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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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 naltrindole and naloxone, pertussis toxin, different phosphoinositide 3-kinase (PI3K) inhibitors, and the Akt inhibitor Akti-1/2. Whereas DADLE exposure had no effect on the expression and secretion of vascular endothelial growth factor (VEGF) in BCa cells, an increased abundance of cyclooxygenase-2 (COX-2) and release of prostaglandin E2 (PGE2) was detected. DADLE-induced COX-2 expression was also observed in three-dimensional cultured MCF-7 cells and impaired by PI3K/Akt inhibitors and the HIF-1α inhibitor echinomycin. Supernatant from DADLE-treated MCF-7 cells triggered sprouting of endothelial (END) cells, which was blocked when MCF-7 cells were pretreated with echinomycin or 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 trigger END 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 (WHO), 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-1) is a heterodimeric transcription factor, consisting of two subunits, HIF-1α and HIF-1β. HIF-1α is a master of the hypoxic response, which in turn regulates the expression of genes associated with angiogenesis, cell proliferation, and survival. The hypoxic-inducible factor 1 (HIF-1) is a heterodimeric transcription factor, consisting of two subunits, HIF-1α and HIF-1β. HIF-1α is a master of the hypoxic response, which in turn regulates the expression of genes associated with angiogenesis, cell proliferation, and survival.
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., 2002; Fukuda et al., 2002) as well as G protein-coupled thrombin and angiotensin II receptors has been shown to induce HIF-1α accumulation (Görlichen, 2007; 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 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 x glioma NG108-15 hybrid cells, stimulation of DORs was shown to induce transcription of IGF-1 receptors and PI3K/Akt activation (Heiss et al., 2009). Moreover, DOR stimulation in human breast cancer cells was shown to induce activation of the Akt pathway and increase the expression of HIF-1α mRNA (Dorland et al., 2011). Activation of DORs might represent a potential proangiogenic effect of opioids.

**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 Vojdan 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-(Falcon, Corning, 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-Ale³,β-Leu⁴]-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), BRM12 5-2,5-dimorpholino-4-pyridinyl-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-quinolinyl)-1H-imidazol-4,5-c]-quinolin-1-yl)-α-dimethyl-benzeneacetonitrile; 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. Celexocib (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-04418948 (1-(4-fluorobenzo-3-)[1-(6-methoxy-2-naphthalenyl)]oxymethyl)-3-azetidincarboxylic 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, 0.1% bromophenole blue), denatured by 95°C for 3 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, precLab; VWR International GmbH, Erlangen, Germany), which was subsequently blocked with 5% non-fat milk powder (Carl Roth GmbH, Karlsruhe, Germany) and cultured for 5 days in complete medium. For detection of HIF-1α accumulation under normoxic conditions, membranes were 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 #4060; CST), rabbit monoclonal COX-2 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# 7076; Cell Signaling Technology) or anti-mouse IgG (Cat# 7076; Cell Signaling Technology) for 60 minutes at room temperature. Membranes were finally exposed to Clarity Western Blotting Touch and Image Laboratory Software (Bio-Rad Laboratories, Inc.).

**Real-Time Quantitative PCR.** Total RNA was isolated usingpeqGOLD 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.
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'-ATGGCAGGACCTGACGTCCTT-3' and reverse 5'-TGG GGTTGCTTTCACACACA-3', RPS18 (reference gene #2: ribosomal protein S18; NM_022551.2): forward 5'-GGTCCTTTTC ACCAGCA-3' and reverse 5'-TGCCTAGGACCTGCTATGTC-3', VEGF-A total (NM_001025366.2), VEGF-A121 (NM_001025370.2), and VEGF-A165 (NM_001287044.1): forward 5'-GGATGAGATCGAGTACATC-3' and reverse 5'-ACCAGGATGACCTGAC-3' (VEGF-A total), 5'-GCCTCGTGTGCTACATTTC-3' (VEGF-A121), and 5'-CAAGGGC CACAGGAGATTTC-3' (VEGF-A165). 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 \( \Delta \Delta C_t \) 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 manufacturer’s instructions. PGE2 ELISA. MCF-7 and T47D cells were grown in a six-well plate and incubated with 1 μM DADLE for 24 hours. Cell culture supernatant was collected, cleared from cells by centrifugation, and stored at -20°C until being analyzed for PGE2 concentrations. Quantification of PGE2 was performed in duplicates from each sample by using the Prostaglandin E2 Parameter Assay Kit (Cat# KGE004B; R&D Systems, Waltham, MA).

**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 1000 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/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 minutes, blocked with 1.5% normal goat serum (Sigma Aldrich) and incubated with rabbit monoclonal COX-2 antibody (1:500, CloneSp21, Cat# RM-9121; Thermo Fisher Scientific). Sections were washed and exposed to anti-rabbit poly-horseradish peroxidase secondary antibody (BrightVision Immunologic, Duiven, The Netherlands) and 3,3’-diaminobenzidine-tetrahydrochloride substrate (Sigma Aldrich) solved in Tris-HCl buffer pH 7.4 and 0.03% H2O2 as chromogen. Finally, slides were washed with distilled water, counterstained with haemalum, dehydrated, and mounted by using xylene-soluble medium (DPX; Sigma Aldrich). Negative controls were performed by substitution of the primary antibody with PBS. Sections were examined using the Polysvar light microscope (Reichert-Jung, Vienna, Austria) with a digital D8-F11 camera (Nikon, Vienna, Austria) and Nikon NIS elements software.

**Sprouting Assay.** Five-day-old spheroids from murine END cells were transferred from nonadherent U-bottom to flat bottom 96-well plates coated with collagen I rat protein (1 mg/ml; Thermo Fisher Scientific) and exposed to supernatant collected from MCF-7 cells treated with 1 μM DADLE in presence or absence of indicated inhibitors for 24 hours. In a second approach, END cell spheroids were treated with PF-04418948 before being exposed to supernatant from DADLE-treated MCF-7 cells. END cell spheroids were cultured for 24 hours, photographed by using the Olympus IX71 microscope (Olympus K.K., Tokyo, Japan) with an Olympus DP72 camera (Olympus K.K.) and Cellsens Dimension software (Olympus K.K.), and assessed for sprouting area by using ImageJ.

**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 (Khrmante 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 exposure to 1 μM DADLE.

![Fig. 1. HIF-1α accumulation in MCF-7 and T47D cells treated with DADLE.](image-url)

(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 naltrindole 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).
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 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.

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, and 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).

Fig. 2. Role of PI3K/Akt signaling in DADLE-regulated HIF-1α accumulation. (A) Akt activation by DADLE in breast cancer cells. MCF-7 and T47D cells were treated with 1 μM DADLE for indicated time periods. Cells pretreated with 2.5 μM wortmannin (30 minutes; wortm), 10 μM LY294002 (30 minutes), or 100 μM Akti-1/2 (15 minutes; Akt-i) were exposed to 1 μM DADLE for 10 minutes. Cells were lysed and subjected to Akt (Akt) and phospho-Serine-473-Akt (pAkt) analysis by immunoblotting. (B) HIF-1α accumulation is prevented by PI3K and Akt inhibitors. MCF-7 and T47D cells were pretreated with wortmannin (2.5 μM; 30 minutes; wortm), LY294002 (10 μM; 30 minutes), Akti-1/2 (100 μM; 15 minutes), Akti-1/2, BEZ235 (1 μM; 10 minutes), or BKM120 (1 μM; 10 minutes) and then exposed to 1 μM DADLE for 1 hour. Control cells (cn) were pretreated for 30 minutes with 1% DMSO as drug solvent control. Cell lysates were subjected to immunoblotting and probed for HIF-1α expression. HSC70 served as loading control. Shown is one representative immunoblot from three independent approaches (n = 3).
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\textsubscript{DADLE}) and used it for incubation of END cells spheroids (Fig. 7A). END cell spheroids exposed to CM\textsubscript{DADLE} for 24 hours showed multiple sprouts, whereas END cells treated with CM from nontreated MCF-7 cells (CM\textsubscript{NT}) 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\textsubscript{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 naloxone (Satoh and Minami, 1995), the DOR-selective antagonist naltrindole (Portoghese et al., 1988), and the Gi/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 as reported previously (Heiss et al., 2009). Inhibition of Akt phosphorylation by wortmannin and LY294002, but also BEZ235 and BKM120, two alternative PI3K inhibitors (Rodriguez et al., 2016), which let us suppose that DADLE-induced HIF-1α, PI3K/Akt turned out to be the central driver and thus a potential target to interfere with DADLE-induced HIF-1α.

Although VEGF expression is a central response of HIF-1α activation (Forsythe et al., 1996), DADLE had no effect on transcription of VEGF-A including its most common isoforms, VEGF-A121 and VEGF-A165, or its secretion as indicated by the unchanged amount of VEGF peptide in the supernatant of treated and nontreated cells. Likewise, the release of CXCL16, Serpin E1, endothelin 1, and FGF-7 was unaffected. Interestingly, these paracrine factors are alternative HIF-1α targets (Yamashita et al., 2001; Chaturvedi et al., 2014; Rouillard et al., 2016), which have previously been demonstrated to trigger expression and secretion of these angiogenic factors in MCF-7 and T47D cells. MCF-7 and T47D cells are characterized by the expression of ER and amplification of these mechanisms, which allow constitutive expression and release of these factors in MCF-7 and T47D cells.
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 PGE₂ in mammary tumors in mice (Farooqui et al., 2007), whereas the DOR selective agonist BW373U86 (6-(1(S*),2a,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 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 Gbg subunit (Khan et al., 2013). Alternatively, PKA is activated by G protein-coupled receptors as a result of IkB 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 suggests 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 spheroid sprouting. Cells were exposed to CM obtained from MCF-7 cells treated with 1 μM DADLE alone (CMDADLE) 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 (CMcn). In addition, END cells were treated with 10 μM PF-04418948 (+PF) for 30 minutes before being exposed to CMDADLE. Pictures show representatives END cell spheroids from each treatment group for 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 CMcn 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.

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Authorship Contributions

Participated in research design: Fux.

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References


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_{DADLE}) or together with 10 µM naloxone (nalox), 10 µM naltrindole (nalt), 10 nM echinomycin (CM_{echino/DADLE}) or 50 µM celecoxib (CM_{cele/DADLE}). CM collected from non-treated T47D cells served as control (CM_{cn}). In addition, END cells were treated with 10 µM PF-04418948 (PF) for 30 min before being exposed to CM_{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_{cn} by unpaired Welch’s t-test.