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Minireviews

Targeting Epigenetic Mechanisms for Chronic Pain: A Valid Approach for the Development of Novel Therapeutics

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ABSTRACT

Chronic pain is a multifaceted and complex condition. Broadly classified into somatic, visceral, or neuropathic pain, it is poorly managed despite its prevalence. Current drugs used for the treatment of chronic pain are limited by tolerance with long-term use, abuse potential, and multiple adverse side effects. The persistent nature of pain suggests that epigenetic machinery may be a critical factor driving chronic pain. In this review, we discuss the latest insights into epigenetic processes, including DNA methylation, histone modifications, and microRNAs, and we describe their involvement in the pathophysiology of chronic pain and whether epigenetic modifications could be applied as future therapeutic targets for chronic pain. We provide evidence from experimental models and translational research in human tissue that have enhanced our understanding of epigenetic processes mediating nociception, and we then speculate on the potential future use of more specific and selective agents that target epigenetic mechanisms to attenuate pain.

Introduction

Acute pain signals real or potential tissue damage, making it an important protective sensation that influences behavior to prevent further injury and promote healing. Acute pain can be mild or severe, with a relatively short duration, and typically resolves with the treatment or healing of the damaged tissue. By contrast, chronic pain is a pathologic state that does not serve a protective function and is considered harmful to the organism. Defined as pain persisting for 6 months after the resolution of, or in the absence of, an injury, chronic pain affects approximately one-fifth of adults in the United States and is associated with a significantly reduced quality of life and an increased risk of mental health disorders (Breivik et al., 2006; Tsang et al., 2008; Goldberg and McGee, 2011). The economic effects of chronic pain are equally profound, with an estimated cost of $300 billion in the United States alone (Institute of Medicine, 2011).

The precise mechanisms underlying the transition from acute to chronic pain are not well understood, although adaptations in numerous structures within pain pathways, such as peripheral neurons, dorsal root ganglia (DRG), spinal cord neurons, and the brain, are known to be involved (Woolf and Salter, 2000; Kuner, 2010). This plasticity, which is essential for the development of chronic pain, involves significant changes in neurotransmitters and other molecules, cells, and neural networks and is maintained, in part, by epigenetic processes (Gräff et al., 2011; Buchheit et al., 2012; Karpova, 2014). Indeed, epigenetic processes, comprising DNA methylation, chromatin remodeling, and noncoding RNA, have been increasingly implicated in the development of chronic pain in recent years, thus highlighting new potential targets for drug development and pain management.

Although current therapeutics are effective at relieving acute pain, drugs used to manage chronic pain are typically less efficacious, with the development of novel pharmacologic therapies experiencing little progress in recent decades. Indeed, chronic pain is still predominantly treated with two classes of drugs: nonsteroidal anti-inflammatory drugs (NSAIDs) and opioids. Both NSAIDs and opioids, along with

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ABBREVIATIONS: 5-aza, 5′-aza-2′-deoxycytidine; BDNF, brain-derived neurotrophic factor; C646, 4-[4-[[5-(4,5-dimethyl-2-nitrophenyl)-2-furanyl]methylene]-4,5-dihydro-3-methyl-5-oxo-1*H*-pyrazol-1-yl]benzoic acid; CCI, chronic constriction injury; CeA, central nucleus of the amygdala; CFA, complete Freund's adjuvant; COX, cyclooxygenase; DNMT, DNA methyltransferase, DRG, dorsal root ganglia; GR, glucocorticoid receptor; HAT, histone acetyltransferase; HDAC, histone deacetylase; IBS, irritable bowel syndrome; lncRNA, long noncoding RNA; miRNA, microRNA; MS-275, *N*-[[4-[[(2-aminophenyl)amino]carbonyl]phenyl]methyl]-3-pyridinylmethyl ester, carbamic acid; ncRNA, noncoding RNA; NSAID, nonsteroidal anti-inflammatory drug; PSNL, partial sciatic nerve ligation; SAHA, suberoylanilide hydroxamic acid; SCN, sciatic nerve; SNL, spinal nerve ligation; TET, ten-eleven translocation; Trpv1, transient receptor potential cation channel subfamily V member 1; TSA, trichostatin A.

the small number of other drugs that do not fall into these categories, produce a number of adverse side effects and, critically, often fail to provide adequate long-term relief in many chronic conditions (Johnson and Greenwood-Van Meerveld, 2014). Given these limitations, the need for improved therapeutic options for the management of chronic pain is apparent.

This review briefly summarizes the pathways of chronic pain, categorized as somatic, visceral, or neuropathic pain, and the currently available therapies. We then describe the primary mechanisms of epigenetic regulation and review the recent findings in the field of epigenetics and chronic pain. Finally, we discuss the epigenetic drugs and their usefulness in the context of pain management and highlight the potential approaches for targeting epigenetic mechanisms in a specific and selective manner.

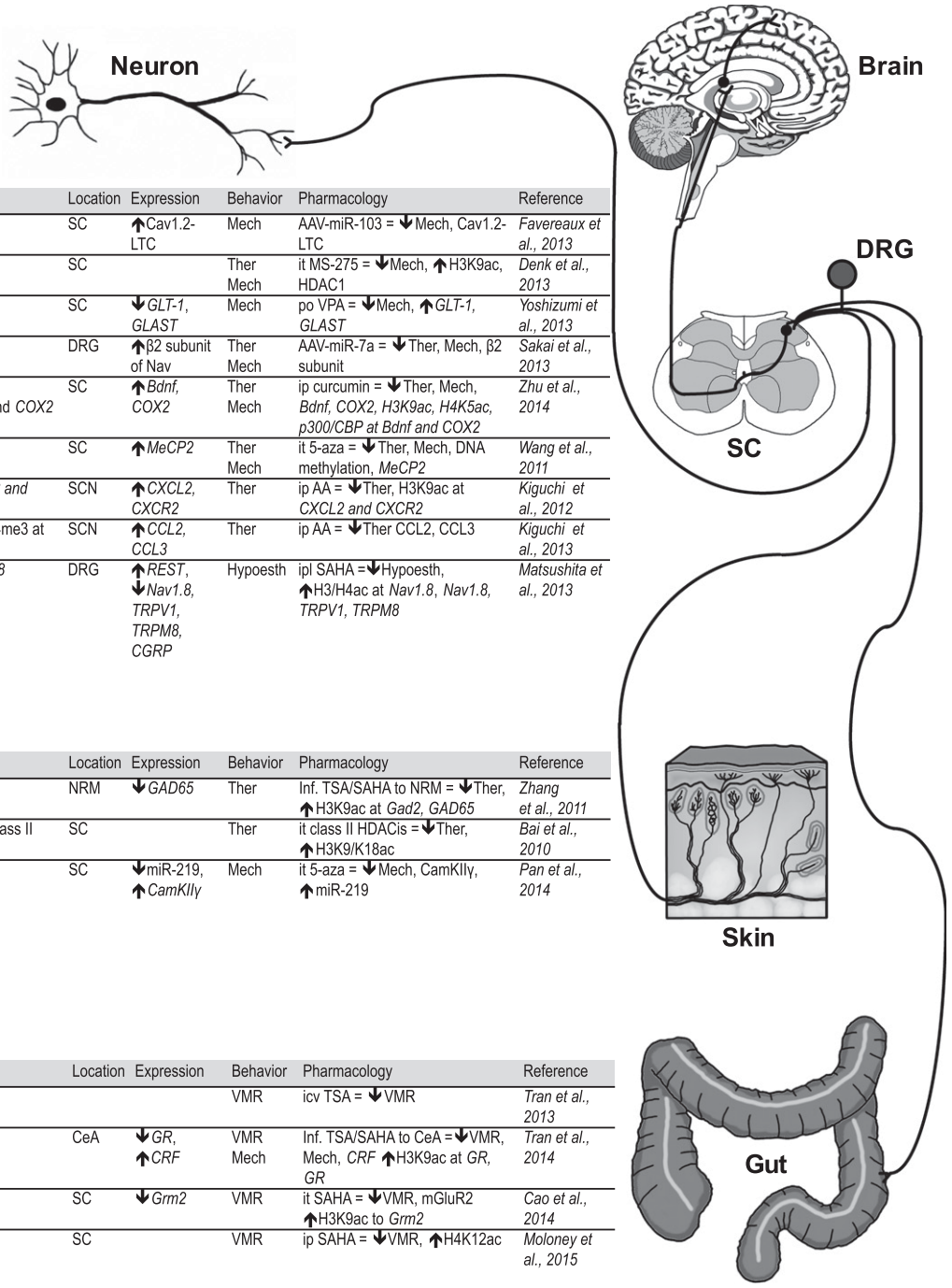
Chronic Pain

Chronic pain pathways involve stimuli originating from skin, skeletal muscle, joints, or visceral organs. These pathways and the mechanisms of their sensitization have been expertly described in several excellent reviews (Besson, 1999; Almeida et al., 2004; Wilder-Smith, 2011; Woolf, 2011) Briefly, the classic acute pain pathway involves the activation of primary nociceptive afferents within the periphery, which then send the stimulus to the dorsal horn of the spinal cord (Almeida et al., 2004). After synapsing with the dorsal horn, the signal is then transmitted across the midline to the anterolateral tract of the spinal cord, where it ascends to the thalamus in the brain. From the thalamus, the signal is relayed to the somatosensory cortex for localization. Ascending nociceptive signals traveling via the spinoparabrachial and spinoreticular tract activate limbic structures, such as the amygdala, to produce an emotional response to the stimulus. The remaining constituent regions of the central pain matrix (prefrontal cortex, cingulate, and parietal cortex) define the magnitude and quality of the pain signal. Pathways composed of motor cortex and brain stem areas are then activated, contributing to descending modulation of the pain signal. Although the exact mechanisms vary depending on site and pathology, sensitization of this acute pain pathway occurring at the level of the periphery, spinal cord, or central pain matrix leads to the development of chronic pain. In the periphery, after tissue damage or immune stimulation, primary afferent nociceptors are sensitized due to the release of a myriad of algesic molecules (cytokines, histamine, prostaglandins, substance P, etc.) by local tissue or immune cells participating in the healing process. In addition, activation of G protein–coupled receptors on the primary afferent nociceptors induces second-messenger pathways that change intracellular calcium, modify existing receptors, and alter receptor expression, all of which lead to further sensitization of the nociceptor. The second site of sensitization occurs within the dorsal horn of the spinal cord, where the sensitized primary nociceptive afferent releases neurotransmitters [including glutamate, substance P, brain-derived neurotrophic factor (BDNF), and others] that stimulate the second-order neuron. Sensitization is promoted through changes in gene regulation that shift the balance of receptors, leading to an increased excitably of the neuron—through changes in α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid, potassium, and metabotropic glutamate receptors. The final hypothesized mechanism that produces chronic pain is supraspinal hypersensitivity. Central sensitization at the level of supraspinal sites, specifically regions encompassing the pain matrix discussed above (thalamus, prefrontal cortex, amygdala), alter the descending control of pain responses and thus maladaptive, chronic nociceptive behaviors occur (Cervero, 1995, 2000). Indeed, brain imaging studies have revealed not only gross structural changes (decreased gray matter, cortical thickness) (DaSilva et al., 2008; Cauda et al., 2014) but altered connectivity between regions in this matrix (Ellingson et al., 2013; Mansour et al., 2013; Irimia et al., 2015). Moreover, it has been proposed that long-term potentiation and thus plasticity occurs to maintain central sensitization (Reichling and Levine, 2009; Luo et al., 2014).

Epigenetic Mechanisms

The term *epigenetics* describes phenotypic trait variations resulting from developmental or environmental cues rather than alterations to the genomic DNA sequence itself (Waddington, 1942). The most thoroughly investigated mechanisms through which these variations arise involve modifications that regulate chromatin, which is made up of combinations of DNA, histones, and other proteins. These modifications, which are dynamic and reversible, lead to the structural remodeling of chromatin and result in the differential expression of genes. Epigenetic mechanisms include DNA methylation and the post-translational modification of histones, with the entirety of these different modifications referred to as the epigenome (Bernstein et al., 2007). More recently, epigenetic mechanisms involving RNAs that do not encode protein or participate in translation have been identified. Only approximately 1.5% of the human genome encodes protein, whereas the noncoding elements of the genome serve to regulate the expression of the coding regions through various mechanisms such as long noncoding RNAs (lncRNAs) and microRNAs (miRNAs). miRNAs are a subset of small noncoding RNAs (ncRNAs) that inhibit gene expression by targeting specific mRNAs for degradation (Farh et al., 2005; ENCODE Project Consortium, 2012). lncRNAs are ncRNAs with a length greater than 200 nucleotides that can regulate transcription via a number of different mechanisms. Aside from directly targeting mRNA, lncRNAs have also been shown to interact with transcription factors, chromatin-modifying complexes, and various other molecules to alter gene transcription (Bonasio and Shiekhattar, 2014). Although miRNAs and lncRNAs do not directly modify chromosomal regions themselves, they can confer altered activity states of genes in response to environmental cues and therefore are generally considered epigenetic regulators.

Histone Modifications. Chromatin structure is significantly affected by post-translational modifications at the freely accessible N-terminal tails of histones, particularly on histones H3 and H4. These modifications can take the form of lysine acetylation, serine/threonine phosphorylation, lysine/arginine methylation, ubiquitination, and ADP-ribosylation. In general, the presence of acetyl or phospho groups promotes active transcription states by decreasing the affinity between histones and DNA, resulting in greater availability of DNA to interact with transcriptional machinery (Géranton and Tochiki, 2015a). Histone methylation, however, can have both activating and silencing effects on gene expression depending



Neuropathic Pain

Model	Mark/Enzyme	Location	Expression	Behavior	Pharmacology	Reference
SNL	↓miR-103	SC	↑Cav1.2-LTC	Mech	AAV-miR-103 = ↓Mech, Cav1.2-LTC	*Favereaux et al., 2013*
SNL		SC		Ther Mech	it MS-275 = ↓Mech, ↑H3K9ac, HDAC1	*Denk et al., 2013*
SNL		SC	↓*GLT-1, GLAST*	Mech	po VPA = ↓Mech, ↑*GLT-1, GLAST*	*Yoshizumi et al., 2013*
SNL/ CCI	↓miR-7a	DRG	↑β2 subunit of Nav	Ther Mech	AAV-miR-7a = ↓Ther, Mech, β2 subunit	*Sakai et al., 2013*
CCI	↑H3K9ac, H4K5ac, p300/CBP at *Bdnf* and *COX2*	SC	↑*Bdnf, COX2*	Ther Mech	ip curcumin = ↓Ther, Mech, *Bdnf, COX2, H3K9ac, H4K5ac, p300/CBP at Bdnf and COX2*	*Zhu et al., 2014*
CCI	↑DNA methylation	SC	↑*MeCP2*	Ther Mech	it 5-aza = ↓Ther, Mech, DNA methylation, *MeCP2*	*Wang et al., 2011*
PSNL	↑H3K9ac at *CXCL2 and CXCR2*	SCN	↑*CXCL2, CXCR2*	Ther	ip AA = ↓Ther, H3K9ac at *CXCL2 and CXCR2*	*Kiguchi et al., 2012*
PSNL	↑H3K9ac and H3K4me3 at *CCL2 and CCL3*	SCN	↑*CCL2, CCL3*	Ther	ip AA = ↓Ther CCL2, CCL3	*Kiguchi et al., 2013*
PSNL	↓H3/H4ac at *Nav1.8*	DRG	↑*REST*, ↓*Nav1.8, TRPV1, TRPM8, CGRP*	Hypoesth	ipl SAHA =↓Hypoesth, ↑H3/H4ac at *Nav1.8, Nav1.8, TRPV1, TRPM8*	*Matsushita et al., 2013*

Somatic Pain

Model	Mark/Enzyme	Location	Expression	Behavior	Pharmacology	Reference
CFA	↓H3K9ac at *Gad2*	NRM	↓*GAD65*	Ther	Inf. TSA/SAHA to NRM = ↓Ther, ↑H3K9ac at *Gad2, GAD65*	*Zhang et al., 2011*
CFA	↓H3K9/K18ac, ↑class II HDACs	SC		Ther	it class II HDACis =↓Ther, ↑H3K9/K18ac	*Bai et al., 2010*
CFA	↑DNA methylation	SC	↓miR-219, ↑*CamKIIγ*	Mech	it 5-aza = ↓Mech, CamKIIγ, ↑miR-219	*Pan et al., 2014*

Visceral Pain

Model	Mark/Enzyme	Location	Expression	Behavior	Pharmacology	Reference
WAS				VMR	icv TSA = ↓VMR	*Tran et al., 2013*
CORT	↓H3K9ac at *GR*	CeA	↓*GR*, ↑*CRF*	VMR Mech	Inf. TSA/SAHA to CeA =↓VMR, Mech, *CRF* ↑H3K9ac at *GR, GR*	*Tran et al., 2014*
E2	↓H3ac	SC	↓*Grm2*	VMR	it SAHA = ↓VMR, mGluR2 ↑H3K9ac to *Grm2*	*Cao et al., 2014*
MS	↓H4K12ac	SC		VMR	ip SAHA = ↓VMR, ↑H4K12ac	*Moloney et al., 2015*

Fig. 1. Summary of epigenetic changes during various chronic pain conditions and the effects of pharmacological treatment. Downward arrows indicate downregulate or silence, whereas upward arrows indicate upregulate or induce. AA, anacardic acid; AAV, adeno-associated virus; CBP, CREB-binding protein; CORT, corticosterone; CCL, CC-chemokine ligand; CRF, corticotrophin releasing factor; CXCL, CXC chemokine ligand; CXCR, CXC chemokine receptor; E2, estradiol; GLAST, solute carrier family 1 (glial high affinity glutamate transporter), member 3; GLT-1, glutamate transporter-1; Hypoesth, hyoesthesia; icv, intracerebroventricular; Inf, infusion; ip, intraperitoneal; ipl, intraplantar; it, intrathecal; LTC, L-type calcium channel; Mech, mechanical hypersensitivity; mGluR, metabotropic glutamate receptor; MS, maternal separation; NRM, nucleus raphe magnus; po, by mouth; PSNL, partial sciatic nerve ligation; REST, RE1-silencing transcription factor; SC, spinal cord; Ther, thermal hypersensitivity; TRPM, transient receptor potential cation channel subfamily M; WAS, water avoidance stress; VMR, visceromotor response; VPA, valproate.. Modified public domain images (commons.wikimedia.org) of the sagittal brain and neuron are from users Nickbyrd and Looxix, respectively.

on the histone residue modified. For instance, H3K4, K36, and K79 methylation is indicative of active transcriptional states, whereas methylated H3K9 and H4K20 are signifiers of condensed and inactive chromatin (Ng et al., 2009). It is important to note that genes can demonstrate both active and repressive modifications, representing a poised state requiring additional external cues to promote either increased expression or gene silencing.

There a number of enzymes dedicated to modifying histones. Histone acetyltransferases (HATs) are responsible for transferring acetyl groups to histone tail lysine residues. Acetylation is reversed by histone deacetylases (HDACs).

There are four known classes of HDACs: the zinc-dependent classes I, II, and IV, and class III (or sirtuins), which are NAD dependent (Géranton and Tochiki, 2015b). Similarly, there are several known enzymes dedicated responsible for methylating histone residues. Histone methyltransferases generally fall into two classes: lysine methyltransferases and the less well understood protein arginine *N*-methyltransferases (Izzo and Schneider, 2010). Initially thought to be an irreversible modification, histone methylation has been shown to be a dynamic process, with the recent discovery of a number histone demethylases (Cloos et al., 2008).

DNA Modifications. Another key epigenetic mechanism of chromatin regulation and, consequently, gene expression is methylation of cytosines in genomic DNA to produce 5-methylcytosine. Cytosine methylation occurs predominantly at CpG dinucleotides, particularly those within intergenic regions and repetitive sequences such as long and short interspersed nuclear elements (Zamudio and Bourc'his, 2010). Typically, methylation in the regulatory regions of promoters silences gene transcription by preventing transcription factor binding or by recruiting gene-silencing complexes. However, DNA methylation is not an exclusively repressive mark. As with histone modifications, DNA methylation is a complex mechanism that has been shown to promote both gene activation and silencing depending on the surrounding epigenome (Smith and Meissner, 2013).

DNA methylation occurs via DNA methyltransferases (DNMTs). DNMT1 is responsible for the maintenance of methylation patterns as cells divide, whereas DNMT3A and DNMT3B are the enzymes that engage in de novo DNA methylation in response to environmental cues (Smith and Meissner, 2013). DNA demethylation, however, is a much more complex process and is much less understood. DNA methylation was long thought a static mechanism but it has recently been recognized as a more plastic process after the identification of demethylation-mediating proteins such as Gadd45a and the ten-eleven translocation (TET) family proteins, among others (Chen and Riggs 2011).

Evidence for Epigenetic Changes in Preclinical Studies of Pain

In recent years, a significant amount of research examining the involvement of epigenetic processes in human disease has been conducted, resulting in the development of a handful of novel therapeutic agents that target these processes. However, the science of pain epigenetics is still very much in its infancy, with understanding of the links between epigenetics and the transition to, and maintenance of, chronic pain only beginning to emerge (Fig. 1). Consequently, it is not yet clear whether targeting these epigenetic mechanisms is a practical method by which chronic pain can be managed.

Somatic Pain. Most studies investigating epigenetic mechanisms involved in chronic somatic pain have been performed in animal models of inflammatory pain. Generally, inflammation-induced histone modifications contribute to hypersensitivity via dysregulation of HDAC and HAT activity and expression, resulting in hypoacetylation at promoter regions of antinociceptive genes or genes critical to proper pain circuit functionality and the silencing of these genes (Zhang et al., 2011). In the case of DNA methylation, inflammation is capable of inducing hypermethylation at the promoter region of antinociceptive genes and consequently silencing these genes (Pan et al., 2014). Other studies have observed hypomethylation of pronociceptive genes and, therefore, increased expression of those genes in models of inflammatory pain (Qi et al., 2013). Alterations in the levels of epigenetic enzymes such as methylated CpG binding proteins have also been reported in models of inflammatory pain (Zhang et al., 2014).

Epigenetic modifying enzymes themselves (i.e., HDACs, HATs) have also implicated in somatic pain modulation and can affect downstream expression of both pro- and antinociceptive genes. Crow et al. (2015) showed that HDAC4 was essential for appropriate transcriptional responses after injury. Expression of pronociceptive genes Calca and transient receptor potential cation channel subfamily V member 1 (Trpv1) was consistently lower within the DRG sensory neurons in HDAC4 conditional knockout animals compared with their littermate controls (Crow et al., 2015). Furthermore, this downregulation of HDAC4 reduced the sensitivity to capsaicin in vitro and reduced thermal hypersensitivity in the complete Freund's adjuvant (CFA) model of inflammatory pain (Crow et al., 2015). The CFA model has also revealed changes in specific miRNAs. CFA significantly reduced miRNA-219 expression in mice spinal neurons, with bisulfite sequencing revealing CFA-induced hypermethylation of CpG islands in the miR-219 promoter (Pan et al., 2014). Moreover, overexpression of spinal miR-219 prevented and reversed thermal hyperalgesia and mechanical allodynia (Pan et al., 2014).

Other gene targets shown to be epigenetically regulated in the CFA model include BDNF, whereby histone H3 acetylation at the *bdnf* gene promoter was reduced significantly 3 days after CFA injection, with concomitant increases in bdnf mRNA levels and BDNF protein levels (Tao et al., 2014). Others have implicated cystathionine-β-synthetase in the pathophysiology of CFA-induced inflammatory pain in which its promoter was differentially methylated in DRG samples from inflamed rats versus controls (Qi et al., 2013). Further examination revealed significant upregulation of methyl-binding domain protein 4 and growth arrest and DNA damage–inducible protein 45α in inflamed rats (Qi et al., 2013), further implicating DNA methylation as a key mechanism underlying CFA-induced inflammatory pain. A translational study of note that examines DNA methylation utilized a rodent model of lower back pain and reported DNA methylation-induced downregulation of SPARC (secreted protein, acidic, rich in cysteine), an extracellular matrix protein that has been linked to age-dependent disc degeneration (Tajerian et al., 2011).

The most commonly investigated drugs in the context of chronic somatic pain are HDAC inhibitors. Studies indicate that HDAC inhibition or the promotion of histone acetylation in these models is typically analgesic. A study by Zhang et al. (2011) showed that 3 days after intraplantar CFA administration, animals exhibited decreased acetylated H3 at the *Gad2* promoter in the nucleus raphe magnus of the brain resulting in the downregulation of GAD65, an enzyme essential for normal GABAergic neuron functionality. After repeated infusion of HDAC inhibitors such as trichostatin A (TSA) or suberoylanilide hydroxamic acid (SAHA) into the nucleus raphe magnus, CFA-induced thermal hyperalgesia was attenuated and H3 acetylation at *Gad2* was restored

(Zhang et al., 2011). A second study utilizing a mouse CFA pain model found that inflammation promoted upregulation of class II HDACs and downregulation of acetylated H3K9/K18 in the spinal cord. These epigenetic changes, along with inflammatory thermal hyperalgesia, could be prevented with a single intrathecal dose of a number of class II HDAC inhibitors 30 minutes prior to CFA administration or reversed with an intrathecal dose of these inhibitors at 1, 5, and 25 hours after CFA administration (Bai et al., 2010). Treatment with demethylation agent 5′-aza-2′-deoxycytidine (5-aza) has also shown efficacy in the CFA model, with marked reductions in pain behavior and spinal neuronal sensitization (Pan et al., 2014); however, further data on the therapeutic potential of DNA methylation are limited.

Visceral Pain. Few studies have addressed the epigenetics of chronic visceral pain. Similar to somatic pain, evidence suggests that the maintenance of chronic visceral pain is a combination of histone modifications and DNA methylation at various levels of the pain pathway. For example, studies investigating models of stress or pharmacologically induced visceral hypersensitivity have found changes in acetylated histone-promoter interactions in the brain and spinal cord and concomitant dysregulation of the related pro- and antinociceptive genes in these tissues (Tran et al., 2013, 2015; Hong et al., 2015). Similarly, stress-induced visceral pain has also been linked to alterations in DNA methylation patterns within the brain, leading to increased expression of pronociceptive neurotransmitters (Tran et al., 2013).

There have also been some recent insights into the role that miRNAs play in experimental visceral pain models of chronic cystitis and esophageal reflux disease, with several miRNAs identified in the development of chronic visceral pain (Sengupta et al., 2013; Zhang and Banerjee, 2015). However, evidence directly linking these miRNAs to visceral pain behaviors is currently lacking. In another study, Zhou et al. (2009) investigated the effects of miR-29 on increased intestinal permeability, which has previously been associated with visceral hypersensitivity (Zhou and Verne, 2011; Camilleri et al., 2012). After experimentally inducing colitis or exposing wild-type mice to a stressor they observed an upregulation of miR-29a and miR-29b along with increased intestinal permeability in these animals. In *Mir29*$^{-/-}$ mice, however, this colitis- or stress-induced intestinal permeability was greatly diminished. Finally, in microarray and permeability experiments, they showed that miR-29a/b target Claudin-1 and nuclear factor-κB–repressing factor mRNA for degradation, thus increasing intestinal permeability (Zhou et al., 2015a).

HDAC inhibitors are the most common epigenetic drugs to be investigated as potential therapeutics for chronic visceral pain. The studies examining HDAC inhibitors report that these drugs significantly improve outcomes in these models. Intrathecal administration of SAHA to rats with 17β-estradiol–induced visceral hypersensitivity stimulated hyperacetylation of H3 and increased binding of H3K9ac to the promoter region of the metabotropic glutamate receptor 2 gene *Grm2*. This increased association between H3K9ac and *Grm2*, in conjunction with binding of activated estrogen receptor α, leads to the upregulation of metabotropic glutamate receptor 2 in the spinal cord and the attenuation of visceral hypersensitivity (Cao et al., 2015). Tran et al. (2013) showed that visceral hypersensitivity in rats resulting from chronic water avoidance stress could be prevented by daily intracerebroventricular infusions of TSA during the course of the stress paradigm. In a second study, this group used a pharmacologically induced model of visceral hypersensitivity to examine histone deacetylation in the brain. This study showed that prolonged exposure of the central nucleus of the amygdala (CeA) to corticosterone to produce visceral hypersensitivity is associated with deacetylation of H3K9 and its decreased association with the 1_7 region of the glucocorticoid receptor (GR) promoter within the CeA, leading to a downregulation of GR and, in turn, upregulation of the pronociceptive corticotrophin releasing factor. Bilateral infusions of TSA and SAHA into the CeA reversed these changes to the epigenome and attenuated visceral hypersensitivity (Tran et al., 2015). Another study examining the role of epigenetic modulation of GR in visceral pain showed that water avoidance stress increases methylation of the GR promoter and reduces its expression in a regional-specific manner in DRG neurons. The authors also found that stress upregulated DNMT1-associated methylation of the cannabinoid receptor promoter, increased expression of the HAT EP300, increased histone acetylation at the TRPV1 promoter, and increased expression of the TRPV1 receptor in DRG neurons. They also showed that knockdown of both DNMT1 and EP300 in L6-S2 DRG neurons reduced both DNA methylation and histone acetylation, respectively, which prevented stress-induced visceral pain (Hong et al., 2015). Finally, chronic visceral hypersensitivity induced by early-life stress has been shown to induce histone deacetylation in the lumbosacral spinal cord, with maternally separated rats showing a decrease in H4K12 acetylation that correlated with visceral hypersensitivity in adulthood. Moreover, peripheral treatment with SAHA attenuated the stress-induced effects (Moloney et al., 2015).

Neuropathic Pain. Many studies have investigated epigenetic modulation in models of neuropathic pain. To date, most have focused on histone modifications and report changes at all levels of the pain pathway. Typically, nerve injury induces alterations in acetylation status of H3 and H4, leading to the dysregulation of a myriad of genes responsible for proper neuronal function and pain perception. For example, the upregulation of pronociceptive genes has been linked to histone hyperacetylation in the spinal cord after nerve injury (Zhu et al., 2014). Other studies have shown that injury causes neuroinflammation-induced neuropathic pain through marked histone modifications and increased expression of multiple proinflammatory genes in leukocytes infiltrating the injured tissue (Kiguchi et al., 2012, 2013). Injury-induced neuropathic pain has also been linked to histone hypoacetylation in the DRG, which leads to decreased expression of genes essential to C-fiber functionality (Matsushita et al., 2013). In addition to changing histone acetylation patterns, nerve injury also alters histone methylation. Specifically, Laumet et al. (2015) showed that spinal nerve ligation (SNL) decreases the expression of several potassium channels and their related genes through increased expression of the histone methyltransferase G9a, resulting in neuropathic pain symptoms.

As with the previously outlined studies, HDAC inhibitors and HAT inhibitors are the most commonly used epigenetic drugs in neuropathic pain studies. Although the mechanisms underlying the various models of neuropathic pain are varied

and complex, the administration of HDAC inhibitors has generally produced positive outcomes in regard to pain behaviors. It has been demonstrated that partial sciatic nerve ligation (PSNL)–induced hypoesthesia could be prevented by administration of the HDAC inhibitors valproate and TSA. The investigators report that PSNL downregulates ion channels Nav1.8 and Kv4.3, which are extensively involved in pain perception, as well as *TRPV1*, transient receptor potential cation channel subfamily M member 8, and calcitonin gene-related peptide gene expression in DRGs. Pretreatment with HDAC inhibitors maintained H3 and H4 acetylation at these genes, thereby promoting their expression and normal C-fiber functionality (Matsushita et al., 2013). Another study showed that intrathecal administration of HDAC inhibitor MS-275 (*N*-[[4-[[(2-aminophenyl)amino]carbonyl]phenyl]methyl]-3-pyridinylmethyl ester, carbamic acid) prevented SNL-induced mechanical and thermal hyperalgesia by increasing acetylation of H3K9 and altering HDAC1 expression in the dorsal horn of the spinal cord (Denk et al., 2013). Finally, valproate attenuated SNL-induced mechanical hyperalgesia via the restoration of glutamate transporter-1 in the spinal cord, although the authors did not specifically investigate epigenetic changes in this study (Yoshizumi et al., 2013). HAT inhibitors have also proven to be particularly effective at improving outcomes in models of neuropathic pain. After PSNL, the HAT inhibitor anacardic acid reportedly decreased acetylation of H3K9 at the promoters of macrophage inflammatory protein 2 and CXC chemokine receptor type 2 in macrophages and neutrophils infiltrating the injured tissue, thereby attenuating PSNL-induced thermal hyperalgesia (Kiguchi et al., 2012). The same authors also demonstrated that CC-chemokine ligands 2 and 3, two other important contributors to peripheral sensitization after injury, could be downregulated by anacardic acid through a similar epigenetic mechanism involving H3K9 and H3K4me3 (Kiguchi et al., 2013).

In a separate study, the chronic constriction injury (CCI) rat model revealed that p300 (transcriptional coactivator and HAT E1A binding protein) expression was increased in the lumbar spinal cord on day 14 after CCI. The treatment with intrathecal p300 short hairpin RNA or C646 (4-[4-[[5-(4,5-dimethyl-2-nitrophenyl)-2-furanyl]methylene]-4,5-dihydro-3-methyl-5-oxo-1*H*-pyrazol-1-yl]benzoic acid), an inhibitor of p300 acetyltransferase, reversed CCI-induced mechanical allodynia and thermal hyperalgesia (Zhu et al., 2012). This work was then expanded on in a following study wherein curcumin, which has known HAT inhibitory properties, was shown to effectively attenuate neuropathic pain by silencing pronociceptive genes *Bdnf* and cyclooxygenase (COX)-2 by reducing the binding of p300/CREB-binding protein, H3K9ac, and H4K5ac to their promoters (Zhu et al., 2014). To date, only one study has investigated the effects of targeting DNA methylation in the context of neuropathic pain models. This study primarily focused on the use of 5-aza to antagonize DNMTs after injury, and the authors showed that 5-aza attenuated mechanical and thermal hyperalgesia by reversing CCI-induced expression of methyl CpG binding protein 2 and global DNA methylation (Wang et al., 2011).

Several studies have examined the effects of targeting specific ncRNAs in the treatment of neuropathic pain, although only a few have directly linked the expression of these RNAs to pain behavior. Sakai and Suzuki (2014) observed a decrease in miR-7a in the DRGs of SNL and CCI rats. Using an adeno-associated virus vector to restore miR-7a in DRGs, they were able to attenuate mechanical and thermal hypersensitivity in both models and identified the $\beta 2$ subunit of the voltage-gated sodium ion channel as a potential target for miR-7a (Sakai and Suzuki, 2014). Another investigation showed that miR-103 expression was decreased in the dorsal horn of SNL rats, whereas the expression of the Cav1.2-comprising L-type calcium channel was increased. The investigators then found that miR-103 regulates the expression of three subunits of the Cav1.2 L-type calcium channel and that knockdown of miR-103 using small interfering RNA in naïve rats results in mechanical hypersensitivity. Moreover, intrathecal administration of miR-103 significantly reduced SNL-induced hypersensitivity (Favereaux et al., 2011). lncRNAs have also been implicated as contributors to neuropathic pain. Specifically, the lncRNA identified as antisense RNA for voltage-dependent potassium channel *Kcna2* mRNA was increased in the DRGs of SNL rats. Mimicking this increase in Kcna2 antisense in naïve animals produced neuropathic pain symptoms, whereas blocking the increase attenuated the development of nerve injury–induced neuropathic pain (Zhao et al., 2013).

Evidence for Epigenetic Changes in Clinical Studies of Pain

The data from clinical studies to date are sparse, with few publications specifically demonstrating changes in the epigenetic signature of human subjects. Interestingly, epigenetic processes themselves, specifically DNA methylation, have been shown to occur after chronic opioid use in pain patients. The study by Doehring et al. (2013) showed increased DNA methylation in a cohort of opioid-treated versus nonopioid-treated pain patients.

Changes in DNA methylation were apparent in whole blood from 50 healthy identical twins with discordant thermal pain sensitivities compared with 50 unrelated individuals (Bell et al., 2014). The authors identified that nine differentially methylated regions in the twin cohort correlated with pain sensitivity. These included targets previously implicated in pain processing (transient receptor potential channels glutamate receptor, ionotropic, N-methyl D-Aspartate 1, doublecortin-like kinase 1) but also new targets (ankyrin-3). To advance these exciting findings, future studies could apply similar approaches in patients with various forms of chronic pain to further catalog epigenetic marks. These studies would begin to investigate whether epigenetic changes can explain chronic pain in specific patient populations.

A limited body of evidence exists to support altered epigenetic processes in chronic visceral pain disorders. Gastrointestinal visceral pain such as that associated with irritable bowel syndrome (IBS) has also been associated with altered epigenetic processes linked to pronociceptive gene expression. Colonic biopsies from this patient population revealed reduced miR-199a/b expression in patients with diarrhea-predominant IBS compared with controls. Moreover, this correlated directly with both increased visceral pain scores and TRPV1 expression (Zhou et al., 2015b). Other miRNAs have also been implicated in patients with IBS, including hsa-miR-150 and hsa-miR-342-3p, which were both

found to be significantly increased in the whole blood of patients with IBS versus healthy controls (Fourie et al., 2014). Both of these miRNAs are implicated in pain processes and inflammation. In another condition characterized by severe visceral pain, Wu et al. (2006) proposed that endometriosis is a epigenetic disease, showing that the promoter region of progesterone receptor B, but not progesterone receptor A, is hypermethylated. Moreover, Wu et al. (2005) previously showed aberrant methylation of HOXA10 in the eutopic endometrium of women with endometriosis. Although these findings do not directly involve pain circuitry, they provide further evidence for altered epigenetic processes in chronic pain disorders.

In patients with lower back pain caused by disc degeneration, reduced SPARC expression was apparent in the intervertebral discs and DNA methylation was altered (Tajerian et al., 2011). The authors show that within the promoter region of the SPARC gene, there are significant increases in DNA methylation, which may underpin decreases in the SPARC gene expression. Following on from this ex vivo work, the authors performed in vitro experiments aimed to further tease apart the exact mechanism, showing that methylation of both the human and murine promoter silences SPARC promoter activity (Tajerian et al., 2011).

Current Approaches to Treat Chronic Pain

As alluded to earlier, the etiology of chronic pain is complex and thus treatment has many obstacles due to its persistent nature. Current therapeutic approaches have modest efficacy and poor side effect profiles and often fall short in directly treating the underlying pathologic nociceptive signaling. NSAIDs are the most common treatment for both acute pain and chronic pain. These compounds act through inhibition of COX-1 and COX-2 activity, thus preventing the synthesis of prostaglandins and thromboxanes (Buvanendran and Lipman, 2010; Buvanendran, 2013). Some of the most commonly used NSAIDs include aspirin, ibuprofen, ketoprofen, and naproxen. The most typical side effects of NSAIDs include heartburn and nausea. However, in the context of chronic pain, frequent or long-term use of NSAIDs may lead to stomach ulcers or high blood pressure. Acetaminophen is another widely used pain medication with a mode of action that involves inhibition of COX-1 and COX-2 (Graham et al., 2013). However, acetaminophen is not classified as an NSAID because it exhibits only modest anti-inflammatory activity. However, when administered in combination with opioid analgesics, acetaminophen is used in the management of more severe pain. Although it is well tolerated,

TABLE 1
Summary of HDAC and DNMT inhibitors

Epigenetic Modifier	Classification	Compound	Chemical Name	Target
HDAC inhibitors	Hydroxamates	SAHA (vorinostat)		Pan inhibitor
		PXD101 (belinostat)	(*E*)-*N*-hydroxy-3-[3-(phenylsulfamoyl) phenyl]prop-2-enamide	Pan inhibitor
		LBH589 (panobinostat)	(*E*)-*N*-hydroxy-3-[4-[[2-(2-methyl-1*H*-indol-3-yl)ethylamino]methyl]phenyl] prop-2-enamide	Classes I and II
		ITF2357 (givinostat)	[6-(diethylaminomethyl)naphthalen-2-yl]methyl-*N*-[4-(hydroxycarbamoyl) phenyl]carbamate;hydrate;hydrochloride	Pan inhibitor
		4SC-201 (resminostat)	(*E*)-3-[1-[4-[(dimethylamino)methyl] phenyl]sulfonylpyrrol-3-yl]-*N*-hydroxyprop-2-enamide	Pan inhibitor
		PCI-24781 (abexinostat)	3-[(dimethylamino)methyl]-*N*-[2-[4-(hydroxycarbamoyl)phenoxy] ethyl]-1-benzofuran-2-carboxamide	Classes I and II
	Cyclic peptides	Depsipeptide/FK228	(1*S*,4*S*,7*Z*,10*S*,16*E*,21*R*)-7-ethylidene-4, 21-di(propan-2-yl)-2-oxa-12,13-dithia-5, 8,20,23-tetrazabicyclo[8.7.6]tricos-16-ene-3,6,9,19,22-pentone	Class I
	Benzamides	MS-275 (entinostat)	*N*-[[4-[[(2-aminophenyl)amino]carbonyl] phenyl]methyl]-3-pyridinylmethyl ester, carbamic acid	Class I
		MGCD0103 (mocetinostat)	*N*-(2-aminophenyl)-4-[[(4-pyridin-3-y lpyrimidin-2-yl)amino]methyl]benzamide	Class I
		M344	4-(dimethylamino)-*N*-[7-(hydroxyamino)-7-oxoheptyl]benzamide	Class I
	Aliphatic fatty acids	Valproate		Classes I and IIa
		Butyrate		Classes I and IIa
	Unknown mechanism	CI-994	4-acetamido-*N*-(2-aminophenyl) benzamide	HDAC1, HDAC2
		BML-210	*N*′-(2-aminophenyl)-*N*-phenyloctanediamide	HDAC 1–5 and 7
		NVP-LAQ824	(*E*)-*N*-hydroxy-3-[4-[[2-hydroxyethyl-[2-(1*H*-indol-3-yl)ethyl]amino]methyl] phenyl]prop-2-enamide	Unknown
DNMT inhibitors		5-Azacitidine		Pan inhibitor
		5-aza-2′-deoxycytidine		Pan inhibitor
		1-β-D-arabinofuranosyl-5-azacytosine		Pan inhibitor
		Dihydro-5-azacytidine		Pan inhibitor
		MG98		DNMT1

acetaminophen can alter liver function when combined with alcohol, and acute overdoses of acetaminophen can cause potentially fatal liver damage (Jaeschke et al., 2014).

For moderate to severe chronic pain, opioidergic compounds (de Leon-Casasola, 2013), including morphine and oxycodone, are typically prescribed. Working through the μ-δ heterodimer, these compounds are generally effective (Pasternak and Pan, 2011). However, common side effects, including constipation, dizziness, lightheadedness, drowsiness, nausea, and vomiting, severely limit their usefulness. More importantly, the long-term daily use of opioid analgesics leads to physical dependence and even hyperalgesia (Bruehl et al., 2013).

Alternative approaches for chronic pain management include antidepressants (serotonin-norepinephrine reuptake inhibitors), calcium channel blockers, α_2-adrenergic receptor agonists, and GABA receptor agonists (Eisenberg and Peterson, 2010; Jackson and Argoff, 2010; Murinson, 2013; Nicholson, 2013). A spectrum of side effects is associated with these compounds; the most common include sedation, dizziness, dry mouth, edema, withdrawal symptoms if discontinued, and severe hypotension. Taken together, the current treatment options for chronic pain are unsatisfactory with low efficacy and are associated with a host of adverse side effects, thus the necessity for the development of novel therapeutics remains an urgent medical need.

Epigenetic Modifiers as Therapeutic Targets for Chronic Pain

Epigenetics offers the opportunity to remodel an aberrant signaling cascade, which may underpin the persistent experience of pain. Over the last 2 decades, there has been rapid advancement of pain genetics and these studies have provided a solid foundation for the emergence of pain epigenetics. However, there are still many obstacles to overcome to develop this concept into an effective treatment approach. Here we will summarize the potential of epigenetic therapies but also the current limitations. The concept of using epigenetic therapies for the treatment of chronic pain remains unproven but evidence to date suggests that this approach may offer more benefit to patients over the current analgesic regiments. Identifying a specific epigenetic mark or landscape that is unique to the disease state is critical for the development of an effective therapy. The idea that an epigenetic therapeutic that could target a specific pathway to rectify the underlying cause of chronic pain, as opposed to simply treating the symptom, is very attractive. Identifying a discrete epigenetic signature, which is responsible for chronic pain in a patient population, and designing compounds to directly target this signature will undoubtedly be a huge advancement in the field. Epigenetic drugs offer the opportunity to rectify the underlying pathology of chronic pain and not just attenuate the symptom.

Currently, the application and availability of epigenetic-based therapies used clinically for a variety of disorders and diseases is limited. Both HDAC inhibitors and DNMT inhibitors are being investigated as anticancer agents; however, therapies for the treatment of non–life-threatening states of persistent pain have yet to be developed. Therapies that manipulate single epigenetic marks that subsequently target a specific gene should be considered for development. Over the last decades, investigators focused on single gene expression differences or mutations that are involved in nociception. Future approaches should focus on the development of locally acting therapeutics targeting the epigenetic mechanism(s) that have been identified to contribute to chronic pain. For example, identifying specific genes within the nociceptive circuitry will allow us to use tools such as small interfering RNA to target the aberrant gene in a discrete manner. Moreover, the epigenome itself could be targeted with designer DNA binding proteins developed from transcriptional activator-like effectors or zinc finger proteins (Day, 2014). The use of miRNA-based therapies is also of interest. Indeed, a limited number of studies have identified specific miRNAs that are altered in chronic pain and are amenable to manipulation via mimics to induce analgesic effects (Sun et al., 2012; Willemen et al., 2012; Pan et al., 2014; Lu et al., 2015).

The current epigenetic modifying compounds are nonspecific and nonselective, acting both centrally and peripherally as well as at many epigenetic sites. The changes in the epigenome during the development of persistent pain are also extraordinarily complex and dynamic. Moreover, the resulting epigenetic mark largely depends on the injury or insult sustained as well as the past experiences of each individual. With this in mind, the current epigenetic drugs in development and in use for the treatment of cancer (Copeland et al., 2009; New et al., 2012) that may potentially be investigated in the context of pain are highly nonspecific HDAC inhibitors and DNMT inhibitors (summarized in Table 1), which have numerous side effects and seem unsuitable for long-term treatment of chronic pain.

Summary

Chronic pain represents a large unmet medical need and it is clear that alternative therapies are required with novel mechanisms of action. Having reviewed the primary mechanisms of epigenetic regulation and the recent findings in the field of epigenetics and chronic pain, it is apparent that new therapies targeting epigenetic marks represent a legitimate approach. However, this strategy for treating chronic pain is currently limited by the paucity of selective compounds with a side effect profile that is suitable to support chronic use by patients often with non–life- threatening but severely debilitating chronic pain. Thus, continuing to build upon our knowledge of genetic and epigenetic mechanisms in pain pathways will undoubtedly aid in our understanding and development of novel therapeutics to treat chronic pain disorders.

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Wrote or contributed to the writing of the manuscript: Ligon, Moloney, Greenwood-Van Meerveld.

References

Almeida TF, Roizenblatt S, and Tufik S (2004) Afferent pain pathways: a neuroanatomical review. *Brain Res* **1000**:40–56.

Bai G, Wei D, Zou S, Ren K, and Dubner R (2010) Inhibition of class II histone deacetylases in the spinal cord attenuates inflammatory hyperalgesia. *Mol Pain* **6**: 51.

Bell JT, Loomis AK, Butcher LM, Gao F, Zhang B, Hyde CL, Sun J, Wu H, Ward K, and Harris J, et al.; MuTHER Consortium (2014) Differential methylation of the TRPA1 promoter in pain sensitivity. *Nat Commun* **5**:2978.

Bernstein BE, Meissner A, and Lander ES (2007) The mammalian epigenome. *Cell* **128**:669–681.

Besson JM (1999) The neurobiology of pain. *Lancet* **353**:1610–1615.

Bonasio R and Shiekhattar R (2014) Regulation of transcription by long noncoding RNAs. *Annu Rev Genet* **48**:433–455.
Breivik H, Collett B, Ventafridda V, Cohen R, and Gallacher D (2006) Survey of chronic pain in Europe: prevalence, impact on daily life, and treatment. *Eur J Pain* **10**:287–333.
Bruehl S, Apkarian AV, Ballantyne JC, Berger A, Borsook D, Chen WG, Farrar JT, Haythornthwaite JA, Horn SD, and Iadarola MJ, et al. (2013) Personalized medicine and opioid analgesic prescribing for chronic pain: opportunities and challenges. *J Pain* **14**:103–113.
Buchheit T, Van de Ven T, and Shaw A (2012) Epigenetics and the transition from acute to chronic pain. *Pain Med* **13**:1474–1490.
Buvanendran A (2013) Nonsteroidal anti-inflammatory drugs, in *Comprehensive Treatment of Chronic Pain by Medical, Interventional, and Integrative Approaches* (Deer TR, Leong MS, Buvanendran A, Gordin V, Kim PS, Panchal SJ, and Ray AL eds) pp 35–44, Springer-Verlag, New York.
Buvanendran A and Lipman AG (2010) Nonsteroidal anti-inflammatory drugs and acetaminophen, in *Bonica's Management of Pain*, 4th ed (Fishman SM, Ballantyne JC, and Rathmell JP, eds) pp 1157–1171, Lippincott Williams & Wilkins, Baltimore, MD.
Camilleri M, Madsen K, Spiller R, Greenwood-Van Meerveld B, and Verne GN (2012) Intestinal barrier function in health and gastrointestinal disease. *Neurogastroenterol Motil* **24**:503–512.
Cao DY, Bai G, Ji Y, and Traub RJ (2015) Epigenetic upregulation of metabotropic glutamate receptor 2 in the spinal cord attenuates oestrogen-induced visceral hypersensitivity. *Gut* **64**:1913–1920.
Cauda F, Palermo S, Costa T, Torta R, Duca S, Vercelli U, Geminiani G, and Torta DM (2014) Gray matter alterations in chronic pain: A network-oriented meta-analytic approach. *Neuroimage Clin* **4**:676–686.
Cervero F (1995) Visceral pain: mechanisms of peripheral and central sensitization. *Ann Med* **27**:235–239.
Cervero F (2000) Visceral pain-central sensitisation. *Gut* **47** (Suppl 4):iv56–iv57; discussion iv58.
Chen ZX and Riggs AD (2011) DNA methylation and demethylation in mammals. *J Biol Chem* **286**:18347–18353.
Cloos PA, Christensen J, Agger K, and Helin K (2008) Erasing the methyl mark: histone demethylases at the center of cellular differentiation and disease. *Genes Dev* **22**:1115–1140.
Copeland RA, Solomon ME, and Richon VM (2009) Protein methyltransferases as a target class for drug discovery. *Nat Rev Drug Discov* **8**:724–732.
Crow M, Khovanov N, Kelleher JH, Sharma S, Grant AD, Bogdanov Y, Wood JN, McMahon SB, and Denk F (2015) HDAC4 is required for inflammation-associated thermal hypersensitivity. *FASEB J* **29**:3370–3378.
DaSilva AF, Becerra L, Pendse G, Chizh B, Tully S, and Borsook D (2008) Colocalized structural and functional changes in the cortex of patients with trigeminal neuropathic pain. *PLoS One* **3**:e3396.
Day JJ (2014) New approaches to manipulating the epigenome. *Dialogues Clin Neurosci* **16**:345–357.
de Leon-Casasola OA (2013) Opioids for chronic pain: new evidence, new strategies, safe prescribing. *Am J Med* **126** (Suppl 1):S3–S11.
Denk F, Huang W, Sidders B, Bithell A, Crow M, Grist J, Sharma S, Ziemek D, Rice AS, and Buckley NJ, et al. (2013) HDAC inhibitors attenuate the development of hypersensitivity in models of neuropathic pain. *Pain* **154**:1668–1679.
Doehring A, Oertel BG, Sittl R, and Lötsch J (2013) Chronic opioid use is associated with increased DNA methylation correlating with increased clinical pain. *Pain* **154**:15–23.
Eisenberg E and Peterson D (2010) Neuropathic pain pharmacotherapy, in *Bonica's Management of Pain*, 4th ed (Fishman SM, Ballantyne JC, and Rathmell JP, eds) pp 1194–1207, Lippincott Williams & Wilkins, Baltimore, MD.
Ellingson BM, Mayer E, Harris RJ, Ashe-McNally C, Naliboff BD, Labus JS, and Tillisch K (2013) Diffusion tensor imaging detects microstructural reorganization in the brain associated with chronic irritable bowel syndrome. *Pain* **154**: 1528–1541.
ENCODE Project Consortium (2012) An integrated encyclopedia of DNA elements in the human genome. *Nature* **489**:57–74.
Farh KK, Grimson A, Jan C, Lewis BP, Johnston WK, Lim LP, Burge CB, and Bartel DP (2005) The widespread impact of mammalian MicroRNAs on mRNA repression and evolution. *Science* **310**:1817–1821.
Favereaux A, Thoumine O, Bouali-Benazzouz R, Roques V, Papon MA, Salam SA, Drutel G, Léger C, Calas A, and Nagy F, et al. (2011) Bidirectional integrative regulation of Cav1.2 calcium channel by microRNA miR-103: role in pain. *EMBO J* **30**:3830–3841.
Fourie NH, Peace RM, Abey SK, Sherwin LB, Rahim-Williams B, Smyser PA, Wiley JW, and Henderson WA (2014) Elevated circulating miR-150 and miR-342-3p in patients with irritable bowel syndrome. *Exp Mol Pathol* **96**:422–425.
Géranton SM and Tochiki KK (2015a) Could targeting epigenetic processes relieve chronic pain states? *Curr Opin Support Palliat Care* **9**:138–146.
Géranton SM and Tochiki KK (2015b) Regulation of gene expression and pain states by epigenetic mechanisms. *Prog Mol Biol Transl Sci* **131**:147–183.
Goldberg DS and McGee SJ (2011) Pain as a global public health priority. *BMC Public Health* **11**:770.
Gräff J, Kim D, Dobbin MM, and Tsai LH (2011) Epigenetic regulation of gene expression in physiological and pathological brain processes. *Physiol Rev* **91**: 603–649.
Graham GG, Davies MJ, Day RO, Mohamudally A, and Scott KF (2013) The modern pharmacology of paracetamol: therapeutic actions, mechanism of action, metabolism, toxicity and recent pharmacological findings. *Inflammopharmacology* **21**: 201–232.
Hong S, Zheng G, and Wiley JW (2015) Epigenetic regulation of genes that modulate chronic stress-induced visceral pain in the peripheral nervous system. *Gastroenterology* **148**:148.e7–157.e7.
Institute of Medicine (2011) *Relieving Pain in America: A Blueprint for Transforming Prevention, Care, Education, and Research*, National Academies Press, Washington, DC.
Irimia A, Labus JS, Torgerson CM, Van Horn JD, and Mayer EA (2015) Altered viscerotopic cortical innervation in patients with irritable bowel syndrome. *Neurogastroenterol Motil* **27**:1075–1081.
Izzo A and Schneider R (2010) Chatting histone modifications in mammals. *Brief Funct Genomics* **9**:429–443.
Jackson KC and Argoff CE (2010) Skeletal muscle relaxants and analgesic balms, in *Bonica's Management of Pain*, 4th ed (Fishman SM, Ballantyne JC, and Rathmell JP, eds) pp 1188–1193, Lippincott Williams & Wilkins, Baltimore, MD.
Jaeschke H, Xie Y, and McGill MR (2014) Acetaminophen-induced liver injury: from animal models to humans. *J Clin Transl Hepatol* **2**:153–161.
Johnson AC and Greenwood-Van Meerveld B (2014) Stress-induced pain: a target for the development of novel therapeutics. *J Pharmacol Exp Ther* **351**:327–335.
Karpova NN (2014) Role of BDNF epigenetics in activity-dependent neuronal plasticity. *Neuropharmacology* **76**:709–718.
Kiguchi N, Kobayashi Y, Maeda T, Fukazawa Y, Tohya K, Kimura M, and Kishioka S (2012) Epigenetic augmentation of the macrophage inflammatory protein 2/C-X-C chemokine receptor type 2 axis through histone H3 acetylation in injured peripheral nerves elicits neuropathic pain. *J Pharmacol Exp Ther* **340**:577–587.
Kiguchi N, Kobayashi Y, Saika F, and Kishioka S (2013) Epigenetic upregulation of CCL2 and CCL3 via histone modifications in infiltrating macrophages after peripheral nerve injury. *Cytokine* **64**:666–672.
Kuner R (2010) Central mechanisms of pathological pain. *Nat Med* **16**:1258–1266.
Laumet G, Garriga J, Chen SR, Zhang Y, Li DP, Smith TM, Dong Y, Jelinek J, Cesaroni M, and Issa JP, et al. (2015) G9a is essential for epigenetic silencing of K(+) channel genes in acute-to-chronic pain transition. *Nat Neurosci* **18**:1746–1755.
Lu Y, Cao DL, Jiang BC, Yang T, and Gao YJ (2015) MicroRNA-146a-5p attenuates neuropathic pain via suppressing TRAF6 signaling in the spinal cord. *Brain Behav Immun* **49**:119–129.
Luo C, Kuner T, and Kuner R (2014) Synaptic plasticity in pathological pain. *Trends Neurosci* **37**:343–355.
Mansour AR, Baliki MN, Huang L, Torbey S, Herrmann KM, Schnitzer TJ, and Apkarian AV (2013) Brain white matter structural properties predict transition to chronic pain. *Pain* **154**:2160–2168.
Matsushita Y, Araki K, Omotuyi Oi, Mukae T, and Ueda H (2013) HDAC inhibitors restore C-fibre sensitivity in experimental neuropathic pain model. *Br J Pharmacol* **170**:991–998.
Moloney RD, Stilling RM, Dinan TG, and Cryan JF (2015) Early-life stress-induced visceral hypersensitivity and anxiety behavior is reversed by histone deacetylase inhibition. *Neurogastroenterol Motil* **27**:1831–1836.
Murinson BB (2013) The role of antidepressants in the treatment of chronic pain, in *Comprehensive Treatment of Chronic Pain by Medical, Interventional, and Integrative Approaches* (Deer TR, Leong MS, Buvanendran A, Gordin V, Kim PS, Panchal SJ, and Ray AL eds) pp 45–51, Springer-Verlag, New York.
New M, Olzscha H, and La Thangue NB (2012) HDAC inhibitor-based therapies: can we interpret the code? *Mol Oncol* **6**:637–656.
Ng SS, Yue WW, Oppermann U, and Klose RJ (2009) Dynamic protein methylation in chromatin biology. *Cell Mol Life Sci* **66**:407–422.
Nicholson BD (2013) Anticonvulsant medications for the treatment of neuropathic and "functional" pain, in *Comprehensive Treatment of Chronic Pain by Medical, Interventional, and Integrative Approaches* (Deer TR, Leong MS, Buvanendran A, Gordin V, Kim PS, Panchal SJ, and Ray AL eds) pp 53–59, Springer-Verlag, New York.
Pan Z, Zhu LJ, Li YQ, Hao LY, Yin C, Yang JX, Guo Y, Zhang S, Hua L, and Xue ZY, et al. (2014) Epigenetic modification of spinal miR-219 expression regulates chronic inflammation pain by targeting CaMKIIγ. *J Neurosci* **34**:9476–9483.
Pasternak GW and Pan YX (2011) Mix and match: heterodimers and opioid tolerance. *Neuron* **69**:6–8.
Qi F, Zhou Y, Xiao Y, Tao J, Gu J, Jiang X, and Xu GY (2013) Promoter demethylation of cystathionine-β-synthetase gene contributes to inflammatory pain in rats. *Pain* **154**:34–45.
Reichling DB and Levine JD (2009) Critical role of nociceptor plasticity in chronic pain. *Trends Neurosci* **32**:611–618.
Sakai A and Suzuki H (2014) Emerging roles of microRNAs in chronic pain. *Neurochem Int* **77**:58–67.
Sengupta JN, Pochiraju S, Kannampalli P, Bruckert M, Addya S, Yadav P, Miranda A, Shaker R, and Banerjee B (2013) MicroRNA-mediated GABA Aα-1 receptor subunit down-regulation in adult spinal cord following neonatal cystitis-induced chronic visceral pain in rats. *Pain* **154**:59–70.
Smith ZD and Meissner A (2013) DNA methylation: roles in mammalian development. *Nat Rev Genet* **14**:204–220.
Sun Y, Li XQ, Sahbaie P, Shi XY, Li WW, Liang DY, and Clark JD (2012) miR-203 regulates nociceptive sensitization after incision by controlling phospholipase A2 activating protein expression. *Anesthesiology* **117**:626–638.
Tajerian M, Alvarado S, Millecamps M, Dashwood T, Anderson KM, Haglund L, Ouellet J, Szyf M, and Stone LS (2011) DNA methylation of SPARC and chronic low back pain. *Mol Pain* **7**:65.
Tao W, Chen Q, Zhou W, Wang Y, Wang L, and Zhang Z (2014) Persistent inflammation-induced up-regulation of brain-derived neurotrophic factor (BDNF) promotes synaptic delivery of α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor GluA1 subunits in descending pain modulatory circuits. *J Biol Chem* **289**:22196–22204.
Tran L, Chaloner A, Sawalha AH, and Greenwood Van-Meerveld B (2013) Importance of epigenetic mechanisms in visceral pain induced by chronic water avoidance stress. *Psychoneuroendocrinology* **38**:898–906.
Tran L, Schulkin J, Ligon CO, and Greenwood-Van Meerveld B (2015) Epigenetic modulation of chronic anxiety and pain by histone deacetylation. *Mol Psychiatry* **20**:1219–1231.

Tsang A, Von Korff M, Lee S, Alonso J, Karam E, Angermeyer MC, Borges GL, Bromet EJ, Demytteneare K, and de Girolamo G, et al. (2008) Common chronic pain conditions in developed and developing countries: gender and age differences and comorbidity with depression-anxiety disorders. *J Pain* **9**:883–891.
Waddington CH (1942) Canalization of development and the inheritance of acquired characters. *Nature* **150**:563–565.
Wang Y, Liu C, Guo QL, Yan JQ, Zhu XY, Huang CS, and Zou WY (2011) Intrathecal 5-azacytidine inhibits global DNA methylation and methyl- CpG-binding protein 2 expression and alleviates neuropathic pain in rats following chronic constriction injury. *Brain Res* **1418**:64–69.
Wilder-Smith CH (2011) The balancing act: endogenous modulation of pain in functional gastrointestinal disorders. *Gut* **60**:1589–1599.
Willemen HL, Huo XJ, Mao-Ying QL, Zijlstra J, Heijnen CJ, and Kavelaars A (2012) MicroRNA-124 as a novel treatment for persistent hyperalgesia. *J Neuroinflammation* **9**:143.
Woolf CJ (2011) Central sensitization: implications for the diagnosis and treatment of pain. *Pain* **152** (Suppl):S2–S15.
Woolf CJ and Salter MW (2000) Neuronal plasticity: increasing the gain in pain. *Science* **288**:1765–1769.
Wu Y, Halverson G, Basir Z, Strawn E, Yan P, and Guo SW (2005) Aberrant methylation at HOXA10 may be responsible for its aberrant expression in the endometrium of patients with endometriosis. *Am J Obstet Gynecol* **193**:371–380.
Wu Y, Strawn E, Basir Z, Halverson G, and Guo SW (2006) Promoter hypermethylation of progesterone receptor isoform B (PR-B) in endometriosis. *Epigenetics* **1**:106–111.
Yoshizumi M, Eisenach JC, and Hayashida K (2013) Valproate prevents dysregulation of spinal glutamate and reduces the development of hypersensitivity in rats after peripheral nerve injury. *J Pain* **14**:1485–1491.
Zamudio N and Bourc'his D (2010) Transposable elements in the mammalian germline: a comfortable niche or a deadly trap? *Heredity (Edinb)* **105**:92–104.
Zhang J and Banerjee B (2015) Role of microRNA in visceral pain. *J Neurogastroenterol Motil* **21**:159–171.
Zhang Z, Cai YQ, Zou F, Bie B, and Pan ZZ (2011) Epigenetic suppression of GAD65 expression mediates persistent pain. *Nat Med* **17**:1448–1455.
Zhang Z, Tao W, Hou YY, Wang W, Kenny PJ, and Pan ZZ (2014) MeCP2 repression of G9a in regulation of pain and morphine reward. *J Neurosci* **34**:9076–9087.
Zhao X, Tang Z, Zhang H, Atianjoh FE, Zhao JY, Liang L, Wang W, Guan X, Kao SC, and Tiwari V, et al. (2013) A long noncoding RNA contributes to neuropathic pain by silencing Kcna2 in primary afferent neurons. *Nat Neurosci* **16**:1024–1031.
Zhou Q, Costinean S, Croce CM, Brasier AR, Merwat S, Larson SA, Basra S, and Verne GN (2015a) MicroRNA 29 targets nuclear factor- κB-repressing factor and Claudin 1 to increase intestinal permeability. *Gastroenterology* **148**:158. e8–169.e8.
Zhou Q and Verne GN (2011) New insights into visceral hypersensitivity–clinical implications in IBS. *Nat Rev Gastroenterol Hepatol* **8**:349–355.
Zhou Q, Yang L, Larson S, Basra S, Merwat S, Tan A, Croce C, and Verne GN (2015b) Decreased miR-199 augments visceral pain in patients with IBS through translational upregulation of TRPV1. *Gut* DOI: [published ahead of print].
Zhou Q, Zhang B, and Verne GN (2009) Intestinal membrane permeability and hypersensitivity in the irritable bowel syndrome. *Pain* **146**:41–46.
Zhu X, Li Q, Chang R, Yang D, Song Z, Guo Q, and Huang C (2014) Curcumin alleviates neuropathic pain by inhibiting p300/CBP histone acetyltransferase activity-regulated expression of BDNF and cox-2 in a rat model. *PLoS One* **9**: e91303.
Zhu XY, Huang CS, Li Q, Chang RM, Song ZB, Zou WY, and Guo QL (2012) p300 exerts an epigenetic role in chronic neuropathic pain through its acetyltransferase activity in rats following chronic constriction injury (CCI). *Mol Pain* **8**:84.

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