



Published in final edited form as:

J Neuroimmune Pharmacol. 2022 June ; 17(1-2): 76–93. doi:10.1007/s11481-021-10046-z.

Opioid Use, Gut Dysbiosis, Inflammation, and the Nervous System

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Abstract

Opioid use disorder (OUD) is defined as the chronic use or misuse of prescribed or illicitly obtained opioids and is characterized by clinically significant impairment. The etiology of OUD is multifactorial as it is influenced by genetics, environmental factors, stress response and behavior. Given the profound role of the gut microbiome in health and disease states, in recent years there has been a growing interest to explore interactions between the gut microbiome and the central nervous system as a causal link and potential therapeutic source for OUD. This review describes the role of the gut microbiome and opioid-induced immunopathological disturbances at the gut epithelial surface, which collectively contribute to OUD and perpetuate the vicious cycle of addiction and relapse.

Keywords

Opioids; OUD; Microbiome; Gut-brain axis; Enteric nervous system

Introduction

According to the 2019 National Survey on Drug Use and Health, non-medical opioid use in the United States is estimated at 2.3% among adolescents (age 12–17), 5.3% among young adults (age 18–25), and 3.6% among adults (age ≥ 26) with the rates of opioid use being significantly higher than that of any other illicit drug (SAMSHA 2020). Consequently, this has resulted in the rise of OUD and a concomitant increase in drug-related overdoses, with increased morbidity and mortality among patients. Additionally, the opioid crisis poses a huge economic burden, partly attributable to higher direct medical costs for patients (Ghate et al. 2010) and indirect costs due to loss of productivity (Reinhart et al. 2018).

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Conflict of Interest All authors declare that they have no conflict of interest in this manuscript.

translocation or alteration in the gut microbiome as is observed with chronic opioid use (Banerjee et al. 2016). Given the complexity and confounders of polydrug use and dietary patterns in humans, animal models are commonly used for phylogenetic and metagenomic analyses to examine mechanisms driving host-gut microbiome interactions and their physiological consequences. Among these animal models, rodents, particularly mice and rats, have commonly been used for economic reasons, with non-human primates (NHPs) also gaining popularity due to their genetic and physiological closeness to humans (Nagpal et al. 2018).

These human and preclinical models have shown considerable variability in describing the microbial composition with opioid use, but altogether consistently point towards microbial dysbiosis (Table 1). Clinical studies of chronic opioid users have shown reduction in the family *Bacteroidaceae* or the genus *Bacteroides* from the phylum Bacteroidetes (Acharya et al. 2017; Xu et al. 2017). However, the abundance of *Prevotella* has varied between studies (Xu et al. 2017; Barengolts et al. 2018). In the phylum, Firmicutes, whereas Clostridiales, particularly *Ruminococcaceae* was decreased in abundance (Acharya et al. 2017), increases in *Ruminococcus* (Xu et al. 2017) and Lactobacillales have also been reported. Additionally, increased abundance of *Bifidobacterium* from phylum Actinobacteria has also been reported (Barengolts et al. 2018). Investigations utilizing NHPs to explore microbial changes with opioid use are few. In one study utilizing NHPs, opioid use primarily resulted in an increase in *Methanobacteriaceae*, and a decrease in abundance of both *Streptococcaceae* and *Ruminococcaceae* from the phylum Firmicutes. Notably, the decrease in *Ruminococcaceae* was consistent with Acharya et al. (2017), though increases in *Ruminococcus* have been found in other human studies (Xu et al. 2017). The vast majority of animal models of opioid exposure have been conducted in rodents, in particular mice. Changes in microbial communities were most consistent between studies based on experimental treatment. For instance, with subcutaneous 25 mg slow release morphine pellets, decreased abundance of Bacteroidetes (Banerjee et al. 2016) and Bacteroidales (Kang et al. 2017) from the phylum Bacteroidetes was observed. In contrast, there was increased abundance in the entire phylum Firmicutes (Banerjee et al. 2016) or specifically the genus *Staphylococcus* and *Enterococcus* (Meng et al. 2015). On the other hand, with a 75 mg slow release pellet, decreased abundance of Clostridiales and Lactobacillales in the phylum Firmicutes, and increased abundance of Enterobacteriales from phylum Proteobacteria was reported (Kang et al. 2017). Intraperitoneal injections consistently resulted in a decrease in *Lactobacillus* or *Lactobacillaceae* (Lee et al. 2018; Zhang et al. 2019) from phylum Firmicutes, but an increased abundance of *Ruminococcus* (Lee et al. 2018). Hydromorphone exposure in mice paralleled findings of opioid exposure in rats, with decreased abundance of Firmicutes and increased abundance of Verrucomicrobia (O'Sullivan et al. 2019; Sharma et al. 2020; Simpson et al. 2020) and Proteobacteria (Sharma et al. 2020; Simpson et al. 2020), though the abundance of Bacteroidetes varied in these studies (O'Sullivan et al. 2019; Simpson et al. 2020).

Which preclinical models lend themselves most relevant to clinical translation of how opioid use affects the human microbiota still remains unclear. Species comparisons and extrapolation to humans is difficult to conduct due to the confounding effects of sampling locations, providers, rearing facilities, genetic backgrounds, geographical settings,

experimental protocols, and sequencing analysis approaches (Hugenholtz and de Vos 2018; Nagpal et al. 2018; Park and Im 2020). This is compounded by the high inter-individual variability in human gut microbial signatures due to dietary behavior and lifestyles. At the phylum level, clinical studies have shown alterations in Bacteroidetes, Firmicutes, and Actinobacteria with opioid use, consistent with rodent studies. In particular, there seems to be a consistently decreased abundance from the phylum Bacteroidetes in both human and rodent studies. Though the overall β -diversity of gut microbiota signatures suggest that the gut microbiota in humans is closer to NHPs than to mice and rats, with mice closer to humans than rats, the limited number of studies utilizing NHP prevented seeing this close association (Nagpal et al. 2018). In contrast, several other studies claim rat microbiome being more closer to human than mice and therefore gut microbiome of humanized rat models provide better representation of human donor than mouse model (Wos-Oxley et al. 2012; Nguyen et al. 2015). Thus, a comprehensive investigation of how opioid use affects the intestinal bacterial diversity and composition in NHPs, along with humans and rodents, is much warranted.

The Gut Microbiome, Metabolome and the CNS in Opioid Use Disorder

Alterations in the gut microbiome have been implicated in various neuropsychiatric disorders, including OUD (Bercik et al. 2011; Kiraly et al. 2016; Han et al. 2018; Meckel and Kiraly 2019; Zhuang et al. 2020). A recent study showed differential alteration in gut microbial communities during acquisition, extinction and reinstatement of morphine conditioned-place preference (CPP) (Zhang et al. 2021). In this study, the gut bacterial community richness in mice was shown to increase following morphine CPP, whereas it decreases with prolonged abstinence. In addition, an increased abundance of *Verrucomicrobia* and decreased *Bacteriodes* abundance was observed during the acquisition stage. Interestingly, this shift in bacterial abundance showed a trend to recovery during the extinction stage. Consistent with these findings, another study found a correlation between the gut microbial composition of rats to their sensitivity to morphine CPP (Zhang et al. 2020a) where the relative abundance of certain taxa such as *Alloprevotella* and *Romboutsia* correlated to the morphine CPP scores. More recently, Thomaz et al. showed an attenuation in morphine withdrawal behavior in mice following antibiotic treatment or fecal microbiota transplant (Thomaz et al. 2021). Together, these studies indicate that the gut microbiome impacts the development of physical dependence to opioids, and that therapeutic interventions aimed at manipulating the gut microbiome may reduce somatic symptoms of opioid withdrawal.

Growing evidence suggest a strong correlation between gut dysbiosis (particularly a decreased Firmicutes to Bacteroides ratio) and neuroinflammation observed in opioid withdrawal (O'Sullivan et al. 2019). In addition, Burma et al. demonstrated that microglial cells mediate opioid withdrawal by activating P2X7 receptors, which triggers the release of ATP through the PANX1 channel and postsynaptic facilitation in the spinal dorsal horn (Burma et al. 2017). In this study, pharmacological blockade of PANX1 channels using probenecid or mefloquine suppressed ATP release and reduced withdrawal severity. The involvement of microglial cells in opioid dependence was further strengthened by a recent study by Reiss et al. who showed a crucial role for the microglial μ -opioid receptors

(MORs) in morphine analgesic tolerance, hyperalgesia and withdrawal in mice (Reiss et al. 2020). In this study, morphine analgesic tolerance in the hot plate assay was delayed in male and female mice lacking MORs in microglia. Interestingly, they also found a sex-dependent contribution of microglial MOR in opioid-induced hyperalgesia and physical dependence.

An increasing body of evidence supports a critical connection between gut microbiota and the development and function of microglia. The importance of this association is evidenced by the global microglial defects observed in mice with a compromised microbiome, including germ-free (GF) mice (Erny et al. 2015), antibiotic-treated mice, and mice exposed to morphine (Lee et al. 2018). GF mice fail to develop microglia with a mature phenotype, indicated by prominent expression of surface molecules such as CSF1R, F4/80, and CD31 that are downregulated over the course of maturity (Erny et al. 2015). Upon histopathological examination, the microglia of GF mice show elongated processes, increases in cell volume and number, and intrusions into neighboring cell territories, among other morphological irregularities (Erny et al. 2015). Analysis of microglial-mRNA expression reveals downregulation of genes associated with cell activation, transcription activation, and pathogen recognition along with upregulation of genes involved with inhibition of transcription and apoptosis, cell cycle stimulation, and cell proliferation (Erny et al. 2015). The consequences of gut dysbiosis on microglia are not limited to development. Perturbations to the gut microbiome caused by chronic treatment of adult mice with antibiotics produce morphological impairments in microglia that are comparable to those seen in GF mice (Erny et al. 2015), suggesting that a healthy and complex gut microbiome is integral not just for the development, but also the homeostasis of microglia. Intermittent treatment with morphine similarly induces a state of gut dysbiosis that is associated with an altered microglial phenotype and behavioral deficits that mirror those observed in antibiotic-treated mice (Lee et al. 2018). The physiological impact of these collective defects in microglia manifests notably in diminished immune responsiveness. GF mice administered with an lipopolysaccharide (LPS) challenge, either intracerebrally or intraperitoneally, show reduced induction of pro-inflammatory cytokines and chemokines as compared to mice with a more complex gut microbiome (Erny et al. 2015). A viral challenge to GF mice similarly results in microglial morphological malformations accompanied by an impaired immune response of pro-inflammatory cytokines (Erny et al. 2015). Collectively, these results suggest that a depleted gut microbiome not only impairs microglial development, but also attenuates resistance to bacterial or viral infection. Remarkably, these impairments are reversible by several manipulations. Microglial defects in mice with a disrupted gut microbiome are at least partly restored by recolonization with a complex microbiome (by microbiota transplant or cohousing with treatment naïve mice), normalizing cell morphology, mRNA levels, and downstream behavioral effects (Erny et al. 2015; Lee et al. 2018). Alternatively, defects in microglial morphology and gene expression can be largely restored with diet supplementation with short chain fatty acids (SCFAs) (Erny et al. 2015), microbial metabolites that are vital to colonic immune cell regulation. The possibility of rescuing microglial deficits by microbe recolonization or SCFA supplementation suggests a potential for therapeutic intervention of microglial pathology in various disease states.

Although the exact mechanisms underlying the gut-microglial axis remain ambiguous, several pathways of cross-talk are recognized. Principally, gut bacteria and their neuroactive

metabolites can interact with the vagus nerve and affect microglial-induced inflammation in the CNS (Forsythe et al. 2014). When an LPS challenge is combined with vagal nerve stimulation, microglial production of pro-inflammatory cytokines is attenuated as compared to an LPS challenge alone (Meneses et al. 2016). This effect is abolished following vagotomy (Meneses et al. 2016). Gut microbiota can also modulate intestinal barrier permeability, enabling the entry of immune-stimulating substances into systemic circulation (Karczewski et al. 2010). Additionally, microbiota can directly stimulate immune cells in the gut, altering peripheral inflammation (Fung et al. 2017; Abdel-Haq et al. 2019). Metabolites of gut microbiota, including neurotransmitters like serotonin (Yano et al. 2015) and acetylcholine, and SCFAs (Conn et al. 1983) can enter circulation and pass the blood brain barrier, altering levels of inflammation in the CNS (Glebov et al. 2015). The relative contributions of gut microbes in influencing pathways involved in microglial activation remain undetermined.

While the relationship between the gut microbiome and microglia is not fully understood, alterations in gut microbiota are strongly implicated in the various stages of OUD. For instance, elevated microglial activation has been observed with drug use and has been shown to play a role in tolerance, anxiety, and withdrawal (Reiss et al. 2020). Accordingly, as gut microbiota can modulate microglial activation, the microbiome may be a mechanism underlying elevated microglia activation both during and after drug use, though this remains to be studied.

Emerging data from research on gut microbiome and its influence on CNS focuses on the role of microbial metabolites in modulating nervous health and behavior (Table 2). Microbial metabolites are absorbed in gut and enters systemic circulation and reach distant organs including brain to exert its effects and acts as a messenger for the “gut-brain-axis”. Opioid treatment has also been reported to change level of bacterial metabolites mainly bile acids (BAs) and SCFA. Primary BA are synthesized from cholesterol in hepatocytes; intestinal bacteria transform primary BA into secondary BA through the use of the bacterial enzymes bile salt hydrolase (BSH) and hydroxysteroid dehydrogenase (HSDH). Firmicutes, Bacteroides, Eubacterium and Clostridium express the BSH enzyme which is required to deconjugate taurine and glycine conjugated primary and secondary BAs. Enteric bacteria expressing the HSDH enzyme required for the conversion of primary to secondary BA includes Bacteroides, Eubacterium, Clostridium, Lactobacillus and Escherichia. Bile acid has been shown to modulate tight junction and altered levels of BAs can lead to blood brain barrier (BBB) permeabilization (Raimondi et al. 2008; Quinn et al. 2014). In rodents, morphine treatment decreases primary and secondary BA levels in the fecal content (Wang et al. 2018). Whereas non-human primate studies consistently show a decrease in primary BA including cholate and glycocholate. In contrast, increases in several secondary BAs have also been reported (Sindberg et al. 2019). Decrease in primary BA after morphine treatment can be a direct host response to morphine treatment. However, since gut bacteria play crucial role for conversion of primary BAs to secondary BAs, therefore, difference in bacterial community changes observed after morphine treatment can account for the contrasting secondary BA profile in both species.

SCFA are bacterial fermentation products; the main SCFA producing bacteria in the human gut belong to the family *Ruminococcaceae* and family *Lachnospiraceae* and in mice, *Muribaculaceae*, *Lachnospiraceae*, and *Ruminococcaceae*. Studies have established the role of SCFA in modulating gastrointestinal function, neuro-immune regulation, host metabolism, BBB integrity (Table 2). In stool samples of individuals on methadone maintenance treatment, reduced levels of SCFAs along with a depletion of SCFA producing bacteria *Bifidobacteria* and *Akkermensia muciphila* have been reported (Cruz-Lebron et al. 2021). Additionally, recent studies further demonstrate the potential role of SCFA in mediating morphine reward pathways (Hofford et al. 2021). Interestingly, antinociceptive tolerance in morphine treated mice has shown to be prevented with oral butyrate treatment, highlighting the impact of SCFA reconstitution following morphine treatment (Akbarali and Dewey 2019; Meng et al. 2019).

Studies exploring the role of other bacterial metabolites including tryptophan and indole derivatives, trimethylamine N-oxide (TMAO), and amino acids are sparse. Additionally, how opioid treatment modulates SCFAs and other bacterial metabolites also remains understudied.

Opioids, Microbiome and Blood Brain Barrier

CNS is protected by the BBB which keeps it safe from different pathogens and toxic molecules. Anatomically, the BBB is formed by the cerebrovascular endothelial cells sealed by tight junctions, pericytes and foot processes of astrocytes. The tight junctions are impermeable for most of the substances and specialized transporters are required for the movement of molecules into the brain (Pardridge 2007). Opioids can cross BBB to exert its analgesic effects mostly by binding to MOR in CNS. P glycoprotein (P-gp) is one of the efflux transporters at BBB and morphine and other opioids act as substrate for P-gp (Bostrom et al. 2008). Long term exposure to morphine can up-regulate expression of P-gp transporter which may contribute towards increased BBB permeability and morphine tolerance (Mahajan et al. 2008; Chaves et al. 2017). An in-vitro study showing morphine treatment reduced the expression of tight junction protein (TJP) zona occludens-1 (ZO-1) in human brain microvascular endothelial cells through platelet derived growth factor (PDGF) and MOR provides mechanistic insight into the role of morphine in BBB damage (Wen et al. 2011). On the contrary, study on Sprague–Dawley rats showed that morphine treatment did not alter BBB permeability during dependence stage, however, morphine withdrawal causes significant breakdown in BBB resulting in neuronal damage seen in animals undergoing withdrawal (Sharma and Ali 2006). BBB structure and function can also be impacted by gut microbial composition and metabolic profile (Braniste et al. 2014). Therefore, changes in gut microbial composition may affect the CNS function through BBB permeability. However, research on the role of dysbiotic community on BBB structure and function is sparse.

The gut microbiome plays key role in maintaining BBB integrity as is indicated in studies where GF mice have been shown to have increased BBB permeability compared to pathogen-free mice with normal gut flora. Braniste et al. have demonstrated that TJPs, occludin and claudin-5 levels were significantly lower in several brain regions of GF mice

compared to control mice which is the contributing factor towards BBB permeability (Braniste et al. 2014). Furthermore, they showed that administration of normal gut flora from pathogen-free mice or oral treatment with the bacterial metabolite sodium butyrate to GF adult mice induced an increase in the expression of occludin (Braniste et al. 2014). Altogether, these observations suggest that the BBB integrity and the expression of tight junction protein occludin in the cerebrovascular endothelial cells are sensitive to changes in the intestinal microflora.

Microbial metabolites, such as SCFAs, and neurotransmitters that enter the systemic circulation and influence different organs including brain. SCFAs can cross the BBB via monocarboxylate transporters located on endothelial cells and influence BBB integrity by upregulating the expression of TJPs (Silva et al. 2020). γ -Aminobutyric acid (GABA) is a very well known inhibitory neurotransmitter in the central nervous system. GABA transporters (GAT2/BGT-1) is present at the BBB and is involved in GABA efflux transport from the brain into the circulating blood across the BBB (Takanaga et al. 2001). However, whether microbial-derived GABA can cross BBB and influx into the brain remains a matter of dispute (Boonstra et al. 2015).

Toll like receptor (TLR) that play a crucial role in recognizing molecules derived from viruses, fungi, bacteria, and protozoa has also been shown to regulate BBB permeability (Nagyoszi et al. 2010; Li et al. 2013; Johnson et al. 2018). Johnson et al. investigated the global responsiveness of human cerebral microvascular endothelial cells (hCMVECs) to a panel of commercial TLR ligands. They observed responses to the TLR3 ligand Poly(I:C), TLR4 ligand LPS and to the TLR7 ligand Imiquimod, but not to any of the other TLR ligands (Johnson et al. 2018). In the same study they measured endothelial barrier function using Electric-cell Substrate Impedance Sensing (ECIS) and demonstrated that Poly(I:C) and LPS both caused an acute reduction in barrier strength, whereas Imiquimod caused an immediate and sustained strengthening of the barrier. Nagyoszi et al. demonstrated the expression of TLR2, TLR3, TLR4 and TLR6 on rat and human cerebral endothelial cells. Oxidative stress significantly upregulated the expression of these receptors whereas tumor necrosis factor- α (TNF- α) upregulated the expression of TLR2 and TLR3. Furthermore, they found, that activation of TLR2/6 leads to an increased permeability which is accompanied by a downregulation of occludin and claudin-5 expression and disappearance of these TJPs from the cell membrane (Nagyoszi et al. 2010). Since morphine treatment has been shown to change expression of TLRs in intestinal tissue, future research should focus on studying how opioids change TLR expression in BBB which can have direct impact on its permeability.

Transport of blood-borne cytokines across the BBB is now known to be an operational pathway by which immune system can directly affect CNS functions (Banks 2005, 2015). Astrocytes through their end-feet provides structural support to BBB and maintain homeostasis in brain (Abbott et al. 2006). In-vitro study using NT2 cell line showed that activation of astrocytes by inflammatory mediators such as TNF α and interleukin-1 β (IL-1 β) lead to transient increase in release of several pro-inflammatory cytokines as well as several leukocytes chemoattractant which lead to astrocyte cell death, compromising BBB integrity (Burkert et al. 2012; van Kralingen et al. 2013). Cellular response of

endothelial cell using human cerebral microvascular endothelial cells (hCMVECs) to the pro-inflammatory mediators TNF α and IL1 β has also been studied. O'Carroll et al. demonstrated that expression of leukocyte adhesion molecules ICAM-1 and VCAM-1 is up-regulated in endothelial cells after TNF α and IL-1 β treatment (O'Carroll et al. 2015). Along with that they also observed an increased secretion of several leukocyte recruitment chemokines after stimulation with TNF α or IL-1 β .

Opioid-Induced-Gut-Dysbiosis in Epithelial Damage (Tight Junctions), Gut Permeability, Systemic Translocation and Regeneration

On a microscopic level, opioid induced gut dysbiosis has also been shown to contribute to tolerance and withdrawal behaviors, originating from structural changes to the gut epithelium itself. Multiple studies have shown that opioid treatment compromises intestinal barrier function and promotes inflammatory responses in cecal ligation, puncture-induced sepsis, and dextran sulfate sodium (DSS)-induced colitis models (Meng et al. 2015; Sharma et al. 2020). Interactions between the gut microbiota and the gut epithelial barrier play an important role in host homeostasis; compromised gut barrier integrity allow bacteria and their toxic products to enter systemic circulation, triggering a systemic inflammatory response and neuroinflammation. Such neuroinflammation has been shown to contribute to the development of withdrawal and tolerance associated with chronic opioid use (Taylor et al. 2015; Lee et al. 2018; Zhang et al. 2019).

While the effects of opioids on the integrity of intestinal barrier have not been fully elucidated, abundant evidence implicates intracellular cross talk between MOR signaling and tight junction dynamics through TLR signaling (Fig. 1) (Meng et al. 2013; Zhang et al. 2020b). Intestinal barrier integrity is regulated by multiple factors including the organization of TJPs and the renewal of the epithelium by intestinal stem cells. TJPs between intestinal epithelial cells selectively allow the transport of nutrients, electrolytes, water, and some macromolecules, while excluding potentially harmful substances (Camilleri et al. 2012; Buckley and Turner 2018). TJPs include transmembrane and paracellular proteins. The transmembrane molecules such as the claudin family members and the occludin are responsible for sealing the paracellular pathway between the epithelial cells. The scaffold proteins such as ZO-1 and ZO-2 cross-link and anchor the transmembrane proteins (Peterson and Artis 2014). Disruption of TJP organization compromises the intestinal barrier function and is associated with a variety of infectious and inflammatory diseases such as Crohn's disease, ulcerative colitis and celiac disease (Schulzke et al. 2009). Of note, TLR signaling is well known to regulate intestinal permeability by modulating intestinal TJP organization through direct and indirect mechanisms. For example, activation of TLR4 by LPS increases the permeability of the intestinal cell monolayer by disrupting the complex consisting of TJPs, F-actins and myosin in a myosin light chain kinase (MLCK) dependent manner (Forsythe et al. 2002). TLR signaling is also involved in gut barrier modulation indirectly by regulating the expression levels of different proinflammatory cytokines such as TNF- α , IL-1 β , interferon- γ (IFN- γ), and interleukin-6 (IL-6), which leads to increased permeability by altering the expression and localization of TJPs (Desai et al. 2002; Bruewer et al. 2003; Tazuke et al. 2003; Utech et al. 2005; Suzuki et al. 2011). Interestingly, previous

studies have shown that morphine can disrupt intestinal barrier function and damage TJP organization via modulation of MLCK in a TLR dependent manner (Meng et al. 2013).

Increased epithelial cell death and deficient crypt tissue repair also contribute to disruption of the normal intestinal barrier. The role of opioid agonists in intestinal tissue recovery are complex. In humanized bone marrow-liver-thymus (HuBLT) mice, morphine treatment inhibits the proliferation of crypt stem cells by inhibiting Notch signaling (Meng et al. 2019). In contrast, MOR-specific agonist [D-Arg2,Lys4] dermorphin-(1,4)-amide (DALDA) has also been shown to attenuate intestinal injury in DSS-induced colitis and ischemia reperfusion models (Goldsmith et al. 2013). Such different outcomes might be explained by pathway-selective signaling of the opioid receptor. In line, many studies have shown that different opioid agonists can differentially activate various signaling pathways, although all opioid agonists bind to the MOR (Zheng et al. 2010). Therefore, further studies are needed to understand how microbiota modulate different opioid signaling pathways and specifically, the consequence to intestinal physiology.

Globally, opioid-induced gut epithelial damage has been associated with lowered host defenses to various diseases. For instance, opioid treatment in mice has been shown to disrupt the gut epithelial barrier resulting in systemic bacterial translocation to the spleen, liver and peritoneum (Hilburger et al. 1997; Meng et al. 2015). In line, multiple clinical studies have also reported that opioid exposure is associated with intestinal barrier dysfunction, increased intestinal permeability, and increased morbidity when exposed to various infectious diseases. For example, a retrospective analysis indicated that opioid-treated patients hospitalized with a diagnosis of sepsis had a significantly higher risk of death (Zhang et al. 2018). Animal studies have further shown that both morphine treatment and morphine withdrawal lower host defense to enteric bacteria including *Salmonella enterica*, *Pseudomonas aeruginosa*, and *Citrobacter rodentium* (a murine mucosal pathogen that shares the similar virulence factors with the related human pathogens enteropathogenic *Escherichia coli* and enterohemorrhagic *E. coli*) (Feng et al. 2006; Breslow et al. 2010; Babrowski et al. 2012; Wang et al. 2020a). Interestingly, opioid antagonist naltrexone has been shown to block acute endotoxic shock by inhibiting the production of proinflammatory cytokine TNF- α (Greenelch et al. 2004). Thus, exploring mechanisms underlying disrupted epithelial barrier function caused by morphine treatment is of great interest.

Opioid Modulation of the Gut Microbiome and its Impact on Immune System

Opioids are well known to affect the innate and adaptive immune system through direct interactions with immune cells via opioid receptors or indirect interactions via bacterial metabolites. Immune cells have been reported to express μ -, κ - and σ - opioid receptors along with non-classical opioid like receptors, allowing them to mount varied responses in immune cell types. Additionally, human peripheral blood mononuclear cells (PBMCs) and platelets have been shown to have morphine binding mu opioid receptors (Mehrishi and Mills 1983). In the past few decades, there has been increasing efforts to elucidate mucosal immune responses to opioids.

Such investigations have shown that opioids can directly affect cells principally involved in innate immunity. For instance, opioids can alter chemokine production in macrophages, with studies showing increased IL-6, IL-12 and TNF α production after morphine treatment (Roy et al. 1998; Peng et al. 2000). MOR agonist treatment in human PBMCs also show a significant increase in MCP-1, RANTES, and IP-10 chemokine RNA and protein levels (Wetzel et al. 2000). Recent studies using methadone, a widely used opioid receptor agonist, show reduced expression of interferons and interferon stimulated anti-HIV genes in macrophages (Wang et al. 2020b). Signaling through μ -, κ - and σ - opioid receptors has also been shown to exert varied immune responses in dendritic cells (DCs) (Makarenkova et al. 2001; Kirst et al. 2002). κ -opioid receptors agonists dynorphin A and U50,488H suppress the ability of DCs to induce T-cell proliferation in a concentration dependent manner (Kirst et al. 2002). However, antigen uptake and maturation of DCs remained unchanged. Recent studies have further shown that morphine treatment exerts immuno-stimulatory effects on DCs and enhanced T cell stimulatory capacity of LPS matured DCs, further showing significant modulation of innate immune cells by opioids (Messmer et al. 2006).

Additionally, there is great consensus that acute and chronic opioid treatment significantly affects adaptive immunity. For instance, chronic morphine treatment leads to an increase in circulating Treg cells and the functional activity of Th17 cells (Cornwell et al. 2013). Prolonged opioid treatment has long been associated with impaired T-cell function, increased T-cell apoptosis, modified T cell differentiation and altered cytokine response (Bryant and Roudebush 1990; Singhal et al. 1999, 2001; Sacerdote et al. 2000; Han et al. 2020). Contrary to the previously believed immunosuppressive role of opioids, recent research indicates a dual effect of opioids. Activation of different opioid receptors on immune cells might demonstrate contrasting and inverse effects on immune cells. Furthermore, different opioid drugs have been shown to have differential immunomodulatory properties. For example, MOR signaling in T cell lymphocytes by fentanyl, methadone and beta endorphins results in strong induction of IL4, whereas treatment with morphine and buprenorphine leads to significantly lowered levels of IL4 mRNA and protein, which suggests agonist biased MOR signaling in T cells (Borner et al. 2013). Opioids have also been shown to affect B lymphocytes, which are major contributors of humoral immunity. In rodent models, morphine pelleting or intraperitoneal morphine treatment causes reduced mitogenic response to bacterial LPS in B cells (Bryant et al. 1988; Bhargava et al. 1994). Furthermore, in regards to B cell function, opioids have been reported to have variable effects on immunoglobulin production, which may be dependent on specific opioid receptor agonists. In an *in-vivo* study, μ -opioid receptor agonist treatment resulted in an increase in IgM and IgG; on the contrary treatment with an σ -opioid receptor agonist lead to immunosuppression with reduced IgG and IgM production (Cheido et al. 2014). Rodent studies have also shown that morphine treatment reduces major histocompatibility complex II (MHCII) expression levels on B lymphocytes by 33% and that this effect is mediated by the hypothalamic–pituitary–adrenal (HPA) axis (Nugent et al. 2011). Since MHCII is an important cell communicator for immune cells, morphine mediated decrease in MHCII expression may contribute to the immunosuppressive effects of morphine.

Apart from direct interactions of opioids on immune cells through opioid receptors, opioids can also influence immune cells indirectly through bacterial metabolites. Most attention has

been paid to the role of BAs and SCFAs in modulating immune cell response. BAs directly participate in gut mucosal defense due to their bactericidal properties (Watanabe et al. 2017). The role of BA signaling in regulating intestinal homeostasis is further confirmed by the development of severe colitis in BA receptor knock out TGR5^{-/-} as well as FXR^{-/-} mouse models (Renga et al. 2013; Biagioli et al. 2017).

Other bacterial metabolites such as SCFA also have essential roles in regulating mucosal immune homeostasis. SCFA are transported across intestinal epithelial cells via monocarboxylate transporter (MCT1) and slc58a (SMCT) to enter systemic circulation (Iwanaga et al. 2006). SCFA receptors including G-protein coupled receptors (GPCR) known as free fatty acid receptors (FFAR 2 or GPCR 43), FFAR 3 (GPCR 41) GPR 109A and olfactory receptor 78 (OLF 78) have been shown to be present on intestinal L-cells and innate as well as adaptive immune cells (Kimura et al. 2011; Tolhurst et al. 2012; Singh et al. 2014; Luu et al. 2018). SCFA not only acts as a major source of energy for intestinal epithelial cell, but they also promote intestinal epithelial barrier function (Kelly et al. 2015; Park et al. 2016). SCFAs, particularly butyrate also have been shown to have several immunomodulatory functions that have been extensively studied and reviewed (Cox et al. 2009; Arpaia et al. 2013; Chang et al. 2014; Singh et al. 2014; Nastasi et al. 2015; Deleu et al. 2021; Simpson et al. 2021) and fecal SCFA levels in inflammatory bowel disease (IBD) samples have shown to be reduced (Kaczmarczyk et al. 2021).

So far, opioid treatment has been established to alter levels of SCFA and BAs but the impact of opioids on other bacterial metabolites is still understudied. Additionally, the impact of metabolic environment on host immune response further needs to be explored. With current gaps in knowledge, future research should focus on identifying key metabolites markers changing after opioid use which can be targeted therapeutically for OUD.

Opioids, Gut Microbiota and the Enteric Nervous System (ENS)

Opioid use and the gut microbiota may also influence ENS functions at the gut epithelium. The gastrointestinal (GI) tract is innervated by a complex network of neurons and glial cells, which are bundled together in the submucosal (Meissner) and the myenteric (Auerbach) plexus (Laranjeira and Pachnis 2009; Furness 2012). These neurons and glial cells of the ENS are derived from the neural crest cells that colonize the embryonic gut at E9-E9.5 in mice (Rothman et al. 1986; Heanue and Pachnis 2007; Coelho-Aguiar et al. 2015). In the ENS, the differentiation of enteric neurons starts prior to the start of enteric glial cells (EGCs). However, EGCs outnumber neurons, and the ratio of enteric neurons to EGC in the submucosal and myenteric plexus varies from 1:4 to 1:10 depending on the species (Savidge et al. 2007; Hoff et al. 2008; Esposito et al. 2016). Both enteric neurons and EGCs play a crucial role in the regulation of intestinal epithelial barrier functions including nutrient absorption and protection from gut microbial pathogens.

A number of studies have verified the expression of μ -, κ - and σ - opioid receptors in myenteric and submucosal plexus neurons (Bagnol et al. 1997; Sternini et al. 2004; Poole et al. 2011; Lay et al. 2016; DiCello et al. 2020) suggesting a potential direct effect of opioids on the enteric neuronal functions. The myenteric plexus neurons regulate GI motor activity

and peristalsis, whereas neurons in the submucosal plexus, which are in close proximity to the epithelial cells, regulate blood flow, immune cell migration, and various mucosal functions in the epithelium (Bertrand et al. 1998; Furness et al. 1998). In addition, the submucosal plexus consists of two types of secretomotor neurons, the ascending cholinergic neurons (immunoreactive for neuropeptide Y; NPY) and the descending non-cholinergic neurons, which through the release of Acetylcholine (ACh) and vasoactive intestinal polypeptide (VIP), respectively, control epithelial cell secretion (Cooke and Carey 1985; Keast et al. 1985a, b). These neuronal mediators also regulate epithelial barrier integrity. For example, ACh and NPY have been shown to increase epithelial permeability (Neunlist et al. 1998; Gareau et al. 2006; Overman et al. 2012). Consistently, increased NPY levels have been reported in mouse models of colitis, whereas NPY knockout mice show improved barrier function and developed less severe colitis (Chandrasekharan et al. 2008, 2013). In contrast, VIP decreases intestinal permeability, promotes epithelial cell proliferation, stimulates mucus production, regulates ZO-1 tight-junction protein expression and induces production of interleukin-8 (a chemokine that attracts immune cells) in epithelial cells, and thereby contributes to both maintenance and immune surveillance of the epithelial barrier (Farack et al. 1987; Neunlist et al. 1998, 2003; Toumi et al. 2003, 2004; Foong et al. 2010; De Quelen et al. 2011). Opioid receptor activation at the enteric circuitry has been shown to suppress neuronal excitability, decrease GI secretion, promote water and electrolyte absorption and cause impairments in peristalsis. These effects of opioids are partly mediated through inhibition of the release of neuronal mediators including VIP, ACh, substance P and nitric oxide (De Luca and Coupar 1996; Iwata et al. 2007; Brock et al. 2012).

The protective effects of EGCs at the gut epithelium may be impaired by chronic opioid use. EGCs like astrocytes in the CNS, are crucial for the development and survival of enteric neurons (Abdo et al. 2010, 2012; De Giorgio et al. 2012), and therefore may also regulate neuron-controlled epithelial barrier function. Regulation by EGCs of the intestinal epithelium was demonstrated in a study by Neunlist et al. that showed a significant increase in crypt hyperplasia after ablation of EGCs (Neunlist et al. 2007). In another study, ablation of EGCs by targeting the glial fibrillary acidic protein (GFAP) caused fatal jejuno-ileitis in mice (Bush et al. 1998; Cornet et al. 2001). Together, these studies suggest that EGCs could directly or indirectly control epithelial cell proliferation and self-renewal. Consistently, EGCs produce various trophic factors including glia derived neurotrophic factor (GDNF), which through the induction of ZO-1 protein may promote intestinal barrier function (Xiao et al. 2014; Meir et al. 2015; Bauman et al. 2017). Other EGC-derived factors that promotes epithelial barrier integrity include proEGF (Van Landeghem et al. 2011), TGF- β 1 (Neunlist et al. 2007), S-nitrosoglutathione (Savidge et al. 2007; Flamant et al. 2011; Li et al. 2016), 15-hydroxyeicosatetraenoic acid (Pochard et al. 2016) and 15-deoxy-delta-12,14-prostaglandin J2 (Abdo et al. 2012; Coquenlorge et al. 2016).

In a recent study, we demonstrated that morphine treatment reduces the barrier-enhancing effects of EGCs on intestinal epithelial cells in vitro, and that this effect of morphine was associated with a decrease in GDNF mRNA and protein levels in EGCs (Bauman et al. 2017). In addition, accumulating evidence implicates a central role for EGCs in the development of abdominal pain, mainly through production of immunoregulatory signals and modulation of nociceptors within the myenteric plexus (Morales-Soto and Gulbransen

2019). EGCs, like glial cells of the CNS, may regulate opioid-induced hyperalgesia through altered purinergic signaling (Watkins et al. 2005; Morales-Soto and Gulbransen 2019). Consistently, long-term exposure of mice to morphine increases purinergic P2X receptor activity in EGCs (Bhave et al. 2017). Of note, under inflammatory conditions of the gut, EGCs may acquire a reactive phenotype, exhibit properties of antigen presenting cells (by expressing MHC class II), recruit immune cells, and contribute to the epithelial damage through production and release of S100 β , nitric oxide, IL-6 and IL-1 β (Esposito et al. 2006, 2007; Cirillo et al. 2009, 2011; Xiao et al. 2011). Additionally, we have previously reported that chronic exposure of mice to morphine increases the expression of IL-6, IL-1 β and TNF α in the small intestine (Meng et al. 2013; Zhang et al. 2019). The morphine-treated mice also showed severe disruption of the gut epithelium and subsequent translocation of gut bacteria into mesenteric lymph node and liver (Meng et al. 2013). Whether or not these detrimental effects of morphine at the gut epithelium are a consequence of a phenotypic switch (from trophic to reactive) in the EGCs remains unclear. In a recent study, the reactive phenotype of EGCs in a mouse model of Gulf War illness was associated with TLR4 activation (Kimono et al. 2019). In this study, EGC reactivity in Gulf War chemical exposed mice was reduced following antibiotic treatment, suggesting a direct modulation of EGC function through TLR4 by the gut microbiota. In line, interestingly, morphine-induced gut epithelial damage is significantly reduced in TLR4 deficient mice (Meng et al. 2013). In addition, TLR4-deficient mice did not develop opioid-induced bowel dysfunction (Beckett et al. 2018). Collectively, these studies suggest that EGCs under physiological conditions confer protection to both enteric neurons and the gut epithelium, and that a perturbation of the gut epithelial homeostasis (that is, microbial dysbiosis and TLR4 activation) following chronic opioid use may trigger EGCs to cause detrimental effects in the ENS.

Emerging evidence indicates an important role of the gut microbiota in ENS development. For example, De Vadder et al. showed that the gut microbiota regulates maturation of the ENS through a mechanism involving serotonin (5-HT) receptor activation (De Vadder et al. 2018). In this study, there was an increase in proliferation of enteric neuronal progenitors when GF mice were colonized with microbiota from conventionally raised mice. Another study by Kabouridis et al. showed that the gut microbiota is essential for postnatal development of EGCs of the intestinal mucosa (Kabouridis and Pachnis 2015). Microbial metabolites may be directly responsible for migration of EGCs to lamina propria and maturation of enteric neurons in the ENS. This is further supported with the observation that microbiota plays a role in mediating opioid-induced damage and inflammation at the gut epithelium as well as in antinociceptive tolerance (Zhang et al. 2019). Taken together, understanding the relationship between the gut microbiota and the ENS is crucial to identifying novel therapeutic targets in opioid-induced bowel dysfunction (Camilleri and Boeckxstaens 2017).

Summary and Conclusion

A substantial amount of research has been conducted in past few decades oriented towards understanding how the gut microbiome influences the gut-brain-axis under health and disease states. Environmental factors, including the use of illicit drugs, have been shown to cause dramatic changes in gut microbial composition; specifically, they are known to

shift the gut microbiome towards a more pathogenic state. Accumulating evidence has further shown that changes in the gut microbiome often coincide with changes in microbial metabolites. Importantly, molecular information in the form of microbial metabolites play an important role in maintaining central as well as enteric nervous system health. For instance, opioid-mediated alterations in microbial metabolites such as SCFAs and BAs may have direct effects on CNS and ENS maturation and function (Fig. 2). This altered metabolic profile also contributes towards dysregulated immune homeostasis. Collectively, these changes may contribute towards neurological disorders as well as opioid induced co-morbidities.

Recent studies also identify contributions of gut microbiota in ENS maturation through modulation of neurotransmitters. The bi-directional facet of the gut-brain axis is also reflected by the fact that secretory factors such as GDNF by enteric glia also regulate microbial homeostasis through mucosal immune system maturation as well as by strengthening epithelial tight junction functions. Opioid mediated decreases in the expression of GDNF are also associated with increased intestinal permeability and altered immune surveillance at the intestinal mucosal surface. Altogether, these factors contribute to maintaining the pro-inflammatory environment observed with opioid treatment, leading to downstream opioid-associated comorbidities such as opioid tolerance, dependence, and withdrawal (Fig. 2). Furthermore, opioid-inhibited-release of neuronal mediators (e.g., VIPs, ACh, NO) from enteric neurons cause decreased GI secretion, increased water and electrolyte absorption, and decreased peristalsis, leading to opioid-induced constipation which further contributes to microbial dysbiosis following opioid use (Fig. 2). In conclusion, while pharmacological treatments for OUDs are available, they are not effective for all patients. It is therefore important that we improve our understanding of the role of the microbiome in OUDs, as new discoveries may elucidate novel targets for future therapeutics. These therapies could target pathways involved in microbial signaling within the gut-brain axis either by manipulating the composition of the gut microbiome or by manipulating its products via drugs designed to alter and exploit microbial metabolism. In particular, while no clinical trials exist of microbiome modulation in opioid-dependent patients, murine studies using fecal microbial transplant (FMT) or probiotics have shown much promise. For instance, FMT from naïve mice donors to antibiotic treated mice was shown to restore normal reward behavior, microglia morphology, sensitivity to pain, and to attenuate naloxone-precipitated opioid withdrawal in morphine-dependent mice (Lee et al 2018; Thomaz et al 2021). Additionally, others have shown that the VSL#3 probiotic cocktail attenuated morphine analgesic tolerance and hyperalgesia in opioid dependent mice, suggesting the beneficial effects of probiotic pretreatment in prolonging the analgesic properties of morphine (Zhang et al 2019). Still, much work needs to be done in this field, together with elucidating how prebiotics or synbiotics may improve GI and neuropsychiatric pathology in opioid-dependent patients. Indeed, while these potential therapeutics may not prove a panacea, they have enormous potential to be developed as or supplement existing therapies (Fig. 2).

Acknowledgements

This work was supported by the National Institutes of Health Grants (R01DA044582, R01DA043252, R01DA050542, R01DK117576, and T32DA045734) awarded to SR, by the Miami Center for AIDS Research (CFAR) via a pilot grant (P30AI073961) awarded to SM, and by the University of Miami Scientific Awards Committee (UM SAC) pilot grant (PG013459) and the Miami CFAR pilot grant (GR009434) to US.

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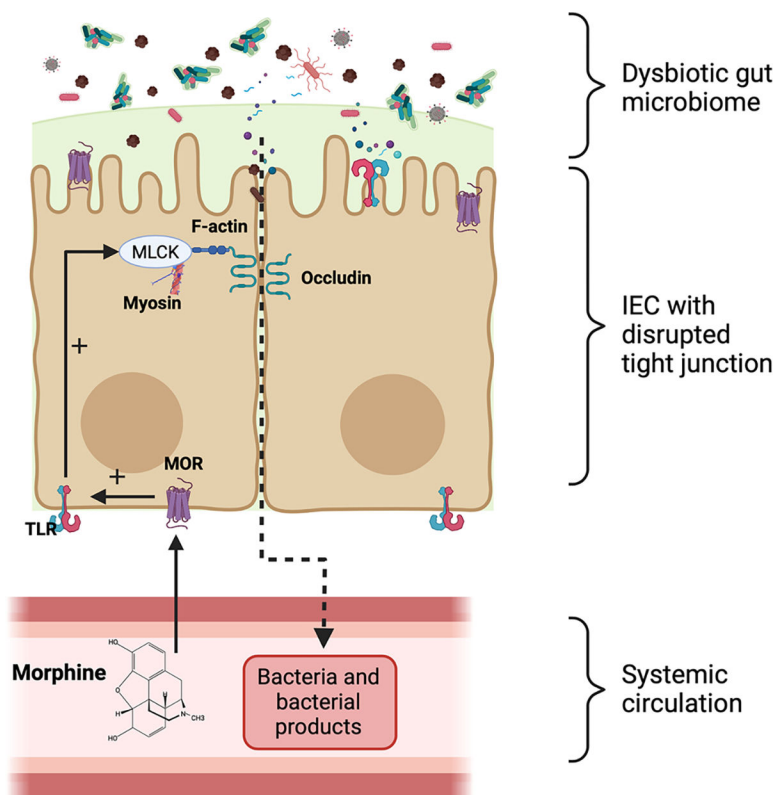


Fig. 1. Morphine treatment upregulates TLR expression in intestinal tissue. Increased TLR signaling in intestinal epithelial cells leads to MLCK induced tight junction redistribution and increase intestinal permeability. (Adapted and modified from Meng et al. 2013). (IEC, Intestinal epithelial cell)

Healthy state

Opioid Use Disorder

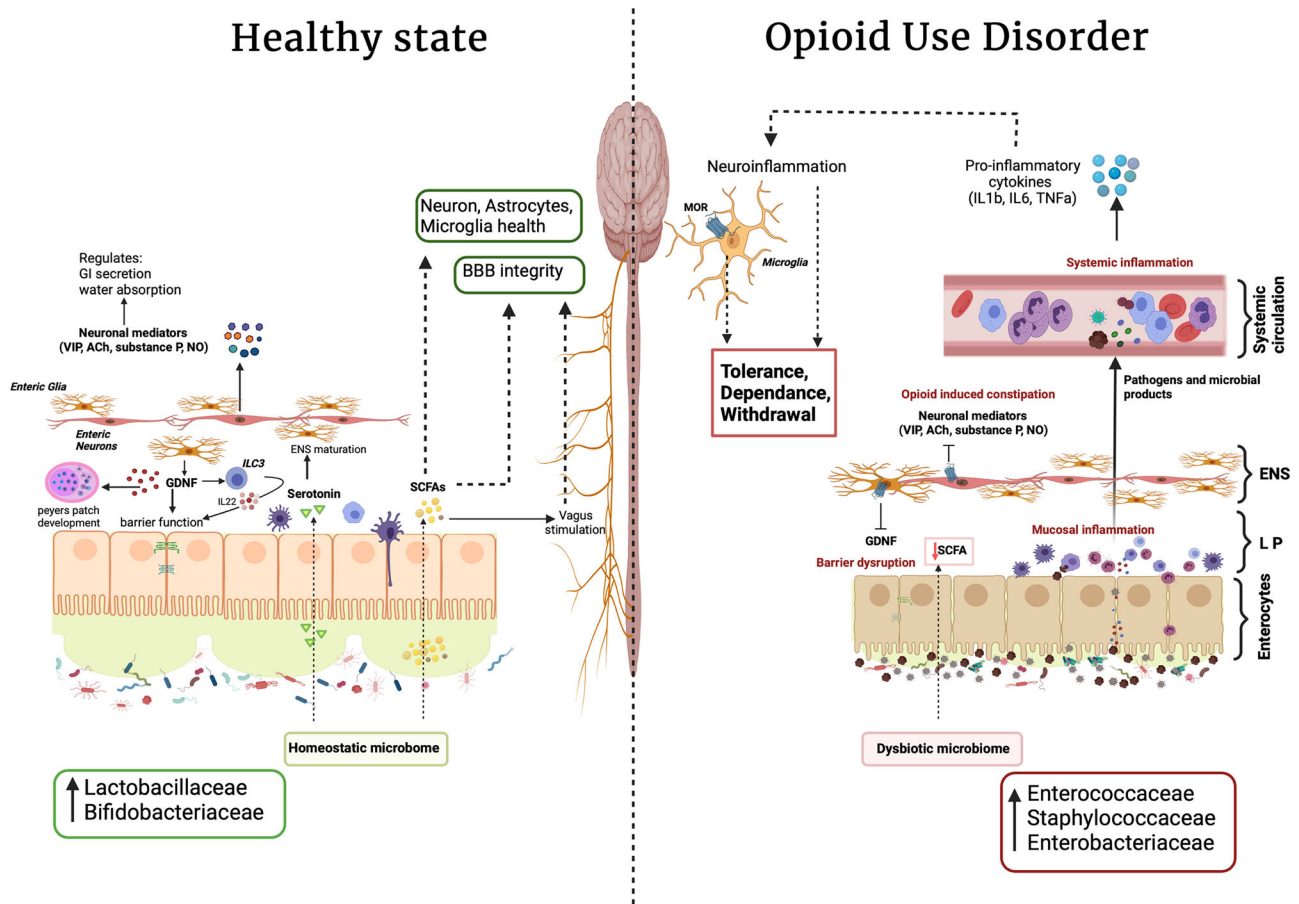


Fig. 2. Opioid use and gut-brain axis: opioid induced gut dysbiosis leads to mucosal, systemic, and neuroinflammation which contributes to opioid associated comorbidities such as tolerance, dependence and withdrawal. (GDNF, glia derived neurotropic factor; SCFA, short-chain fatty acid; BA, bile acid; ACh, Acetylcholine; VIP, vasoactive intestinal polypeptide; NO, nitric oxide; ENS, enteric nervous system; MOR, μ opioid receptor; LP, lamina propria; ILC3, innate lymphoid cells 3; BBB, blood brain barrier)

Table 1

Summary of studies indicating opioid use associated alteration in gut microbiota and its phenotypic response

Substance used	Species	Treatment/stage	Change in Microbiome	Phenotypic response	Reference
Multi-opioids	Human	Chronic user outpatients and Inpatients	↓ <i>Bacteroidaceae</i> ↓ Clostridiales XI ↓ <i>Ruminococcaceae</i>	Cirrhosis and readmissions	(Acharya et al. 2017)
Multi-opioids	Human	Chronic user outpatients	↑ <i>Bifidobacterium</i> ↓ <i>Prevotella copri</i> ↑ Lactobacillales	Type 2 diabetes (T2D) and psychiatric conditions	(Barengolts et al. 2018)
Multi-opioids	Human	Chronic user	↓ <i>Bacteroides</i> ↓ <i>Prevotella</i> ↑ <i>Ruminococcus</i>	Substance use addiction	(Xu et al. 2017)
Morphine	NHP	Intramuscular Injections (21d)	↑ <i>Methanobacteriaceae</i> ↓ <i>Streptococcaceae</i> ↓ <i>Ruminococcaceae</i>	Increase inflammation	(Sindberg et al. 2019)
Morphine	Mouse	Subcutaneous slow release pellet (25 mg, 3d)	↑ <i>Staphylococcus</i> ↑ <i>Enterococcus</i>	Inflammation and sepsis	(Meng et al. 2015)
Morphine	Mouse	Intraperitoneal injections (10 mg/kg, every 12 h, 4 d)	↑ <i>Ruminococcus</i> ↓ <i>Lactobacillus</i>	Hyperalgesia, and impaired reward response	(Lee et al. 2018)
Morphine	Mouse	Subcutaneous slow release pellet (75 mg, 5d)	↓ Clostridiales ↓ Lactobacillales ↓ Bacteroidales ↑ Enterobacteriales	Morphine antinociceptive tolerance	(Kang et al. 2017)
Morphine	Mouse	Subcutaneous slow release pellet (25 mg, 3d)	↑ <i>Enterococcus faecalis</i>	Augment analgesic tolerance	(Wang et al. 2018)
Morphine	Mouse	Intraperitoneal injections (15 mg/kg, 8d)	↓ <i>Bifidobacteria</i> ↓ <i>Lactobacillaceae</i>	Develop morphine analgesic tolerance	(Zhang et al. 2019)
Morphine	Mouse	Subcutaneous slow release pellet (25 mg, 2d)	↑ <i>Firmicutes</i> ↓ Bacteroidetes	Gut barrier disruption and systemic inflammation	(Banerjee et al. 2016)
Morphine	Rat	Subcutaneous slow release pellet (75 mg)	↓ <i>Firmicutes</i> ↑ Bacteroidetes ↑ Actinobacteria ↑ Verrucomicrobia	Opioid withdrawal	(O'Sullivan et al. 2019)
Hydromorphone	Mouse	Intraperitoneal injections (7.5 mg/kg, every 12 h, 7 d)	↓ Firmicutes ↑ Proteobacteria ↑ Verrucomicrobia	Increase gut and systemic inflammation	(Sharma et al. 2020)
Oxycodone	Rat	Subcutaneous injections (2 mg/ kg, every 12 h for 5 d)	↓ Bacteroidetes ↓ Firmicutes ↑ Cyanobacteria ↑ Proteobacteria ↑ Verrucomicrobia	Opioid dependence	(Simpson et al. 2020)

Table 2

Summary of studies showing role of bacterial metabolites on nervous health and behavior

Bacterial metabolite	Class	Study Model	Host response	Reference
CDCA and DCA	Bile Acid	BA injection in Sprague Dawley rats	Increased BBB permeability	(Quinn et al. 2014)
Obeticholic acid (OCA)	Bile Acid	Oral gavage of BA in HFHS (high fat, high sugar) fed mice	Improve metabolic disorder driven Anxiety	(Wu et al. 2021)
Sodium propionate, sodium butyrate and sodium acetate	SCFA	Added to drinking water in mice	Increased microglial maturation and function	(Erny et al. 2015)
Sodium butyrate	SCFA	BTBR autism mouse model	Attenuates social behavior deficits	(Kratsman et al. 2016)
Sodium butyrate	SCFA	Chronic mild stress model in Wistar rats	Anti-depressant and anti-manic properties	(Resende et al. 2013)
Propionate	SCFA	Experimental autoimmune encephalomyelitis	Ameliorate experimental autoimmune encephalomyelitis (EAE) disease course	(Haghikia et al. 2015)
P-cresol	Aromatic acid metabolite	BTBR autism mouse model	Triggers anxiety and hyperactivity at lower doses and exacerbate autism like behavior at higher dose	(Pascucci et al. 2020)
TMAO	Amine oxide	C57Bl/6 mice on low-choline diet supplemented with TMAO	Induced neuroinflammation and decline in cognitive function	(Brunt et al. 2021)
Tryptophan	Amino acid	EAE mouse model of multiple sclerosis	Decreased neuroinflammation and decreased EAE score	(Rothhammer et al. 2016)