy of coupling of GABA$_B$-R with G-proteins shortly after the birth (at PD1 and PD2) is related to some other effectors but AC-cAMP system. Ionic channels and electrophysiological effects of GABA$_B$-R stimulation mediated by $G_o\alpha$ and Gβ subunits represent the obvious choice (Newberry *et al.* 1984a,b, Gähwiler *et al.* 1985, Bormann 1988, Bowery *et al.* 1989).

Comparison of EC_{50} values of agonist-stimulated [^{35}S]GTPγS binding indicated no significant difference in PM isolated from 2-, 14- and 90-day-old rats for

baclofen, but EC_{50} values of SKF97541 were clearly increased from the birth to adulthood (Table 1). This result suggests a developmental decrease in affinity of $GABA_B$-R response for the latter agonist and it is compatible with electrophysiological studies of brain function indicating the differences in sensitivity of $GABA_B$-R to individual agonists (Bernasconi *et al.* 1992, Hosford *et al.* 1992, Lin *et al*. 1992, Marescaux *et al.* 1992). Furthermore, epileptological studies of brain function indicated that anticonvulsant action of baclofen was unchanged during postnatal period (Kubová *et al.* 1996) but the detailed ontogenetic profile of anticonvulsant action of SKF97541 was not identical with that of baclofen (Mareš 2008). The time-span between PD12 and PD18 represented the most critical period in this respect.

Conclusions

Our data indicate significant intrinsic efficacy of $GABA_B$-receptors in rat brain cortex already at the birth (PD1, PD2). Subsequently, baclofen and SKF97541-stimulated G-protein activity, measured by high-affinity [^{35}S]GTPγS binding assay, was increased; the highest level of agonist-stimulated [^{35}S]GTPγS binding was detected between PD10 and PD15. In older rats, both baclofen- and SKF97541-stimulated [^{35}S]GTPγS binding was continuously decreased so, that level in adult, 90-days old animals was not different from that in newborn animals. This profile of ontogenetic development of $GABA_B$-R was similar to the maturation of AC activity (Ihnatovych *et al.* 2002).

The potency of G-protein response to baclofen (characterized by EC_{50} values) was high at birth and unchanged by further development. An individual variance among different agonists was observed in this respect as the potency of SKF97541 response was decreased when compared in 2- and 90-days old rats. Surprisingly, the plasma membrane density of $GABA_B$-R, determined by saturation binding assay as maximum binding capacity (B_{max}) for specific antagonist [^{3}H]CGP54626, was highest in 1-day old and then decreased in 13- and 90-days old animals.

Conflict of Interest

There is no conflict of interest.

Acknowledgements

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Abbreviations

AC, adenylyl cyclase; cAMP, cyclic 3´,5´-[α-^{3}H] adenosine monophosphate, baclofen, β-p-chlorophenyl-GABA; GABA, γ-aminobutyric acid, $GABA_B$-R, metabotropic receptor for GABA, GPCR, G-protein-coupled receptor; G-proteins, heterotrimeric guanine nucleotide-binding regulatory proteins; NS, not significant; PD, postnatal day; PBS, phosphate-buffered saline; PM, plasma membrane, PMSF, phenylmethylsulfonyl fluoride; PTX, pertussis toxin; SKF97541, aminopropyl (methyl) phosphinic acid; w.w., wet weight, TCA, trichloroacetic acid.

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Morphine, opioid-receptor signaling cascades and plasma membrane structure in rat cerebral cortex and model cell lines

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Summary

Large number of extracellular signals is received by specific plasma membrane receptors which, upon activation, transduce information into the target cell interior *via* trimeric G-proteins (G-protein-coupled receptors, GPCR) and induce activation or inhibition of adenylylcyclase enzyme activity (AC). Receptors for opiopid drugs such as morphine (μ-OR, δ-OR and κ-OR) belong to rhodopsin family of GPCR. Our recent results indicated a specific up-regulation of adenylylcyclases I (8x) and II (2.5x) in plasma membranes (PM) isolated from rat brain cortex exposed to increasing doses of morphine (10-50 mg/kg) for 10 days. Increase of ACI and II represented the specific effect as the amount of ACIII-ACIX, of prototypical PM marker Na, K-ATPase and of trimeric G protein α and β subunits was unchanged. The up-regulation of ACI and ACII faded away after 20 days since the last dose of morphine.

Proteomic analysis of these PM indicated that the brain cortex of morphine-treated animals can not be regarded as being adapted to this drug as significant up-regulation of

proteins functionally related to oxidative stress and alternation of brain energy metabolism occurred. The number of δ-OR was increased 2x and their sensitivity to monovalent cations altered. Characterization of δ-OR-G-protein coupling in model HEK293 cell line indicated high ability of lithium to support potency /affinity of δ-OR response to agonist stimulation.

Our studies of plasma membrane structure and function in context with desensitization of GPCR action were extended by data indicating participation of cholesterol-enriched membrane domains /rafts in agonist-specific internalization of δ-OR. In HEK293 cells stably expressing δ-OR-$Gi_1\alpha$ fusion protein, depletion of PM cholesterol was associated with decrease (by two-orders of magnitude) in affinity /potency of G-protein-response to agonist stimulation; maximum response was unchanged. Hydrophobic interior of isolated PM became more "fluid", chaotically organized and more accessible to water molecules. Validity of this conclusion was supported by analysis of an immediate PM environment of cholesterol molecules in living δ-OR-$Gi_1\alpha$-HEK293 cells by fluorescent probes 22- and 25-NBD-cholesterol. Alternation of plasma membrane structure by decrease of cholesterol made the membrane more hydrated.

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key-words: GPCR, morphine, μ-, δ- and κ-opioid receptors, rat brain cortex, adenylyl cyclase I and II, proteomic analysis, monovalent cations, agonist-induced internalization, plasma membrane structure, cholesterol, membrane domains, fluorescent probes.

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Introduction

Hormones, neurotransmitters and growth factors, bind to the cell surface membrane receptors, which may be divided into the three main families: i) coupled with guanine nucleotide-binding regulatory proteins (GPCR), ii) ionic channels, and iii) tyrosine-kinases. Binding of hormones or neurotransmitters to the stereo-specific site of receptor molecules, located at extracellular side of plasma membrane, represents the first step in complicated sequence of molecular events transmitting the signal into the cell interior and initiating the ultimate physiological response. In G-protein-mediated cascades, ligand binding induces conformational change of receptor molecule, which, in the next step, induces dissociation of trimeric G protein-complex (non-active) into the free, active Gα and Gβγ subunits. Subsequently, both Gα and Gβγ subunits activate variety of enzyme activities and/or ionic channels which regulate intracellular concentrations of secondary messengers such as cAMP, cGMP, diacylglycerol, IP_3, DAG, arachidonic acid, sodium, potassium or calcium cations (Svoboda et al., 2004; Drastichova et al., 2008).

Receptors for opiopid drugs, μ-OR, δ-OR and κ-OR were classified as members of rhodopsin family of GPCR. All these receptors are known to inhibit adenylyl cyclase activity in pertussis-toxin-dependent manner by activation of Gi/Go class of trimeric G proteins. These proteins (Gi1, Gi2, Gi3, Go1, Go2) are present in brain in large quantities and inhibit adenylyl cyclase activity or regulate ionic channels in pertussis-toxin-dependent manner.

Morphine binds to all three types of OR (μ-, and κ-OR) and represents one of the most effective painkillers. Repeated exposure of experimental animals to morphine results in *tolerance* to this drug, development of physical *dependence* and a *chronic relapsing disorder – drug addiction* [Contet et al., 2004]. Physical dependence contributes to a drug seeking behavior and the continuous drug use with the aim to prevent the onset of unpleasant *withdrawal* symptoms [Preston et al., 1991]. Morphine *withdrawal* generates a set of

symptoms like retches, vomiting, blood pressure increase, insomnia, intestines dysfunctions, body shaking and teeth chatter.

Drug addiction to morphine is characterized by a complex etiology including changes in psychology of experimental animals as well as physiology of their brain function. These changes proceed mainly in brain stem and hippocampus [Connor and Christie, 1999; Law et al., 2000; Chen et al., 2007; Law and Loh, 2000], however, some of the long-term behavioral consequences of repeated morphine exposure were related to reorganized patterns of synaptic connectivity in forebrain [Robinson et al., 1999]. Morphine-induced changes of brain function were also associated with alternations of neurotransmission, specific signaling cascades, energy metabolism and stability of protein molecules [Miller et al., 1972; Kim et al., 2005; Li et al., 2006; Li et al., 2009].

Hyper-sensitization or super-activation of adenyl cyclase (AC) activity by prolonged exposure of cultured cells or mammalian organism to morphine has been demonstrated in previous studies of mechanism of action of this drug [Contet et al. 2004; Preston 1991; Connor and Christie, 1999; Law et al., 2000; Law et al., 2004] and considered as biochemical basis for development of opiate *tolerance* and *dependence*.

Our previous work on isolated Percoll membranes (PM) prepared from brain cortex of rats exposed to morphine for 10 days (10-50 mg/kg) indicated a desensitization of G-protein response to μ-OR (DAMGO) and δ-OR (DADLE) stimulation [Bourova et al., 2010] and specific increase of ACI (8x) and ACII (2.5x) isoforms [Ujcikova et al., 2011]. The κ-OR (U-23554)-stimulated [^{35}S] GTPγS binding and expression level of ACIII-X in PM was unchanged. Behavioral tests of morphine-treated animals indicated that these animals were fully drug-dependent (*opiate abstinence syndrome*) and developed tolerance to subsequent drug addition (a*nalgesic tolerance* detected by hot-plate and hind paw withdrawal tests). The

increase of ACI and ACII was interpreted as a specific compensatory response to prolonged stimulation of brain cortex OR by morphine.

Proteomic analysis of membrane proteins in rat brain cortex; *changes induced by the long-term exposure to increasing doses to morphine*

The aim of the next step of our work was the description of an over-all change of membrane protein composition and recognition of proteins exhibiting the largest morphine-induced change. This was performed by proteomic analysis of post-nuclear supernatant (PNS) and plasma-membrane-enriched fraction isolated in Percoll gradient (PM). PNS was analyzed because it contains proteins of mitochondrial, endoplasmic reticulum, plasma membrane and cytoplasmic origin. Rats were adapted to morphine for 10 days [10 mg/kg (day 1 and 2), 15 mg/kg (day 3 and 4), 20 mg/kg (day 4 and 5), 30 mg/kg (day 6 and 7), 40 mg/kg (day 9) and 50 mg/kg (day 10)] and sacrificed 24 hours after the last dose (group +M10). Control animals were sacrificed in parallel with morphine-treated (group −M10). Post-nuclear supernatant fraction (PNS) was prepared from brain cortex of both groups and resolved by 2D-ELFO. The gels were stained by Coomassie brilliant blue (CBB) and the altered proteins detected by PDQuest software analysis.

The 10 up (↑)- or down (↓)-regulated proteins exhibiting the ***largest morphine-induced change*** were selected, excised manually from 2D-gel and identified by MALDI-TOF MS/MS. The identified proteins were: 1-(gi|148747414, Guanine deaminase), ↑2.5x; 2-(gi|17105370, Vacuolar-type proton ATP subunit B, brain isoform), ↑2.6x; 3-(gi|1352384, Protein disulfide-isomerase A3), ↑3.4x; 4-(gi|40254595, Dihydropyrimidinase-related protein 2), ↑3.6x; 5-(gi|149054470, N-ethylmaleimide sensitive fusion protein, isoform CRAa), ↑2.0x; 6-(gi|42476181, Malate dehydrogenase, mitochondrial precursor), ↑1.4x; 7-(gi|62653546, Glyceraldehyde-3-phosphate dehydrogenase), ↑1.6x; 8-(gi|202837, Aldolase A), ↑1.3x; 9-(gi|31542401, Creatine kinase B-type), ↓0.86x; 10-(gi|40538860, Aconitate

hydratase, mitochondrial precursor), ↑1.3x. Thus, the 10 most highly altered proteins in PNS were of cytoplasmic (1, 4, 5, 7, 9), cell membrane (2), endoplasmic reticulum (3) and mitochondrial (6, 8, 10) origin and the 9 of them were significantly increased by morphine, 1.3-3.6x. Correlation with functional properties of these proteins indicated up-regulation of proteins related to guanine degradation (1), vacuolar acidification (2), apoptotic cell death (3), oxidative stress (4, 6, 7, 10), membrane traffic (5) and glycolysis (8). The role in apoptosis has been also described for Glyceraldehyde-3-phosphate dehydrogenase (7), already mentioned as major target protein in oxidative stress [Hwang et al, 2009]. All together, the spectrum of altered proteins suggests a major change of energy metabolism of brain cortex tissue when exposed to increasing doses of morphine. Judged from functional point of view, the most significant change was up-regulation of proteins related to oxidative stress (4, 6, 7, 10) and apoptotic cell death.

We could therefore conclude that the brain cortex of rats exposed to increasing doses of morphine (10-50 mg/kg) for 10 days can not be regarded as being adapted to this drug. Significant up-regulation of proteins functionally related to oxidative stress and apoptosis indicates the state of severe "discomfort" of brain cells or even damage.

Identification of an *active*, minority pool of trimeric Gβ subunits responding to chronic morphine in rat brain cortex; *proteomic analysis of Percoll-purified membranes*

In Percoll-purified membranes (PM), the altered proteins were of plasma membrane [BASP1, Brain acid soluble protein, down regulated (↓) 2.1x; GBB, Guanine nucleotide-binding protein subunit beta-1, (↓) 2.0x], myelin membrane [MBP, Myelin basic protein S, (↓) 2.5x], cytoplasmic [KCRB, Creatine kinase B-type (EC 2.7.3.2), (↓) 2.6x; AINX, alpha-internexin, up-regulated (↑) 5.2x; DPYL2, Dihydropyrimidinase-related protein 2, (↑) 4.9x; SIRT2, NAD-dependent deacetylase sirtuin-2, (↑) 2.5x; SYUA, Alpha-synuclein, (↑) 2.0x; PRDX2, Peroxiredoxin-2, (↑) 2.2x; TERA, Transitional endoplasmic reticulum ATPase, (↑)

2.1x; UCHL1, Ubiquitin carboxyl-terminal hydrolase L1, (↑) 2.7x; COR1A, Coronin-1A, down 5.4x, SEP11, Septin-11, (↑) 2.2x; RL12, 60S ribosomal protein L12, (↑) 2.7x] and mitochondrial [DHE3, Glutamate dehydrogenase 1, (↑) 2.7x; SCOT1, Succinyl-CoA:3-ketoacid-coenzyme A, (↑) 2.2x; AATM, Aspartate aminotransferase**,** down 2.2x; PHB, prohibitin, (↑) 2.2x] origin.

The only member of GPCR-initiated signaling cascades identified by LC-MS/MS in PM was trimeric Gβ subunit (**2**-GBB) which was decreased 2x in samples of morphine-adapted rats. Similarly, proteomic analysis of protein alternations induced by long-term stimulation of HEK cells stably expressing TRH-receptor and G11α protein by TRH, indicated the change of 42 proteins, but not even one of these proteins represented the plasma membrane protein functionally related to G-protein mediated signaling cascades [Drastichova et al., 2010].

The immunoblot analysis of the same PM resolved by 2D-ELFO indicated that the "active" pool of Gβ subunits effected by morphine, which was decreased 2x, represented just a minor fraction of the total signal of Gβ subunits in 2D-gels (**Fig. 1**). The total signal of Gβ was decreased 1.2x only and dominant /major part of the total signal was unchanged. Accordingly, the immunoblot analysis of Gβ after resolution by 1D-SDS-PAGE in 10% w/v acrylamide/0.26% w/v bis-acrylamide or 4-12% (InVitroGene) gradient gels indicated no change of this protein. *We could therefore conclude that proteomic analysis represents a valuable tool for identification of membrane proteins. However, analysis of low-abundance proteins of OR-initiated signaling cascades in plasma membranes has to be accompanied by specific immublot analysis. Identification of an "active", minority pool of Gβ subunits down-regulated by morphine represents an original finding which has not been described in up-to-date literature dealing with drug addiction and morphine effect on mammalian brain.*

The effect of lithium and other monovalent ions on ligand binding and efficiency of δ-opioid receptor-G-protein coupling

Lithium is still one of the most effective therapies for depression. Comparison of the effect of lithium, sodium and potassium on δ-opioid receptor was studied in HEK293 cells stably expressing PTX-insensitive δ-OR-$G_i1\alpha$ (Cys^{351}-Ile^{351}) fusion protein. δ-OR-$G_i1\alpha$ (C^{351}-I^{351}) cells represent useful experimental tool as the covalent bond between δ-OR and $G_i1\alpha$ (C^{351}-I^{351}) provides the permanent and fixed, 1:1 stoichiometry and C^{351}-I^{351} mutation provides resistance to PTX together with extraordinary high efficacy of coupling between δ-OR and $G_i1\alpha$ (C^{351}-I^{351}) protein (Bourova et al. 2003; Brejchova et al. 2011).

Agonist [^{3}H]DADLE binding was decreased with the order: $Na^+ \gg Li^+ > K^+ > (+)$ NMDG. When plotted as a function of increasing NaCl concentrations, binding was best-fitted with a two phase exponential decay considering the two Na^+-responsive sites (r^2 = 0.99). High-affinity Na^+-sites were characterized by K_d = 7.9 mM and represented 25% of the basal level determined in the absence of ions. Remaining 75% represented the low-affinity sites (K_d = 463 mM). Inhibition of [^{3}H]DADLE binding by lithium, potassium and (+)-NMDG proceeded in low-affinity manner only. Preferential sensitivity of δ-OR-$G_i1\alpha$ to sodium was thus clearly manifested.

Surprisingly, the *affinity/potency* of DADLE-stimulated [^{35}S]GTPγS binding, quantitatively characterized by comparison of dose-response curves in different ion media (EC_{50} values), was increased in the reversed order: $Na^+ < K^+ < Li^+$. This result was demonstrated in PTX-treated as well as PTX-untreated cells (**Table 1**). Therefore, this finding is not restricted to $G_i1\alpha$ present in fusion protein, but is also valid for stimulation of endogenous G-proteins of Gi/Go family.

This surprising but fully reproducible result may be considered in connection with clinical usage of lithium in treatment of manic depression. In electrically active cells, Li^+

enters the intracellular compartment via “fast“ sodium channel (Richelson, 1977) and also via oubabain-sensitive K^+-influx catalyzed by Na,K-ATPase. However, the efflux of Li^+ via Na,K-ATPase is limited because ATP+Mg+Na-dependent phosphorylation proceeding at inner side of plasma membrane and out-ward oriented efflux of Na^+ cations via Na+-pump is strictly specific for sodium. Thus, if available in extracellular space, the intracellular Li^+ concentration will be slowly increased. It is reasonable to assume that such conditions may arise in neuronal or glial cells of depressive patients as the effective range of plasma concentrations of Li^+ used clinically is 0.6-1.0 mM. The 2 mM LiCl is regarded as toxic. In comparison with our results, this is exactly the concentration range in which the first significant inhibition of the basal level of [^{35}S]GTPγS binding was detected. The first significant decrease of the basal level of [^{35}S]GTPγS binding measured in the absence of cations was noticed at 1-2 mM NaCl, KCl and LiCl; the 50% inhibition was reached at 62 mM NaCl, 88 mM LiCl and 92 mM KCl, respectively (Vosahlikova and Svoboda, 2011). Thus, in treatment of acute depression, competitive effect of Li^+ on inverse agonist-like effect of Na^+ on δ-OR and, in parallel, on G_i/G_o class of G-proteins, might be considered as one plausible possibility for mechanism of action of lithium, i.e., besides numerous other effects on overall cell metabolism (Young, 2009).

The role of cholesterol, cholesterol depletion and membrane domains/rafts in structural organization of plasma membrane and trans-membrane signaling through G-protein-coupled receptors

Cholesterol constitutes a major component of mammalian plasma (cell) membrane. Its correct distribution among plasma membrane and intracellular membrane compartments is essential for the homeostasis of mammalian cells and intracellular membrane traffic plays a major role in the correct disposition of internalized cholesterol and in the regulation of cholesterol efflux (Scheidt et al., 2003; Maxfield and Wustner, 2002). Furthermore, lateral

and trans-bilayer organization of cholesterol molecules in the plasma membrane determines plasma membrane structure and dynamics. However, neither its intracellular pathways of trafficking nor its precise lateral organization in cholesterol-enriched microdomains such as membrane rafts and *caveolae* is fully understood. The same applies to the trans-bilayer distribution between the two leaflets of biological membranes (Simons and Ikonen, 1997; Brown and London, 1998; Anderson and Jacobson, 2002).

Cholesterol- and sphingolipid-enriched membrane domains, characterized by high content of cholesterol, saturated phospholipids, glycolipids and sphingomyelin, have been described as lipid platforms capable to harbor and confine trimeric G-proteins in high amounts (Simons and Ikonen, 1997; Brown and London, 1998; Anderson, 1998; Anderson and Jacobson, 2002; Moffett et al., 2000; Oh and Schnitzer, 2001; Pike, 2004; Quinton et al., 2005). Considering the function of trimeric G-proteins in membrane domains containing caveolin, heterologous desensitization of GPCR signaling was described as specific binding of G-proteins to caveolin (Murthy and Maclouf, 2000).

These structures were also reported to play an important role in both positive and negative regulation of trans-membrane signaling through G-protein-coupled receptors (Klein et al., 1995; Feron et al., 1997; De Weerd and Leeb-Lundberg, 1997; Gimpl et al., 1995; Gimpl and Farenholz, 2002; Schwencke et al., 1999; De Luca et al., 2000; Dessy et al., 2000; Lasley et al., 2000; Igarashi and Michel, 2000; Ostrom et al., 2000, 2001; Rybin et al., 2000, 2003; Ushio-Fukai et al., 2001; Sabourin et al., 2002; Ostrom and Insel, 2004; Pucadyil and Chattopadhyay, 2004, 2007; Monastyrskaya et al., 2005; Savi et al., 2006; Xu et al., 2006; Allen et al., 2007; Ostasov et al., 2007, 2008; Chini and Parenti, 2009). More specifically, the functional significance of OR presence in membrane domains is far from being understood as cholesterol reduction by methyl-β-cyclodextrin attenuated δ-OR-mediated signaling in neuronal cells but enhanced it in non-neuronal cells (Huang at al., 2007).

In HEK293 cells stably expressing δ-OR-$Gi_1α$ fusion protein, depletion of PM cholesterol was associated with decrease (by two-orders of magnitude) in affinity /potency of G-protein-response to agonist stimulation. The maximum response was unchanged (Brejchova et al., 2011). Hydrophobic interior of isolated PM became more "fluid", chaotically organized and more accessible to water molecules. Analysis of PM environment of fluorescent derivatives of cholesterol (22- and 25-NBD-cholesterol) in living δ-OR-$Gi_1α$-HEK293 cells confirmed these results as it indicated that alternation of plasma membrane structure by decrease of cholesterol makes the membrane more hydrated (Ostasov et al., 2013). Our data also indicated that small perturbation of PM structure by low, non-ionic detergent concentrations increased GPCR-G-protein coupling, while the high concentrations were strictly inhibitory (Sykora at al., 2009). The close-to-zero level of basal and agonist-stimulated G-protein activity is the typical feature of detergent-resistant membrane domains (DRMs) prepared at high detergent concentrations, 0.5-1% Triton X100 (Bourova at al., 2003).

Agonist-induced internalization of δ-opioid receptors

The first evidence for agonist-induced internalization of GPCR was brought by subcellular fractionation studies of cell homogenate using differential or sucrose density gradient centrifugation. The internalized, endosomal pool of receptor molecules was separated from the major pool of receptor molecules in plasma membranes and found to be increased by agonist stimulation (Waldo et al., 1983; Stadel et al., 1983; Hertel et al., 1985; Clark et al., 1985; Sibley et al., 1987). In intact cells, the specific, agonist-induced sequestration and internalization of GPCR was detected by immuno-fluorescence microscopy of cells expressing $β_2$-adrenergic receptors. $β_2$-AR were transferred from clathrine-coated pitts (in plasma membrane) to clathrine-coated vesicles, rab5-containing early endosomes and back to the plasma membrane (Zastrow and Kobilka, 1992, 1994; Moore et al., 1995; Pippig et al.,

1995). Cellular and molecular mechanisms of GPCR internalization are in focus of OR studies as one the leading theories of drug addiction is directly based on atypical parameters of μ-OR internalization (Whistler and von Zastrow, 1998; Whistler et al., 1999). When exposed to morphine, μ-OR remain at PM and in this way elude desensitization by β-arrestin.

Our analysis of HEK293 cells transiently expressing Flag-epitope tagged version of δ-OR indicated that cholesterol depletion alone induced transfer of receptor molecules into the cell interior (compare **Fig. 2A,** upper right and left panels). Incubation of cells with 10 mM β-CDX (30 minutes) caused significant increase of intracellular fluorescence ($p < 0.05$), while in control, β-CDX-untreated cells, the small intracellular signal distributed among numerous faint fluorescent patches was unchanged in the course of 30 min of incubation in serum-free medium alone (**Fig. 2B**). Massive transfer of receptor molecules from the cell surface (plasma membrane) into the intracellular compartments was noticed after agonist stimulation (100 nM DADLE). This transfer was decreased in β-CDX-treated cells (compare **Fig. 2A,** lower right and left panels). Difference between β-CDX-treated and β-CDX- plus DADLE-treated samples was highly significant, $p < 0.01$ (**Fig. 2B**).

We could therefore conclude that treatment of HEK293 cells with β-CDX alone, i.e., degradation of membrane domains, induced destabilization of HEK293 plasma membrane structure manifested as spontaneous transfer of a portion of δ-OR molecules into the cell interior. Massive internalization of δ-OR proceeding in the presence of specific agonist was suppressed by β-CDX. This part of internalized receptor molecules may be regarded as functionally related to membrane domains.

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Table 1

DADLE-stimulated [^{35}S]GTPγS binding in membranes prepared from PTX-treated and PTX-untreated δ-OR-$G_i1\alpha$ - HEK293 cells

A PTX-treated

	EC_{50}		%		B_{basal}		B_{max}		Δ_{max}	
NaCl	5.1×10^{-8} M	**	350	**	0.143	**	0.499	*	0.356	**
KCl	9.6×10^{-9} M	* **	216	NS **	0.241	NS **	0.520	** NS	0.279	NS **
LiCl	5.4×10^{-9} M		231		0.209		0.481		0.272	

B PTX-untreated

	EC_{50}		%		B_{basal}		B_{max}		Δ_{max}	
NaCl	6.5×10^{-8} M	**	327	*	0.178	**	0.582	*	0.404	**
KCl	2.0×10^{-8} M	* **	237	NS *	0.222	NS **	0.526	NS *	0.304	NS **
LiCl	8.4×10^{-9} M		248		0.211		0.523		0.312	

[^{35}S]GTPγS binding was measured in P2 membrane fraction isolated from PTX-treated (A) or PTX-untreated cells (B) as described in methods. Binding assays were performed in 200 mM NaCl, KCl or LiCl. EC_{50} (M) and B_{max} (pmol x mg^{-1}) values were calculated by GraphPad*Prizm4*. B_{max} values were also expressed as the ratio (%) between maximum DADLE-stimulated (B_{max}) and the basal level (B_{basal}) of binding. Net-increment of agonist stimulation (Δ_{max}) was calculated as the difference between B_{max} and B_{basal} values. Numbers represent the means ± SEM of 3 binding assays, each performed in triplicates. Data were analyzed by one-way ANOVA followed by Neuman-Keuls post test (* $p<0.05$, ** $p<0.01$, NS non-significant).

(A) In PTX-treated membranes, [^{35}S]GTPγS binding in the absence of ions was 0.622 pmol × mg^{-1} and this level was decreased to 0.143 (NaCl), 0.241 (KCl) and 0.209 (LiCl) pmol × mg^{-1} by addition of 200 mM NaCl, KCl or LiCl, respectively.

(B) In PTX-untreated membranes, [^{35}S]GTPγS binding in the absence of ions was 0.809 pmol × mg^{-1} and this level was decreased to 0.178 (NaCl), 0.222 (KCl) and 0.211 (LiCl) pmol × mg^{-1} by addition of 200 mM NaCl, KCl or LiCl, respectively.

Figure legends

Fig. 1

Trimeric Gβ subunit protein; *immunoblot analysis of 2D-gels.*

A Two-dimensional resolution of Gβ protein content in PM isolated from control and morphine-adapted rats. PM protein (400 μg) was resolved by 2D electrophoresis using the pI range 3-11 for isoelectric focusing in the first dimension. The white small circle shows the small fraction of the total signal of Gβ which was taken into consideration when analyzed by LC-MS/MS. The second dimension was performed by SDS-PAGE in 10% w/v acrylamide/0.26% bis-acrylamide gels (Hoefer SE 600). Gβ was identified by immunoblotting with specific antibody oriented against C-terminal decapeptide of Gq/G11α. Numbers 1-8 represent spots of Gβ subunits which were subsequently analyzed by LC-MS/MS.

B The average of 3 immunoblots ± SEM. Difference between (-M10) and (+M10) was analyzed by Student´s *t*-test using GraphPad*Prizm4* and found not significant, NS ($p > 0.05$).

Fig.2

Agonist (DADLE)-induced internalization of δ-OR is attenuated by cholesterol depletion

HEK293T cells transiently transfected with FLAG-tagged δ-OR were *in vivo* labeled with the corresponding anti-tag antibodies, exposed to serum-free DMEM (Control), 10 mM β-CDX in serum-free DMEM (CDX), 100 nM DADLE (DADLE), or 10 mM β-CDX plus 100 nM DADLE in serum-free DMEM (CDX+DADLE) for 30 minutes, and fixed. After fixation the cells were subjected to indirect immunofluorescence with Alexa Fluor 488-conjugated secondary antibodies and imaged with laser scanning confocal microscopy.

Left panels **(A)** show representative micrographs of cells expressing FLAG-tagged δ-OR and treated as described above. Right panel (**B**) displays results from quantification of micrographs performed by ImageJ software. Fraction of internalized receptors was calculated as a ratio of intracellular to total signal determined in 8 cells per each condition, averaged and

normalized to values obtained by agonist (DADLE) stimulation. Data represent the average of 3 experiments, i.e., 3 independent transfections, ± S.E.M.. Statistical analysis was performed using one-way ANOVA repeated measurements with Bonferroni post test. *, **, represent the significant difference, $p<0.05$, $p<0.01$.

Fig.1

Morphine-induced decrease of trimeric Gβ subunits in plasma-membrane-enriched fraction; *resolution by 2D-electrophoresis*

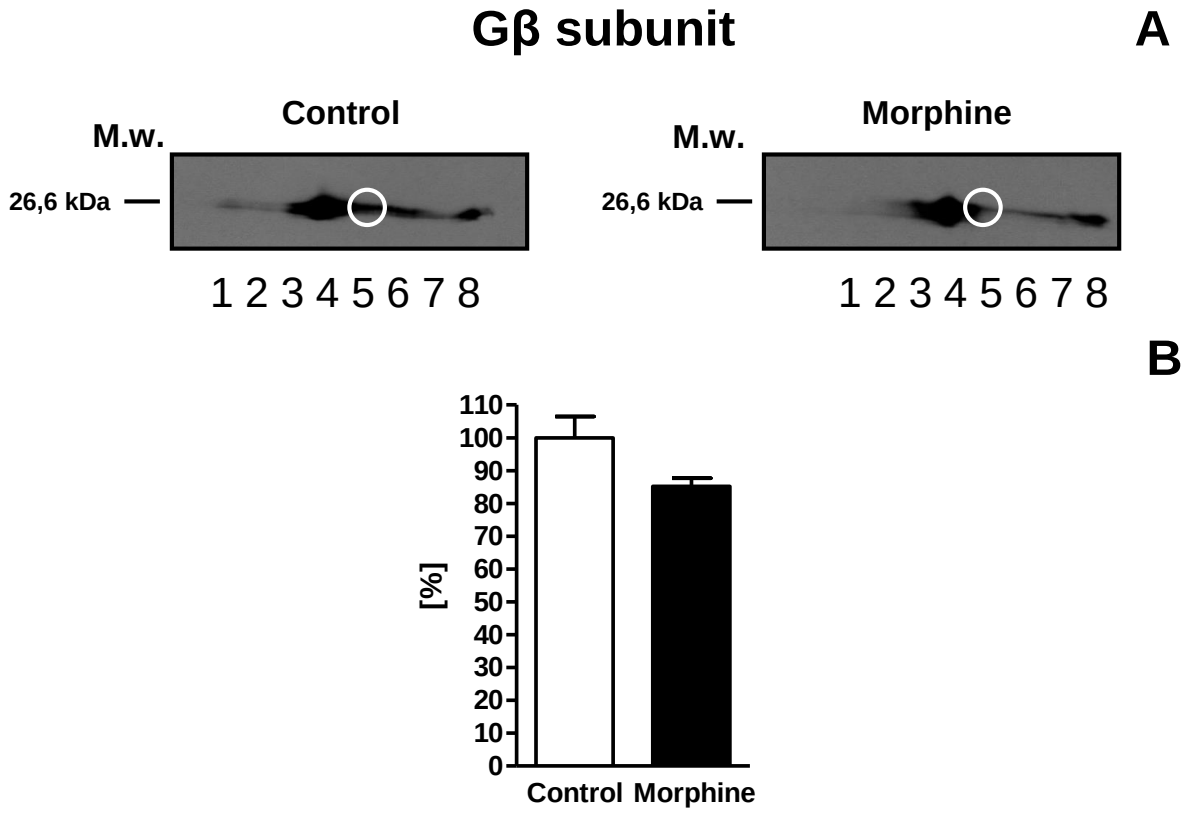
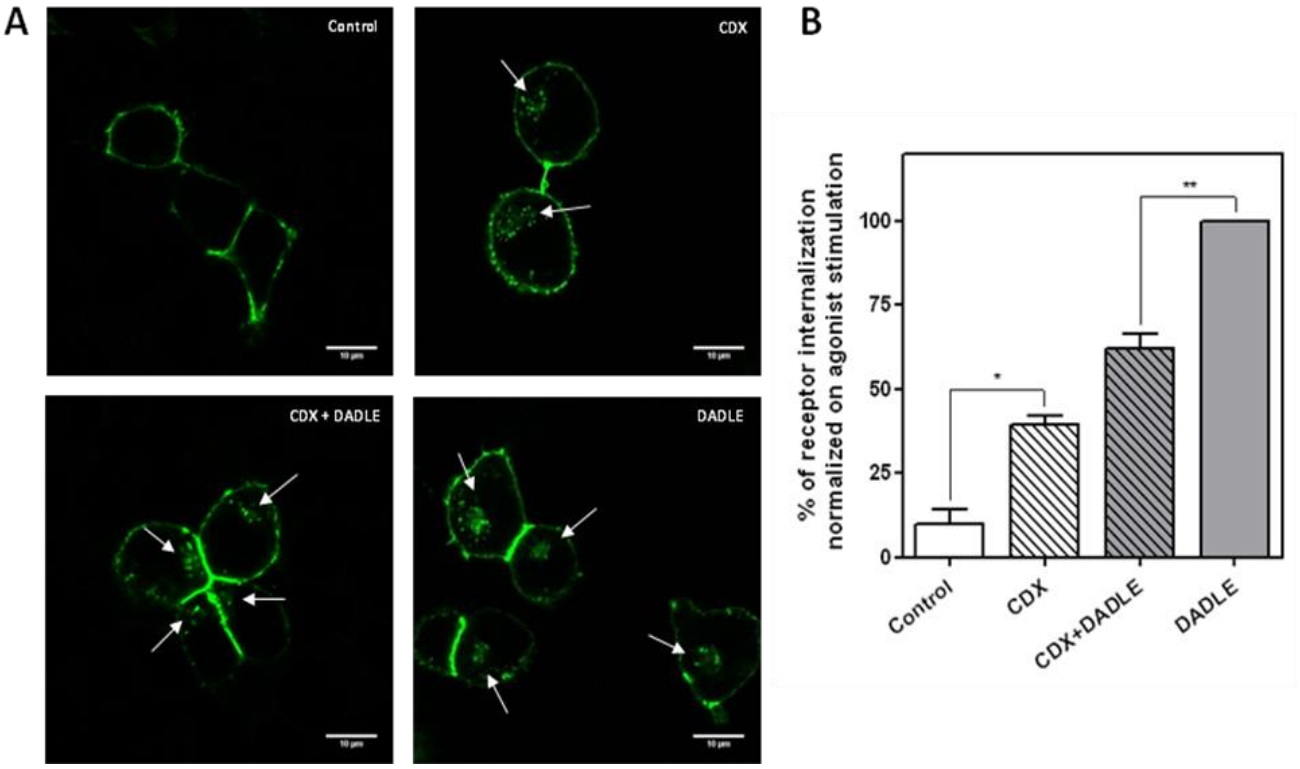


Fig. 2

Agonist-induced internalization of δ-opioid receptors in HEK cells transiently transfected with Flag-δ-OR



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Up-regulation of adenylylcyclases I and II induced by long-term adaptation of rats to morphine fades away 20 days after morphine withdrawal

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ABSTRACT

Background: Activation of adenylyl cyclase (AC) by prolonged exposure of mammalian organism to morphine was demonstrated in previous studies of mechanism of action of this drug. However, expression level of individual AC isoforms was not analyzed in crucial cell structure, plasma membrane (PM).
Methods: Rats were adapted to morphine for 10 days and sacrificed 24 h (group + M10) or 20 days (+M10/−M20) after the last dose. Control animals were sacrificed in parallel with morphine-treated (groups − M10 and (−M10/−M20)). Percoll®-purified PM were isolated from brain cortex and analyzed by immunoblotting and specific radioligand binding.
Results: ACI (ACII) was increased 8× (2.5×) in morphine-adapted rats (+M10) when compared with controls (−M10). Increase of ACI and II by long-term adaptation to increasing doses of morphine represented a specific effect as the amount of ACIII–ACIX, of prototypical PM marker, Na, K-ATPase and of trimeric G protein α and β subunits was unchanged. Increase of ACI and II was not detected in PM isolated from group (+M10/−M20). Thus, the marked increase of ACI and ACII faded away 20 days since the last dose of morphine.
Conclusions: We assume that the specific increase in expression level of ACI and ACII in brain cortex of morphine-adapted rats proceeds as a compensatory, homeostatic response to prolonged exposure to inhibitory drug, morphine.
General significance: Our findings demonstrate that the *dramatic and specific* change of the crucial component of the opioid receptor cascade in brain cortex, manifested as an increase in PM level of ACI and II, is reversible.

1. Introduction

Physiological action of opioid drugs requires an initial interaction with opioid receptors [1]. These receptors, MOR (μ-OR), DOR (δ-OR) and KOR (κ-OR) [2–9] are classified as members of rhodopsin family of G-protein coupled receptors, GPCRs. All these receptors are known to inhibit adenylyl cyclase activity in pertussis-toxin-dependent manner by activation of G_i/G_o class of trimeric G proteins [10]. These proteins (G_i1, G_i2, G_i3, G_o1, G_o2) are present in brain in large quantities and inhibit adenylyl cyclase activity or regulate ionic channels in pertussis-toxin-dependent manner [11–15].

Hyper-sensitization or super-activation of AC enzyme activity by prolonged exposure of cultured cells or mammalian organisms to morphine has been demonstrated in previous studies of mechanism of action of this drug representing the non-selective OR agonist [1,7,8,16–26]. Adenylyl cyclase is regulated by trimeric G-proteins, so any significant change of AC activity should be preceded by alternation of trimeric G-protein activity.

In our previous work [27], the purified membranes from brain cortex were used for determination of DAMGO (μ-OR)-, DADLE (δ-OR)-, and U-23554 (κ-OR)-stimulated [^{35}S] GTPγS binding which was used as an estimate of trimeric G protein activity. Membranes were isolated from forebrain cortex of control and morphine-treated rats. Results of this study indicated a clear desensitization of DAMGO- and DADLE-stimulated G protein response in membranes prepared from

Abbreviations: AC, adenylyl cyclase; β-AR, β-adrenergic receptor; DADLE, [2-D-alanine, 5-D-leucine]enkephalin = Tyr-D-Ala-Gly-Phe-D-Leu; DAMGO, [2-D-alanine, 4-N-methylphenylalanine, 5-glycinol]enkephalin = Tyr-D-Ala-Gly-N-methyl-Phe-Gly-ol; DOR, δ-opioid receptor; GPCR, G protein-coupled receptor; G proteins, heterotrimeric guanine nucleotide-binding regulatory proteins; $G_s\alpha$, G protein α subunit stimulating adenylyl cyclase activity; $G_i/G_o\alpha$, G protein α subunits inhibiting adenylyl cyclase activity in pertussis-toxin sensitive manner; $G_q/G_{11}\alpha$, G protein α subunits stimulating phoshoplipase C in pertussis-toxin independent manner; [^{35}S]GTPγS, guanosine-5′-[γ-^{35}S] triphosphate; KOR, κ-opioid receptor; PM, plasma (cell) membranes; MOR, μ-opioid receptor; Na,K-ATPase, sodium- plus potassium-activated, ouabain-dependent adenosine triphosphatase (EC 3.6.1.3); P_i, inorganic phosphate; OR, opioid receptor; PBS, phosphate-buffered saline; PM, plasma membrane; PMSF, phenylmethylsulfonyl fluoride; PTX, pertussis toxin; SLB, sample loading buffer; TBS, Tris-buffered saline; w.w., wet weight

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morphine-treated rats [27]. U-23554-stimulated [^{35}S] GTPγS binding was unchanged. Our results were fully in line with data of Sim et al. [28], Sim-Selley et al. [29] and Maher et al. [30] indicating the desensitization of G protein response in specific areas of brain stem and hippocampus in morphine- as well as heroine-adapted rats.

In our present work, we have analyzed the content of *all* types of adenylyl cyclase protein molecules (ACI–IX) in PM isolated in the same way from morphine-adapted rats because the previous analyses of AC in drug-addicted state were preferentially oriented to functional assays of AC only and not to the quantitative determination of different isoforms of this enzyme in plasma membranes. Recent histochemical analysis of ACI–IX mRNA levels indicated that the expression level of ACI and II in rat brain cortex is high [31].

2. Material and methods

2.1. Chemicals

[^{3}H]-ouabain (30 mCi/mmol, NET211001MC), [^{3}H]DADLE (39.1 Ci/mmol, NET648250UC) and [^{3}H]DPDPE (45 Ci/mmol; NET922050UC) were purchased from Perkin Elmer. [α-^{32}P] ATP (adenosine-5′-[α-^{32}P] triphosphate, cat. no. 32007.2) was purchased from MP Biomedicals. [^{3}H]cAMP (cyclic 3′,5′-[α-^{3}H] adenosine monophosphate, cat. no. TRK498) was from Amersham. Complete protease inhibitor cocktail was from Roche Diagnostic, Mannheim, Germany (cat. no. 1697498). All other chemicals were of highest purity available.

2.2. Antisera

$G_i\alpha$ and $G_o\alpha$ subunit proteins were identified by antipeptide antibodies as originally described by Gierschik et al. [11], Goldsmith et al. [12], Backlund et al. [13] and Milligan [15]. Production of the rabbit polyclonal antisera anti-$G_i1/G_i2\alpha$, anti-$G_i3\alpha$, anti-G_o and anti-$G_q/G_{11}\alpha$ was performed according to Mitchell et al. [32,33], Mullaney and Milligan [34] and Mullaney et al. [35–37]. These antisera were previously characterized in our laboratory by Ihnatovych [38]. $G_s\alpha$ (G-5040) antibody was from Sigma. Rabbit polyclonal antibodies $G_z\alpha$ (I-20, sc-388), Gβ (T-20, sc-378), ACI (V-20, sc-586), ACII (C-20, sc-587), ACIII (C-20, sc-588), ACIV (C-20, sc-589), ACV/VI (C-17, sc-590), ACVII (M-20, sc-1966), ACVIII (C-17, sc-32131), ACIX (N-18, sc-8576) were purchased from Santa Cruz Biotechnology. Antibody oriented against α subunit of Na, K-ATPase (H-300, sc-28800) was also from Santa Cruz. Caveolin-1-oriented antibody C13630 was purchased from Transduction Laboratories [39].

2.3. Animals

All experiments were performed in accordance with the European Council Directive (86/609/EEC). Male Wistar rats (220–250 g) were killed by decapitation under ether narcosis, the frontal brain was rapidly removed, washed intensively from the remaining blood and cooled to 0 °C. The cerebral cortex was separated on the pre-cooled plate, snap frozen in liquid nitrogen and stored at −70 °C until use.

2.4. Morphine treatment of experimental animals

The animals were exposed to morphine by intra-muscular application according to the following protocol: 10 mg/kg (days 1 and 2), 15 mg/kg (days 3 and 4), 20 mg/kg (days 5 and 6), 30 mg/kg (days 7 and 8), 40 mg/kg (day 9) and, finally 50 mg/kg (day 10). The morphine-adapted rats were sacrificed 24 h (group + M10) or 20 days (group (+M10/−M20)) after the last dose of the drug. Control animals were injected with sterile PBS and sacrificed in parallel with morphine-adapted rats, i.e. 24 h (−M10) or 20 days (−M10/−M20) after the last dose.

An independent group of animals was exposed to the single dose (injection) of 10 mg/kg, 15 mg/kg, 20 mg/kg, 30 mg/kg, 40 mg/kg or 50 mg/kg of morphine (group + M1) and sacrificed for 24 h later. Control animals were injected with sterile PBS (group − M1). The aim of this *short term morphine exposure* experiment was to obtain an independent set of data on ACI and II levels in PM with the aim to compare these data with those collected from *morphine-adapted* rats for 10 days (group + M10).

2.5. Isolation of plasma membrane-enriched fraction from rat brain cortex

Rat brain cortex was minced with razor blade on pre-cooled plate and diluted in STEM medium containing 250 mM sucrose, 20 mM Tris–HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.6, fresh 1 mM PMSF plus protease inhibitor cocktail. It was then homogenized mildly in loosely-fitting Teflon-glass homogenizer for 5 min (2 g w. w. per 10 ml) and centrifuged for 5 min at 3500 rpm. Resulting post-nuclear supernatant (PNS) was filtered through Nylon nets of decreasing size (330, 110 and 75 mesh, Nitex) and applied on top of Percoll in Beckman Ti70 tubes (30 ml of 27.4% Percoll in STE medium). Centrifugation for 60 min at 30,000 rpm (65,000×*g*) resulted in the separation of two clearly visible layers [40]. The upper layer represented plasma membrane fraction (PM); the lower layer contained mitochondria (MITO). The upper layer was removed, diluted 1:3 in STEM medium and centrifuged in Beckman Ti70 rotor for 90 min at 50,000 rpm (175,000×*g*). Membrane sediment was removed from the compact, gel-like sediment of Percoll and re-homogenized by hand in a small volume of 50 mM Tris–HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.4 (TME medium).

2.6. SDS-PAGE and immunoblotting

The aliquots of membrane fractions were mixed 1:1 with 2× concentrated Laemmli buffer (SLB) and heated for 3 min at 95 °C. Standard (10% w/v acrylamide/0.26% w/v bis-acrylamide) SDS electrophoresis was carried out as described before [41–43]. Molecular mass determinations were based on pre-stained molecular mass markers (Sigma, SDS 7B). After SDS-PAGE, proteins were transferred to nitrocellulose and blocked for 1 h at room temperature in 5% (w/v) low-fat milk in TBS-Tween buffer [10 mM Tris–HCl, pH 8.0, 150 mM NaCl, 0.1% (v/v) Tween 20]. Antibodies were added in TBS-Tween containing 1% (w/v) low-fat milk and incubated for at least 2 h. The primary antibody was then removed and the blot washed extensively (3×10 min) in TBS-Tween. Secondary antibodies (donkey anti-rabbit IgG conjugated with horse-radish peroxidase) were diluted in TBS-Tween containing 1% (w/v) low-fat milk, applied for 1 h and after three 10 min washes the blots were developed by ECL technique using Super Signal West Dura (Pierce) as substrate. The developed blots were scanned with an imaging densitometer ScanJett 5370C (HP) and quantified by Aida Image Analyzer v. 3.28 (Ray test).

When indicated, membrane fractions were also analyzed by NuPAGE system (Invitrogen). Aliquots of membrane fractions were solubilized in NuPAGE LDS Sample Buffer (4×) with addition of NuPAGE Sample Reducing Agent (10×) according to manufacturer's instructions. Samples were heated at 70 °C for 10 min, loaded at 10 μg/well and resolved by NuPAGE 4–12% or 10% Bis-Tris polyacrylamide gels (10 wells,1 mm thick) using 3-(N-morpholino) propane sulfonic acid (MOPS), sodium dodecyl sulfate (SDS) running buffer with NuPAGE Antioxidant prior to blotting on nitrocellulose membranes (Protran, Schleicher & Schuell). Western blotting was carried out as described above.

2.7. Na, K-ATPase

All membrane preparations were screened for the content of PM marker, sodium- plus potassium-activated magnesium-dependent adenosine triphosphatase (EC 3.6.1.3). Na, K-ATPase was determined

by binding of radioactively labeled, selective inhibitor of this enzyme, [^{3}H]ouabain as described before by Svoboda et al. [44]. Membranes (50 μg) were incubated with 5 nM [^{3}H]ouabain for 90 min at 30 °C in total volume of 0.4 ml of 5 mM $NaHPO_4$, 5 mM $MgCl_2$, 50 mM Tris–HCl, pH 7.6 at 37 °C. Binding reaction was terminated by dilution with 5 ml of ice-cold buffer and filtration through Whatman GF/B filters. The filters were washed twice, dried overnight at laboratory temperature and the radioactivity was determined by liquid scintillation. Non-specific binding was determined in the presence of 1 μM unlabelled ouabain.

Membrane density of Na, K-ATPase molecules was detected by immunoblotting with antibodies oriented against α-subunit of this enzyme (sc-28800, Santa Cruz) as described above.

2.8. Adenylyl cyclase

Adenylyl cyclase enzyme activity was determined as described before by Bourova et al. [45]. Reaction mix was prepared according to Salomon [46]; separation of cyclic AMP from other nucleotides and inorganic phosphate was performed by dry alumina column chromatography as described by White [47].

2.9. δ-opioid receptors

Saturation binding experiments were performed using [^{3}H]DADLE or [^{3}H]DPDPE according to Bourova et al. [45] and Moon et al. [48]. The assay medium contained membrane protein (120 μg per tube) diluted in final volume of 100 μl of binding mix containing 50 mM Tris–HCl, 10 mM $MgCl_2$, 1 mM EDTA, pH 7.4 ± 100 mM NaCl plus increasing radioligand concentrations ([^{3}H]DADLE 0.1–34.4 nM; [^{3}H]DPDPE 0.1–57.3 nM). Specific binding of the radioligand was obtained as the difference between binding in the absence and presence of nonradioactive 10 μM DADLE or DPDPE. After incubation for 60 min at 30 °C, samples were diluted with 3 ml of ice-cold Mg-HEPES buffer, immediately filtered and washed 3× with 3 ml of Mg-HEPES buffer. Whatman GF/B filters mounted in Brandel cell harvester were used for separation of bound and free radioactivity. Radioactivity remaining on the filters was determined by liquid scintillation. Data were analyzed by GraphPad*Prizm4*.

2.10. Protein determination

The method of Lowry was used for determination of membrane protein. Bovine serum albumin (Sigma, Fraction V) was used as standard. Data were calculated by fitting the data with calibration curve as quadratic equation.

3. Results

3.1. Morphine-induced increase in plasma membrane density of adenylylcyclases I and II

The amount of adenylylcyclases I and II was determined first in plasma membrane fraction (PM) isolated from frontal brain cortex of rats adapted to increasing doses of morphine for 10 days and compared with PM isolated from control animals. Data presented in Fig. 1A (left panels) indicate clearly a large increase in membrane density of ACI. Quantitative analysis of 32 immunoblots performed with 50 μg or 100 μg of PM protein applied per gel indicated a highly significant difference between the two sets of data, $p<0.001$. Membranes isolated from morphine-adapted rats (group + M10) exhibited 8× higher density of ACI than membranes isolated from control animals (group − M10). The same type of analysis, when performed with ACII oriented antibody indicated 2.5× increase of this enzyme protein in membranes prepared from morphine-adapted rats when compared with controls (Fig. 1A, middle panels). The difference between the two groups was again highly significant, $p<0.01$.

The increased level of ACI and ACII in PM samples prepared from morphine-adapted animals was not observed in membranes isolated from animals exposed to morphine for 10 days but sacrificed 20 days since the last dose of morphine (group (+M10/−M20)), Fig. 1B. These samples exhibited the same amount of ACI and ACII as corresponding controls (group (−M10/−M20)); (compare left and middle panels in Fig. 1B). Thus, in drug addicted state, PM density of AC molecules was dramatically increased mainly as far as ACI isoform was involved. This increase, being clearly disproportionate between ACI (8×) and ACII (2.5×), faded away 20 days since application of the last dose of morphine. Obviously, the withdrawal of the drug for sufficiently long period of time resulted in reversal of the pathological change back to "normal" state as far as the levels of these two isoforms of AC were involved.

The increase of ACI and II observed after 10 days of adaptation to increasing doses of morphine represented the specific phenomenon as the PM level of ACIII, IV, V/VI, VII, VIII and IX was unchanged (Fig. 2A). Furthermore, analysis of ACI and II in membranes prepared from animals exposed to the same doses of morphine but for 24 h only, i.e. to the *single* injection of morphine 10, 15, 20, 30, 40 and 50 mg/kg (see Material and methods for details), indicated that this short-term exposure had no effect on the membrane density of ACI and ACII in brain cortex PM (Fig. 2B). Thus, the dramatic and specific increase of ACI (8×) observed after 10 days of step-wise adaptation to increasing doses of morphine does not represent an acute phenomenon and may be regarded as the long-term adaptation of experimental animals to this drug.

3.2. Unchanged level of Na, K-ATPase

The next part of our work was oriented to analysis of other PM signaling molecules distinct from AC. Therefore, in parallel membrane samples to those used for determination of ACI and ACII, the specific content of Na, K-ATPase was measured as a negative standard and prototypical plasma membrane marker which should not be affected by morphine treatment, (Fig. 1A–C, right panels). Quantitative analysis of immunoblot signals corresponding to α subunit of this enzyme indicated that the expression level of this protein in PM was unchanged after adaptation to morphine for 10 days (Fig. 1A). Accordingly, the membrane content of Na, K-ATPase in samples isolated from rats sacrificed 20 days after the last dose of morphine was the same as in controls (Fig. 1B, right panel).

Data obtained by immunoblot analysis of Na, K-ATPase protein content in PM were extended and verified by analysis of "functional" parameter of this marker molecule, the number and affinity of binding sites for its selective inhibitor [^{3}H] ouabain. The maximum number (B_{max}) and affinity (K_d) of binding of this radioligand represents the highly selective and sensitive method for detection of Na, K-ATPase molecules in a given membrane sample. Virtually the same results as those obtained by immunoblot analysis were obtained (Fig. 3). Maximum binding capacity B_{max} and dissociation constant K_d of this radioligand binding to membranes isolated from morphine-adapted rats ($B_{max} = 35.5 \pm 2.1$ pmol . mg^{-1}; $K_d = 20.8 \pm 2.3$ nM) were not different from those determined in membranes prepared from control animals ($B_{max} = 36.6 \pm 2.1$ pmol . mg^{-1}; $K_d = 26.2 \pm 3.1$ nM).

3.3. Unchanged level of trimeric G protein α and β subunits

Determination ACI–IX and Na, K-ATPase presented in the previous paragraphs (Figs. 1–3) was accompanied by analysis of G protein content in PM preparations isolated from the same rats as those used for determination of ACI and ACII. The reason why we have performed this analysis was that the change in functional activity of a given set of signaling molecules does not necessarily mean the change in its expression level or membrane density. As already mentioned in introduction section, our previous data indicated the desensitization of G

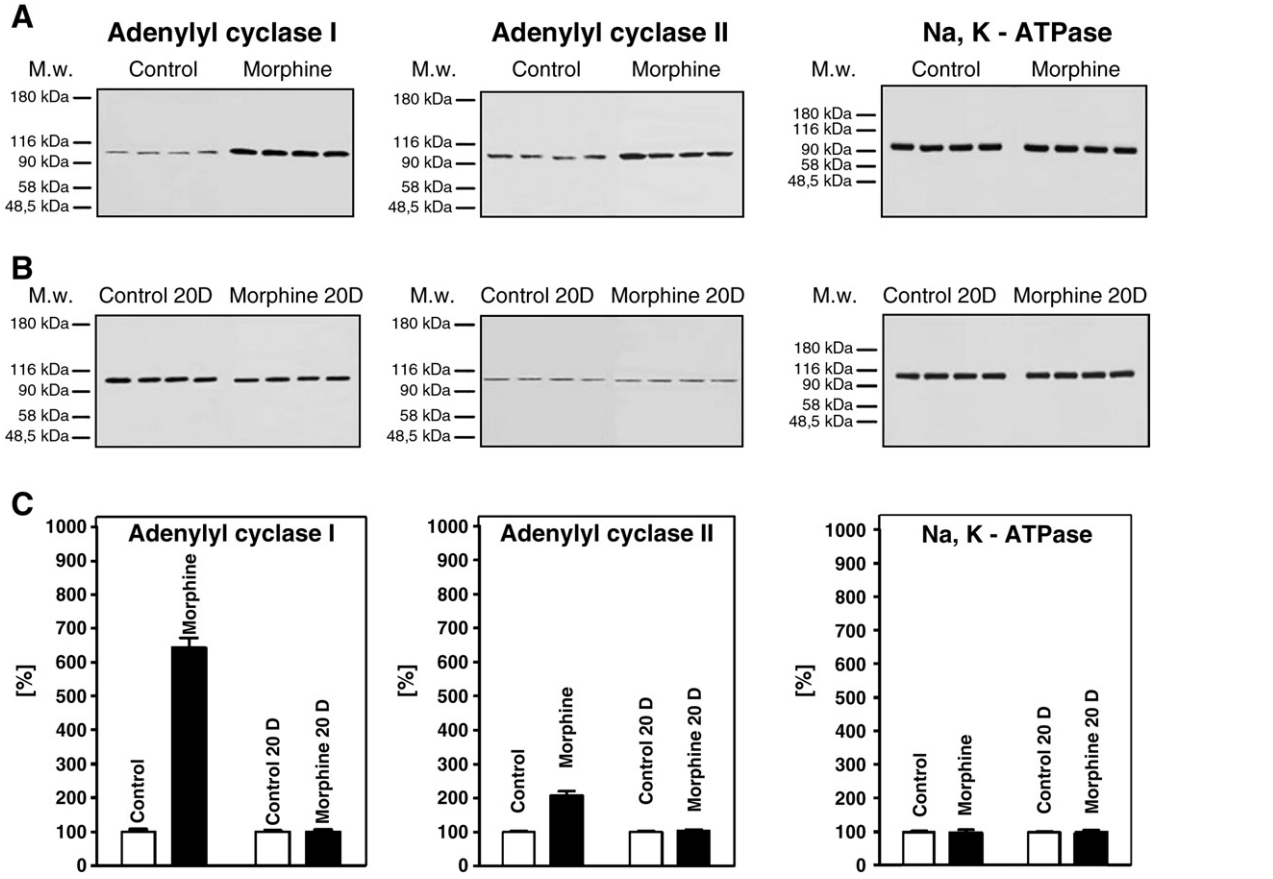

Fig. 1. Adenylyl cyclases I, II and Na, K-ATPase; *immunoblot analysis*. A. Membrane content of ACI (left), ACII (middle) and Na,K-ATPase (right panels) was determined by quantitative immunoblotting in PM isolated in parallel from brain cortex of control rats (group − M10) and rats adapted to increasing doses of morphine for 10 days (group + M10). Adaptation was performed according to the following protocol: 10 mg/kg (days 1 and 2), 15 mg/kg (days 3 and 4), 20 mg/kg (days 5 and 6), 30 mg/kg (days 7 and 8), 40 mg/kg (day 9) and 50 mg/kg (day 10). Control animals were injected with PBS at the same time intervals. Resolution of control and morphine-adapted samples by SDS-PAGE was always performed on the same gel and subsequently transferred to the same nitrocellulose sheet. Typical immunoblots performed with the same amount of protein in the two types of PM are shown: 4×(−M10) samples followed by 4×(+M10) samples from left to right. Control, membranes isolated from group (−M10); Morphine, membranes isolated from group (+M10). B. PM had been isolated from animals adapted to morphine according to the same protocol but further nurtured for 20 days in the absence of this drug (group (+M10/−M20)). Corresponding controls were represented by PM isolated from animals designated as (−M10/−M20), see Material and methods. Animals in this group were injected with PBS for 10 days and subsequently nurtured in the absence of any additions/injections for 20 days. Typical immunoblots performed with the same amount of PM protein resolved in the same gel [4×(−M10) plus 4×(+M10) samples] are shown. Control 20D, membranes isolated from group (−M10/−M20); Morphine 20D, membranes isolated from group (+M10/−M20). C. Statistical analysis of immunoblot signals collected from 32 (ACI), 26 (ACII) and 12 (Na, K-ATPase) immunoblots [4×(−M10) plus 4×(+M10) samples in each gel/blot]. Numbers represent the average + M10/−M10 ratio ± SEM expressed as% of control values, 100%.

protein response to OR stimulation in membranes isolated from morphine-adapted rats [27].

Data presented in Fig. 4 indicated clearly the unchanged level of all the major classes of trimeric G protein α and β subunits: $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_o\alpha$, $G_z\alpha$, $G_s\alpha$, $G_q/G_{11}\alpha$ and Gβ. When normalized and compared in at least 3 immunoblots performed with different amounts of protein, the difference between morphine-treated and control samples (100%) was not significant: $G_i1/G_i2\alpha$ (100 ± 10%), $G_i3\alpha$ (109 ± 5%), $G_o\alpha$ (105 ± 2%), $G_z\alpha$ (100 ± 6%), $G_s\alpha$ (98 ± 4%), $G_q/G_{11}\alpha$ (96 ± 4%), Gβ (101 ± 7%). Membrane density of caveolin-1 was also unchanged — the level of this PM marker in morphine-adapted samples represented 89 ± 6% of the control level. The difference between control and morphine treated rats was analyzed by Student's *t*-test and expressed as% of control level. The numbers represent the average ± SEM of densitometric scans carried out in triplicate.

Results presented in Fig. 4 may be regarded as an additional support for desensitization mechanism of morphine action as more drastic adaptation should result in decrease of the amount of the cognate G protein α subunits in PM isolated from morphine-treated rats. This phenomenon, known as *down-regulation* of G proteins is well known, has been originally described by Milligan and Green [49] in white fat cells and later demonstrated in numerous GPCR-stimulated cascades both in cultured cells and intact tissue [35,36,49–56].

3.4. Adenylyl cyclase activity in morphine-adapted rats

The question, to what extend the increase of ACI and ACII in brain cortex of morphine-adapted rats (group + M10) is associated with or reflected in change of an overall adenylyl cyclase enzyme activity, was tested in parallel PM samples as those used before in immunoblot analysis of ACI–IX, Na, K-ATPase and G protein subunits. Data shown in Fig. 5 indicated that inhibitory effect of MOR and DOR agonists DAMGO and DADLE, which was manifested in control animals (group − M10), was not detected in morphine-adapted rats (group + M10). This result, demonstrated for basal as well as Forskolin-stimulated AC, supports the previously published data describing the decrease (desensitization) of G protein response to opioid stimulation in drug-addicted state [27–30,32] and is directly relevant and in agreement with principal finding of He and Whistler [57] indicating that chronic morphine resulted in a significant attenuation of the DAMGO-mediated inhibition of AC activity.

3.5. Increase in number of δ-opioid receptors (DOR)

In crude membrane preparations of monkey cortex and thalamus, the magnitude of MOR-, DOR- and KOR-stimulated G protein responses was proportional to the corresponding receptor densities

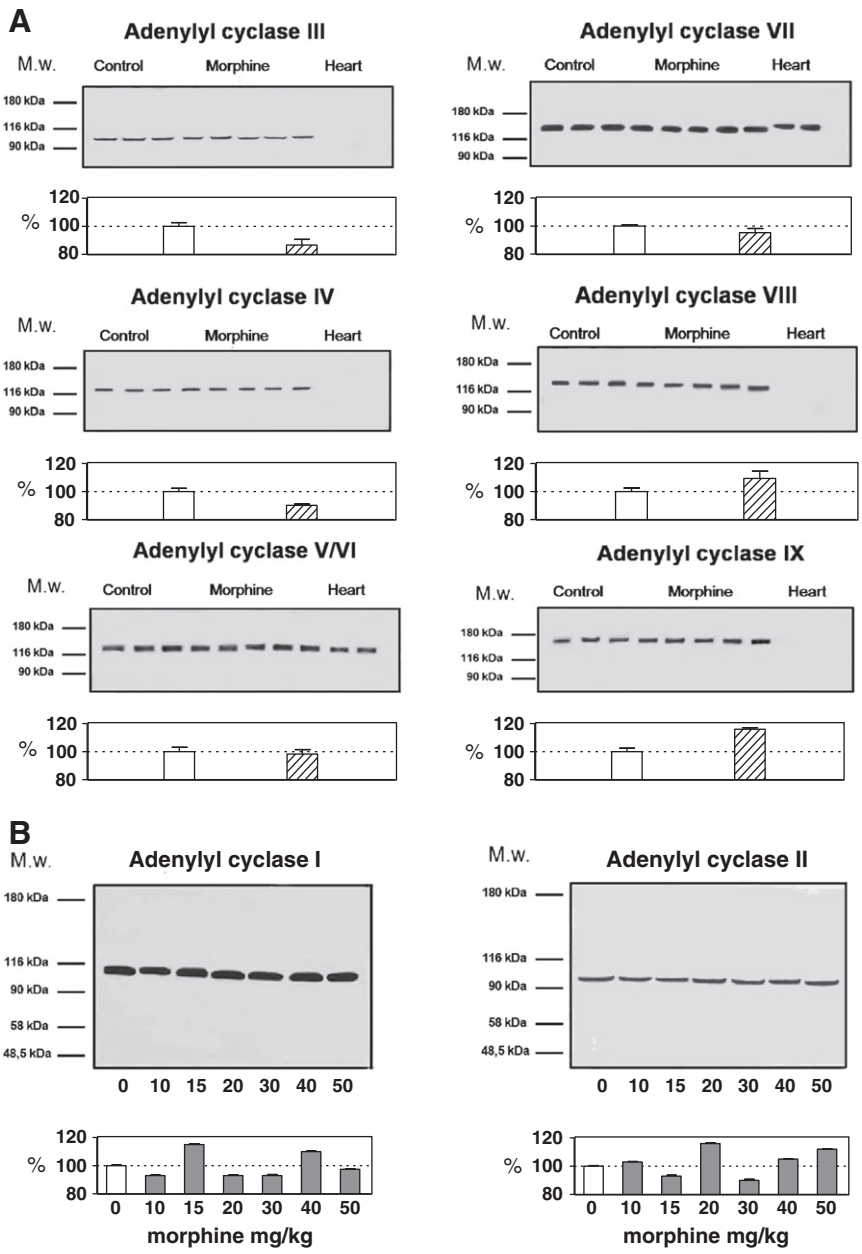

Fig. 2. Adenylyl cyclases III, IV, V/VI, VII, VIII and IX; *immunoblot analysis*. A. Membrane content of ACIII–IX was determined in PM isolated from brain cortex of morphine-adapted (group + M10) and control rats (group − M10) by quantitative immunoblotting. Typical immunoblots performed with the same amount of PM protein resolved in the same gel [4 × (− M10) plus 4 × (+ M10) samples] are shown. Statistical analysis was based on analysis of 3 immunoblots [4 × (− M10) plus 4 × (+ M10) samples in each gel/blot]. Numbers represent the average + M10/− M10 ratio ± SEM expressed as% of control (− M10) values, 100%. B. PM were isolated from animals exposed to the same doses of morphine (10, 15, 20, 30, 40 and 50 mg/kg) as in long-term adaptation experiment (Fig. 1), but for 24 h only (group + M1). Control animals were exposed to the single injection of PBS and sacrificed after 24 h (group − M1). As before, immunoblotting was performed with the same amount of PM protein resolved in the same gel [4 × (− M1) plus 4 × (+ M1). samples]. Both types of samples were run in parallel. Statistical analysis was based of comparison of (− M1) and (+ M1) samples in 3 immunoblots. Numbers represent the average + M1/− M1 ratio ± SEM expressed as% of control values, 100%.

[58]. Accordingly, the studies dealing with MOR in CHO cells [59] and in brain [60,61] indicated that the relationship between MOR occupancy and G protein activation depends on the receptor density [59–61]. As these studies were primarily oriented to MOR we decided to compare DOR density in PM prepared from control and morphine-adapted rat brain cortex.

DOR receptors in control (− M10) and morphine-treated (+ M10) brain cortex were characterized by saturation binding studies with DOR agonists [^{3}H]DADLE and [^{3}H]DPDPE. Saturation binding curves were measured in 0.1–34.4 nM ([^{3}H]DADLE) and 0.1–57.3 nM ([^{3}H] DPDPE) range of agonist concentrations in the presence or absence of 100 mM NaCl.

As shown in Fig. 6, maximum number of [^{3}H]DADLE binding sites in membranes isolated from morphine-adapted rats ($B_{max} = 0.115$ pmol . mg^{-1}) was 1.4× higher than in membranes isolated from control rats ($B_{max} = 0.083$ pmol . mg^{-1}). Surprisingly, 100 mM sodium chloride had no effect on [^{3}H]DADLE binding in morphine-adapted samples, but, as expected, it did inhibit radioligand binding to control membranes.

Morphine-induced increase of ligand binding to DOR was substantially higher when more specific ligand, [^{3}H] DPDPE, was

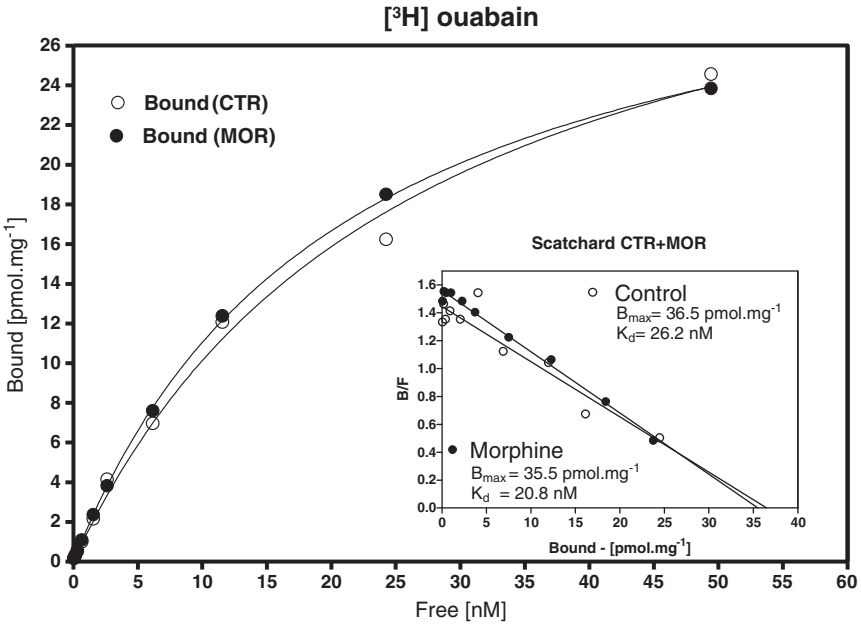

Fig. 3. Maximum binding capacity (B_{max}) and dissociation constant (K_d) of [^{3}H] ouabain binding sites in PM isolated from control and morphine-treated rats. Binding of selective Na, K-ATPase inhibitor [^{3}H] ouabain to PM isolated from brain cortex of control (−M10) and morphine-treated (+M10) rats was determined as described in Material and methods. Data were analyzed by GraphPad*Prism4*. B_{max} and K_d values represent the average of 3 experiments, each performed in triplicates.

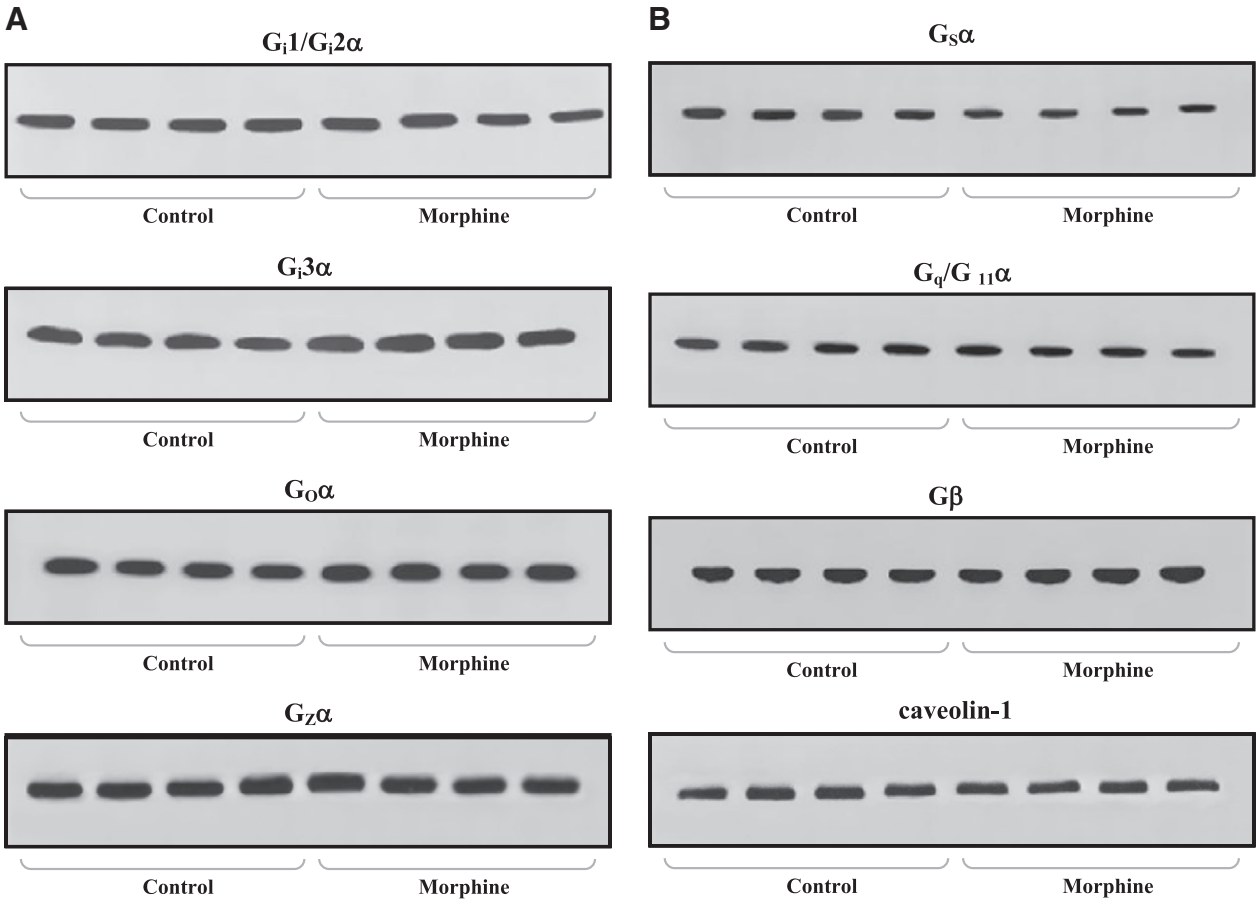

Fig. 4. Comparison of G protein content in PM isolated from control and morphine-adapted rats; $G_i1/G_i2\alpha$, $G_i3\alpha$, $G_z\alpha$, $G_s\alpha$, $G_q/G_{11}\alpha$, $G\beta$. PM protein (10 μg per well) was resolved by standard SDS-PAGE in Bio Rad Mini Protean II or by NuPAGE system (Invitrogen). G protein α and β subunits were identified by immunoblotting with specific antibodies as described in Material and methods. Caveolin-1 was determined as a marker of membrane domains. Data represent the typical immunoblots. $G_z\alpha$ and Gβ were resolved by NuPAGE electrophoretic system (Invitrogen); all other proteins were resolved by standard SDS-PAGE (BioRad). Statistical analysis was based on analysis of 3 immunoblots [4×(−M10) plus 4×(+M10) samples in each gel/blot]. Numbers represent the average + M10/−M10 ratio ± SEM expressed as% of control (−M10) values, 100%.

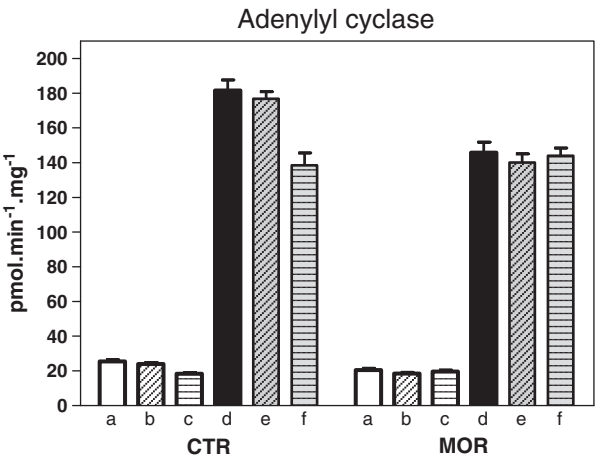

Fig. 5. Adenylyl cyclase enzyme activity. AC activity was measured in the absence (a, b, c) or presence of 10 μM Forskolin (d, e, f) in PM isolated from control (CTR, group − M10) or morphine-adapted (MOR, group + M10) rats as described in Material and methods. (a, d), basal activity, i.e. no additions; (b, e), 10 μM DADLE (δ-opioid agonist); (c, f), 10 μM DAMGO (μ-opioid agonist). Data represent the average of 3 experiments ± SEM.

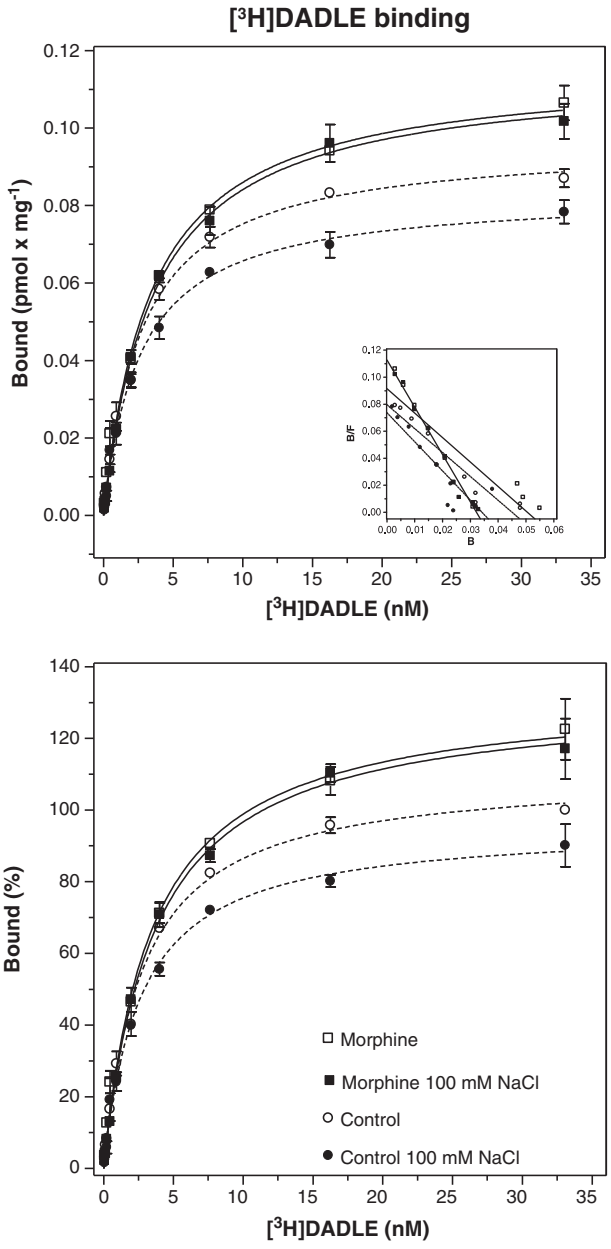

Fig. 6. Agonist binding characteristics of DOR; [^{3}H] DADLE. Saturation of specific [^{3}H] DADLE binding sites in control (− M10) and morphine-adapted (+ M10) plasma membrane samples was measured in 0.15–35 nM range of radioligand concentrations in the presence (+ NaCl) or absence (− NaCl) of 100 mM NaCl. The B_{max} and K_d values were calculated by GraphPad*Prizm4*. The data represent the average of three experiments performed in triplicates ± SEM. (○), controls, − NaCl; (●), controls, + NaCl; (□), morphine-adapted, − NaCl; (■), morphine-adapted, + NaCl.

used for determination of DOR in brain membranes. Maximum number of [^{3}H]DPDPE binding sites in morphine-treated membranes ($B_{max} = 0.057$ pmol . mg^{-1}) was 2.1× higher than in control ($B_{max} = 0.027$ pmol . mg^{-1}), Fig. 7. The effect of sodium chloride on [^{3}H]DPDPE binding was similar to that on [^{3}H]DADLE binding: inhibition was detected in control membranes only.

The difference between the two radioligands may be explained by higher specificity of [^{3}H]DPDPE to DOR in samples prepared from brain as the brain tissue contains, besides δ-opioid-receptors, high amount of μ- and κ-receptors [58]: maximum number of radioligand binding sites occupied by [^{3}H]DADLE was significantly higher than that recognized by [^{3}H]DPDPE. Therefore, morphine-induced increase of DOR detected by [^{3}H] DPDPE (2.1×) represents a "better estimate" of the actual increase of DOR density in PM isolated from morphine-adapted rats.

Sodium ions have been described as efficient inhibitors of agonist binding to numerous GPCR including OR causing the shift of receptor molecules towards the non-active state and uncoupling DOR from the cognate G protein, i.e. inverse agonist effect [62–65]. Sodium ions also decrease the basal GDP/GTP exchange of G_i/G_o proteins [66]. The low sensitivity of DOR to inhibitory effect of NaCl in morphine-adapted samples may be therefore interpreted as disturbance of equilibrium between active and non-active forms of receptor molecules.

4. Discussion

Opioid *addiction* has been long recognized as neurological disease involving the development of complex behavior characterized by drug tolerance, dependence and craving for the drug. The efforts to elucidate the molecular and cellular mechanisms of opioid *addiction* extend over many years and their results may be classified into two main hypotheses [1]:

(a) According to *homeostasis theory*, the drug disturbs cellular homeostasis and its effects are compensated by the activation of pathways that produce opposite effects and thus restore homeostasis.
(b) According to *desensitization theory*, the change of the drug–receptor interaction, receptor–G protein interaction or of some other, down-stream steps of OR-stimulated cascade renders the receptor less sensitive to the drug [1,7,57,67].

The *homeostasis* model involves an alteration of the amount of macromolecules in the cell, while the *desensitization* hypothesis does not because the negative change of drug–receptor interaction or subsequent steps of OR-initiated cascade may proceed with unchanged level of down-stream effectors. Our previous data [27] indicated that long-term adaptation of rats to increasing doses of morphine (according to the same protocol as that used in this work, group + M10) induces the *desensitization* of trimeric G protein response to MOR and DOR agonists (high-affinity GTPase and GTPγS binding assays). Desensitization of G protein response was demonstrated in plasma-membrane fraction isolated from rat brain cortex [27,40]. Furthermore, behavioral studies performed with the same group of animals indicated that these animals were fully "*drug*

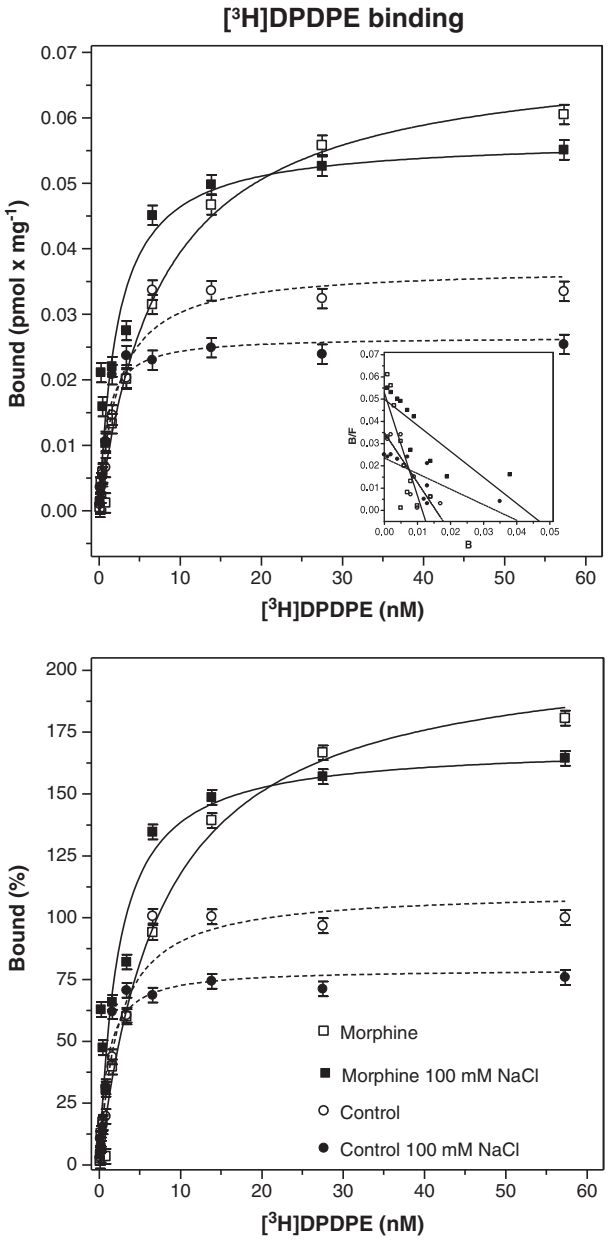

Fig. 7. Agonist binding characteristics of DOR; [^{3}H] DPDPE. Saturation of specific [^{3}H] DPDPE binding sites in control (−M10) and morphine-treated (+M10) plasma membrane samples was measured in 0.15–35 nM range of radioligand concentrations in the presence (+NaCl) or absence (−NaCl) of 100 mM NaCl. The B_{max} and K_d values were calculated by GraphPad*Prizm4*. The data represent the average of three experiments performed in triplicates ± SEM. (○), controls, −NaCl; (●), controls, +NaCl; (□), morphine-adapted, −NaCl; (■), morphine-adapted, +NaCl.

adapted" (*hot-plate* and *hind paw withdrawal* tests of tolerance). The state of *drug dependence* was also manifested by ptosis, chewing, diarrhea, increased sensitivity to touch and teeth clattering after drug withdrawal [27].

These results were fully compatible with data reported earlier by other authors who used auto-radiographic detection of the high-affinity [〈35〉S] GTPγS binding sites in different brain regions, mainly in specific areas of brain stem [28–30]. Thus, the decrease in functional response of G proteins persists in brain of animals fully adapted to morphine for prolonged period of time [27–30] and proceeds at the unchanged level of all the main classes of G proteins (Fig. 4). Accordingly, determination of AC activity in PM isolated from morphine-adapted rats indicated that inhibitory effect of opioid agonists, clearly manifested in control animals (group−M10), was *not* present in morphine-adapted rats (group+M10). This result has been demonstrated for basal as well as Forskolin-stimulated AC activity (Fig. 5) and was in full agreement with the data of He and Whistler [57].

Significance of the dramatic increase of ACI (8×) and ACII (2x) described in this work (Fig. 1A) was strongly supported by additional data indicating the specificity of this increase as the level of all other AC isoforms (AC III–IX) was unchanged (Fig. 2A) and that the increase of ACI and II was not detected in membranes exposed to the same doses of morphine, but for 24 h only (Fig. 2B).

It may be assumed that desensitization of G protein response for prolonged period of time (10 days) serves as an impulse for induction of compensatory response — proteosynthesis leading to specific increase of ACI and II in PM of morphine-adapted rats. This interpretation is fully in line with characteristics of molecular mechanisms of opioid tolerance and addiction as an example for homeostatic control aiming to keep the performance of target cell metabolism at unchanged level [1]. Finally, after withdrawal of the drug for 20 days, AC levels return back to the normal state (Fig. 1B).

Data presented in this work thus fall in line between the two above mentioned hypotheses of drug addiction as homeostatic mechanisms and activation of specific proteosynthetic pathways are obviously responsible for increase in plasma membrane density of ACI and ACII, simultaneously, the decrease of G protein response to OR stimulation detected in the same type of membranes [27], may be regarded as a part of desensitization mechanism of morphine action.

In brain, ACI and ACII represent the highly expressed and physiologically important species of this crucial regulatory enzyme of cAMP-dependent signaling cascades [31,68–70]. Sensitization, activation or over-shoot of AC activity after prolonged exposure of cultured cells or brain tissue to morphine has been demonstrated in previous studies of mechanism of action of this drug [1,7,8,16–23,26]. These data, however, were up to now not accompanied by the detailed analysis of the individual subtypes of AC protein molecules in plasma membranes isolated from brain cortex. Furthermore, the efforts to explain the molecular mechanism of the increase of AC activity by long-term morphine treatment have not so far resulted in a commonly accepted interpretation as widely different and even contradictory results were obtained [1,7,21,22,28,29,57].

The increase of ACI and II which has been clearly demonstrated in this work has to be considered together with the unchanged level of all other types of AC molecules and PM markers Na,K-ATPase, trimeric G protein subunits and caveolin-1. The unchanged level of these PM proteins brings strong evidence for the *specificity* of the long-term morphine effect on ACI and II. *Therefore, data presented in this work bring new and original evidence which so far has not been presented in the up-to-date literature and help for better understanding of the complicated pathological phenomenon denominated as drug addiction.*

We suggest that the positive as well as negative regulatory circuits exist at different steps of OR-induced signaling pathways when responding to prolonged exposure to morphine in the course of full adaptation to this drug. Decrease of G protein response to OR stimulation, *desensitization*, persists in animals adapted to morphine for 10- or 12 days [27–30], while the levels of all the main classes of G proteins remained unchanged (Fig. 4). Consequently, the decrease in inhibitory effect of G proteins on AC activity was measured in PM isolated from morphine-adapted rats (Fig. 5). It may be therefore assumed that the synthesis of new ACI and II molecules represents the *specific*, compensatory response leading to the increased plasma membrane density of these protein molecules (Fig. 1A, left panels).

Our results and interpretation are also relevant to analysis of drug tolerance and addiction states of mammalian organism as behavioral tests performed under in vivo conditions indicated that morphine-adapted animals have been fully *drug dependent* and developed *tolerance* to subsequent drug addiction [27].

Explanation why ACI and ACII differ when responding to the long-term morphine treatment can hardly be clear-cut and unequivocal as these two isoforms differ substantially when responding to different GPCR agonists and activated forms of G proteins [25,68–70]. ACI is known to be inhibited by free $G_o\alpha$ and $G\beta\gamma$ subunits [10,68,70], while ACII activity is dramatically activated/potentiated by $G\beta\gamma$ in the presence free $G_s\alpha$ subunits [21,22,25,69]. Nevertheless, we assume that the decreased response of PTX-sensitive G proteins of G_i/G_o family to MOR and DOR agonists in morphine-adapted rats (desensitization) represents the primary impulse for subsequent compensatory response increasing the expression level of ACI and II. Preferential increase of ACI (Fig. 1A) and attenuation of DAMGO-mediated inhibition of AC activity (Fig. 5) [57] suggests the primary involvement of "classical, inhibitory pathway" proceeding via MOR and inhibition of ACI activity [68,70].

5. Conclusions

Data presented in this work extend the knowledge and bring more close view to understanding of the long-term adaptation of mammalian organism to morphine and widely studied phenomena of drug addiction and tolerance.

We have found that:

- plasma membrane density of ACI and II molecules was increased largely and this increase was disproportionate between ACI (8×) and ACII (2.5×) in rats adapted to increasing doses of morphine for prolonged period of time, 10 days,
- increase of ACI and II represented the specific effect as the level of ACIII–IX was unchanged,
- levels of plasma membrane marker Na, K-ATPase and caveolin-1 were unchanged,
- membrane density of all the major classes of trimeric G proteins was unchanged;
- number of δ-opioid receptors was increased 2× and agonist binding to these receptor sites was not affected by sodium ions;
- difference in responsiveness of different AC isoforms to the long-term morphine treatment may be interpreted as preferential activation of specific synthetic pathway leading to production of new ACI and AC II molecules,
- increase of ACI and II was not detected in PM prepared from rats exposed to the same doses of morphine, but for 24 h only (short-term exposure),
- analysis of PM isolated from animals adapted to morphine for 10 days and subsequently nurtured for 20 days in the absence of the drug indicated that membrane density of both ACI and ACII returned fully to the control level observed in morphine-unexposed rats. *Thus, the major reorganization of the complement of AC molecules in plasma membrane, arising as a compensatory response to the long-term adaptation to morphine, was fully reversible.*

Acknowledgements

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Proteomic analysis of post-nuclear supernatant fraction and percoll-purified membranes prepared from brain cortex of rats exposed to increasing doses of morphine

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Abstract

Background: Proteomic analysis was performed in post-nuclear supernatant (PNS) and Percoll-purified membranes (PM) prepared from fore brain cortex of rats exposed to increasing doses of morphine (10–50 mg/kg) for 10 days.

Results: In PNS, the 10 up (↑)- or down (↓)-regulated proteins exhibiting the *largest morphine-induced change* were selected, excised manually from the gel and identified by MALDI-TOF MS/MS: **1**-(gi|148747414, Guanine deaminase), ↑2.5×; **2**-(gi|17105370, Vacuolar-type proton ATP subunit B, brain isoform), ↑2.6×; **3**-(gi|1352384, Protein disulfide-isomerase A3), ↑3.4×; **4**-(gi|40254595, Dihydropyrimidinase-related protein 2), ↑3.6×; **5**-(gi|149054470, N-ethylmaleimide sensitive fusion protein, isoform CRAa), ↑2.0×; **6**-(gi|42476181, Malate dehydrogenase, mitochondrial precursor), ↑1.4×; **7**-(gi|62653546, Glyceraldehyde-3-phosphate dehydrogenase), ↑1.6×; **8**-(gi|202837, Aldolase A), ↑1.3×; **9**-(gi|31542401, Creatine kinase B-type), ↓0.86×; **10**-(gi|40538860, Aconitate hydratase, mitochondrial precursor), ↑1.3×. The identified proteins were of cytoplasmic (**1, 4, 5, 7, 9**), cell membrane (**2**), endoplasmic reticulum (**3**) and mitochondrial (**6, 8, 10**) origin and 9 of them were significantly increased, 1.3-3.6×. The 4 out of 9 up-regulated proteins (**4, 6, 7, 10**) were described as functionally related to oxidative stress; the 2 proteins participate in genesis of apoptotic cell death.
In PM, the 18 up (↑)- or down (↓)-regulated proteins were identified by LC-MS/MS and were of *plasma membrane* [Brain acid soluble protein, ↓2.1×; trimeric Gβ subunit, ↓2.0x], *myelin membrane* [MBP, ↓2.5×], *cytoplasmic* [Internexin, ↑5.2×; DPYL2, ↑4.9×; Ubiquitin hydrolase, ↓2.0×; 60S ribosomal protein, ↑2.7×; KCRB, ↓2.6×; Sirtuin-2, ↑2.5×; Peroxiredoxin-2, ↑2.2×; Septin-11, ↑2.2×; TERA, ↑2.1×; SYUA, ↑2.0×; Coronin-1A, ↓5.4×] and *mitochondrial* [Glutamate dehydrogenase 1, ↑2.7×; SCOT1, ↑2.2×; Prohibitin, ↑2.2×; Aspartate aminotransferase, ↓2.2×] origin. Surprisingly, the immunoblot analysis of the same PM resolved by 2D-ELFO indicated that the "active", morphine-induced pool of Gβ subunits represented just a minor fraction of the total signal of Gβ which was decreased 1.2x only. The dominant signal of Gβ was unchanged.

Conclusion: Brain cortex of rats exposed to increasing doses of morphine is far from being adapted. Significant up-regulation of proteins functionally related to oxidative stress and apoptosis suggests a major change of energy metabolism resulting in the state of severe brain cell "discomfort" or even death.

Keywords: Morphine, Long-term adaptation, Fore brain cortex, Isolated plasma membranes, Post-nuclear supernatant, 2D electrophoresis

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Background

Morphine is one of the most effective painkillers. Repeated exposure of experimental animals to morphine results in tolerance to this drug, development of physical dependence and a chronic relapsing disorder – drug addiction [1-5]. Physical dependence contributes to a drug seeking behavior and the continuous drug use with the aim to prevent the onset of unpleasant withdrawal symptoms. To name just few, morphine-induced changes of brain function were associated with alternations of synaptic connectivity [6], neurotransmission [7], specific signaling cascades [8], energy metabolism [9] and stability of protein molecules [10].

Hyper-sensitization or super-activation of adenyl cyclase (AC) activity by prolonged exposure of cultured cells or mammalian organism to morphine has been demonstrated in previous studies of mechanism of action of this drug [1-5] and considered as biochemical basis for development of opiate *tolerance* and *dependence*.

Our previous work on isolated Percoll® membranes (PM) prepared from brain cortex of rats exposed to morphine for 10 days (10–50 mg/kg) indicated a desensitization of G-protein response to μ-OR (DAMGO) and δ-OR (DADLE) stimulation [11] and specific increase of ACI (8x) and ACII (2.5×) isoforms [12]. The κ-OR (U-23554)-stimulated [^{35}S] GTPγS binding and expression level of ACIII-IX in PM was unchanged. Behavioral tests of morphine-treated animals indicated that these animals were fully drug-dependent (opiate abstinence syndrome) and developed tolerance to subsequent drug addition (analgesic tolerance - hot-plate and hind paw withdrawal tests). The increase of ACI and ACII was interpreted as a specific compensatory response to prolonged stimulation of brain cortex OR by morphine.

Proteomic analysis represents a useful approach for an investigation of the overall changes of protein composition induced by the short-term or prolonged use of drugs. The aim of our present work was to identify proteins which are significantly altered in brain cortex of rats exposed to the increasing, high doses of morphine for prolonged period of time (10 days). For this aim, the post-nuclear supernatant fraction (PNS) was analyzed because it contains proteins of mitochondrial, endoplasmic reticulum, plasma membrane as well as cytoplasmic origin. In the second part of our work, we extended these studies by analysis of protein composition in membrane fraction isolated in Percoll gradient (PM).

Results

Two-dimensional electrophoresis and protein identification in post-nuclear supernatant prepared from brain cortex of control and morphine-treated rats; *analysis by MALDI-TOF MS/MS*

Samples of PNS were extracted in ice-cold aceton/TCA/96% ethanol, resolved by 2D-ELFO in linear IPG strips (pH 3–11) and 10% w/v acrylamide/0.26% w/v bis-acrylamide gels as described in methods and stained with silver or colloidal Coomassie blue. The stained 2D gels were scanned with an imaging densitometer and quantified by PDQuest software.

About 440 protein spots were recognized by silver staining and PDQuest analysis of gels in both types of PNS (Figure 1, left panels); when stained in colloidal Coomassie blue, about 200 spots were recognized. In CBB-stained gels, proteins 1–10 with different mobility in (+M10) and (−M10) samples were selected for identification by MALDI-TOF MS/MS as described in methods (Figure 1, right panels). The detailed list of the altered and identified proteins is presented in Additional file 1: Table S1 and Table 1. These tables also include description of the subcellular localization and function of these proteins.

The identified proteins were of cytoplasmic (**1**-Guanine deaminase, ↑2.5×; **4**-Dihydropyrimidinase-related protein 2,↑3.6×; **5**-N-ethylmaleimide sensitive fusion protein, isoform CRAa, ↑2.0×; **7**-Glyceraldehyde-3-phosphate dehydrogenase, ↑1.6×; **9**-Creatine kinase B-type, ↓0.86), cell membrane (**2**-Vacuolar-type proton ATPase, subunit B, brain isoform), ↑2.6x), endoplasmic reticulum (**3**-Protein disulfide-isomerase A3, ↑3.4×) and mitochondrial (**6**-Malate dehydrogenase, mitochondrial precursor, ↑1.4x; **8**-Aldolase A, ↑1.3×; **10**-Aconitate hydratase, mitochondrial precursor, ↑1.3x) origin. The 9 of them were significantly increased, 1.3-3.6x. Correlation with functional properties of these proteins indicated up-regulation of proteins related to guanine degradation (**1**), vacuolar acidification (**2**), apoptotic cell death (**3**), oxidative stress (**4, 6, 7, 10**), membrane traffic (**5**) and glycolysis (**8**). All together, the spectrum of the altered proteins suggests a major alternation of brain cortex tissue when exposed to increasing doses of morphine. *The most significant change from functional point of view was up-regulation of proteins related to oxidative stress (see discussion for further details).*

Two-dimensional electrophoresis and protein identification in Percoll-purified membranes isolated from brain cortex of control and morphine-treated rats; *analysis by LC-MS/MS*

PM samples were resolved by 2D-electrophoresis in the same way as described for PNS. The resolution in 10% w/v acrylamide/0.26% w/v bis-acrylamide gels was used in the case of silver staining; 12.0% w/v acrylamide/0.32% w/v bis-acrylamide gels were used for staining in CBB. About 300 protein spots were recognized by silver (Figure 2, left panels); when stained in CBB, the total number of detected protein spots was 490 (Figure 2, right panels). Proteins 1–18 with an altered mobility in (+M10) versus (−M10) samples were excised from in

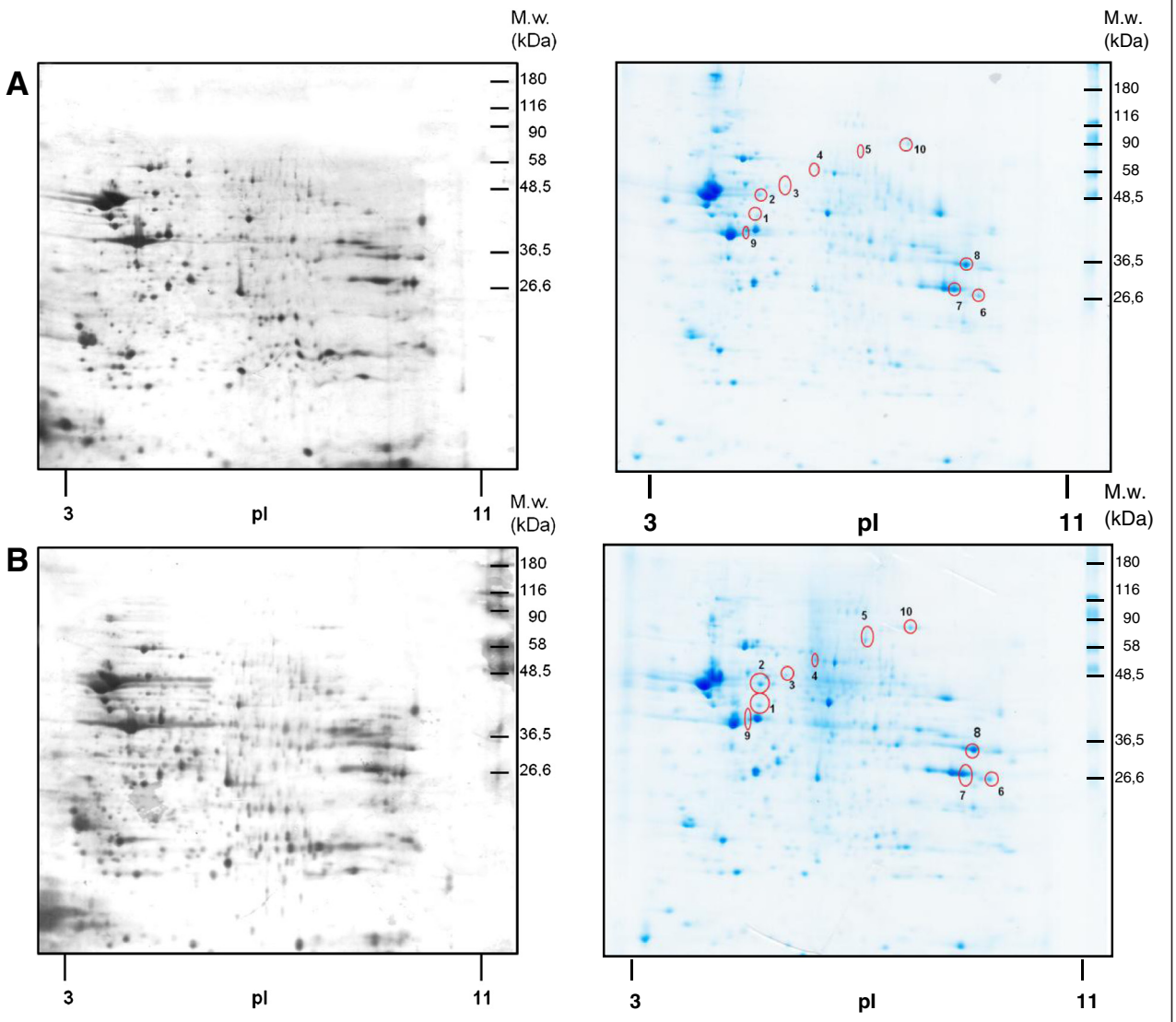

Figure 1 Two-dimensional gel electrophoresis maps of PNS prepared from control (A) and morphine-treated (B) rats. Protein samples (600 μg for both Silver and CBB staining) were separated in the first dimension on pH 3–11 IPG strips. For resolution in the second dimension, SDS-PAGE was performed in 10% w/v acrylamide/0.26% w/v bis-acrylamide gel. The stained 2D gels were scanned in an imaging densitometer and quantified by PDQuest software. The process of quantification of the difference between morphine-treated (+M10) and control (–M10) samples included spot detection, gel matching and spot quantification. Master gel was constructed for each group (+M10) or (–M10) as a synthetic image that contains the spot data from all the gels in the MatchSet. At least four replicates were performed for each group/sample. All matched and unmatched spots were then checked in a manual manner. Protein levels altered at least two-fold were taken into consideration. About 200 protein spots totally were recognized by CBB silver staining by PDQuest analysis. Proteins 1–10 with an altered mobility in (+M10) versus (–M10) samples were excised from in CBB-stained gels and identified by MALDI TOF/TOF analyzer as described in methods. *Left panels*, Silver staining; *Right panels*, CBB staining.

CBB-stained gels and identified by LC-MS/MS. The list of altered and identified proteins is presented in Additional file 2: Table S2 and Table 2. These tables also include a brief description of subcellular localization and function of these proteins as well as quantitative estimate of their relative change induced by morphine-treatment.

The identified up (↑)- or down (↓)-regulated proteins were of *plasma membrane* [**1**-BASP1, Brain acid soluble protein 1, ↓2.1×; **2**-GBB1, Guanine nucleotide-binding protein subunit beta-1, ↓2.0×], *myelin membrane* [**17**-MBP, Myelin basic protein S, ↓2.5×], *cytoplasmic* [**3**-KCRB, Creatine kinase B-type (EC 2.7.3.2), ↓2.6x; **4**-AINX, Alpha-internexin, ↑5.2×; **5**-DPYL2, Dihydropyrimidinase-related protein 2, ↑4.9×; **6**-SIRT2, NAD-dependent deacetylase sirtuin-2, ↑2.5×; **7**-SYUA, Alpha-synuclein, ↑2.0×; **8**-PRDX2, Peroxiredoxin-2, ↑2.2×; **9**-TERA, Transitional endoplasmic reticulum ATPase, ↑2.1×; **13**-UCHL1,

Table 1 Functional significance of proteins identified in PNS as altered by chronic morphine

Protein name	Change (dependence vs.control)	Subcellular localization	Functional category	Protein characterization - PNS
Guanine deaminase	Up-regulated	Cytoplasm	Metabolism	Purine metabolism, guanine degradation [13]
V-type proton ATP subunit B, brain isoform	Up-regulated	Cell membrane	Trafficking	ATP hydrolysis coupled proton transport, vacuolar acidification [14]
Protein disulfide-isomerase A3	Up-regulated	Endoplasmatic reticulum lumen	Cellular development and regulation	Up-regulation of this protein causes apoptotic cell death [15], alterations in its level were revealed during neurodegenerative processes [16]
Dihydropyrimidinase-related protein 2	Up-regulated	Cytoplasm	Neuronal development and regulation	Neuronal development and polarity [8], cone collapse and cell migration; one of major determinants in the control of oxidative stress [17]
N-ethylmaleimide sensitive fusion protein, isoform CRA_a	Up-regulated	Cytoplasm	Trafficking	ATP binding, regulating protein membrane trafficking, involved in vesicle priming [18]
Malate dehydrogenase, mitochondrial precursor	Up-regulated	Mitochondrion matrix	Metabolism	L-malate dehydrogenase activity, protein self-association; up-regulation of the mitochondrial malate dehydrogenase is caused by oxidative stress [19]
Glyceraldehyde-3-phosphate dehydrogenase	Up-regulated	Cytoplasm	Metabolism	Glyceraldehyde-3-phosphate dehydrogenase and nitrosylase activities; surprising role in apoptosis [20]; is known as a major target protein in oxidative stress [21]
Aldolase A	Up-regulated	Mitochondrion	Metabolism	Role in glycolysis and gluconeogenesis, scaffolding protein; potential role in regulating the free intracellular concentration of InsP3, and subsequently intracellular calcium dynamics[22,23]; the expression of aldolase A may be regulated by chronic lithium administration [24]
Creatine kinase B-type	Down-regulated	Cytoplasm	Metabolism	Energy-related (skeletal muscle, heart, brain and spermatozoa), brain development [25]
Aconitate hydratase, mitochondrial precursor	Up-regulated	Mitochondrion	Metabolism	Isomerization of citrate to isocitrate via cis-aconitate;an iron-sulfur protein, the particular susceptibility to oxidative damage may be related to the iron-sulfur cluster [4Fe-4S]in its active site [26]

Ubiquitin carboxyl-terminal hydrolase L1, ↓2.0×; **15**-COR1A, Coronin-1A, ↓5.4×, **16**-SEP11, Septin-11, ↑2.2×; **18**-RL12, 60S ribosomal protein L12, ↑2.7×] and *mitochondrial* [**10**-DHE3, Glutamate dehydrogenase 1, ↑2.7×; **11**-SCOT1, Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, ↑2.2×; **12**-AATM, Aspartate aminotransferase**,** ↓2.2×; **14**-PHB, Prohibitin, ↑2.2×] origin.

Thus, the only member of GPCR-initiated signaling cascades identified by LC-MS/MS was trimeric Gβ subunit, which was decreased 2× in PM samples prepared from morphine-adapted rats. The morphine-induced decrease of Gβ subunit in PM was subsequently verified by immunoblot analysis of the same 2D-gels as those used for preparation of samples for LC-MS/MS (Figure 3). The spot 2 (compare with Figure 2) represented just a small fraction of the total signal of Gβ subunits which was distributed over wider range of pI. The total signal of Gβ was decreased 1.2x only. We have divided the signal of Gβ in CBB-stained gels into 8 small spots according to immunoblot signal (Figure 3) in order to verify it. Proteomic analysis was performed by LC-MS/MS and positive signal was detected in spots 3, 4, 5, 7 and 8 (Table 3).

Therefore, the decrease of Gβ determined by proteomic analysis (2×) has to be regarded as an alternation of relatively small fraction of numerous forms of Gβ resolved by 2D-ELFO. Morphine-induced decrease of Gβ is selectively oriented to specific, minority component of this protein; the dominant pool of Gβ subunits is unchanged.

Discussion

Opium extracts from the plant Papaver somniferum have been used for therapeutic and recreational purposes for thousands of years. Opioid alkaloids and related pharmaceuticals are the most effective analgesics for the treatment of acute and chronic pain. They also represent one of the largest components of the illicit drug market worldwide, generating revenue of approximately $70 billion in 2009, much of which supports crime, wars and terrorism. Intravenous use of opioid drugs is a leading cause of death by overdose in Europe and North America, and a major contributing factor to the worldwide AIDS epidemic [50,51].

Morphine and codeine are the main active opioid alkaloids in opium. In humans, they act on the central nervous system to produce a wide range of effects including analgesia, euphoria, sedation, respiratory depression and cough suppression. Chronic opiate administration results

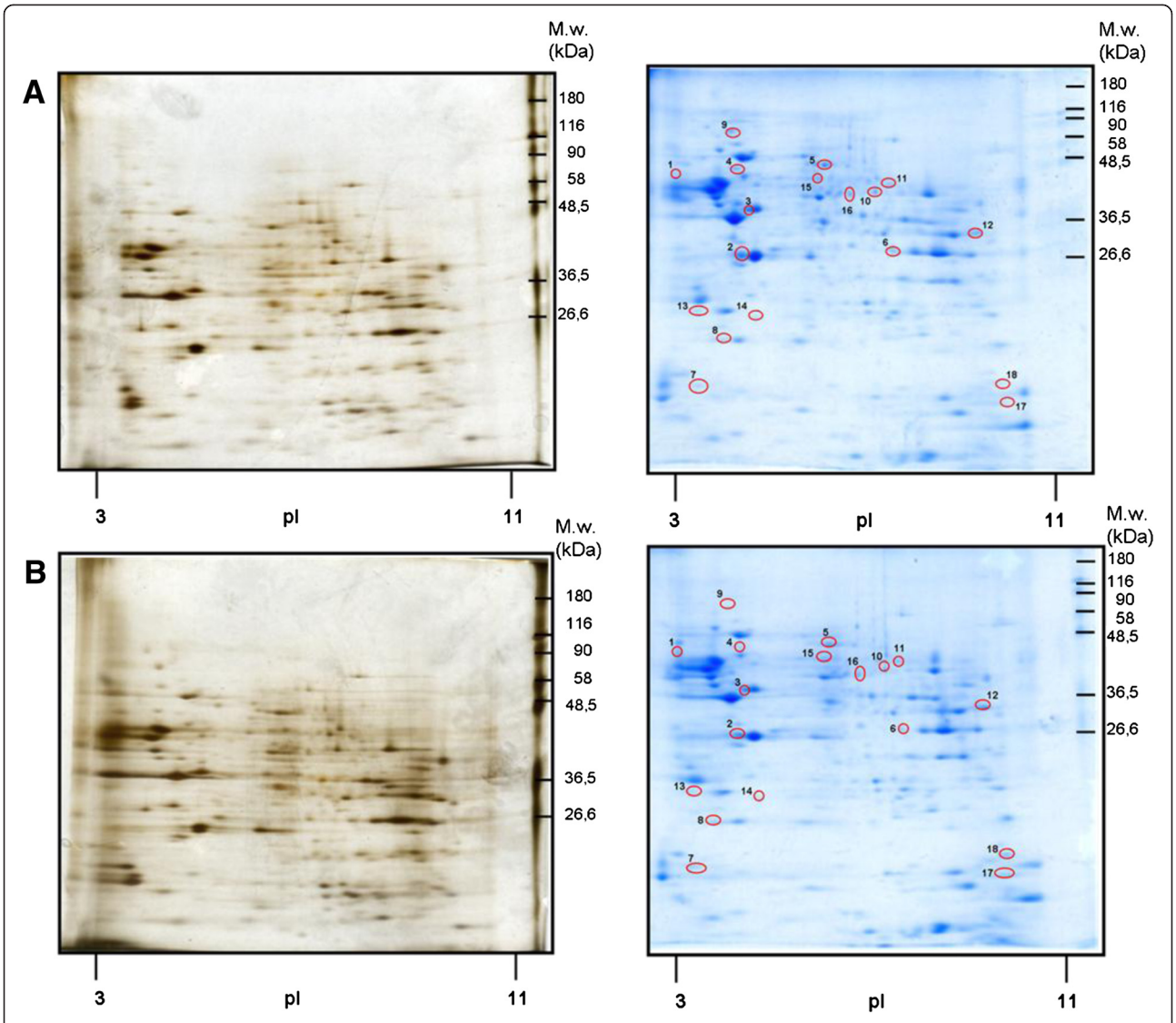

Figure 2 Two-dimensional gel electrophoresis maps of protein extracts prepared from PM of control (A) and morphine-treated (B) rats. Protein samples (400 μg for Silver staining; 2 mg for CBB staining) were separated in the first dimension on pH 3–11 IPG strips. For resolution in the second dimension, SDS-PAGE was performed in 10% w/v acrylamide/0.26% w/v bis-acrylamide gel (silver staining) or in 12.5% w/v acrylamide/0.0625% w/v bis-acrylamide gel (CBB staining). The stained 2D gels were scanned in an imaging densitometer and quantified by PDQuest software. The process of quantification of the difference between morphine-treated (+M10) and control (–M10) samples included spot detection, gel matching and spot quantification. Master gel was constructed for each group (+M10) or (–M10) as a synthetic image that contains the spot data from all the gels in the MatchSet. At least four replicates were performed for each group/sample. All matched and unmatched spots were then checked in a manual manner. Protein levels altered at least two-fold were taken into consideration. About 500 protein spots totally were recognized by CBB staining by PDQuest analysis. Proteins 1–18 with an altered mobility in (+M10) versus (–M10) samples were excised from in CBB-stained gels and identified by LC-MS/MS as described in methods. *Left panels*, Silver staining. *Right panels*, Coomassie staining.

in the development of tolerance and dependence, but the regulation of MOR and DOR function during this process is not clearly understood.

To localize changes of MOR-stimulated G-protein activity in various brain regions after chronic morphine treatment, Sim et al. [52] examined [^{35}S]GTPγS binding to brain sections by in vitro autoradiography. Rats were treated for 12 d with increasing doses (10–320 mg . kg^{-1} . d^{-1}) of morphine. Control rats were injected with either saline or a single acute injection of morphine (20 mg/kg). [^{35}S]GTPγS binding was measured in the presence or absence of MOR-selective agonist DAMGO. In rats injected with a *single acute dose* of morphine, no significant changes were detected in basal or DAMGO-stimulated [^{35}S]GTPγS binding in any brain region. In *chronic morphine-treated rats*, however, DAMGO-stimulated [^{35}S]GTPγS binding in cerebral cortex was significantly decreased when compared with control rats. Similar data were obtained in analysis of

Table 2 Functional significance of proteins identified in PM fraction as altered by chronic morphine

Protein name	Change (dependence vs.control)	Subcellular localization	Functional category	Protein characterization - PM
Brain acid soluble protein 1	Down-regulated	Cell membrane; Lipid anchor	Neuronal development and regulation	Associated with the membranes of growth cones that form the tips of elongating axons, DNA-dependent, localizes in the membrane raft domain with a cholesterol-dependent manner; changes in the localization during the development of neuronal polarity [27]
Guanine nucleotide-binding protein subunit beta-1	Down-regulated	Cell membrane	Signaling	Gβ1 is required for neural tube closure, neural progenitor cell proliferation and neonatal development [28]; stimulated ACII, ACIV, ACVII, inhibited ACI, ACV/VI, ACVIII [29,30]
Creatine kinase B-type	Down-regulated	Cytoplasm	Metabolism	Energy-related (skeletal muscle, heart, brain and spermatozoa), brain development [25], aging [31]; one of major determinants in the control of oxidative stress [17]
Alpha-internexin	Up-regulated	Cytoplasm	Neuronal development and regulation	Copurifies with intermediate filaments from rat spinal cord and optic nerve, developmental protein involved in morphogenesis of neurons [32]
Dihydropyrimidinase-related protein 2	Up-regulated	Cytoplasm	Neuronal development and regulation	Neuronal development and polarity [8], cone collapse and cell migration; one of major determinants in the control of oxidative stress [17]
NAD-dependent deacetylase sirtuin-2	Up-regulated	Cytoplasm	Cellular development and regulation	Colocalizes with microtubules; NAD-dependent deacetylase, involved in the control of mitotic exit in the cell cycle; up-regulation may protect the brain against incurred oxidative damage [33]
Alpha-synuclein	Up-regulated	Cytoplasm	Neuronal development and regulation	Specifically expressed in neuronal cell bodies and synapses, negative regulation of neuron apoptosis, aging; role in the pathogenesis of Parkinson's disease [34]
Peroxiredoxin-2	Up-regulated	Cytoplasm	Neuronal development and regulation	Involved in redox regulation of the cell, negative regulation of neuron apoptosis; the relative abundance appears to protect cellular components by removing the low levels of hydroperoxides and peroxinitrites produced as a result of normal cellular metabolism in the cytosol [35]
Transitional endoplasmic reticulum ATPase	Up-regulated	Cytoplasm Nucleus	Cellular development and regulation	Involved in the formation of the transitional endoplasmatic reticulum, necessary for the fragmentation of Golgi stacks during mitosis and for their reassembly after mitosis [36]; interacts with neurofibromin to control the density of dendritic spines [37]
Glutamate dehydrogenase 1, mitochondrial	Up-regulated	Mitochondrion matrix	Metabolism	Glutamate catabolic process, long-term memory, in rat brain the glutamate dehydrogenase reaction operates in the direction of ammonia production [38]
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	Up-regulated	Mitochondrion matrix	Metabolism	A mitochondrial ketone body-activating enzyme [39]; brain development, response to drug
Aspartate aminotransferase, mitochondrial	Down-regulated	Mitochondrion matrix	Metabolism	Amino acid metabolism, metabolite exchange between mitochondria and cytosol, fatty acid transport; its activity is related with the maintenance of amino acid homeostasis and might be an indicator of mitochondrial injury [40]
Ubiquitin carboxyl-terminal hydrolase isozyme L1	Down-regulated	Cytoplasm Endoplasmatic reticulum membrane	Deubiquitination Neuronal development and regulation	Involved both in the processing of ubiquitin precursors and of ubiquitinated proteins; the ubiquitination/proteasome pathway involved in synaptic plasticity [41]
Prohibitin	Up-regulated	Mitochondrion inner membrane	Cellular development and regulation	Antiproliferative activity, role in regulating mitochondrial respiration activity and aging, response to drug [42-44]; down-regulation of prohibitin renders neurons more vulnerable to injury and reactive oxygen species production, whereas up-regulation appears to be neuroprotective [45]
Coronin-1A	Down-regulated	Cytoplasm	Cellular development and regulation	Invagination of plasma membrane, forming protrusions of plasma membrane involved in cell locomotion; coronin-1A activity is spatially and temporally regulated by phosphoinositides [46]

Table 2 Functional significance of proteins identified in PM fraction as altered by chronic morphine *(Continued)*

Septin-11	Up-regulated	Cytoplasm	Cellular development and regulation	Filament-forming cytoskeletal GTPase, cell division; it is involved in dendritic maturation [47]
Myelin basic protein S	Down-regulated	Myelin membrane	Neuronal development and regulation	Myelination, negative regulation of axonogenesis; morphine exposure colud result in a decreased number of myelinated axons [48]
60S ribosomal protein L12	Down-regulated	Cytoplasm	Regulatory	Binds directly to 26S ribosomal RNA; it accesses the importin 11 pathway as a major route into the nucleus [49]

MOR-stimulated [^{35}S]GTPγS binding after chronic heroin administration [53,54]. Accordingly, our analysis of PM isolated from cerebral cortex of rats exposed to morphine for 10 days (10–50 mg/kg) indicated significant desensitization of G-protein response to MOR and DOR stimulation [11] and up-regulation of ACI and II [12].

Proteome changes after prolonged morphine exposure have been so far investigated in "frozen tissue powders" of the rat cerebral cortex, hippocampus, striatum [55,56] and nucleus accumbens [7] or in the "whole-cell lysates" of striatal neuronal cell cultures [57]. Therefore, the aim of our work was to perform proteomic analysis in *more defined* preparations: post-nuclear supernatant (PNS) and membranes isolated in Percoll® gradient (PM). The morphine-induced changes in protein composition (proteom) of PNS and PM were determined by 2D-electrophoresis resolution and PDQuest analysis; the altered proteins were identified by MALDI-TOF MS/MS or LC-MS/MS.

Proteomic analysis of PNS indicated a marked increase of proteins of mitochondrial and cytoplasmic origin (Additional file 1: Table S1 and Table 1). The 9 out of 10 proteins exhibiting the largest morphine-induced change in Coomassie stained gels were increased *by* morphine: **1**-Guanine deaminase, ↑2.5×; **2**-Vacuolar-type proton ATP subunit B, brain isoform ↑2.6×; **3**-Protein disulfide-isomerase A3, ↑3.4×; **4**-Dihydropyrimidinase-related protein 2, ↑3.6x; **5**-N-ethylmaleimide sensitive fusion protein, isoform CRAa, ↑2.0×; **6**-Malate dehydrogenase, mitochondrial precursor, ↑1.4×; **7**-Glyceraldehyde-3-phosphate dehydrogenase, ↑1.6×; **8**-Aldolase A, ↑1.3×; **10**-Aconitate hydratase, mitochondrial precursor, ↑1.3×**.** The 4 out of 9 up-regulated proteins (**4**, **6**, **7**, **10**) were described as functionally related to manifestation of oxidative stress conditions [17,19,21,26]. Marked increase of Protein disulfide-isomerase A3 (**3**) causing apoptotic cell death [15] should be also noticed. The role in apoptosis has

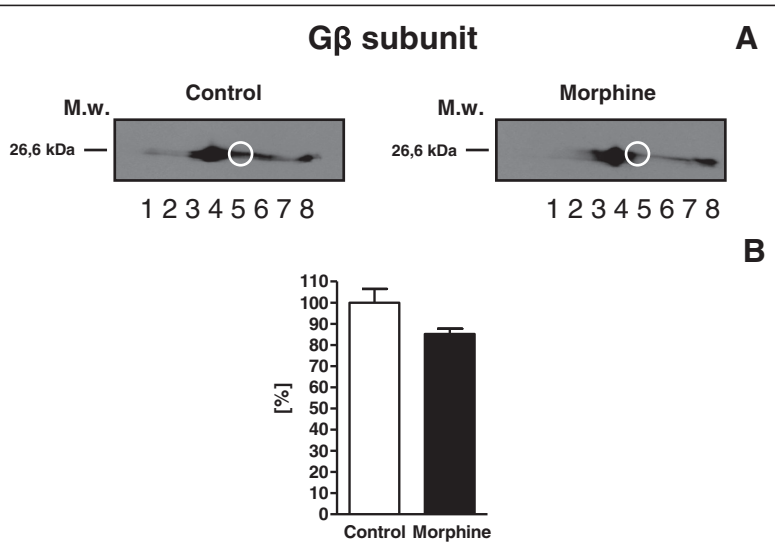

Figure 3 Gβ subunit protein; ***immunoblot analysis of 2D-gels.*** **A** Two-dimensional resolution of Gβ protein content in PM isolated from control and morphine-adapted rats. PM protein (400 μg) was resolved by 2D electrophoresis using the pI range 3–11 for isoelectric focusing in the first dimension. The white small circle shows the small fraction of the the total signal of Gβ which was taken into consideration when analyzed by LC-MS/MS. The second dimension was performed by SDS-PAGE in 10% w/v acrylamide/0.26% bis-acrylamide gels (Hoefer SE 600). Gβ was identified by immunoblotting with specific antibody as described in Material and methods. The numbers 1–8 represent spots of Gβ subunits which were subsequently analyzed by LC-MS/MS. **B** The average of 3 immunoblots ± SEM. Difference between (–M10) and (+M10) was analyzed by Student's *t*-test using GraphPad*Prizm4* and found not significant, NS ($p > 0.05$).

Table 3 Proteomic analysis of Gβ subunits isolated from brain cortex of control and morphine-treated rats

Spot	Accession number	Protein name	Mascot score	Matched peptides	Peptides	SC[a] [%]	MW[b] (kDa)	pI[c]
3	GBB1_RAT	**Guanine nucleotide-binding protein subunit beta-1**	184.3	6	R.LFDLR.A R.LLVSASQDGK.L K.LWDVR.E K.IYAMHWGTDSR.L + Oxidation (M) K.ACADATLSQITNNIDPVGR.I K.VHAIPLR.S	16.8	37.4	5.6
4	GBB1_RAT	**Guanine nucleotide-binding protein subunit beta-1**	471	12	K.ACADATLSQITNNIDPVGR.I R.LFVSGACDASAK.L K.IYAMHWGTDSR.L + Oxidation (M) R.LFDLR.A K.IYAMHWGTDSR.L R.LLVSASQDGK.L K.LWDVR.E R.KACADATLSQITNNIDPVGR.I R.LLLAGYDDFNCNVWDALK.A K.VHAIPLR.S K.LIIWDSYTTNK.V R.ELAGHTGYLSCCR.F	32.9	37.4	5.6
4	GBB2_RAT	**Guanine nucleotide-binding protein subunit beta-2**	413.9	10	R.TFVSGACDASIK.L K.ACGDSTLTQITAGLDPVGR.I K.IYAMHWGTDSR.L + Oxidation (M) R.LFDLR.A K.IYAMHWGTDSR.L R.LLVSASQDGK.L K.LWDVR.D K.VHAIPLR.S K.LIIWDSYTTNK.V R.LLLAGYDDFNCNIWDAMK.G + Oxidation (W)	14.4	37.3	5.6
5	GBB1_RAT	**Guanine nucleotide-binding protein subunit beta-1**	199.1	5	R.AGVLAGHDNR.V R.LFVSGACDASAK.L R.LFDLR.A K.IYAMHWGTDSR.L + Oxidation (M) R.LLVSASQDGK.L	14.1	37.4	5.6
5	GBB2_RAT	**Guanine nucleotide-binding protein subunit beta-2**	188.7	5	R.AGVLAGHDNR.V R.TFVSGACDASIK.L R.LFDLR.A K.IYAMHWGTDSR.L + Oxidation (M) R.LLVSASQDGK.L	3.5	37.3	5.6
7	GBB (1–4)_RAT	**Guanine nucleotide-binding protein subunit beta-3**	22.4	1	K.LLVSASQDGK.L	2.9	37.2	5.4
8	GBB (1–4)_RAT	**Guanine nucleotide-binding protein subunit beta-3**	34.7	1	K.LLVSASQDGK.L	2.9	37.2	5.4

[a]Sequence coverage.
[b]Theoretical molecular weight.
[c]Theoretical isoelectric point.

been also described for Glyceraldehyde-3-phosphate dehydrogenase (**7**), already mentioned as major target protein in oxidative stress [21]. The 4 out of 9 up-regulated proteins (**4**, **6**, **7**, **10**) were thus functionally related to manifestation of the state of oxidative stress/oxidative damage in brain of morphine-exposed rats and 2 proteins were related to apoptotic cell death.

More detailed analysis of Percoll-purified membranes indicated a complex reorganization of PM protein composition. The list of proteins presented in Additional file 2: Table S2 and Table 2 indicates that morphine-induced alternation included increase as well as decrease of wide range of proteins functionally and structurally related to plasma, myelin, endoplasmic reticulum and mitochondrial membranes. Numerous soluble enzymes present in soluble, cytosol fraction or in mitochondrial matrix were also altered by chronic morphine. Surprisingly, with the exception of trimeric Gβ subunit, not just one of these proteins was functionally related to GPCR- or ionic-channel-activated signaling cascades. Similarly, proteomic analysis of protein alternations induced in the long-term TRH-treatment of HEK cells expressing TRH-R and G11α protein indicated the change of 42 proteins, but not even one of these proteins represented plasma membrane protein functionally related to GPCR-initiated signaling cascades [58].

Our results indicate that the energy metabolism of rat brain cortex exposed to increasing doses of morphine (10–50 mg/kg, 10 days) is shifted far from the normal, physiological state. Using other words, brain cortex of rats exposed to morphine according to our protocol is far from being adapted. It may be suggested that the both neuronal and glial cells undergo a drastic reorganization as consequence of cell discomfort and, subsequently, oxidative stress. Simultaneous activation of all types of opioid receptors (μ-, δ- and κ-OR) by high doses of morphine results in high energy demand of neurons [59,60]. Consequently, glycogen in astrocytes as the single largest energy reserve in the brain is mobilized with the aim to match these increased energy requirements [61]. After depletion of glycogen in astrocytes, the state of oxidative stress appears [62] as the full supply of oxygen to brain mitochondria is not accompanied by transfer of the sufficient number of "reducing equivalents" into the mitochondrial matrix.

Conclusions

Proteomic analysis of rat brain cortex of rats exposed to morphine for 10 days (10–50 mg/kg) indicated a significant morphine-induced change of membrane protein composition. Changes in *post-nuclear supernatant* were exclusively based on increase (1.3-3.6×) of proteins of mitochondrial and cytoplasmic origin. In isolated *plasma membranes* (PM), morphine-induced alternation included increase as well as decrease of wide range of proteins functionally and structurally related to plasma, myelin, endoplasmic reticulum and mitochondrial membranes. Numerous soluble enzymes present in soluble, cytosol fraction or in mitochondrial matrix were also altered by chronic morphine. The only member of GPCR-initiated signaling cascades identified by LC-MS/MS in Percoll-purified membranes was trimeric Gβ subunit (**2**-GBB) which was decreased 2x in samples prepared from morphine-adapted rats. This "active" component of Gβ subunits, however, represented a minor pool of total complement of Gβ molecules in PM, which was unchanged.

Material and methods

Chemicals

Acrylamide, bis-acrylamide and Coomassie Blue G-250 were from SERVA (Heidelberg, Germany), nitrocellulose membrane was from Whatman (Germany). Immobiline Dry-Strips, Pharmalyte buffer, and secondary anti-rabbit antibody labeled with horseradish peroxidase were purchased from GE Healthcare (Piscataway, NJ). Complete protease inhibitor cocktail was from Roche Diagnostic, Mannheim, Germany (cat. no. 1697498). All others chemicals were from Sigma-Aldrich and were of highest purity available. Primary antibody oriented against trimeric Gβ subunit protein (T-20, sc-378) was from Santa Cruz.

Animals

Male Wistar rats (220-250 g) were killed by decapitation under ether narcosis, the frontal brain was rapidly removed, washed intensively from the remaining blood and cooled to 0°C. The cerebral cortex was separated on the pre-cooled plate, snap frozen in liquid nitrogen and stored at −70°C until use. The experiments were approved by Animal Care and Use Committee of the Institute of Physiology, Academy of Sciences of the Czech Republic to be in agreement with Animal Protection Law of the Czech Republic as well as European Comunity Council directives 86/609/EEC.

Morphine treatment of experimental animals

The animals were exposed to morphine by intra-muscular application according to the following protocol: 10 mg/kg (day 1 and 2), 15 mg/kg (day 3 and 4), 20 mg/kg (day 4 and 5), 30 mg/kg (day 6 and 7), 40 mg/kg (day 9) and, finally 50 mg/kg (day 10). The *morphine-adapted* rats were sacrificed 24 hours after the last dose of the drug (group + M10). Control animals were injected with sterile PBS and sacrificed in parallel with morphine-treated rats, i.e. 24 hours (group – M10) after the last dose [12].

Subcellular fractionation of rat brain cerebral cortex; preparation of post-nuclear supernatant (PNS) and percoll-purified membranes (PM)

Rat brain cortex was minced with razor blade on pre-cooled plate and diluted in STEM medium containing 250 mM sucrose, 20 mM Tris–HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.6, fresh 1 mM PMSF plus protease inhibitor cocktail. It was then homogenized mildly in loosely-fitting Teflon-glass homogenizer for 5 min (2 g w. w. per 10 ml) and centrifuged for 5 min at 3500 rpm (1200 × *g*). Resulting post-nuclear supernatant (PNS) was filtered through Nylon nets of decreasing size (330, 110 and 75 mesh, Nitex) and applied on top of Percoll in Beckman Ti70 tubes (30 ml of 27.4% Percoll in STE medium). Centrifugation for 60 min at 30000 rpm (65000 × *g*) resulted in the separation of two clearly visible layers (Bourova et al., 2009). The upper layer represented plasma membrane fraction (PM); the lower layer contained mitochondria (MITO). The upper layer was removed, diluted 1:3 in STEM medium and centrifuged in Beckman Ti70 rotor for 90 min at 50000 rpm (175000 × *g*). Membrane sediment was removed from the compact, gel-like sediment of Percoll and re-homogenized by hand in a small volume of 50 mM Tris–HCl, 3 mM $MgCl_2$, 1 mM EDTA, pH 7.4 (TME medium).

SDS-PAGE and immunoblotting

The aliquots of membrane fractions were mixed 1:1 with 2x concentrated Laemmli buffer (SLB) and heated for 3 min at 95 °C. Standard (10% w/v acrylamide/0.26% w/v bis-acrylamide) SDS electrophoresis was carried out as described before [63-65]. Molecular mass determinations were based on pre-stained molecular mass markers (Sigma, SDS 7B). After SDS-PAGE, proteins were transferred to nitrocellulose and blocked for 1 h at room temperature in 5% (w/v) low-fat milk in TBS-Tween buffer [10 mM Tris–HCl, pH 8.0, 150 mM NaCl, 0.1% (v/v) Tween 20]. Antibodies were added in TBS-Tween containing 1% (w/v) low-fat milk and incubated for at least 2 h. The primary antibody was then removed and the blot washed extensively (3x10 min) in TBS-Tween. Secondary antibodies (donkey anti-rabbit IgG conjugated with horseradish peroxidase) were diluted in TBS-Tween containing 1% (w/v) low-fat milk, applied for 1 h and after three 10 min washes, the blots were developed by ECL technique using Super Signal West Dura (Pierce) as substrate. The developed blots were scanned with an imaging densitometer ScanJett 5370C (HP) and quantified by Aida Image Analyzer v. 3.28 (Ray test).

Sample preparation for isoelectric focusing

Samples of PNS or PM containing 400–600 μg protein or 2 mg protein, respectively, were precipitated with ice cold aceton overnight at – 20°C. After centrifugation at 16 000 × *g* for 20 min at 4°C, the supernatant was removed and the pellet was precipitated with ice-cold 6% TCA for 1.5 h on ice. After centrifugation at 16 000 × *g* for 10 min at 4°C, the supernatant was discarded and the pellet washed with 400 μl of ice-cold 96% ethanol for 1 h at room temperature. The mixture was centrifuged at 16 000 × *g* for 10 min at 4°C and the remaining pellet was solubilizated with 250 μl IEF sample buffer containing 7 M urea, 2 M thiourea, 4% CHAPS, 1% DTT, 1% ampholines pH 3–10 and 0.01% bromphenol blue for 3 h at room temperature. After a brief centrifugation (16 000 × *g*, 1 min), the sample was transferred into a groove of the Immobiline DryStrip Reswelling Tray (GE Healthcare).

Two-dimensional electrophoresis (2D-ELFO)

Immobiline DryStrips (linear pH gradient 3–11 NL, 13 cm) were placed into the Immobiline DryStrip Reswelling Tray containing protein samples and rehydrated overnight.

Isoelectric focusing was performed using the Multiphor II system (GE Healthcare) at 15°C in the following manner: 150 V for 5 h, 500 V for 1 h, 3500 V for 12 h and 500 V for 3 h. The focused strips were stored at – 20°C or immediately used.

Strips were rinsed thoroughly with ultrapure water, dried quickly on filter paper and equilibrated in 4 ml of equilibration buffer (50 mM Tris–HCl pH 6.8, 6 M urea, 0.1 mM EDTA, 2% SDS, 30% glycerol and 0.01% bromophenol blue) containing 1% DTT for 15 min in order to reduce disulphide bridges and other oxidized groups. Subsequently, the strips were alkylated in equilibration buffer containing 2.5% iodoacetamide for 15 min. Molecular weight markers were loaded onto a piece of filter paper and placed close to the alkaline side of the strip. The strip and molecular marker were covered with 0.5% agarose. Gels were run vertically at a constant current of 10 mA for 20 min and then at 80 mA for 2 h till the bromophenol blue dye reached the end of the gel. The apparatus was cooled to 15°C using the Hoefer SE 600 unit (GE Healthcare).

Silver staining

Silver staining was performed by ProteoSilver™ Plus Silver Stain Kit (Sigma-Aldrich) according to the manufacturer's instructions [66-68]. Briefly, the gel was fixed in 40% ethanol/10% acidic acid overnight and then washed by 30% ethanol for 10 min and once by ultrapure water for 10 min. The gels were incubated for 10 min with 1% Sensitizer solution and washed twice with 200 ml of ultrapure water for 10 min. The gels were submerged in 1% Silver solution for 10 min, washed with 200 ml of ultrapure water for 1 min and developed with 100 ml of the Developer solution until the desired

intensity of spots was attained. The ProteoSilver Stop solution was added to the Developer solution and gels were incubated for 5 min. All steps were carried out at room temperature on an orbital shaker at 60 to 70 rpm. The gels were stored in fresh, ultrapure water or dried in 3% glycerol/25% methanol.

Colloidal coomassie staining

For MS analysis, the gels were stained by colloidal Coomassie Blue G-250 [69]. The gel was fixed in 40% methanol/5% orthophosphoric acid for 12 h and incubated with colloidal Coomassie Blue (17% ammonium sulphate, 34% methanol, 3% orthophosphoric acid and 0.1% Coomassie G-250) for 48 h. After staining, the gels were kept in 1% acetic acid at 4°C.

Image analysis

The stained 2D gels were scanned with an imaging densitometer ScanJett 5370C (HP) and quantified by PDQuest software (Bio-Rad, version 7.3.1). The process included spot detection, gel matching and spot quantification. Master gel was constructed as a synthetic image that contains the spot data from all the gels in the MatchSet. At least four replicates were performed for each sample. All matched and unmatched spots were then checked in a manual manner. Protein levels altered at least two-fold were taken into consideration.

Preparation of samples for MALDI-TOF MS/MS; *analysis of post-nuclear fraction*

Mass spectrometric analysis MALDI-TOF was performed as described before [58]. The peak lists from the MS spectra were generated by 4000 Series Explorer V 3.5.3 (Applied Biosystems/MDS Sciex) without smoothing, peaks with local signal to noise ratio greater than 5 were picked and searched by local Mascot v. 2.1 (Matrix Science) against nonredundant NCBI database of protein sequences (11186807 sequences; 3815639892 residues). Database search criteria were as follows-enzyme: trypsin, taxonomy: *Rattus norvegicus* (66703 sequences), fixed modification: carbamidomethylation, variable modification: methionine oxidation, peptide mass tolerance: 120 ppm, one missed cleavage allowed. Only hits that were scored as significant ($P < 0.001$) were included.

In-gel digestion and preparation of samples for LC-MS/MS; *analysis of percoll-purified membranes (PM)*

Protein spots (from 2-DE: ca 1–2 mm in diameter) were excised from the Coomassie-stained gels, and then processed as described by Shevchenko et al. [70]. Briefly, the spots were first destained by incubation in 100 μl of 100 mM ammonium bicarbonate/acetonitrile (1:1, v/v) with occasional shaking for 1 hour. After destaining, the gel pieces were shrunk by dehydration in 500 μl of acetonitrile, which was then removed and the gel pieces were dried in a vacuum centrifuge. In further step, 100 μl of 10 mM DTT in 100 mM ammonium bicarbonate was added, and the proteins were reduced for 1 hour at 56°C. After cooling to room temperature, the DTT solution was replaced by roughly the same volume of 55 mM iodoacetamide in 100 mM ammonium bicarbonate, and the gels were incubated at ambient temperature for 45 min in the dark. Then the gel pieces were washed with 100 μl of 100 mM ammonium bicarbonate, and dehydrated by addition 500 μl of acetonitrile. Subsequently, the liquid phase was removed and the gel pieces were dried in a vacuum centrifuge.

Before the in-gel digestion, the gel pieces were cooled in an ice-cold bath and swollen in a 100 μl of digestion buffer containing trypsin (20 μg/ml) in 50 mM ammonium bicarbonate, and the gel pieces were sonicated (5 min), placed to air circulation thermostat, and incubated overnight at 37°C. The volumes of solutions needed for processing of the protein bands were four-fold larger than the volumes for processing of the spots. The supernatant of each spot was then transferred to a new vial. The in-gel digestion was performed once more the same way. The resulting tryptic peptides were extracted with sonication (15 min) by 150 μl of extraction buffer (5% formic acid/acetonitrile, 1:2, v/v). Then the solution was spun, the supernatants were transferred, pooled and concentrated to dryness by lyophilization. Dried extracts were stored at −80°C before analysis.

Analysis of tryptic digests with LC-MS/MS

Dried protein digests were dissolved in 20 μl of 1% formic acid, centrifuged (10 000 × *g*, 5 min, 4°C) and the supernatant transferred to inserts in vials. The nano-HPLC apparatus used for protein digests analysis was a Proxeon Easy-nLC (Proxeon, Odense, Denmark) coupled to a maXis Q-TOF (quadrupole – time of flight) mass spectrometer with ultrahigh resolution (Bruker Daltonics, Bremen, Germany) by nanoelectrosprayer. The nLC-MS/MS instruments were controlled with the software packages HyStar 3.2 and micrOTOF-control 3.0. The data were collected and manipulated with the software packages ProteinScape 2.0 and DataAnalysis 4.0 (Bruker Daltonics).

The 3 μl of the peptide mixture were injected into a NS-AC-11-C18 Biosphere C18 column (particle size: 5 μm, pore size: 12 nm, length: 150 mm, inner diameter: 75 μm), with a NS-MP-10 Biosphere C18 pre-column (particle size: 5 μm, pore size: 12 nm, length: 20 mm, inner diameter: 100 μm), both manufactured by NanoSeparations (Nieuwkoop, Netherlands).

The separation of peptides was achieved via a linear gradient between mobile phase A (water) and B (acetonitrile), both containing 0.1% (v/v) formic acid. Separation was

started by running the system with 5% mobile phase B, followed by gradient elution to 30% B at 70 min. The next step was gradient elution to 50% B in 10 min, and then a gradient to 100% B in 8 min was used. Finally, the column was eluted with 100% B for 2 min. Equlibration before the next run was achieved by washing the column with 5% mobile phase B for 10 min. The flow rate was 0.25 μl min^{-1}, and the column was held at ambient temperature (25°C).

On-line nano-electrospray ionization (easy nano-ESI) in positive mode was used. The ESI voltage was set at +4.5 kV, scan time 1.3 Hz. Operating conditions: drying gas (N_2), 1 l min^{-1}; drying gas temperature, 160°C; nebulizer pressure, 0.4 bar. Experiments were performed by scanning from 100 to 2200 m/z. The reference ion used (internal mass lock) was a monocharged ion of $C_{24}H_{19}F_{36}N_3O_6P_3$ (m/z 1221.9906). Mass spectra corresponding to each signal from the total ion current chromatogram were averaged, enabling an accurate molecular mass determination. All LC-MS/MS analyses were done in duplicates.

Database searching

Data were processed using ProteinScape software. Proteins were identified by correlating tandem mass spectra to SwissProt databases, using the MASCOT searching engine (http://www.matrixscience.com); *Rattus norvegicus* as species. Trypsin was chosen as the enzyme parameter. One missed cleavage was allowed, and an initial peptide mass tolerance of ±10.0 ppm was used for MS and ±0.05 Da for MS/MS analysis. Cysteines were assumed to be carbamidomethylated, proline and lysine to be hydroxylated, serine, threonine and tyrosine to be phosphorylated, and methionine was allowed to be oxidated. All these possible modifications were set to be variable. Monoisotopic peptide charge was set to 1+, 2+ and 3+. The Peptide Decoy option was selected during the data search process to remove false-positive results. Only significant hits (MASCOT score ≥60, http://www.matrixscience.com) were accepted.

Statistical analysis

In immunoblot assays, the significance of difference between data collected in control and morphine-treated samples was analyzed by Student's t-test by GraphPad-*Prizm4*. Results represent the average ± S.E.M.

Protein determination

The method of Lowry was used for determination of membrane protein. Bovine serum albumin (Sigma, Fraction V) was used as standard. Data were calculated by fitting the data with calibration curve as quadratic equation.

Additional files

Additional file 1: Table S1. Proteomic analysis of post-nuclear supernatant prepared from brain cortex of control and morphine-treated rats.

Additional file 2: Table S2. Proteomic analysis of PM fraction isolated from brain cortex of control and morphine-treated rats.

Abbreviations

AC: Adenylyl cyclase; CBB: Coomassie brilliant blue; d: Day; DAMGO: [(2-D-alanine2-4-methylphenylalanine-5-glycineol)-enkefalin]; DADLE: [(2-D-alanine-5-D-leucine)-enkefalin]; DOR: δ-opioid receptor; DTT: Dithiothreitol; EDTA: Ethylenediamine-tetraacetic acid; ELFO: Electrophoresis; GPCR: G protein-coupled receptor; G proteins: Heterotrimeric guanine nucleotide-binding regulatory proteins; CHAPS: 3-[(3-cholamidopropyl) dimethylammonio]-1-propanesulfonate; DTT: Dithiothreitol; IEF: Isoelectric focusing; KOR: κ-opioid receptor; LC-MS/MS: Liquid chromatography–mass spectrometry; MALDI-TOF MS/MS: Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry; MOR: μ-opioid receptor; PBS: Phosphate-buffered saline; PM: Percoll®-purified membranes; PMSF: Phenylmethylsulfonyl fluoride; PNS: Post-nuclear supernatant; SLB: Sample loading buffer; TBS: Tris-buffered saline; w.w.: Wet weight; TCA: Trichloroacetic acid; TRH-R: Thyrotropin-releasing hormone receptor.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

HU performed the experiments, analyzed the data and participated in writing the manuscript. AE performed proteomic analysis of plasma membrane proteins by LC-MS/MS. DK and LB were responsible for application of morphine to rats according to experimental protocol described in Methods and prepared membrane fractions by differential or density gradient centrifugation. PS conceived the study, designed the experiments and wrote the manuscript. All authors have read and approved the final manuscript.

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Early postnatal development of rat brain is accompanied by generation of lipofuscin-like pigments

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Abstract The increased generation of free radicals results in the formation of fluorescent end-products of lipid peroxidation, lipofuscin-like pigments (LFPs). The authors observed that LFPs are generated in rat brain after a normal birth during 5 postnatal days. The experimental design of the study comprised 10 groups of animals. The authors measured prenatal values 1 day and 7 days before birth, and then the animals were sampled on postnatal day 1, 2, 5, 10, 15, 25, 35, and 90. Maximum LFP concentration is achieved on the postnatal day 2. Starting from postnatal day 10, LFP concentration returns to prenatal values. A new rise in LFP concentration is observed at 3 months of age. This is associated with the beginning of the aging process. LFPs were characterized by fluorescence spectroscopy using tridimensional excitation spectra, synchronous spectra and their derivatives, and HPLC with fluorescence detection. It was possible to discern several tens of fluorescent compounds of unknown structure that are generated and metabolized during early development. The authors suggest that LFPs are formed after respiratory burst of microglia phagocytosing apoptotic cells.

Keywords Brain · Early development · Lipofuscin-like pigments · Fluorescence · Rat

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Introduction

The increased generation of free radicals and non-radical intermediates of oxygen reduction, collectively known as reactive oxygen species (ROS), constitutes the condition of oxidative stress that is considered as a major factor in the aging process and has formed the basis for explaining the mechanism of aging [1, 2]. The main quantitative source of ROS in mammalian organism is represented by mitochondria [3]. The effect of oxidative stress on the aging process is therefore widely recognized [4] in the brain tissue containing abundant mitochondria and highly active respiratory enzymes [5].

Immediately after birth, brain oxygen concentration undergoes dramatic changes that, from the quantitative point of view, are comparable to the exposure of experimental animals to hyperoxia. This pathological state was documented as a cause of brain oxidative damage [6], and an increase in ROS production in brain after birth is, therefore, to be expected.

As earlier studies indicated that brain mitochondrial enzymes in rats are fully active only after postnatal day 10 [7, 8], the direct role of mitochondria in neonatal ROS production is uncertain. Another possible source of ROS is represented by brain phagocytes, microglia. During mammalian brain development, both neurons and glia are produced in overabundance, and approximately half of them are eliminated by apoptosis [9]. Apoptotic cells are phagocytosed by microglia with concomitant production of ROS. Superoxide was detected by staining living brain slices with nitroblue tetrazolium, and microglial respiratory burst was revealed in vivo using a fluorescent probe [10].

There are many products formed during oxidative free radical damage to cells. Widely used as markers of free radical attack are the aldehydes originating from membrane

lipid peroxidation, especially malonaldehyde and 4-hydroxynonenal [11]. These aldehydes are relatively short-lived because of their high reactivity, and their determination by the thiobarbituric acid assay has several draw-backs. The most serious problem is the fact that positive reaction is also given by substances not related to free radicals [12]. A more reliable group of markers of free radical damage is represented by lipophilic fluorescent end-products, originally termed lipofuscin-like pigments (LFPs) [13]. They are relatively stable and long-lived. LFPs were originally named on the basis of the similarity of their fluorescence properties with those of lipofuscin—the pigment of old age. However, later studies showed that they are not directly related to lipofuscin formation but are rather the result of free radical-initiated oxidative damage to membrane lipids [14].

The presence of LFP has been widely used as an indicator of oxidative damage in various biological systems induced by such diverse triggers as hyperoxia or hypoxia [6, 15, 16], ionizing radiation [17–19], phagocytosis of oxidized proteins [20], and physical activity [21].

The aim of this study was to investigate the formation of LFP in frontal rat brain cortex in the neonatal period and during early development to assess the extent of oxidative damage after birth. For a more detailed characterization of fluorescent properties of LFP, the authors used various spectral methods comprising tridimensional spectral arrays, synchronous fluorescence spectra, and their derivatives. The LFPs were resolved into several fractions by means of HPLC with fluorescence detection. The results confirm that the highest accumulation of oxidative products takes place immediately after birth; they also indicate that brain LFPs constitute a complex mixture of chemical compounds whose composition is changing during development.

Methods

The study was conducted in accordance with the *Guide for the Care and Use of Laboratory Animals* published by the US National Institutes of Health (NIH publication No. 85-23, revised 1996).

Animals

A total of 70 pregnant female Wistar rats were used throughout the experiments. They had free access to water and standard laboratory diet. The offsprings of both sexes were divided into 10 groups. Group A (110 foetuses) was sampled 7 days before birth, group B (110 foetuses) 1 day before birth, group C (50 animals) on postnatal day 1, group D (50 animals) on postnatal day 2, group E (50 animals) on postnatal day 5, group F (50 animals) on postnatal day 10, group G (50 animals) on postnatal day 15, group H (30 animals) on postnatal day 25, group I (30 animals) on postnatal day 35, and group J (20 animals) 3 months after birth. The animals were euthanized by decapitation in ether narcosis. The frontal brain was rapidly removed, separated from white matter if possible, snap-frozen in liquid nitrogen, and stored at −70°C until use.

LFP fluorescence measurement

The technique described by Goldstein and McDonagh [22], modified in [16], was used for the analysis of LFP in brain homogenates. Approximately 30 mg of frozen brain sample was weighed, chopped to fine pieces, and transferred into a glass-stoppered test tube containing 6 ml of chloroform–methanol mixture (2:1, v/v). After 1-h extraction on a motor-driven shaker, 2 ml of double distilled water was added, the sample was agitated, and the ensuing mixture was centrifuged (400 g, 10 min). After centrifugation, the lower chloroform phase was separated and used for measurements.

Fluorescence excitation and synchronous spectra were measured on an Aminco-Bowman series 2 spectrofluorometer and recorded and analyzed using AB-2 computer program that also organized the spectra into tridimensional spectral arrays. The excitation spectra were measured in the range of 250–400 nm for emission adjusted between 400 and 500 nm in steps of 10 nm. The quantitative estimation of LFP was based on excitation and emission maxima found in tridimensional spectral arrays. The authors identified three major fluorophores F325/380, F335/410, and F355/440 (excitation/emission, nm). The fluorometer was calibrated based on the standard No. 5 of the instrument manufacturer, and the LFP concentration was expressed in arbitrary units per mg tissue wet weight. The statistical evaluations were made using ANOVA with Scheffe post-hoc test, and the results are shown as means ± SEM.

The synchronous emission spectra were measured in the range of 350–550 nm, with a constant difference of 50 nm between excitation and emission wavelengths. Their second derivatives were obtained using the AB-2 software.

HPLC analysis

Brain chloroform extracts were evaporated under the stream of nitrogen. The evaporated sample was dissolved in approximately 1 ml of running phase used in isocratic HPLC separation. A mixture of acetonitrile–methanol–water (50:10:40, v/v) was used for separation of LFP. A Jasco HPLC instrument equipped with fluorescence detector was set at the excitation and emission maxima of the three major fluorophores. A C18 column (4 × 250 mm)

was used for the analysis. Isocratic elution gave optimum separation at 0.2 ml/min.

Results

Fluorescence measurements

In the first step of our study, the authors analyzed the chloroform extracts obtained from brains of animals of different age by measuring tridimensional fluorescence spectral arrays. These spectral arrays are capable of revealing many fluorophores contained in the studied mixture. Each age group was characterized by a specific spectral pattern. For the sake of illustration, Fig. 1 shows the examples of spectra of whole-brain chloroform extracts from animals 7 days before birth (A), 2 days after birth (D), and then 3 months old (J). The shapes of the spectra indicate the presence of many fluorophores and their changes in the course of development. The general appearance of the spectra is a sort of a "fingerprint" characteristic for given mixture. Thus, even a subtle difference between groups A and D indicates a change in composition. This conclusion is further confirmed by the second derivatives of synchronous spectra shown in Fig. 3.

Figure 2 documents the evolution of the three major fluorophores used for the quantitation—F325/380, F335/410, and F355/440 (excitation/emission)—during the development. It is apparent that the pattern of changes is similar for all of them. On the postnatal day 1 (group C), there is an increase in concentration that is statistically significant in relation to prenatal group A. On the postnatal day 2 (group D), the concentration reaches its maximum, and on postnatal day 5 (group E), it is still significantly increased in relation to prenatal situation. Starting from postnatal day 10 (group F) up to day 35 (group I), the concentrations of the fluorophores are decreased to prenatal levels. A new rise of fluorophore concentration appears at 3 months of age (group J).

As the shape of the spectra of Fig. 1 implies the presence of several fluorophores, the authors attempted to further resolve the mixture by spectral and chromatographic techniques. Figure 3 presents the synchronous fluorescence spectra in the left-hand panels and their second derivatives in the right-hand panels. Especially the second derivative of the synchronous spectra has a great resolving power. The vertical arrows indicate the emission maxima of major peaks. It is apparent from the comparison of prenatal (group A) and 2-day-old animals (group D) that the greatest changes are observed between emissions in the range of 410–470 nm, i.e., in the region characteristic for fluorescent products of lipid peroxidation. Comparison with 5-day-old animals (group E) indicates dynamic changes in the fluorophore composition that persist until 90 days of age (group J).

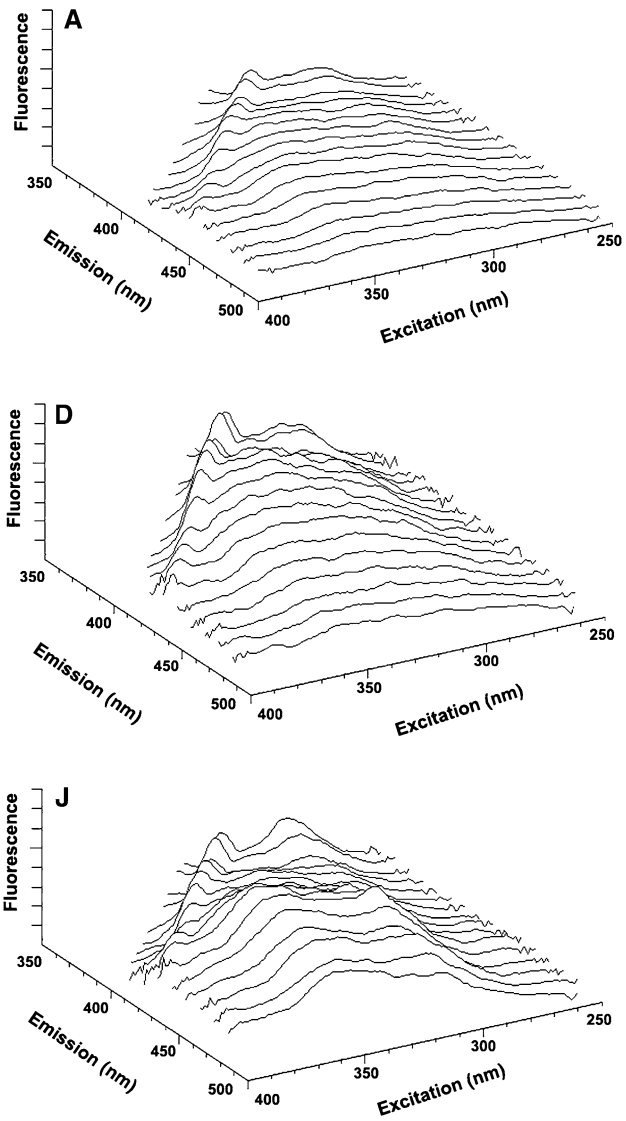

Fig. 1 Examples of 3D fluorescence excitation spectra of brain chloroform extracts. **A** 7 days before birth, **D** postnatal day 2, **J** 3-month-old animals

HPLC analysis

The authors further resolved spectrally characterized fluorophores by HPLC. Figure 4 documents that one fluorophore can be resolved into several chromatographically distinct species. Again, the fractionation pattern is different throughout the development indicating changes in the composition of these free radical products. Figure 4 illustrates the fractionation of the fluorophore F355/410, but other fluorophores can also be fractionated in a similar way. This means that several tens of fluorescent radical

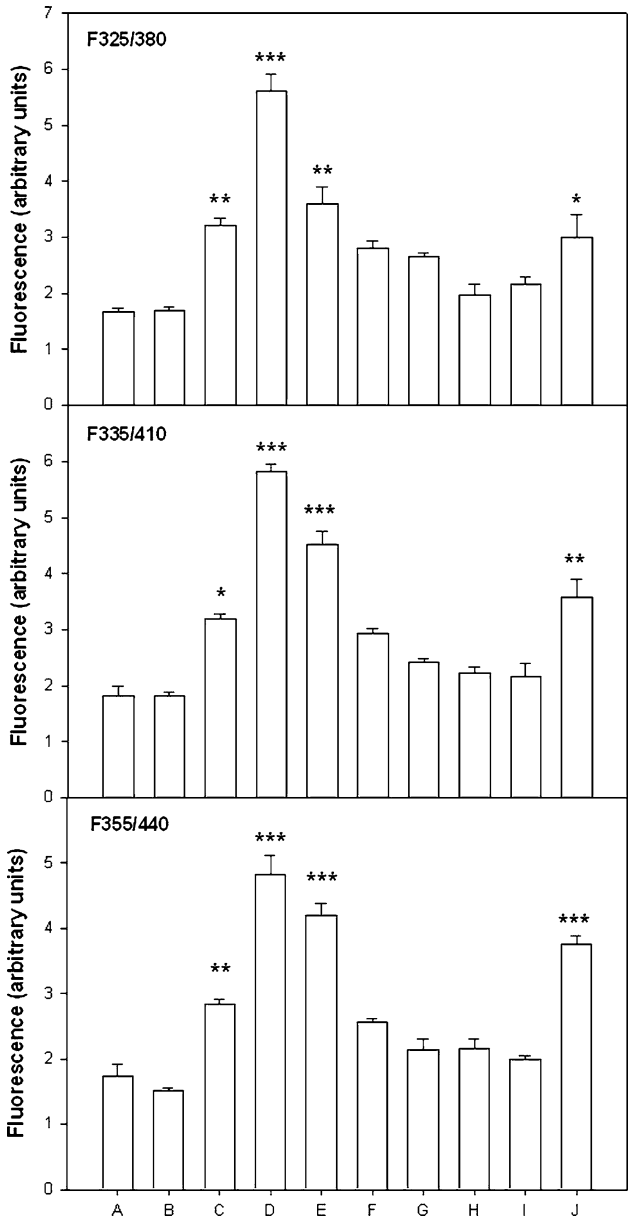

Fig. 2 Quantitative presentation of three major LFP fluorophores found in 3D spectra. For the group description, see Methods section. Statistical significance related to group A: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$

products are generated and metabolized during brain development.

Discussion

Although the increased free radical generation after birth is to be expected because of rapid increase in oxygen concentration, the problem has not been extensively studied. An important study in this regard showed ROS-mediated oxidative damage to DNA in rat liver, kidney, and skin during the first few hours after normal birth. Lungs were not affected. The lesions were considered substantial, having been similar to or exceeding the levels in 24-month-old rats [23]. The concept of oxidative stress after normal birth was supported by the finding of pronounced neonatal decreases in the hepatic GSH/GSSG ratio in rats [24, 25]. Also the product of membrane lipid peroxidation, malonaldehyde, exhibited a transient rise after birth in rat liver and kidney [26]. The tissue specificity of oxidative damage may be explained by differences in both oxidative metabolism and antioxidant protection. Unfortunately, no such studies were undertaken in brain.

Our results indicate a transient accumulation of oxidative products occurring in neonatal rat brain. LFPs, which represent the end-products of membrane lipid peroxidation, appeared on the day 1 after birth, were at a maximum on the day 2, and decreased to prenatal concentrations after postnatal day 5. A new rise of LFP production appeared in 3-month-old animals. Thus, our results correlate with oxidative damage to DNA observed in a previous study [23]. The fact that all fluorophores have similar, though not identical, kinetics is biologically relevant. It might mean that they originate from the same kind of processes or are localized to the same compartment.

In a parallel study, the authors have investigated LFPs in neonatal rat heart, and found that the kinetics is similar to that of brain. The manuscript is in preparation for publication.

Though mitochondria are the first suspects when it comes to ROS generation in brain, their role in early postnatal brain is uncertain, as previous studies have documented fully active mitochondrial enzymes only after postnatal day 10 [7, 8]. It suggests that mitochondria are not responsible for the aforementioned oxidative damage. It appears that the real culprit might be microglia phagocytosing apoptosed brain cells. In mice, it was shown that maximum phagocytosis associated with ROS production occured on postnatal day 3 [10]. This time period corresponds well with maximum LFP production between postnatal day 1 and day 5 in this study. Thus, the authors suggest that the early production of LFP in brain is connected with the activity of microglia. Transition from hypoxia to normoxia triggers increased production of free radicals [16]. Delivery is accompanied with the increase in oxygen partial pressure which might support free radical generation. In that case, LFPs would increase immediately after birth; however, the authors have found maximum LFP formation on the postnatal day 2. It is possible that hypoxic/normoxic transition can contribute to the process of LFP formation, but it will not be the major factor.

The patterns of tridimensional spectral arrays, synchronous spectra, and their derivatives all indicate the presence of many fluorescent species belonging to the category of

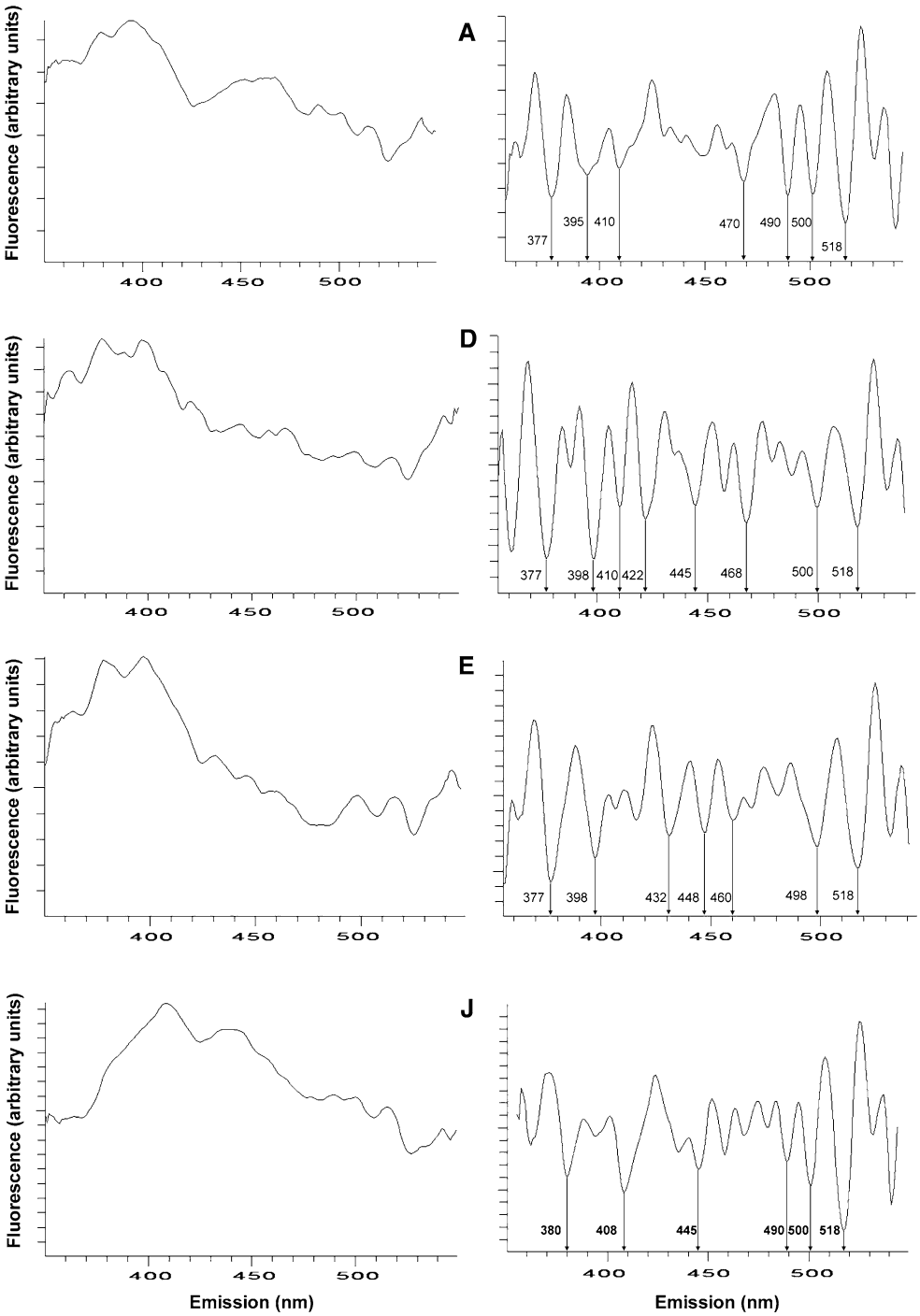

Fig. 3 Examples of synchronous fluorescence spectra (*left-hand panels*) and their second derivatives (*right-hand panels*). **A** 7 days before birth, **D** postnatal day 2, **E** postnatal day 5, **J** 3-month-old animals. *Vertical arrows* in the second derivatives of the spectra indicate the emission maxima of the resolved fluorophores

LFP. Each spectrally characterized species can be further resolved into several chromatographically distinct compounds. Taken together, LFPs represent several tens of unknown compounds that are related to brain oxidative damage after normal birth in rats. The changes in their concentration are accompanied by dynamic changes in their composition. Apparently, therefore, there is a dynamic metabolism of these compounds in the neonatal period. Unfortunately, the chemical composition of these compounds is not known, nor are their biological effects. Further studies should, therefore, be aimed at their detailed characterization that would enable us elucidate on their biological role.

The formation of LFPs in 3-month-old animals, when aging starts in rats, might depend on ROS generated by mitochondria [5]. Since that time, these products only cumulate [27]. The levels of LFP generated in the early neonatal period are higher than in 3-month-old animals,

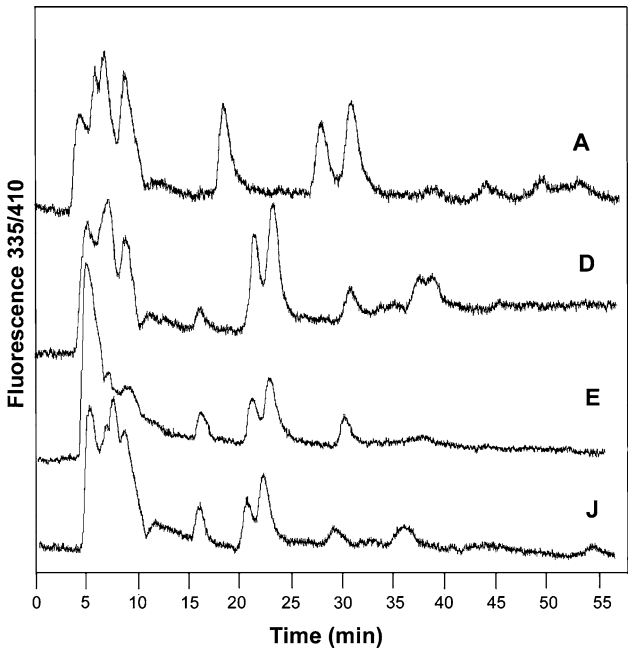

Fig. 4 Examples of the HPLC tracings of the fluorophore F355/410 in brain chloroform extracts of animals of different age: (*A*) 7 days before birth, (*D*) postnatal day 2, (*E*) postnatal day 5, (*J*) 3-month-old animals

but they return to basal value on day 10. The authors believe that this effect is caused by short-term ROS production. When apoptosis is terminated, newly growing brain cells—not producing ROS—"dilute" LFP generated during the respiratory burst. In our opinion, this kinetics support our view that early LFPs are the by-products of microglial phagocytosis of apoptosed brain cells.

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