Activation of HIF-1α by δ-Opioid Receptors Induces COX-2 Expression in Breast Cancer Cells and Leads to Paracrine Activation of Vascular Endothelial Cells

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Received February 14, 2019; accepted June 24, 2019

ABSTRACT

Opioids promote tumor angiogenesis in mammary malignancies, but the underlying signaling mechanism is largely unknown. The current study investigated the hypothesis that stimulation of δ-opioid receptors (DOR) in breast cancer (BCa) cells activates the hypoxia-inducible factor 1α (HIF-1α), which triggers synthesis and release of diverse angiogenic factors. Immunoblotting revealed that incubation of human MCF-7 and T47D breast cancer cells with the DOR agonist D-Ala²,D-Leu⁵-enkephalin (DADLE) resulted in a transient accumulation and thus activation of HIF-1α. DADLE-induced HIF-1α activation preceded PI3K/Akt stimulation and was blocked by the DOR antagonist D-Ala²,D-Leu⁵-enkephalin (DADLE) and the COX-2 inhibitor celecoxib. Also no sprouting was observed when END cells were exposed to the PGE₂ receptor antagonist PF-04418948. The findings together indicate that DOR stimulation in BCa cells leads to PI3K/Akt-dependent HIF-1α activation and COX-2 expression, which triggers endothelial cell sprouting by paracrine activation of PGE₂ receptors. These findings provide a potential mechanism of opioid-driven tumor angiogenesis and thus therapeutic targets to combat the tumor-angiogenic opioid effect.

SIGNIFICANCE STATEMENT

Opioids are indispensable analgesics for treating cancer-related pain. However, opioids were found to promote tumor growth and metastasis, which questions the use of these potent pain-relieving drugs in cancer patients. Enhanced tumor vascularization after opioid treatment implies that tumor progression results from angiogenic opioid effects. Thus, understanding the signaling mechanism of opioid-driven tumor angiogenesis helps to identify therapeutic targets to combat these undesired tumor effects. The present study reveals that stimulation of δ-opioid receptors in breast cancer cells leads to an activation of HIF-1α and expression of COX-2 via PI3K/Akt stimulation, which results in a paracrine activation of vascular endothelial cells by prostaglandin E₂ receptors.

Introduction

Therapy of breast cancer is associated with pain in many ways. In addition to intra- and postoperative pain, pain caused by the tumor itself, by metastases, or by chemo- and radiotherapy requires the use of adequate analgesic drugs. For the relief of moderate and severe cancer pain, opioid analgesics are recommended (World Health Organization, 1996). However, there is growing evidence that the use of these potent analgesics is associated with adverse side effects in breast cancer patients. Different studies revealed that opioids may promote progression, metastasis, recurrence, growth, and angiogenesis of human mammary tumors (Gupta et al., 2002; Exadaktylos et al., 2006; Bimonte et al., 2015), and thus question the clinical use of opioids. As tumor angiogenesis—the formation of new vessels from the existing vasculature—contributes essentially to cancer growth and metastasis (Bielenberg and Zetter, 2015), understanding the still largely unknown mechanism of opioid-promoted vessel formation may help to find therapeutic targets to combat the tumor-supporting effects of opioids.

The hypoxia-inducible factor 1 (HIF-1α) is a heterodimeric transcription factor, consisting of two subunits, HIF-1α and HIF-1β.

Supplemental material to this article can be found at: http://jpet.aspetjournals.org/content/suppl/2019/07/12/jpet.119.257501.DC1

Abbreviations: BCa, breast cancer; CM, conditioned medium; CM₄₄, conditioned medium from untreated MCF-7 cells; CM₄₄DADLE, conditioned medium from DADLE-treated MCF-7 cells; COX-2, cyclooxygenase-2; 3D, three-dimensional; DADLE, D-Ala²,D-Leu⁵-enkephalin; DOR, δ-opioid receptors; END, cells, endothelial cells; ER, estrogen receptor; FCS, fetal calf serum; GSK3, glycogen synthase kinase 3; HIF-1α, hypoxia-inducible factor 1α; IGF, insulin-like growth factor; MAPK, mitogen-activated protein kinase; OR, opioid receptor; PCR, polymerase chain reaction; PGE₂, prostaglandin E₂; PDE, phosphodiesterase domain; PI3K, phosphoinositide 3-kinase; PKA, protein kinase A; PTX, pertussis toxin; VEGF, vascular endothelial growth factor.
HIF-1α. Whereas HIF-1β is constitutively expressed, presence of HIF-1α is regulated by oxygen-sensitive prolyl hydroxylase domain enzymes (PHDs). In the presence of oxygen, HIF-1α is hydroxylated by PHDs and rapidly degraded by proteasomes (Huang et al., 1998; Schofield and Ratcliffe, 2004). At low oxygen concentrations (hypoxia), HIF-1α eludes from hydroxylation and degradation, translocates from the cytoplasm into the nucleus, and dimerizes with HIF-1β to gain full transcriptional activity (Dengler et al., 2014). HIF-1 regulates the expression of several proangiogenic factors, including the vascular endothelial growth factor VEGF-A (Krock et al., 2011), which is released as paracrine molecule to stimulate endothelial cell proliferation, migration, and tube formation (Hoeben et al., 2004). As HIF-1α knockout in breast cancer (BCa) cells significantly reduces VEGF expression and tumor vascularization (Schwab et al., 2012), HIF-1α is considered a key player in the process of breast cancer angiogenesis.

Oxygen-independent mechanisms may also stabilize and thus activate HIF-1α. In addition to inhibition of PHDs by cobalt chloride (CoCl₂) or desferrioxamine (Schofield and Ratcliffe, 2004), stimulation of receptor tyrosine kinases for the epidermal growth factor or insulin-like growth factor (IGF-1) (Zhong et al., 2000; Fukuda et al., 2002) as well as G protein-coupled thrombin and angiotensin II receptors has been shown to induce HIF-1α accumulation (Görler et al., 2001; Pagé et al., 2002). Moreover, activation of phosphoinositide 3-kinase (PI3K)/Akt (Zundel et al., 2000) or cyclin-dependent kinase CDK1 (Warfel et al., 2013) allows HIF-1α activation by various stimuli under normoxic conditions.

Classic opioid effects such as analgesia, bradycardia, and constipation are mediated through the stimulation of μ-, δ-, or κ-opioid receptors (Connor and Christie, 1999; Kieffer and Evans, 2009; Pathan and Williams, 2012). Opioid receptors belong to the family of G protein-coupled receptors and trigger different signaling pathways, resulting in modulation of ion conductance, regulation of adenyl cyclase activities, or stimulation of mitogen activated protein kinases (MAPK) (Al-Hasani and Bruchas, 2011). Opioid receptors are expressed in neuronal and diverse non-neuronal cells, including breast cancer cells and tissues (Zagon et al., 1987; Hatzoglou et al., 1996; Gach et al., 2011; Kharmate et al., 2013). A recent study showed that DOR expression in human breast tumors correlates with breast cancer stage, incidence of metastasis, and mortality rate (Wei et al., 2016), which implies a role of the opioid receptor type in mammary malignancies. In neuroblastoma × glioma NG108-15 hybrid cells, stimulation of DORs was shown to induce transactivation of IGF-1 receptors and PI3K/Akt activation (Heiss et al., 2009). Moreover, DOR stimulation in human heart tissue was found to trigger cellular effects that are similar to that induced by hypoxia (Bell et al., 2000). As hypoxia, IGF-1 receptor and PI3K/Akt signaling are closely related to HIF-1α activation, HIF-1α might represent a potential DOR downstream effector. To test the thesis, we examined here the effect of DOR stimulation on HIF-1α accumulation in human breast cancer cells and analyzed whether HIF-1α regulation may account for angiogenic opioid function.

**Material and Methods**

**Cell Culture.** Human breast cancer MCF-7 (ATCC HTB-22; American Type Culture Collection, Manassas, VA) and T47D cells (ATCC HTB-133) were cultured in Dulbecco’s modified Eagle’s medium (Sigma-Aldrich, St. Louis, MO) supplemented with 10% fetal calf serum (FCS; HyClone UK Ltd., Thermo Scientific, Northumberland, UK), 1% penicillin (100 U/ml), and 100 µg/ml streptomycin (Sigma-Aldrich). Cells were tested to be free of mycoplasma by polymerase chain reaction (PCR) using genus-specific primers according to Vojdani et al. (1998). Murine endothelial (END) cells (Gotthardt et al., 2016) were routinely grown in Roswell Park Memorial Institute medium (Sigma-Aldrich) supplemented with 10% FCS, 1% penicillin (100 U/ml), and 100 µg/ml streptomycin. All cells were cultured at 37°C in a humidified atmosphere in presence of 5% CO₂. For experiments, cells were grown in 6- (Palcon, Coning, NY) or 12-well culture plates (SPL Life Sciences Co. Ltd., Gyeonggi-do, Korea). For 3D cell culture, MCF-7 or END cells (10⁵/ml) were seeded into nonadherent, U-bottom 96-well microtiter plates (BRAND GmbH & Co. KG, Wertheim, Germany) and cultured for 5 days in complete medium.

**Cell Treatments.** To test HIF-1α accumulation under normoxic conditions, MCF-7 and T47D cells were exposed to 100 µM cobalt chloride (CoCl₂; Sigma-Aldrich) or 1 µM [α-Aga²,δ-Leu⁷]-enkephalin (DADLE) (Sigma-Aldrich). Activation of DORs was blocked by cell treatment with 10 µM naltrindole (Sigma-Aldrich) or 10 µM naloxone for 10 minutes prior to DADLE exposure. The role of Gαs proteins was examined by cell pretreatment with 100 ng/ml pertussis toxin (PTX; Thermo Fisher Scientific, Waltham, MA) for 18 hours. To analyze the role of Akt signaling, cells were pretreated with the Akt inhibitor Akti-1/2 (100 µM, 15 minutes; Selleckchem, Munich, Germany) or the PI3K inhibitors wortmannin (2.5 µM, 30 minutes; Sigma-Aldrich), LY294002 2-(4-Morpholinyl)-8-phenyl-1(4H)-benzopyran-4-one (10 µM, 30 minutes; Sigma-Aldrich), BRK120 5-(2,6-dimorpholinopyrimidin-4-yl)-4-(trifluoromethyl)pyridin-2-amine (1 µM, 10 minutes; Sigma-Aldrich), or BEZ235 (4-[2,3-dihydro-3-methyl-2-oxo-8-(3-quinoxalinyl)-1H-imidazo[4,5-c]quinolin-1-yl]-α,α-dimethyl-benzensactonitrile; 1 µM, 10 minutes; Sigma-Aldrich). To inhibit HIF-1α activity, cells were pretreated with 10 nM echnomycin (Calbiochem; EMD Chemicals, Inc., San Diego, CA) for 10 minutes. Celecoxib (50 µM; 30 minutes; Torcis Bioscience, Bio-Techne Ltd., Minneapolis, MN) was used to inhibit cyclooxygenase 2 (COX-2) activity, whereas prostaglandin E receptor was blocked by PF-04419848 (1-(4-fluorobenzoyl)-3-[[6-methoxy-2-naphthalenyl]oxy][methyl]-3-azetidinecarboxylic acid; 10 µM, 30 minutes; Torcis Bioscience).

**Western Blotting.** MCF-7 and T47D cells were lysed by addition of Laemmli sample buffer (62.5 mM Tris-Cl, pH 6.8, 2% SDS, 50 mM DTT, 10% glycerol, 0.01% bromophenol blue), denatured at 95°C for 5 minutes and subjected to sodium dodecyl sulfate polyacrylamide gel electrophoresis using 8% or 10% polyacrylamide gels. Proteins were transferred to a polyvinylidene fluoride membrane (PVDF Blotting Membrane, perlab; VWR International GmbH, Erlangen, Germany), which was subsequently blocked with 5% non-fat milk powder (Carl Roth GmbH + Co. KG, Karlsruhe, Germany) dissolved in Tris-buffered saline with 0.1% Tween-20 (TBST) for 60 minutes. Membranes were then incubated with rabbit monoclonal HIF-1α antibody (1:1000, Cat# 14179; Cell Signaling Technology (CST), Inc., Danvers, MA), rabbit monoclonal phospho-Serine-473-Akt antibody (1:1000, Cat# 4690; CST), rabbit polyclonal Akt antibody (1:1000, Cat# 9272; CST), rabbit monoclonal COX-2 antibody (1:1000, Cat# 12282; CST), or mouse monoclonal HSC70 antibody (1:1000, Cat# SC7298; Santa Cruz Biotechnology, Dallas, TX) at 4°C overnight. After being washed with TBST, membranes were incubated with horseradish-peroxidase conjugated anti-rabbit (Cat# 7074; Cell Signaling Technology) or antimouse IgG (Cat# 7076; Cell Signaling Technology) for 60 minutes at room temperature. Membranes were finally exposed to Clarity Western Blotting Detection Reagent (Bio-Rad, Hercules, CA) at 4°C overnight. Membranes were then subjected to X-ray film detection using epeGOLD TriFast (VWR International GmbH, Life Science Competence Center, Darmstadt, Germany) according to the manufacturer’s protocol. One microgram of total RNA was subjected to reverse transcription-quantitative polymerase chain reaction (RT-qPCR) using pegGOLD TriFast (VWR International GmbH, Life Science Competence Center, Darmstadt, Germany) according to the manufacturer’s protocol.

**Real-Time Quantitative PCR.** Total RNA was isolated using RNeasy Mini Kit (Qiagen). First-strand cDNA was synthesized from 1 µg total RNA using SuperScript III Reverse Transcriptase and 5 µM random primers. Quantitative PCR was performed using iQ SYBR Green Supermix (Bio-Rad) and the iCycler iQ5 (Bio-Rad). The following primer sets were used: 18S (forward TCGACAGGACCTGGCTCTT, reverse GTACGTTGCTCCTCCTACA), MUC1 (forward 5'-AAGTTGCGCTTGGAGTCTA-3', reverse 5'-TAGTTGGGTGGTGCGAGACAT-3'), and GAPDH (forward 5'-GAGGACAGGTTTGCTGTGG-3', reverse 5'-TGGGTTGCTGTIACTGACCTCA-3'). The relative expression of each target gene was normalized to the expression of GAPDH. The data were analyzed using the 2⁻ΔΔCT method.
transcription using the iScript cDNA Synthesis Kit (Bio-Rad Laboratories, Inc.). Amplifications were run on a CFX96 Real-Time System C1000Touch Thermal Cycler (Bio-Rad Laboratories, Inc.) using SsoAdvanced Universal SYBR Green Supermix (Bio-Rad Laboratories, Inc.). Primers used were as follows: HPRT1 (reference gene #1: hypoxanthine phosphoribosyltransferase 1; NM_000194): forward 5′-AGTGACAGGACCTGAACTGTTT-3′ and reverse 5′-TGG GTGCTCTCTTTCACAGCA-3′, RPS18 (reference gene #2: ribosomal protein S18, NM_022551.2): forward 5′-ATTAAGGTTGTOGCGCCA AG-3′ and reverse 5′-TGGCTAGGACCTGGCGGTAT-3′; VEGF-A/total, VEGF-A121 (NM_001025366.2), VEGF-A121 (NM_001025370.2), and VEGF-A165 (NM_001287044.1): forward 5′-ACCGCCTCGGCTTGTCAC-3′ and reverse 5′-ACCGCCTCGGCTTGTCAC-3′ (VEGF-A/total), 5′-GGCTCCTGTGCATCTTCT-3′ (VEGF-A121, NM_001025366.2), and 5′-CAAGGCC CACAGGGATTTC-3′ (VEGF-A165, NM_001287044.1). Controls without reverse transcription or without template cDNA were included in each assay. Results were normalized to reference genes HPRT1 and RPS18. Relative gene expression levels were obtained using the ΔΔCt method (Livak and Schmittgen, 2001) and the Bio-Rad CFX Manager Software.

**Human Angiogenesis Array.** MCF-7 and T47D cells were incubated with 1 µM DADLE for 24 hours in FCS-reduced medium. Cell culture supernatant was collected and analyzed for VEGF and other angiogenic factors by using Human Angiogenesis Array Kit (Cat# ARY007, Proteome Profiler Array; R&D Systems, Minneapolis, MN) according to manufacturers’ instructions.

**PGE2 ELISA.** MCF-7 and T47D cells were treated with DADLE for 1 hour and exposed to supernatant collected from MCF-7 cells treated with DADLE for 24 hours. Culture supernatant was collected and analyzed for VEGF and other angiogenic factors by using Human Angiogenesis Array Kit (Cat# ARY007, Proteome Profiler Array; R&D Systems, Minneapolis, MN) according to manufacturers’ instructions.

**Immunohistochemistry.** Three-dimensional cultured MCF-7 cells were exposed to 1 µM DADLE in presence and absence of BE2235 or BKM120 for 3 hours, collected by centrifugation for 2 minutes at 2000 rpm, washed two times with Dulbecco’s phosphate-buffered saline, fixed with 4% formaldehyde (48 hours; 4°C), and embedded in Paraplast medium (Vogel, Giessen, Germany). Serial sections of 3 µm thickness were cut and mounted on 3-aminopropyltriethoxysilane/Paraplast medium (Vogel, Giessen, Germany). Serial sections of 3 µm thickness were cut and mounted on 3-aminopropyltriethoxysilane/glutaraldehyde-coated slides. After a drying period of 12 hours, sections were exposed to 0.6% H2O2 in methanol for 15 minutes at room temperature and incubated with 0.01 M citrate buffer (pH 6.0) for 30 minutes in a steamer for antigen retrieval. Sections were then washed with PBS for 5 minute, blocked with 1.5% normal goat serum for 30 minutes in a steamer for antigen retrieval. Sections were then dried under 12 hours, photographed by using the Olympus IX71 microscope (Olympus, Tokyo, Japan) with an Olympus DP72 camera (Olympus K.K.) and CellSens Dimension software (Olympus K.K.), and assessed for sprouting area by using Image J.

**Data Analysis.** Data are presented as mean ± S.E.M., and analyzed by using GraphPad Prism 5.0 for Windows (GraphPad Software Inc., La Jolla, CA). To assess statistical significance, an unpaired Student’s t-test with Welch correction was used. A P value <0.05 was considered statistically significant.

**Results**

**DADLE Induces HIF-1α in Human Breast Cancer Cells.** The effect of DOR stimulation on HIF-1α was examined in human MCF-7 and T47D breast cancer cells, which do endogenously express DORs (Kharmate et al., 2013). To evaluate whether DOR activation leads to HIF-1α activation, MCF-7 and T47D cells were exposed to 1 µM DADLE for 1–6 hours, and examined for HIF-1α protein by immunoblotting (Fig. 1A). As a positive control, cells were incubated with 100 µM CoCl2 for 3 hours (Yuan et al., 2003). Compared with nontreated cells, incubation with CoCl2 resulted in a prominent increase of HIF-1α in both BCa cell lines. Also cell exposure to 1 µM DADLE enhanced the amount of HIF-1α protein: an increase of HIF-1α protein was observed after a 1-hour DADLE treatment. (A) MCF-7 and T47D cells were treated with 1 µM DADLE for 1–6 hours and examined for HIF-1α protein expression by immunoblotting. Controls (cn) were left untreated. Cells treated with 100 µM CoCl2 for 3 hours were used as positive HIF-1α controls; HSC70 served as loading control. (B) Cells were pretreated with 10 µM naloxone or 10 µM naltrexone for 10 minutes or 100 ng/ml PTX for 18 hours followed by exposure to 1 µM DADLE for 1 hour. Controls (cn) were pretreated with sterile water as drug solvent control for 10 minutes. Subsequently, cells were lysed and examined for HIF-1α expression by immunoblotting. HSC70 served as loading control. Shown is one representative blot from three independent experiments (n = 3).

**Fig. 1.** HIF-1α accumulation in MCF-7 and T47D cells treated with DADLE. (A) MCF-7 and T47D cells were treated with 1 µM DADLE for 1–6 hours and examined for HIF-1α protein expression by immunoblotting. Controls (cn) were left untreated. Cells treated with 100 µM CoCl2 for 3 hours were used as positive HIF-1α controls; HSC70 served as loading control. (B) Cells were pretreated with 10 µM naloxone or 10 µM naltrexone for 10 minutes or 100 ng/ml PTX for 18 hours followed by exposure to 1 µM DADLE for 1 hour. Controls (cn) were pretreated with sterile water as drug solvent control for 10 minutes. Subsequently, cells were lysed and examined for HIF-1α expression by immunoblotting. HSC70 served as loading control. Shown is one representative blot from three independent experiments (n = 3).
In presence of wortmannin, LY294002 and Akti-1/2, DADLE
itors and analyzed for HIF-1
MCF-7 and T47D cells were pretreated with PI3K/Akt inhib-
ished by the PI3K inhibitors BEZ235 or BKM120 (Fig. 2B). To evaluate
the impact of DADLE-induced Akt regulation for HIF-1
DADLE-mediated Akt phosphorylation (Fig. 2A). To evaluate
MCF-7 and T47D cells with the PI3K inhibitors wortmannin
for 5–15 minutes increased the amount of Ser-473 phosphory-
lated Akt in both BCa cell lines (Fig. 2A). Pretreatment of
MCF-7 and T47D cells with the PI3K inhibitors wortmannin
and LY294002, or with the Akt inhibitor Akti-1/2 prevented
DADLE-mediated Akt phosphorylation (Fig. 2A). To evaluate the
impact of DADLE-induced Akt regulation for HIF-1α, MC
C-7 and T47D cells were pretreated with PI3K/Akt inhibi-
tors and analyzed for HIF-1α after DADLE exposure for 1 hour.
In presence of wortmannin, LY294002 and Akti-1/2, DADLE
incubation failed to induce HIF-1α accumulation (Fig. 2B).
Moreover, DADLE-triggered HIF-1α accumulation was abol-
ished by the PI3K inhibitors BEZ235 or BKM120 (Fig. 2B).

**Inhibition of PI3K/Akt Prevents DADLE-Induced
HIF-1α Accumulation.** HIF-1α may be induced by PI3K/ Akt signaling under nonhypoxic conditions (Agani and Jiang, 2013). To determine whether the signaling mechanism also account for DADLE-induced HIF-1α, MCF-7 and T47D cells were first tested for Akt activation upon DADLE treatment. Compared with nontreated controls, DADLE exposure for 5–15 minutes increased the amount of Ser-473 phosphorylated Akt in both BCa cell lines (Fig. 2A). Pretreatment of MCF-7 and T47D cells with the PI3K inhibitors wortmannin and LY294002, or with the Akt inhibitor Akti-1/2 prevented DADLE-mediated Akt phosphorylation (Fig. 2A). To evaluate the impact of DADLE-induced Akt regulation for HIF-1α, MCF-7 and T47D cells were pretreated with PI3K/Akt inhibitors and analyzed for HIF-1α after DADLE exposure for 1 hour. In presence of wortmannin, LY294002 and Akti-1/2, DADLE incubation failed to induce HIF-1α accumulation (Fig. 2B). Moreover, DADLE-triggered HIF-1α accumulation was abolished by the PI3K inhibitors BEZ235 or BKM120 (Fig. 2B).

**Effect of DADLE Treatment on VEGF Expression and Release.** To investigate next whether DADLE-stimulated HIF-1α triggers the synthesis of angiogenic factors, MCF-7 and T47D cells were first analyzed for VEGF-A expression by real-time quantitative-PCR. As shown in Fig. 3A, incubation of BCa cells with 1 μM DADLE for 6 hours yielded similar amounts of VEGF-A mRNA as in the nontreated controls. Also, extended DADLE exposure for 12 or 24 hours had no effect on the abundance of VEGF-A mRNA (Fig. 3A). Likewise, the amount of mRNA of the VEGF-A splice variants VEGF-A121 and VEGF-A165 remained unaffected by DADLE treatment.

To evaluate whether DADLE treatment alters the release of VEGF, conditioned medium (CM) from MCF-7 and T47D cells cultured in the absence or presence of 1 μM DADLE for 24 hours were analyzed on an angiogenesis cytokine array. The analysis showed comparable amounts of VEGF in CM from DADLE-treated and nontreated BCa cells (Fig. 3B, red box). In addition, CM from BCa cells contained the proangiogenic factors CXCL16, angiogenin, amphiregulin, serpin E1 (only MCF-7 cells), urokinase plasminogen activator, IGFBP-2, IGFBP-3, and FGF-7 (only T47D cells), and the angiogenesis inhibitors TIMP-1 and thrombospondin (Fig. 3B). Neither qualitative nor quantitative differences were observed for these factors between CM from DADLE-treated and nontreated BCa cells.

**DADLE Treatment Triggers COX-2 Expression and PGE2 Release in Breast Cancer Cells.** An alternative HIF-1α target with angiogenic function is COX-2 (Kaidi et al., 2006). Thus, MCF-7 and T47D cells were treated with 1 μM DADLE for 1–5 hours and analyzed next for COX-2 protein level by immunoblotting. Incubation of both BCa cell lines with DADLE for 1 hour increased the amount of COX-2 protein (Fig. 4A), which remained elevated for 4 hours in MCF-7 and 5 hours in T47D cells.

To further evaluate whether DADLE-induced COX-2 is functionally active, BCa cells were treated with 1 μM DADLE for 24 hours and tested for PGE2 release by ELISA. Compared with CM collected from nontreated controls, the amount of PGE2 was approximately two-times higher in CM from DADLE-treated MCF-7 and T47D cells (Fig. 4B). Pretreatment of BCa cells with the COX-2 inhibitor celecoxib (50 μM, 30 minutes) abolished the DADLE effect in both BCa cell lines. These findings demonstrate that DADLE treatment induced the expression of active COX-2 in MCF-7 and T47D cells.

**Role of PI3K/Akt/HIF-1α Signaling in DADLE-Induced
COX-2 Expression.** To find out whether DADLE-mediated COX-2 expression is linked to PI3K/Akt-regulated HIF-1α, MCF-7, and T47D cells were pretreated with Akti-1/2, BEZ235, or BKM120 and subsequently examined for COX-2 protein level by immunoblotting. Pretreatment of MCF-7 cells with Akti-1/2 (100 μM, 15 minutes) or BEZ235 (1 μM; 10 minutes) enhanced basal level of COX-2 in MCF-7, but not in T47D cells (Fig. 5A). In contrast, incubation with BKM120 (1 μM, 10 minutes) had no effect on basal COX-2 expression. Cell exposure to 1 μM DADLE for 1 hour decreased protein level of COX-2 in MCF-7 cells pretreated with Akti-1/2 and BEZ-235, respectively. In MCF-7 cells pretreated with BKM120, DADLE had no effect on COX-2 protein level (Fig. 5A).

To examine the role of DADLE-induced HIF-1α, MCF-7, and T47D cells were exposed to echinomycin, which inhibits the
binding of HIF-1α to the DNA (Kong et al., 2005). Incubation of BCa cells with 10 nM echinomycin prevented DADLE-induced increase of COX-2 protein in MCF-7 and T47D cells (Fig. 5B).

**Regulation of HIF-1α and COX-2 in 3D-Cultured MCF-7 Cells.** Next, the effect of DADLE on HIF-1α and COX-2 was examined in MCF-7 cells grown as 3D culture. First, 3D-cultured MCF-7 cells were incubated with 1 μM DADLE for 3 or 6 hours and analyzed for HIF-1α protein level by immunoblotting. Nontreated controls exhibited a basal level of HIF-1α protein, which was further increased after DADLE exposure for 3 hours (Fig. 6A); 3D cultures incubated with DADLE for 6 hours exhibited similar HIF-1α protein levels than the nontreated controls. To assess COX-2 regulation, 3D-grown MCF-7 cells were treated with 1 μM DADLE for 3 hours and then subjected to immunohistochemical analysis. Nontreated 3D cultures showed no COX-2 staining, whereas clusters of COX-2-positive cells were observed after DADLE exposure (Fig. 6B). Three-dimensional cultures treated with 1 μM BEZ235 or 1 μM BKM120 alone displayed scattered COX-2-positive cells, which were totally abolished after DADLE treatment.

**Conditioned Medium from DADLE-Stimulated MCF-7 Cells Stimulates END Cells.** We finally asked whether DADLE-induced HIF-1α/COX-2 signaling in breast cancer cells has angiogenic function. To address the question, we isolated CM from MCF-7 cells treated with 1 μM DADLE for 24 hours (CM\textsuperscript{DADLE}) and used it for incubation of END cells spheroids (Fig. 7A). END cell spheroids exposed to CM\textsuperscript{DADLE} for 24 hours showed multiple sprouts, whereas END cells treated with CM from nontreated MCF-7 cells (CM\textsuperscript{nont}) remained in a round shape (Fig. 7B). No sprouts were observed when END cell spheroids were exposed directly to 1 μM DADLE for up to 5 days (Supplemental Fig. 1). Also END cell spheroids pretreated with the EP2 receptor inhibitor PF-04418948 showed no sprouting after incubation with CM\textsuperscript{DADLE} (Fig. 7, B and C). Likewise, CM from MCF-7 cells exposed to DADLE and celecoxib, DADLE and naloxone or naltrindole, or DADLE and echinomycin failed to bring about sprout formation (Fig. 7, B and C). Comparable sprouting activities were also observed for END cell spheroids after incubation with CM from T47D cells treated with DADLE and respective inhibitors (Supplemental Fig. 2).

**Discussion**

Opioids promote breast cancer angiogenesis by a largely unknown mechanism. Here we demonstrate that DADLE induces HIF-1α accumulation in human MCF-7 and T47D breast cancer cells via PI3K/Akt activation. We further show that DADLE treatment enhances COX-2, but not VEGF expression, which triggers paracrine activation of END cells. MCF-7 and T47D cells are classic in vitro models to study human estrogen receptor (ER)-positive breast cancer (Comşa et al., 2015; Yu et al., 2017). Exposure to DADLE enhanced HIF-1α protein levels in both cell lines and was prevented by the nonselective opioid receptor antagonist naltroxone (Satoh and Minami, 1995), the DOR-selective antagonist naltrindole (Portoghese et al., 1988), and the G\textsubscript{i/o} protein inhibitor PTX (Leaney and Tinker, 2000). Thus, HIF-1α regulation results from stimulation of G\textsubscript{i/o} protein-dependent signaling of DORs and is not a cell line-specific DADLE effect. HIF-1α regulation by DORs was also observed in a previous study where fentanyl induced HIF-1α in human SH-SY-5Y neuroblastoma cells (Daijo et al., 2011). This suggests HIF-1α is a DOR downstream target in different human cancer cells and probably also an effector molecule of other G\textsubscript{i/o} protein-coupled receptors.
DADLE induced a transient HIF-1α accumulation within 1 hour in MCF-7 and T47D cells. The fast onset is in large contrast to fentanyl-induced HIF-1α accumulation in SH-SY-5Y cells, which is observed only after 24 hours (Daijo et al., 2011). The fast kinetic in BCa cells suggests a direct DOR-mediated signaling mechanism, which allows HIF-1α induction by DADLE. Transient HIF-1α stimulation further implies that this signaling mechanism is terminated within 2 to 3 hours. It has been shown that stimulation of DORs by DADLE induces receptor desensitization, internalization, and subsequent degradation with comparable kinetics (Cvejic et al., 1996; Yoon et al., 1998; Eisinger et al., 2002). As these processes terminate DOR signaling, rate of DADLE-induced DOR internalization and degradation might account for transient HIF-1α accumulation in BCa cells.

DADLE treatment induced Akt activation in MCF-7 and T47D cells as indicated by Akt Ser-473 phosphorylation (Alessi et al., 1996). Inhibition of Akt phosphorylation by wortmannin and LY294002, two structurally unrelated PI3K inhibitors (Powis et al., 1994; Vlahos et al., 1994), confirms that DADLE-mediated Akt activation depends on PI3K in BCa cells (Powis et al., 1994; Vlahos et al., 1994), indicating that DADLE and LY294002, two structurally unrelated PI3K inhibitors, are characterized by the expression of ER and amplification of PKCε and RAF-1 (Shadeo and Lam, 2006). RAF-1 signaling induces endothelin-1 expression (Cheng et al., 2001), whereas

**Fig. 4.** DADLE stimulates COX-2 expression and PGE2 release. (A) COX-2 expression in DADLE-treated MCF-7 and T47D cells. Cells were treated with 1 μM DADLE for 1–5 hours. Controls (cn) remained untreated. Cells were lysed and analyzed for COX-2 expression by immunoblotting. HSC70 served as loading control. Shown is one representative blot from three independent experiments (n = 3). (B) Analysis of PGE2 released from DADLE-treated MCF-7 and T47D cells. MCF-7 and T47D cells were treated with 1 μM DADLE in presence or absence of 50 μM celecoxib (cele). After 24 hours, conditioned medium was collected and tested for PGE2 concentration (pg/ml) by ELISA. Data represent mean ± S.E.M. from three individual experiments (n = 3). *P < 0.05 compared with non-treated control (cn) by unpaired Welch’s t test.

**Fig. 5.** Role of PI3K/Akt and HIF-1α in DADLE-mediated COX-2 expression. (A) Effect of PI3K and Akt inhibitors on COX-2 expression. MCF-7 and T47D cells were treated with 100 μM Akti-1/2 (15 minutes; Akt-i), 1 μM BEZ235 (10 minutes), or 1 μM BKM120 (10 minutes) before exposure to 1 μM DADLE for 1 hour. Controls (cn) were pretreated with 1% DMSO as solvent control. HSC70 served as loading control. Shown is one representative blot from three independent experiments (n = 3). (B) Echinomycin blocks DADLE-induced COX-2 expression. MCF-7 and T47D cells were pretreated with 10 nM echinomycin for 10 minutes; controls (cn) remained untreated. After incubation with 1 μM DADLE for 1 hour, cells were lysed and tested for COX-2 protein by Western blotting. HSC70 served as loading control. Shown is one representative immunoblot from three independent experiments (n = 3).
PKCα may promote CXCL16 release by ADAM10 activation (Gough et al., 2004; Kohutek et al., 2009). Moreover, activation of ER leads to the expression of VEGF, Serpin E1, and FGF-7 by HIF-1α-independent mechanisms (Ruohola et al., 1999; Smith et al., 2002; Gopal et al., 2012). As our experiments were conducted with medium containing phenol red, which has estrogen activity (Berthois et al., 1986), regulation of these pro-angiogenic factors by DADLE might be covered by the signaling of amplified RAF-1 and PKCα and ER activation in MCF-7 and T47D cells.

In contrast to VEGF, DADLE triggered the expression of catalytically active COX-2 in BCa cells. The ability of opioids to induce COX-2 upregulation has been already observed in vivo. Morphine treatment enhanced the content of COX-2 protein and PGE_2 in mammary tumors in mice (Farooqui et al., 2007), whereas the DOR selective agonist BW373U86 (6)-[1(S*),2α,5b]-4-[(2,5-Dimethyl-4-(2-propenyl)-1-piperazinyl](3-hydroxyphenyl)methyl]-N,N-diethylbenzamide upregulates the expression and activity of COX-2 in the myocardium (Kodani et al., 2002). The in vivo mechanism of opioid-induced COX-2 expression was not further examined. Inhibition of DADLE-induced COX-2 expression by echinomycin, BEZ235, and Akti-1/2 implicates a functional role for PI3K/Akt/HIF-1α signaling in BCa cells. As activation of HIF-1α or PI3K/Akt is associated with COX-2 upregulation in tumor cells (Kaidi et al., 2006; Xia et al., 2010), DADLE-induced PI3K/Akt/HIF-1α signaling is a plausible mechanism for COX-2 expression in BCa cells.

Considering that activation of PI3K/Akt enhances COX-2 expression in tumor cells (St.-Germain et al., 2004; Xia et al., 2010), it was surprising that incubation of BCa cells with the PI3K/Akt inhibitors Akti-1/2 and BEZ235 had the same effect. Interestingly, subsequent DADLE exposure suppressed Akti-1/2 and BEZ235-induced COX-2 expression. As the phenomenon was observed in MCF-7, but not T47D cells, a cell-type specific mechanism seems to trigger COX-2 upregulation after PI3K/Akt inhibition. Enhanced expression of COX-2 after PI3K/Akt inhibition by BEZ235 or Akt inhibitor X was previously observed for microglia (de Oliveira et al., 2012). The effect was suggested to result from an enhanced activity of glycogen synthase kinase 3 (GSK3), which is negatively regulated by PI3K/Akt (Jope et al., 2007). Considering the “GSK3 hypothesis,” our observation implies that DOR signaling may block BEZ235 and Akti-1/2 induced GSK3 activity by a PI3K/Akt-independent mechanism. The activity of GSK3 is not only controlled by Akt (Cross et al., 1995). Also protein kinase A (PKA) terminates GSK3 activity (Fang et al., 2000). Zhang et al. (1999) showed that activation of p38 MAPK by DORs requires PKA activity, which implies that cAMP-dependent PKA may be stimulated by DORs. The mechanism of PKA activation by the opioid receptor has not been investigated so far, but studies revealed several signaling processes, by which G_α protein-coupled receptors may stimulate PKA. For instance, PKA may be activated by cAMP produced by adenylyl cyclase 2 (AC2), AC4, and AC7, which are stimulated by G_{αγ} subunit (Khan et al., 2013). Alternatively, PKA is activated by G_α coupled receptors as a result of IκB degradation upon stimulation of protein kinase C or JNK (Dulin et al., 2001). As DORs can activate AC2, PKC, and JNK (Ho et al., 1999; Kam et al., 2003; Eisinger and Ammer, 2008), several possibilities may be suggested for the signaling cascades leading to DADLE-induced activation of PKA. Independent of the underlying mechanism,
PKA activation by DORs might thus suppress BEZ235- and Akti-1/2-induced COX-2 expression by GSK3 inhibition.

Studies have shown that findings from two-dimensional (2D, monolayer) cultured tumor cells differ from in vivo observations (Horman, 2016). Especially drug-induced regulation of HIF-1α observed in cell culture experiments has to be considered critical as solid tumors are often exposed to hypoxia and thus already feature HIF-1α overexpression (Zhong et al., 1999; Yang et al., 2017). To assess the biologic relevance of in vitro data, testing drug effects in 3D-cultured cells is state-of-the-art in cancer research, because 3D-cultured cells have similar characteristics as in vivo and are considered in vitro microtumor models (Ivascu and Kubbies, 2006). 3D-cultured cells also feature in vivo like oxygen gradients and HIF-1α expression (Chandrasekharan et al., 2002; Riedl et al., 2017), which render the models ideal tools to examine the effect of DADLE under tumor-like conditions. We used 3D-cultured MCF-7 cells, which exhibited a basal level of HIF-1α expression referring to hypoxic conditions in the microtumor model. Also, 3D-cultured MCF-7 cells showed transient increase of HIF-1α and COX-2 expression in response to DADLE treatment. Enhanced COX-2 expression after exposure to PI3K inhibitors and its inhibition by DADLE was observed as well. These findings indicate that DADLE-induced PI3K/HIF-1α/COX-2 signaling axis is not an artifact of 2D-cultured BCa cells but also occurs in microtumors under in vivo-like conditions.

COX-2 has a pivotal role in breast cancer progression (Rozic et al., 2001). Beside growth and metastasis, COX-2 expression is closely related to vascularization of mammary malignancies (Davies et al., 2003; Wang and DuBois, 2004). COX-2 activity was also revealed to promote morphine-mediated angiogenesis in a murine breast cancer model (Farooqui et al., 2007), which suggest DOR-induced PI3K/Akt/HIF-1α/COX-2 signaling in BCa cells a potential mechanism of angiogenic opioid effect. Findings from our END cell sprouting assay support the hypothesis and further suggest a paracrine mechanism underlying opioid-induced angiogenesis. We showed that conditioned medium from DADLE-treated MCF-7 cells triggers sprouting of endothelial cells. (A) Experimental setup. MCF-7 cells were grown as monolayer in a six-well plate filled with 2 ml medium/well and treated with 1 μM DADLE in presence or absence of 50 μM celecoxib (30 minutes), 10 μM naloxone, 10 μM naltrindole, or 10 nM echinomycin (10 minutes) for 24 hours. Subsequently, 1.5 ml culture supernatant was collected and transferred to END cell spheroids placed on a collagen-coated 96-well plate (100 μl/well). After incubation for 24 hours, spheroids were analyzed for sprouting. (B) END cell sprouting. END cells were exposed to CM obtained from MCF-7 cells treated with 1 μM DADLE alone (CM^DADLE) or together with 10 nM echinomycin (echino), 10 μM naloxone (nalox), 10 μM naltrindole (nalt), or 50 μM celecoxib (celecox). CM collected from nontreated MCF-7 served as control (CM^cn). In addition, END cells were treated with 10 μM PF-04418948 (+PF) for 30 minutes before being exposed to CM^DADLE. Pictures show representatives END cell spheroids from each treatment group after 24-hour incubation. (C) Quantification of sprouting areas. Sprouting area was determined from 6 to 15 randomly selected spheroids per experimental group from three independent experiments and presented as mean ± S.E.M. **P < 0.05 compared with CM^cn by unpaired Welch’s t test.
factors mediate END cell sprouting by the PG2 receptor EP2, as the EP2 receptor antagonist PF-04418948 blocked sprout formation. Stimulation of endothelial EP2 receptors has a central role in tumor angiogenesis (Kamiyama et al., 2006), so that paracrine activation by BCa cells in consequence of HIF-1α/COX-2 upregulation represents a possible mechanism of opioid-induced angiogenesis. In summary, the present data elucidate that DOR stimulation in ER-positive BCa cells induces PI3K/Akt/1α/COX-2 signaling, resulting in paracrine activation of endothelial cells via EP2 receptor activation. It remains to be investigated whether the signaling mechanism also applies to other cancer cells expressing DORs, which would render opioid-induced tumor angiogenesis a much more widespread phenomenon in cancer patients. As PI3K inhibitors like BEZ235 and BKM120 are promising anticancer drugs in clinical trials (Martin et al., 2017; Rodon et al., 2018), targeting PI3K/Akt signaling represents a potential therapeutic strategy to combat the proangiogenic opioid effect.

Acknowledgments

The authors thank Felix Holstein and Claudia Höchsmann for technical support.

Authorship Contributions

Participated in research design: Fux.
Conducted experiments: Schoos, Knab, Gabriel, Fux.
Performed data analysis: Schoos, Gabriel, Fux.
Wrote or contributed to the writing of the manuscript: Schoos, Gabriel, Knab, Fux.

References


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Activation of HIF-1α by δ-opioid receptors in breast cancer cells induces COX-2 expression for paracrine activation of vascular endothelial cells

*The Journal of Pharmacology and Experimental Therapeutics*

**Supplemental Figures**

**Fig. 1**

END cell spheroids were exposed to 1 µM DADLE and examined for sprout formation after 5 days. Negative controls (cn) remained untreated. For positive sprouting control, spheroids were treated with 20 ng/ml FGF-2 for 24 h. Pictures show representative spheroids. Sprouting area was determined from 6-8 randomly selected spheroids per experimental group and expressed as mean ± SEM. * p < 0.05 compared to non-treated controls (cn) by unpaired Welch’s t-test.
A) END cells were exposed to CM obtained from T47D cells treated with 1 µM DADLE alone (CM\textsuperscript{DADLE}) or together with 10 µM naloxone (nalox), 10 µM naltrindole (nalt), 10 nM echinomycin (CM\textsuperscript{echino/DA}) or 50 µM celecoxib (CM\textsuperscript{cele/DA}). CM collected from non-treated T47D cells served as control (CM\textsuperscript{cn}). In addition, END cells were treated with 10 µM PF-04418948 (PF) for 30 min before being exposed to CM\textsuperscript{DADLE}. Pictures show representatives END cell spheroids from each treatment group after 5 day-incubation.

B) Quantification of sprouting areas. Sprouting area was determined from 6-10 randomly selected spheroids per experimental group from three independent experiments and presented as mean ± SEM. * p < 0.05 compared to CM\textsuperscript{cn} by unpaired Welch’s t-test.