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Substrate-selective COX-2 inhibition as a novel strategy for therapeutic endocannabinoid augmentation

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Abstract

Pharmacologic augmentation of endogenous cannabinoid (eCB) signaling is an emerging therapeutic approach for the treatment of a broad range of pathophysiological conditions. Thus far, pharmacological approaches have focused on inhibition of canonical eCB inactivation pathways, fatty acid amide hydrolase for anandamide and monoacylglycerol lipase for 2arachidonoylglycerol. Here we review experimental evidence that cyclooxygenase-2-mediated eCB oxygenation represents a third mechanism for terminating eCB action at cannabinoid receptors. We describe the development, molecular mechanisms, and *in vivo* validation of "substrate-selective" COX-2 inhibitors that prevent eCB inactivation by COX-2 without affecting the prostaglandin generation from arachidonic acid. Lastly, we review recent data on the potential therapeutic applications of substrate-selective COX-2 inhibitors with a focus on neuropsychiatric disorders.

The endocannabinoid system

Two decades of intense scientific inquiry have defined a prominent role for central endogenous cannabinoid (eCB) signaling in a variety of physiological and pathophysiological processes [1, 2]. eCBs are arachidonate-containing lipid signaling molecules that exert biological actions via activation of cannabinoid type 1 and 2 receptors

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(CB₁ and CB₂), in addition to other targets including vanilloid receptor 1 (TRPV1), peroxisome proliferator-activated receptor (PPAR), and some ion channels [1]. The two most well studied eCBs, *N*-arachidonoylethanolamide (anandamide, AEA) and 2-arachidonoylglycerol (2-AG), are synthesized and degraded by discrete sets of enzymes [3-5]. Elucidation of the molecular regulation of eCB metabolism has led to the development of pharmacological tools to enhance eCB signaling and probe the therapeutic utility of eCB augmentation for a variety of pathological conditions [6-8].

AEA is primarily degraded by fatty acid amide hydrolase (FAAH), and pharmacological inhibition of FAAH causes robust increases in brain AEA concentrations [9, 10]. However, FAAH also degrades a number of non-cannabinoid N-acylethanolamides (NAEs), which are elevated upon FAAH inhibition and active at molecular targets, such as PPARs [11-13]. In parallel to AEA, 2-AG is primarily degraded by monoacylglycerol lipase (MAGL) [14], which also metabolizes a series of monoacylglycerols (MAGs). Inhibition of FAAH or MAGL have demonstrated preclinical efficacy in models of neuropathic pain, neurodegeneration, anxiety and depression, hyperemesis, and drug withdrawal syndromes, many of which are mediated by CB receptor-dependent mechanisms [6, 15-18]. These studies demonstrate the pleiotropic therapeutic potential of eCB augmentation via FAAH and MAGL inhibition and the resulting augmentation of cannabinoid receptor signaling.

Here we will review the pharmacology and potential therapeutic implications of a *third* eCB metabolic pathway, the oxidative metabolism of AEA and 2-AG by cyclooxygenase-2 (COX-2). We review the molecular biology of COX-2, data defining its role as an eCB-metabolizing enzyme, the roles of eCB-derived COX-2 oxidative metabolites, and compare and contrast COX-2-mediated eCB metabolism with the canonical FAAH- and MAGL-mediated metabolic pathways. We then discuss recent advances in the development of "substrate-selective" COX-2 inhibitors (SSCIs), which prevent eCB oxygenation by COX-2 without inhibiting the oxygenation of arachidonic acid (AA) to prostaglandins (PGs). We review the evidence that this novel pharmacological strategy increases eCB tone without affecting AA-derived PG formation by COX-2 and could have fewer adverse side effects compared to either direct CB receptor activation or PG synthesis inhibition. Lastly, we will describe the development, validation, and proof-of-concept validation of the therapeutic potential of SSCIs in preclinical models of anxiety using the first-generation SSCI, LM-4131, as an example.

Molecular biology of COX-2

COX-2 is a homodimer encoded by *Ptgs-2*, an immediate-early gene that produces a 4 kb mRNA in response to a wide range of stimuli [19]. Upon synthesis, COX-2 localizes to the nuclear envelope and lumen of the endoplasmic reticulum [20, 21]. COX-2 contains two separate active sites: a cyclooxygenase active site, which catalyzes the oxygenation of polyunsaturated fatty acids to hydroperoxy endoperoxides, and a peroxidase active site, which reduces the hydroperoxide to an alcohol [22]. The cyclooxygenase reaction is initiated by the oxidation of the heme prosthetic group by hydroperoxide; the oxidized heme then oxidizes the active site Tyr-385 to the catalytic tyrosyl radical [23-25]. The tyrosyl radical then abstracts the 13-pro-(*S*)-hydrogen from the substrate to form a carbon-centered

radical, which can be trapped at carbon 11 by molecular oxygen to produce an 11-(R)-peroxyl radical. The 11-(R)-peroxyl radical then undergoes two cyclizations to form a bicyclic endoperoxide and an allylic radical between carbons 13 and 15. The allylic radical then reacts with a second molecule of molecular oxygen to form a peroxyl radical at carbon 15. Finally, the peroxyl radical abstracts the phenolic hydrogen of Tyr-385 to generate hydroperoxy endoperoxide prostaglandin G₂ (PGG₂₎ and regenerate the tyrosyl radical, which can further catalyze fatty acid oxygenation. PGG₂ then diffuses out of the cyclooxygenase active site and into the peroxidase active site, where the 15-hydroperoxide group is reduced to an alcohol to form prostaglandin endoperoxide H₂ (PGH₂). COX-2 action is regulated post-translationally by several mechanisms, including degradation by the endoplasmic reticulum-associated degradation system [26] and suicide-inactivation during catalysis [27]. Although COX-2 is generally considered an inducible enzyme, it is constitutively expressed in the brain, kidney, and spinal cord [28-30].

The catalytic activities of both COX-1 and COX-2 lead to the production of PGH₂ from AA. PGH₂ is metabolized by downstream synthases to form prostaglandins E_2 (PGE₂), D_2 (PGD₂), $F_{2\alpha}$ (PGF_{2\alpha}), prostacyclin (PGI₂), and thromboxane A₂ (TxA₂). Thus, COX enzymes catalyze the committed step in the formation of a series of lipid mediators that play crucial roles in immunity, inflammation, and a plethora of other biological responses [31, 32]. Non-steroidal anti-inflammatory drugs (NSAIDs) block the production of PGs from AA by inhibiting the cyclooxygenase reactions of COX-1 and COX-2, and this accounts for their myriad of pharmacological effects [33]. Because of the presence of COX-2 in inflammatory cells and neural tissue, it is the principal target for the anti-inflammatory and analgesic effects of NSAIDs [34].

There are a variety of NSAID scaffolds (**Figure 1a**) that bind to COX-2 in distinct conformations. In the canonical binding mode, carboxylic acid-containing inhibitors form an ion-pair and hydrogen bond with Arg-120 and Tyr-355 at the base of the active site (e.g., flurbiprofen, naproxen, and indomethacin) (**Figure 1b**) [35, 36]. Alternatively, inhibitors can bind in an inverted fashion and form hydrogen bonds between their carboxylates and Tyr-385 and Ser-530 near the top of the active site (e.g., diclofenac and lumiracoxib) (**Figure 1c**) [37, 38]. Neutral NSAIDs, such as the COX-2 selective inhibitors celecoxib and rofecoxib, insert sulfonamide or sulfone groups into a side pocket of the COX-2 active site adjacent to Val-523 [36]. Thus, NSAIDs bind in several conformations within the COX-2 active site and form interactions with multiple residues.

Oxygenation of endocannabinoids by COX-2

In addition to the oxygenation of AA, COX-2 also catalyzes the oxygenation of AEA and 2-AG to form prostaglandin ethanolamides (PG-EAs) [39] and prostaglandin glycerol esters (PG-Gs), respectively (see **Box 1**) [40]. Although PGH₂ is converted to PGE₂, PGD₂, PGF_{2a}, PGI₂, and TxA₂ by downstream synthases, PGH₂-EA and PGH₂-G are not good substrates for thromboxane synthase; thus, they each only form four of the five downstream products [41]. The production of PG-EAs has been demonstrated in several settings, including in FAAH knockout mice treated with exogenous AEA [42], lipopolysaccharide-stimulated mouse dorsal root ganglia cultures [43], mouse renal medulla [44], rat spinal cord

[45], and in mouse adipocytes [46]. PG-Gs have been detected in rat paws [47] and multiple stimulated macrophage cell lines including RAW 264.7 cells [48], resident peritoneal macrophages [49, 50], and J774 macrophages [51]. Several studies have demonstrated that PG-Gs are unstable due to enzymatic hydrolysis to PGs, which may account for the fewer reports of their formation *in vivo* compared to PG-EAs [52-54].

Emerging evidence reveals that PG-EAs and PG-Gs have discrete functions that appear to be mediated by receptors distinct from classical PG receptors (**Box 2**). Therefore, eCB-derived PGs form a bioactive signaling network discrete from AA-derived PGs. Efforts to categorize the effects of eCB-derived PG-EAs and PG-Gs are accelerating in part due to the availability of novel pharmacological tools including $PGF_{2\alpha}$ -EA receptor agonists and antagonists (for review see [55]) as well as COX-2 inhibitors that differentially inhibit PG-EA and PG-G production by COX-2 without affecting AA-derived PGs.

Substrate-selective inhibition of COX-2

SSCIs represent a novel pharmacological approach to COX-2 inhibition by inhibiting the oxygenation of 2-AG and AEA but not AA by COX-2 (**Box 3**) [43, 76, 77]. The discovery of "substrate-selective" inhibition prompted several studies assessing the generalizability of this phenomenon among NSAIDs. The initial report identified ibuprofen, mefenamic acid, and 2'-*des*-methyl indomethacin (but not indomethacin) as SSCIs [76]. A more comprehensive investigation found that all rapidly reversible inhibitors are SSCIs, whereas all slow-tight binding inhibitors are non-SSCIs [43].

The structures of COX-2 complexes with some SSCIs have been determined by X-ray crystallography. The similarities between the structures of the bound SSCIs to analogs that are not SSCIs (e.g., (*R*)-flurbiprofen vs. (*S*)-flurbiprofen; diclofenac vs. lumiracoxib; *des*methylflurbiprofen vs. (*S*)-flurbiprofen) indicate that the basis for substrate-selectivity cannot be elucidated by structural analysis alone. Interestingly, SSCIs can bind in either the canonical conformation, as in the case of (*R*)-flurbiprofen (**shown in Figure 1b**), or the inverted conformation as in the case of lumiracoxib (**shown in Figure 1c**). Comparison of the structures of AA and 1-AG bound in the active site of COX-2 reveal that the conformation of 1-AG is less favorable for catalysis [78]. Thus, even subtle differences in binding between substrate-selective and non-substrate-selective inhibitors could be sufficient to disrupt 1-AG or 2-AG oxidation but not AA oxidation by COX-2. Functional studies of site-directed mutants are underway to test the role of specific active site residues that may be key determinants of substrate-selective pharmacology [38, 43, 79].

Functional analyses of COX-2 inhibition have been used to design novel SSCIs. Sitedirected mutagenesis to remove a hydrogen-bonding interaction between Tyr-355 or Arg-120 of COX-2 and the non-SSCI indomethacin causes it to become a SSCI against these mutant COX-2 proteins [77], suggesting inhibitor interactions with these residues are important for inhibition of AA conversion to PGs. As a corollary, reduction of hydrogenbonding capacity between inhibitor molecules and Tyr-355 and Arg-120 by conversion of the carboxylate of indomethacin to a tertiary amide (e.g., LM-4131) results in a SSCI [77].

Thus, site-directed mutagenesis and functional COX-2 assays using both AA and eCBs as substrates could be used to develop novel SSCIs from a variety of scaffolds.

Different classes of SSCIs have been utilized in cellular settings to study the oxygenation of eCBs by COX-2. In particular, (*R*)-flurbiprofen has been utilized to demonstrate that COX-2 regulates eCB concentrations in stimulated primary dorsal root ganglia [43], that PGF_{2α}-EA negatively regulates adipogenesis [46], and that PGD₂-G has anti-inflammatory effects in macrophages [51]. In addition, LM-4131 increases 2-AG but does not affect AA or PG concentrations in stimulated RAW 264.7 macrophages [77]. These studies have validated the pharmacological profile of SSCIs in cellular settings, as (*R*)-flurbiprofen and LM-4131 selectively inhibit eCB oxygenation by COX-2 while displaying no inhibition of AA oxygenation by COX-2. The existence of multiple structurally diverse SSCIs provides complementary probes for the investigation of the role of COX-2 oxidation of eCBs in cellular systems.

In vivo effects of substrate-selective COX-2 inhibition

Although *in vitro* and cellular studies clearly validate the pharmacology of SSCIs, whether this selectivity is retained *in vivo* is a critical question. Although (*R*)-flurbiprofen is an excellent probe *in vitro*, in mice (but to a lesser extent in rats, humans, or monkeys) it undergoes a unidirectional isomerization to the non-SSCI (*S*)-flurbiprofen, rendering it suboptimal for *in vivo* studies [84]. Therefore, we focused our initial *in vivo* SSCI validation studies on the morpholino amide of indomethacin, LM-4131 [77]. LM-4131 dose-dependently increases brain AEA concentrations to ~150% of control, while only marginally increasing 2-AG concentrations to ~110% of control. The non-selective COX-1/2 inhibitor indomethacin, the parent compound of LM-4131, and the COX-2 selective inhibitor NS398 also increase brain AEA and, to a lesser extent, 2-AG concentrations. Importantly, while all three inhibitors increased eCB concentrations, a clear distinction is evident between their effects on PG production: indomethacin and NS398 reduce brain PG and increase AA concentrations, while LM-4131 has no effect on either analyte [77].

The ability of LM-4131 to increase eCB concentrations is dependent on COX-2 activity because it does not increase eCB concentrations in COX-2^{-/-} mice [77]. Importantly, COX-2^{-/-} mice have basally elevated brain AEA, providing *in vivo* confirmation that COX-2 is a key mediator of basal brain AEA signaling. The effects of LM-4131 are mediated through COX-2 and not alternate mechanisms of action, such as FAAH and MAGL inhibition, because LM-4131 increases AEA concentrations in FAAH^{-/-} mice and produces additive increases in brain AEA concentrations when co-administered with the irreversible FAAH inhibitor PF-3845. Similarly, LM-4131 produces additive increases in 2-AG concentrations when combined with the irreversible MAGL inhibitor JZL-184 [77]. These data provide compelling evidence that LM-4131 exhibits substrate-selective pharmacological properties *in vivo* and can increase eCB concentrations via a COX-2-dependent mechanism.

Comparative analyses of the effects of LM-4131 on NAE and MAG concentrations relative to PF-3845 and JZL-184 revealed divergent effects of COX-2 inhibition compared to FAAH

or MAGL inhibition (**Figure 2**). FAAH inhibition increases concentrations of AEA and several non-cannabinoid NAEs in the brain and FAAH-rich tissues such as the liver. Similarly, MAGL inhibition increases the concentrations of 2-AG and several other non-cannabinoid MAGs. In contrast, LM-4131 only increases AEA and 2-AG concentrations, without affecting other NAEs or MAGs in any tissue. This remarkable selectivity for eCBs relative to non-eCB NAEs and MAGs is likely due to the substrate specificity of COX-2 for arachidonate-containing lipids. In contrast, FAAH catalyzes amidase and MAGL catalyzes esterase cleavages of a variety of fatty acid amides and glycerol esters, respectively. The selectivity of LM-4131 is mirrored by genetic COX-2 deletion, which results in a ~200% increase in brain AEA, but not other NAEs [77]. These data indicate that SSCIs can selectively augment eCB concentrations without affecting non-eCB NAEs or MAGs and highlights distinct differences between these three strategies for eCB augmentation.

In addition to having central effects, LM-4131 increases AEA, but not other NAEs, in a variety of peripheral tissues including the lung, kidney, stomach, and small intestine, but not the liver or heart [77]. Thus, COX-2 plays a role in the regulation of eCBs in multiple peripheral organs. The differential tissue-specific effects likely relate to differences in COX-2 and FAAH expression as well as the differential rates of AEA biosynthesis between tissues. Importantly, LM-4131 does not affect PG concentrations in either central or peripheral tissues, whereas indomethacin profoundly reduces PGs in all tissues examined. Taken together, these data suggest an important role for COX-2 in the metabolism of eCBs and identify a third metabolic pathway for eCB inactivation in the brain and many peripheral tissues.

A growing literature indicates that COX-2 inhibition can enhance prototypical 2-AGmediated forms of retrograde synaptic signaling in the form of depolarization-induced suppression of inhibition or excitation (DSI or DSE) [56, 75, 85]. Both pharmacological and genetic inhibition strategies indicate that COX-2 limits synaptic 2-AG signaling in the hippocampus; however, the role of COX-2 in the regulation of AEA-mediated synaptic plasticity remains to be investigated. One possible explanation for the lackluster effect of pharmacological or genetic inhibition of COX-2 on the concentration of 2-AG in the brain is that the bulk measurement of tissue 2-AG does not accurately reflect the effects of COX-2 inhibition at the cellular or synaptic level. Furthermore, alternative 2-AG metabolic pathways such as MAGL and α/β -hydrolase domain 6 or 12 may mitigate changes in bulk tissue concentrations after COX-2 inhibition [86], but allow for enhanced CB receptor activation prior to hydrolysis. In this scenario, COX-2 inhibition would cause higher concentrations of 2-AG postsynaptically, and increased presynaptic CB₁ receptor activation followed by rapid presynaptic degradation by MAGL or other esterases. Thus, the effects of COX-2 inhibition may be transient and/or highly localized such that bulk tissue measurement does not capture effects that are measured in a more targeted fashion.

Therapeutic implications of SSCIs

Augmenting eCB signaling has shown preclinical efficacy in reducing behavioral signs of anxiety in laboratory animals [10, 87-91]. Seminal studies by Piomelli and coworkers demonstrate that inhibiting FAAH reduces anxiety in multiple preclinical models via a CB₁

receptor-dependent mechanism [10]. Importantly, some studies suggest that COX-2 inhibition may have anxiolytic effects in preclinical models [92, 93], and some clinical studies have identified therapeutic effects of adjunctive COX-2 inhibition in individuals with major depression [94-96].

Based on these data, we tested the hypothesis that the prototypic SSCI, LM-4131, has anxiolytic effects mediated by eCB augmentation and CB receptor activation. Acute treatment with LM-4131 reduces anxiety measures in the open-field assay, elevated plusmaze, and light-dark box exploration assay [77]. Pharmacological and genetic approaches identified that the anxiolytic effects of LM-4131 are mediated via CB₁ receptor activation and are COX-2-dependent [77]. These studies provide the first proof-of-concept support that SSCIs exert behavioral effects mediated via eCB activation of CB₁ receptors.

Although the *in vivo* therapeutic effects of SSCIs have not been examined in detail, given the wide array of pathophysiological processes modulated by eCB signaling, the therapeutic potential of SSCIs could be extensive. Augmentation of eCBs via FAAH or MAGL inhibition has shown therapeutic potential for mitigating drug withdrawal syndromes, neuropathic pain, hyperemesis, neurodegeneration, seizure, excitotoxicity, and tumor progression, among other promising effects [97]. Future studies aimed at determining the changes in COX-2 expression patterns and the therapeutic potential of SSCIs in the treatment of a broad range of disorders will help define the promise of augmenting eCBs by COX-2 inhibition.

Additionally, SSCIs may provide similar therapeutic effects as NSAIDs given their similar molecular target of COX-2. NSAIDs have long been used as analgesic and antipyretic agents [98, 99]. NSAIDs also have potent anti-inflammatory actions and have been utilized clinically in inflammatory disorders including osteoarthritis, rheumatoid arthritis, inflammatory arthropathies, and acute gout [100-103]. COX-2 inhibitors have also been utilized as anti-oncogenic agents in breast, colon, bladder, and prostate cancers, among others [104-107]. COX inhibitors have also shown promise in combating infection and sepsis [108, 109]. A critical fundamental question is whether these diverse therapeutic effects of NSAIDs are mediated by PG inhibition, PG-G and PG-EA inhibition, and/or eCB augmentation. SSCIs are ideal probes to determine the differential impact of exclusively inhibiting PG-EA and PG-G synthesis, and consequently increasing AEA and 2-AG concentrations, while not modulating PGs. The use of SSCIs in combination with tools such as PG receptor knockout animals should help to dissect the importance of COX-2-eCB oxidation in a range of physiological and pathophysiological effects.

Predicting the adverse effect profile of SSCIs in the CNS and beyond

The mechanism of action of SSCIs predicts two potential sets of adverse effects. First, adverse effects such as gastrointestinal and cardiovascular or cerebrovascular toxicity are associated with most NSAIDs and are mediated by the inhibition of PG synthesis by COX-1, COX-2, or both enzymes [110-113]. Second, adverse cognitive, metabolic, and motoric side effects are associated with direct CB_1 receptor activation. The selective inhibition of eCB-

derived PGs but not AA-derived PGs suggests that SSCIs may present a more favorable side effect profile relative to other NSAIDs.

A major clinical concern for the chronic use of COX inhibitors is cardiovascular and cerebrovascular toxicity manifested by an increased incidence of heart attack and stroke. Cardiovascular side effects are exhibited by most NSAIDs, regardless of their selectivity for COX-2, due to a reduction in vascular PGI₂ biosynthesis [114, 115]. As SSCIs do not affect central or peripheral concentrations of PGs, including PGI₂, it is possible that this pharmacological class of inhibitors could be devoid of or exhibit significantly reduced cardio/cerebrovascular toxicity compared to traditional NSAIDs. Indeed, clinical trials conducted with the SSCI (*R*)-flurbiprofen suggest that it does not increase cardiovascular events [116, 117].

Gastrointestinal bleeding is also a well-known adverse effect of COX inhibition and is mediated by inhibition of gastroprotective PG synthesis in the gut [118, 119]. The SSCI LM-4131 does not cause overt gastrointestinal bleeding after acute administration, whereas indomethacin causes significant overt bleeding at the same dose [77]. Additionally, the SSCI (*R*)-flurbiprofen does not display gastrointestinal toxicity in humans [116, 117]. These studies suggest that SSCI's lack of effect on PG synthesis may render them less prone to or even devoid of the complicating side effects of traditional COX inhibitors.

Because SSCIs lead to CB_1 receptor activation in the CNS, and possibly in other tissues, cannabimimetic side effects could occur. Common adverse effects of direct acting cannabinoid agonists include motor suppression, cognitive impairment, hyperphagia, and dependence liability. Initial studies with the SSCI LM-4131 found a notable lack of motor suppression or object recognition memory deficits [77]. This may be in part be due to the relative preference of SSCIs to elevate AEA over 2-AG, since MAGL inhibition or combined MAGL and FAAH inhibition produces cannabimimetic effects such as pronounced motoric inhibition [120].

In addition to the potential lack of adverse cannabimimetic effects of SSCIs, distinct differences in the tissue-specificity of COX-2 relative to FAAH suggests that SSCIs may lack some of the side effects of FAAH inhibition. FAAH inhibition in the liver causes robust increases in AEA and non-eCB NAE concentrations [77]. In contrast, LM-4131 does not affect liver AEA or NAE concentrations [77]. Activation of hepatic CB₁ receptors contributes to diet-induced metabolic pathology [121, 122], and genetic FAAH deletion promotes a pre-diabetic state and adversely affects energy metabolism [123]. The lack of effect of LM-4131 on hepatic AEA indicates that SSCIs may lack adverse metabolic side effects relative to other indirect or direct acting cannabinoid agonists [77]. Moreover, one might predict a general theme that in tissues where FAAH expression is high and can act as an alternate eCB metabolic pathway, adverse cannabimimetic effects of SSCI would likely be minimized. Lastly, AEA is also an agonist at TRPV1 receptors [124], and as such, SSCIs could potentially result in overstimulation of TRPV1 under some conditions. The biological significance of this potential mechanism needs to be evaluated in subsequent studies. Ongoing studies aimed at comparing and contrasting the relative cannabimimetic profiles of

Concluding remarks

Despite the recent elucidation of COX-2 as a key regulator of eCB signaling, several fundamental questions remain unanswered. For example, why is there significant redundancy in eCB metabolic pathways? It is now clear that both FAAH and COX-2 can metabolize AEA; blockade of either enzyme can elevate AEA levels; and the effects of FAAH and COX-2 inhibition are additive. In many cases this occurs in tissues and/or cells where both enzymes are co-expressed, as they are in neurons [125]. These data suggest the intriguing possibility that there are distinct metabolic pools of AEA that are segregated with regard to metabolic pathways; if this were not the case one would not expect to see increases in AEA after COX-2 blockade, since shunting through FAAH would be expected to metabolize the "excess" AEA. What then defines these distinct metabolic pools? Do distinct synthetic pathways determine them or are they physically segregated within cells, or both? An alternative to this differential pool hypothesis could be that COX-2-mediated AEA metabolism represents a salvage pathway operating to limit AEA signaling only under conditions where FAAH activity is already near maximal efficiency. Differentiating between these two possibilities could provide important insight into the basic biology of endocannabinoid signaling and potential differential therapeutic implications of pharmacological FAAH and COX-2 inhibition.

Furthermore, although COX-2 eCB oxidative metabolites have been identified and some of their biological effects elucidated, the vast majority of these findings are based on application of exogenous PG-EAs or PG-Gs to biological systems. We suggest elucidation of the physiological triggers of endogenous PG-EA and PG-G synthesis and degradation are critically important. In addition, elucidation of the receptors by which PG-EAs and PG-Gs exert biological actions represents a key open question that, if answered, could reveal a new network of endogenous bioactive lipid signaling systems amenable to pharmacological manipulation through both inhibition of COX-2 as well as antagonism of these receptors. Modulation of this system could potentially have therapeutic implications for neuropsychiatric, pain, and metabolic disorders.

The data summarized herein highlight the emerging role of COX-2 in the regulation of central and peripheral eCB metabolism and suggest that, in addition to the canonical FAAH and MAGL pathways, COX-2-mediated eCB oxygenation represents a third eCB metabolic mechanism. We propose that SSCIs provide a novel pharmacological strategy to augment eCB signaling without affecting PG formation, which will enhance therapeutic opportunities surrounding eCB augmentation and provide tools to elucidate differential fundamental biology of eCB- and AA-derived COX-2 products. Optimizing the *in vivo* pharmacological profile of SSCIs and elucidating the therapeutic potential of this class of compounds could ultimately have broad implications.

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Highlights

- 1. Endocannabinoid augmentation may have broad therapeutic implications
- 2. COX-2 is a third endocannabinoid metabolic mechanism
- **3.** Substrate-selective COX-2 inhibition increases central endocannabinoid signaling
- 4. Substrate-selective COX-2 inhibition decreases anxiety

Box 1: COX-2 as an eCB-inactivating enzyme

A connection between COX-2 action and eCB inactivation has been suggested by converging data. Inhibition of COX-2 potentiates retrograde eCB synaptic signaling in the hippocampus [56] and decreases excitatory responses in a CB₁-dependent manner [57], revealing a functional tie between COX-2 activity and eCB tone at central synapses. NSAIDs inhibit the metabolism of AEA by rat cerebellar membrane preparations [58] and extend the stability of exogenous AEA in mouse brain [59], suggesting that COX-2 directly metabolizes AEA in vivo. COX-2 is constitutively expressed in the spinal cord and mediates tissue injury-induced hyperalgesia [60]. The NSAIDs indomethacin and nimesulide produce eCB-mediated spinal antinociception as evidenced by the blockade of their antinociceptive effects by the CB1 receptor antagonist AM251 [61, 62]. Moreover, the peripheral antinociceptive effects of AEA and NSAIDs are synergistic [63] and ibuprofen interacts with AEA in both acute and inflammatory pain models [64]. COX-2 selective inhibitors, but not COX-1 selective inhibitors, also reverse spinal neuron hyperexcitability in a CB1 receptor-dependent manner and reduce the breakdown of 2-AG [65]. These studies, combined with the data reviewed below, indicate that COX-2 plays a fundamental role as an eCB-metabolizing enzyme in multiple settings and tissues.

Box 2: Biological targets and actions of PG-EAs and PG-Gs

PG-EAs and PG-Gs have little or no activation of the canonical EP₁₋₄, DP, FP, TP, and IP prostanoid receptors [66, 67], with the exception of PGE₂-EA which binds to the EP₁₋₄ receptors [68], indicating that they form a discrete bioactive signaling network from AA- derived PGs. The receptors that mediate the biological actions of most PG-EAs and PG Gs have not been elucidated, however, the PGF2a-EA receptor has been identified as a heterodimer containing a FP receptor and a FP receptor splice variant [69]. Several studies have identified biological actions of some PG-Gs and PG-EAs. PGE₂-G potently induces calcium mobilization in RAW 264.7 macrophages and H1819 cells [67, 70], induces hyperalgesia through modulation of NF-kB [47], enhances miniature excitatory post-synaptic currents in glutamatergic neurons [71], and exacerbates malonate-induced neurotoxicity [72]. In contrast, PGD₂-G exhibits anti-inflammatory activity in isolated macrophages and in vivo [51]. PGF2a-EA and its analog, bimatoprost, are ocular hypotensive agents used for treating glaucoma [73]. PGF_{2a}-EA has also been shown to negatively regulate adipogenesis [46] and increase the firing of nociceptive neurons and reduce hot plate paw withdrawal latency in mice after spinal application [45]. PGE₂-G, PGD₂-G, PGF_{2a}-G, and PGD₂-EA increase the frequency of miniature inhibitory postsynaptic currents in GABAergic hippocampal neurons [74]. PGE₂-G, PGE₂-EA, and PGF_{2a}-EA elevate long-term potentiation in the hippocampus [75]. Thus, PG-Gs and PG-EAs produce a plethora of biological effects in multiple settings through their activation of as of yet unidentified receptors.

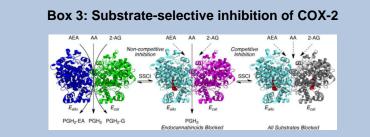


Figure I: Mechanism of substrate-selective inhibition of COX-2. Binding of a SSCI to the allosteric subunit (Eallo) results in non-competitive inhibition of eCB oxygenation in the catalytic subunit (Ecat) but no inhibition of AA oxygenation. Binding of a second SSCI molecule to the catalytic subunit results in inhibition of AA.

The two subunits of COX-2 are sequence homodimers, but the heme prosthetic group binds to only a single monomer, creating functional heterodimers (Figure I). The hemecontaining subunit is the catalytic subunit, whereas the non-heme-containing subunit is the allosteric subunit [80, 81]. Binding of substrates, activators, and inhibitors to the allosteric subunit alters binding in the catalytic subunit through subunit communication via the dimer interface [82]. COX-2 inhibitors bind in one of two kinetic modes, rapidreversible or slow-tight binding. Compounds that are rapid-reversible inhibitors of COX-2 inhibit eCB oxygenation at concentrations that are orders of magnitude lower than the concentrations required for inhibition of AA oxygenation, a phenomenon termed "substrate-selective" COX-2 inhibition [76]. Substrate-selective inhibitors bind in the allosteric subunit and induce a conformational change that blocks eCB oxidation in the catalytic subunit. Binding of a second inhibitor molecule in the catalytic subunit blocks AA oxygenation, but this typically occurs at inhibitor concentrations orders of magnitude higher than the concentrations that block eCB oxygenation [76]. Slow, tight-binding inhibitors bind in the catalytic subunit and block the oxygenation of all substrates at similar concentrations [35, 83].

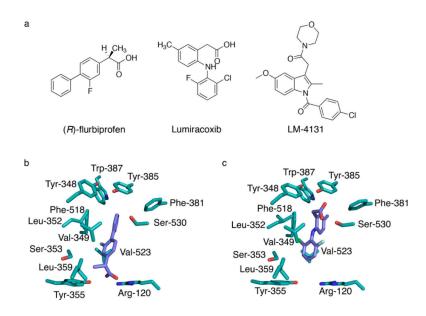


Figure 1. Structures and binding mechanisms of COX-2 inhibitor scaffolds

a) Structures of selected SSCI scaffolds: (*R*)-flurbiprofen, a member of the 2-arylpropionic class, lumiracoxib, a member of the arylacetic acid class, and LM-4131, a member of the arylacetic acid class, demonstrate the structural diversity of NSAIDs. b) Binding mode of the SSCI (*R*)-flurbiprofen to the cyclooxygenase active site of murine COX-2 in a canonical fashion with hydrogen bonding and ion pairing interactions with Arg-120 and Tyr-355 (PDB: 3RR3). c) Crystal structure of lumiracoxib bound to murine COX-2 in an inverted pose with hydrogen bonds to Tyr-385 and Ser-530 (PDB: 4LLZ).

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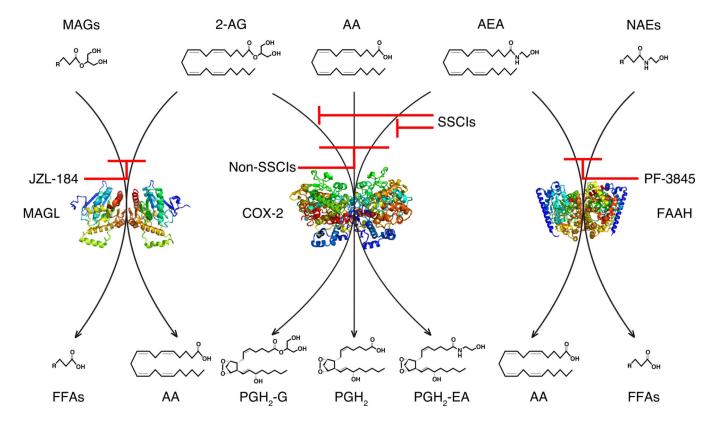


Figure 2. Differential regulation of MAGs, eCBs, and NAEs by MAGL, COX-2, and FAAH MAGL catalyzes the hydrolysis of the glycerol moiety of 2-AG and other MAGs to AA and free fatty acids (left). COX-2 oxygenates AA, 2-AG, and AEA to PGs, PGGs, and PG-EAs, respectively (middle). FAAH catalyzes the hydrolysis of the ethanolamide moiety of AEA and other NAEs to AA and free fatty acids (right). Different classes of eCB degradation inhibitors and their effects on respective lipid metabolic pathways are depicted in red.