

Vitamin D, Testosterone, Epigenetics and Pain an Evolving Concept of Neurosignaling, Neuroplasticity and Homeostasis

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Abstract

The thought of exploring a possible relationship between the broad systems of steroid hormone physiology (specifically vitamin D and testosterone) and nociception was prompted by an unexpectedly frequent personal clinical observation. Patients with chronic pain syndromes or chronic musculoskeletal pain often have low serum levels of vitamin D and testosterone. Mining for relevant information in Pub Med, Medline and Cochrane Systems Review, three concepts repeatedly emerge that provide a common context for understanding the mechanics of these diverse systems—epigenetic, homeostasis and neuroplasticity. Viewing homeostasis within the framework of epigenetics allows reasoned speculation as to how various human systems interact to maintain integrity and function, while simultaneously responding in a plastic manner to external stimuli. Cell signaling supports normal function by regulating synaptic activity, but can also effect plastic change in the central and peripheral nervous system. This is most commonly achieved by post-translational remodeling of chromatin. There is thus persistent epigenetic change in protein synthesis with all the related downstream effects but without disruption of normal DNA sequencing. In itself, this may be considered an example of genomic homeostasis. Epigenetic mechanisms in nociception and analgesia are active in the paleospinothalamic and neospinothalamic tracts at all levels. Physiologic response to a nociceptive insult, whether mechanical, inflammatory or ischemic, is provided by cell signaling that is significantly enhanced through epigenetic mechanisms at work in nociceptors, Gamma-Aminobutyric Acid (GABA) and glutamate receptors, voltage gated receptors, higher order neurons in the various dorsal horn laminae and proximal nociceptive processing centers in the brainstem and cortex. The mediators of these direct or epigenetic effects are various ligands also active in signaling, such as free radicals, substance P, a variety of cytokines, growth factors and G proteins,

stress responsive proteins, matrix and structural proteins such as reelin and the *Jmjd3* gene/enzyme. Calcitriol, the vitamin D receptor and vitamin D Responsive Elements collectively determine regulatory effects of this secosteroid hormone. Agents of homeostasis and plasticity include various D-system specific cytochrome enzymes (CYP 24, CYP 27 A1, B1), as well as more widely active enzymes and protein cell signalers (*Jmjd3*, Calbindin, BMP), many of which play a role in the nociceptive system. While the highlighted information represents an understanding of complex systems that is currently in its infancy, there are clear results from reliable research at a foundational level. These results are beginning to tell a compelling tale of the homeostasis and plasticity inherent in vitamin D and nociception systems.

Keywords

Gamma-Aminobutyric Acid (GABA), Jumonji (*Jmjd3*), Homer Gene, Cholecalciferol, Calcitriol, Neurosteroids, Glutamate, 5-HT

1. Introduction

A Possible Relationship between Nociception, Vitamin D3 and Testosterone

The thought of exploring possible relationships between the broad content domains of vitamin D Metabolism, testosterone related physiology and nociception as regulated by typical and epigenetic mechanics, within the context of homeostasis and neuroplasticity, was prompted by a personal and unexpectedly frequent clinical observation. I have seen that many patients with chronic pain syndromes or chronic musculoskeletal pain have low serum levels of vitamin D and testosterone. Admittedly, this personal observation is inconsistently supported by high-quality scientific investigations, and understandable by a host of plausible mechanisms. Nonetheless the following thought process draws upon an exploding body of knowledge as it pertains to the not so disparate steroids vitamin D and testosterone, and the emerging concepts that are elucidating the processes of nociception and epigenetics.

A body of knowledge, as identified through Cochran systems review, Pubmed and Medline, exists that supports the idea that epigenetics plays a significant role in the nociceptive process, vitamin D dependent systems and testosterone metabolism. The epigenetic influences that affect steroid hormones are also being identified.

At this time, a link between vitamin D function and the nociceptive system seems probable, while a link with testosterone more tenuous. Much of the highlighted information represents an understanding of complex systems that is currently in its infancy, but there are clear results from reliable research at a foundational level and these results are beginning to tell a compelling tale of the homeostasis and plasticity inherent in human physiology.

2. Background

2.1. Epigenetics

Epigenetics is the study of changes gene expression (phenotype) without change in the underlying DNA sequence [1]. This term is used for processes which are both heritable and transient (in a generational sense). In general, the focus of epigenetics is on stable changes maintained across several cell generations [2].

The geneticist Dr. A. Riggs provides a useful operational definition of epigenetics as “the study of mitotically and/or meiotically heritable changes in gene function that cannot be explained by changes in DNA sequence” [3]. In 2008, the consensus definition of epigenetic process was written by a consortium of geneticists as a “stably heritable phenotype resulting from changes in a chromosome without alterations in the DNA sequence” [4]. For the purpose of this paper, epigenetic processes are the non-genomic mechanisms that result in this type of change.

Epigenetics is typically divided into; predetermined and probabilistic epigenesis [5]. Predetermined epigenesis is a one way progression from DNA structure to functional maturation of a protein that is predictable [6]. Probabilistic epigenesis allows a bidirectional structure-function relationship between DNA and protein, with extrinsic factors being key determinants of gene expression.

With epigenetic mechanics, there is no change in the nucleotide sequence. They allow the genome to display both plastic and homeostatic properties, adapting to change across cell generations while maintaining genetic integrity. The resulting ability to differentially express protein synthesis is an integral part of human development and adaptation [7].

Epigenetic change in response to an environmental trigger or stimulus can have tremendous impact on an organism. For example, mice fed supplements that alter expression of the agouti gene show variability in fur color, weight, and propensity to develop cancer [8]. In humans, identical twins with different environmental exposures develop clear differences in the content and genomic distribution of 5-methylcytosine DNA and histone acetylation that is reflected in differences in their medical histories [9].

Epigenetic change is achieved through diverse strategies including DNA methylation and histone modification therefore altering genetic expression and without changing the DNA sequence [10] (Figure 1).

Chromatin (Figure 2) is activated or silenced at either the transcriptional or post-transcriptional level. Transcriptional activation may occur through histone modification and transcriptional silencing is more commonly due to DNA methylation and epigenetic “crosstalk” between the processes may add yet another dimension to epigenetically directed plasticity and homeostasis [11] [12]. Post-transcriptional gene silencing is the result of blocking the mRNA of a particular gene, generally by a small non-coding RNA [13]. The destruction of the mRNA prevents gene-directed protein synthesis.

Chromatin is fundamentally DNA wrapped around histone proteins. The

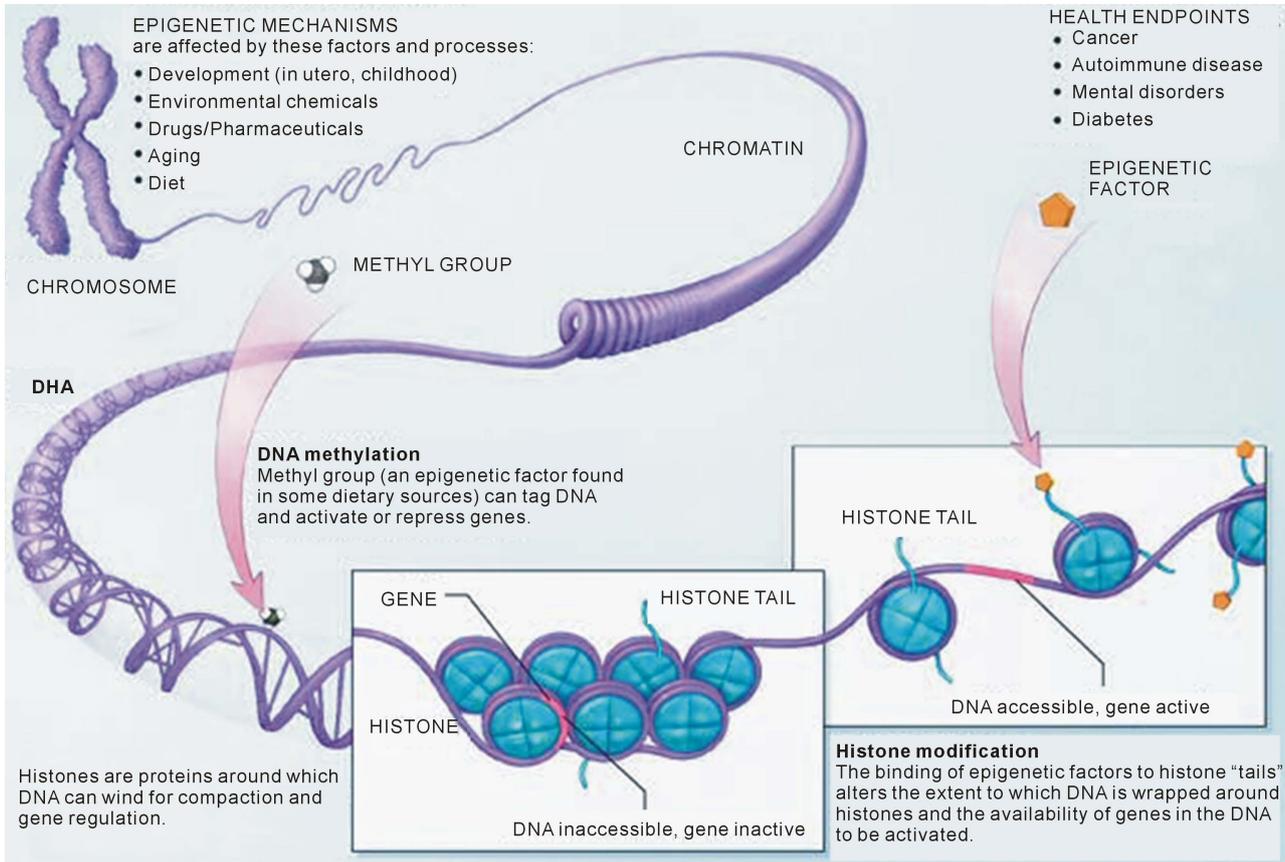


Figure 1. A scientific illustration of how epigenetic mechanisms can affect health (<https://commonfund.nih.gov/epigenomics/figure>).

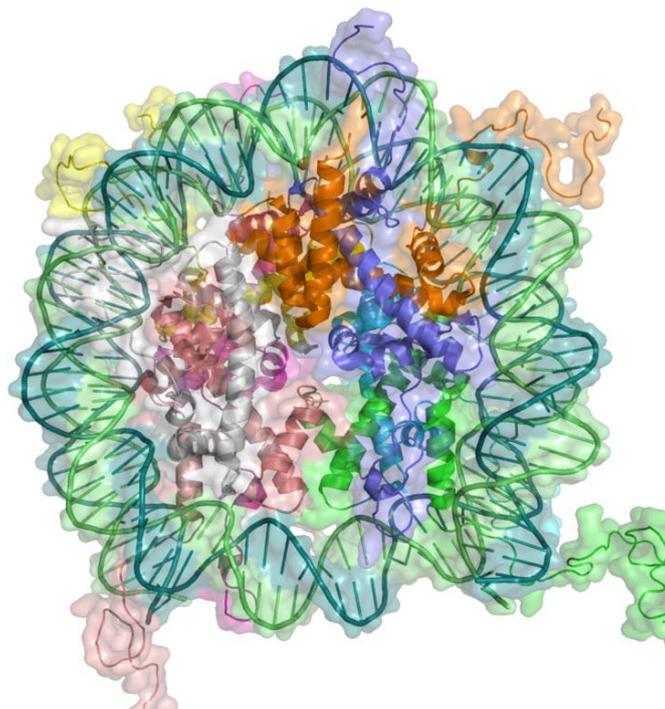


Figure 2. Chromatin-DNA plus histone complex (https://commons.wikimedia.org/wiki/File%3ANucleosome_1KX5_2.png). By Richard Wheeler (Zephyris) 2005.

confirmation of this complex determines a transcription state. Remodelling of the chromatin results in epigenetic, or heritable, transcription states. The change in gene expression is related to the way that histone, or the mated DNA, changes.

Change in the histone component of chromatin, or remodeling change, occurs by post-translational change in the long amino acid chains that form histone proteins. This alters the configuration of the histone, and the histone-DNA complex such that protein synthesis is altered by the change in available DNA loci. In a similar manner, during replication the altered configuration may act as a new template and the altered chromatin is carried forward, although the reality of this heritability is a matter of current controversy.

The way that histone proteins change is through acetylation, methylation, phosphorylation, enzyme binding of the respiratory protein ubiquitin (ubiquitylation) or similar addition of a related protein (small ubiquitin-like modifier; sumoylation) [13] [14] [15]. This is meaningful at the N-terminus (tail) where it impacts transcriptional competence, perhaps by removing the “native” positive charge. This affects the DNA (negative phosphate backbone)-histone (positive nitrogen tail) bond and provides DNA access to transcriptional factors—the cis model of epigenetic function where changes in the histone tail directly affects DNA expression [16] [17]. Histone tail changes may also indirectly impact DNA. In the trans model, the histone modification creates a binding site for chromatin modifying enzymes [18].

The various possible histone modifications appear to produce a variable response that is dependent upon the specific modification, the site of modification and the combination of multiple and varied modifications [19]. This produces a very broad and dynamic range of differential gene expressions (the result of a putative histone code). In most cases, histone modification is most commonly transcriptional activating [20].

Epigenetic change in DNA results from Methylation. Generally this occurs at the sites where cytosine and guanine are bound by a phosphate group, the CpG site [21]. Methylation converts cytosine to 5-methylcytosine. DNA methylation helps to suppress the expression and mobility of transposons (the “jumping genes” or transposable elements within a gene) [22] [23] [24] [25]. This highly methylated areas of the genetic base pairs tend to be less transcriptionally active. DNA methylation occurs in response to an external stimulus through the mediation of multiple independent DNA methyltransferases.

Methylation of histone may also provide a site for transcriptional factor binding. These are most typically inactivating and may silence the involved gene [26] [27]. Methylation may also, incidentally, reveal the lineage of a chromosome as the additional methyl group is passed in a germ cell line, an aspect of genetic imprinting, due to enzymatic preferential affinity for methylated cytosine [28] [29] [30].

Histones H3 and H4 can also be demethylated by histone lysine demethylase

(KDM) at the active site—the Jumonji domain (JmjC). JmjC is involved in demethylating mono-, di-, tri-methylated substrates [31] [32].

Yet another mechanism of chromatin change is via non-coding RNA. From a mechanical perspective these changes have generally been thought to silence gene expression, although their role in gene activation is increasingly identified [33].

Approximately 60% of genes coding for human protein are regulated by micro RNA (miRNAs) and many miRNAs are epigenetically regulated. miRNA genes are repressed by epigenetic methylation. Other miRNAs are epigenetically regulated by histone modifications or by combined DNA methylation and histone modification. Such potentially sophisticated epigenetic regulation of an epigenetic agent is an example of how homeostasis and plasticity interact at a fundamental level in biological systems [34] [35] [36].

More than 2000 miRNAs have been identified to date within humans [37]. And as each miRNA expressed in a cell may down-regulate over one hundred messenger RNAs, the potential impact of epigenetic modification at this level is immense.

Ribozymes, alternately, are catalytic RNA molecules that do not down-regulate messenger RNAs, but rather cleave them, thus silencing gene expression [38] [39] [40].

Additionally, small interfering RNA's represent a vast array of small non-coding RNA's that are involved in epigenetic gene regulation [41].

Epigenetic change can also be effected by various mechanisms that play a significant role in the developing organism. A list of the most common such processes includes paramutation, bookmarking, imprinting and transvection [42] [43]. These processes are largely predetermined, at times latent, epigenetic events. Another mechanism, DNA damage, is epigenetically probabilistic [44].

DNA damage which is frequent, approximately 10,000 times a day per cell due to oxidative damage alone, can produce epigenetic changes at the site of a DNA repair [45] [46].

The most significant damage, a double strand break in DNA, can promote DNA methylation or histone modification that most commonly silences the involved gene [47]. Enzymatic mediators of DNA repair can accumulate and promote chromatin remodeling at adjacent undamaged sites.

Subsequent changes may even affect expression of DNA repair genes and this might have a significant downstream effect, perhaps resulting in an escape from genetic homeostasis [48]. Inflammatory conditions that stimulate nociception can damage DNA and produce epigenetic change.

Free radical generation with the potential to damage DNA results from exposure to many environmental toxins as well as from constitutive processes such as aging [49] [50]. High levels of free radicals foster reaction with DNA. The product of this reaction is 8-hydroxy-2'-deoxyguanosine (8OHdG). This can be used as a biomarker for oxidative DNA damage. Levels of 8OHdG increase following

inflammatory processes [51].

2.2. Nociception

Nociception is the perception of noxious stimuli—stimuli with the potential to effect tissue damage. In a broader sense it is the perception of pain. As such the nociceptive system is a complex sensory neural network that communicates widely with motor, affective, cognitive and other sensory systems. Evidence, subsequently presented, supports the concept of nociceptive homeostatic control, as well as a robust intrinsic ability of the system to provide a plastic response in pathological states, and that this plasticity is realized through epigenetic mechanisms.

Stimulation of a peripheral nociceptor, generally a free nerve ending that reaches firing threshold in response to mechanical, thermal or chemical changes. In turn, the receptor initiates signal propagation along the peripheral nerve which synapses in the posterior horn of the spinal cord. The signal is modified in specific cord laminae by segmental and suprasegmental factors prior to proximal transmission, ultimately to processing centers in the thalamus and cortex [52]. Nociception can also trigger a variety of autonomic mediated responses (diaphoresis, nausea, tachycardia, hypertension and so on) [53].

The nociceptive system is constructed to provide a wide range of variable response, generally subserved through two afferent pathways and multiple efferent pathways or systems [54] [55]. These pathways correlate with specific identification in response to a painful stimulus. There are a wide variety of neurotransmitters involved in the afferent and efferent limbs of the nociceptive system [56].

In the periphery, nociceptors stimulate either fast, myelinated sensory fibers (A delta fibers) or slow, unmyelinated ones (C fibers). These fibers synapse with the second order neuron (of types that vary in electrical sensitivity, inhibiting or facilitating interneuron connections and firing thresholds) located in various laminae of the spinal cord (largely laminae II, IV, and V). At this point the signal enters the spinothalamic tract. Before reaching the brain the spinothalamic tract divides into the lateral neospinothalamic tract in the medial paleospinothalamic tract. Neospinothalamic fibers terminate at the synapse with ventrobasal thalamic neurons. Signals are then projected to the somatosensory cortex. The paleospinothalamic tract receives unmyelinated C fiber which generated signals that are projected to neurons in the reticular formation, thalamus, medulla, pons and periaqueductal gray matter and subsequently are transmitted to many areas of the brain for processing.

The efferent limb of the system incorporates an endogenous analgesia system that regulates nociception and pain responses [57]. Peripheral signal generation can be inhibited prior to central nervous system propagation, and signal transmission can also be inhibited or facilitated centrally (in the spinal cord, periaqueductal gray matter and thalamus) [58] [59].

Analgesia, or inhibition of nociceptive neurons, occurs when opioid receptors

are activated. There are multiple types of opioid receptors and a great deal of genetic, and possibly epigenetic, variability in their characteristics [60].

2.3. Epigenetics of Pain

The impact of epigenetic regulation of the pain system is apparent in the context of both homeostasis and plasticity. The previously described mechanisms, promoting DNA or histone methylation, histone modification and DNA damage, function in homeostatic pain modulation within the nociceptive system. This is particularly evident in cases of neuropathic or chronic pain where sensory neural activity continues in the absence of a peripheral stimulus [61] [62].

2.4. Epigenetics in the Afferent Nociceptive System

Inflammation, ischemia and nerve injury produce local tissue acidosis and are potent inducers of nociceptive activity, possibly via of the mediation of extracellular proteoglycans and G protein ligands [63] [64]. The byproducts of tissue damage (inflammatory cells, histamines, bradykinin, prostaglandins, ATP, nitrous oxide, cytokines and growth factors) electrically activate a peripheral nociceptors. They produce local tissue acidosis, the magnitude of which correlates well with the degree of perceived pain [65] [66]. The production of free radicals, with their potential for DNA damage and gene silencing, is one example probabilistic epigenetic processing in the nociceptive system. Inflammatory products can also contribute to histone modification [67] [68] [69].

Inflammation and pain transduction are associated with the production of multiple peripheral factors such as nerve growth factor (NGF) and brain derived neurotrophic factor (BDNF) that signal transcription of ligands, particularly excitatory nociceptive peptides such as substance P, which is located within the cell body and within the posterior horn [70] [71]. Substance P also activates proton-sensing G-proteins (of these, GTP γ S has been most studied) which in turn potentiate sodium channels (specifically Tetrodotoxin (TTX)-resistant voltage-gated Na (Na (V)) channels) in the paleospinothalamic nociceptive tract [72].

The G proteins however are also resultant in phosphorylative histone remodeling through several intermediaries [73] [74]. The reconfigured chromatin transcribes proteins which lower the threshold for ion-gated nociceptor activation [75]. This is an epigenetically produced bias that favors pain signal transmission. It is also a potential point of departure from a homeostatic to a plastic nociceptive process where changes in protein transcription result in an altered nociception phenotype. The resultant gene expression promotes a lasting decrease in activation threshold and increase in signal duration such as occurs in chronic, deafferented pain states [76].

The stress responsive protein deacytlases (SIRT) are encoded by SIRT genes and function in diverse molecular pathways including inflammatory and DNA repair pathways [77]. Sirtuin-6 (SIRT6) specifically has been identified as a me-

diator of inflammation-induced epigenetic change affecting both histone and DNA [78].

2.5. Epigenetic Mechanisms in the Efferent Limb of the Nociceptive System

DNA methylation can affect the opiate receptor. Endorphins are produced in response to painful stimuli [79]. These peptides bind opioid receptors in the brain (mu, kappa and delta), and dorsal horn of the spinal cord (mu and kappa receptors) to activate GABAergic, glutaminergic, cholinergic, substance P and serotonergic releasing neurons [80]. There is evidence for predetermined (developmental) epigenetic modification of opiate receptors through DNA methylation, and this modification may correlate with individual variations in pain perception, tolerance and related behaviours [81].

In the endogenous inhibitory arm of the nociceptive system, analgesic can be produced by activating the μ -opioid receptor (MOR), a member of the G-protein coupled receptor (GPCR) superfamily. Under homeostatic conditions, signaling is later terminated by intrinsic GTPase activity and a regulator of G protein signaling (RGS) protein [82] [83].

RGS proteins are GTPase-accelerating proteins (GAPs) and therefore reduce G protein mediated signal duration and intensity [84]. Loss of RGS activity results in enhanced endogenous opioid peptide signaling and inhibition of GABA release in periaqueductal gray matter. This introduces the potential of epigenetically mediated variability in the inhibitory arm of the nociceptive system.

DNA methylation can also affect the reelin protein. Reelin is a matrix protein that promotes glutamate receptor maturation [85] [86]. It is present in spinal cord nociceptive processing centers (laminae I, II and V pain) and involved in signal processing and opiate receptor sensitivity [87] [88]. DNA methylation of Reelin gene promoter sequence controls transcription of the protein, and changes in methylation result in altered transcription [89]. This is potentially another example of neuroplasticity and epigenetically directed change in the way that an afferent pain signal can be processed within the CNS [90].

2.6. Epigenetics and Descending Pathways

DNA methylation and resulting changes can affect the inhibitory limb of nociceptive pathways, most commonly through methylation of DNA transcribing neurotransmitters.

Dopamine is an inhibiting neurotransmitter that is present in the basal ganglia, spinal cord, thalamus and periaqueductal gray matter, Dysregulation of dopamine production is associated with chronic pain states and there is evidence that DNA methylation of promoter genes can lead to such dysregulation [91] [92].

There is also evidence of epigenetic control within the nociceptive system through DNA methylation of brain derived nerve growth factor (BDNF) [93].

This nerve factor and the related downstream proteins are essential for nerve cell viability and function. The BDNF-related gene has multiple promoter sites that are susceptible to chromatin alteration, most particularly DNA methylation [94] [95] [96]. Pain has the potential to downregulate BDNF DNA methylation and increase selective production of BDNF isoforms in the dorsal horn and dorsal root ganglion.

The glutamate receptor, NMDA (N methyl D aspartate), controls excitatory synaptic plasticity and memory through ion gated channel control. It is the primary agent of excitatory synapse plasticity within the nociceptive system in the brain and spinal cord [97] [98] [99]. DNA methylation of the promoter gene results in variation of the NMDA receptor expression and activity, favoring either the receptor subtype responsible for rapidly decaying or slowly decaying signals [100]. Receptor subunits have variable binding affinity's for the nociceptive neurotransmitter glutamine. There are further distinctions in the NMDA receptor, with subtypes of subunits, all of which contributes to a highly variability, or the ability to promote a differential response to an afferent pain signal [101] [102] [103] [104].

Epigenetic changes that result from nociceptive stimulation can also occur through the histone modification. Inflammatory conditions that increase IL-1, IL-6, IL-8, and metalloproteinases have demonstrated histone acetylation and phosphorylation [105] [106]. Such changes may impact NMDA receptors gene expression, altering subunits and the nociceptive bias in the brain and spinal cord, as noted above [107].

Histone modification can lead to stimulation of receptors in the posterior horn (brain derived neurotrophic factor (BDNF)/tropomyosin-related kinase receptor B (TrkB), glutamate/NMDA and substance P/NK-1) [108] and results in central sensitization, the ongoing pain response after removal of a painful stimulus.

Intracellular calcium will increase with activation of these receptors [109] and activation of calcium-dependent kinases that phosphorylate nuclear proteins. This is an illustration of the plastic response capability within the nociceptive system.

With the stimulation of C-fibers, activation of intranuclear factors occurs, which then promotes gene transcription V of the calcium-mediated cAMP responsive element binding protein (CREB) [110] [111]. Calcium mediated regulation occurs in the brain and spinal cord through acetylation of histone and phosphorylation of multiple transcription factors, changing chromatin and subsequent protein transcription.

Non-coding miRNA might be another post-translational epigenetic regulatory pathway within the nociceptive system. The mRNAs of inflammatory proteins can be exposed to miRNA modification [112]. With muscle inflammation, the levels of miRNA increase rapidly within a sensory ganglion [113] [114].

There is evidence from both animal and human studies that miRNA di-

rected epigenetic change plays a role in inflammatory pain [115] [116] [117] and that this change is upregulated by the inflammatory cytokines IL-1 and TNF-alpha [118] [119] [120]. Similarly, there is good evidence for miRNA mediated modulation of nociceptive pathways in chronic pain states, with differential signaling based on both nociceptive stimulus and the site of signal processing [121].

Another post-transcriptional epigenetic consideration in the nociceptive system that is a consequence of altered protein production via RNA alteration is the transformation of the protein Homer I to Homer IA [122].

Homer I is a structural protein that promotes pain transmission in the dorsal horn, binding glutamate receptors at the cell membrane. It is a constituent of the signaling complex that releases calcium from intracellular pools. Thus Homer I potentially initiates the downstream effects on ion gated channels in the nociceptive system [123] [124].

The native Homer gene transcription product is differentially deaminated (transforming adenosine into inosine [125] by adenosine deaminase to produce Homer IA, which results in different cellular functions. Homer IA lacks the ability to link with glutamate receptors and so its ligand activity inhibits, rather than facilitates, the transmission of a nociceptive signal.

With peripheral injury, Homer IA is produced in spinal neurons. This is an example of epigenetic homeostasis. If upregulation of the protein fails (failure to deaminate), pain transmission to proximal segments of the nociceptive system become more probable [126].

2.7. 5 Hydroxytryptamine (5-HT) Receptors

Another site where RNA deamination serves a nociceptive epigenetic function is at the serotonin (5-HT) receptor. The receptor receives suprasegmental stimulation. It is another G-protein coupled protein in the dorsal horn and inhibits signal transmission in ascending nociceptive fibers [127] [128] [129]. Alteration of the protein results in hypersensitivity to pain [130].

2.8. Steroids, Neurosteroids, Steroid Hormones, Secosteroids, Vitamin D and Testosterone

A steroid is an organic compound that contains four joined cycloalkane rings. A secosteroid is a steroid with a failure of bonding of B-ring carbon atoms, leaving one "broken ring". Neurosteroids are bioactive steroids that are transcribed in neurons and glial cells in both the central and peripheral nervous systems. The role that they play in nociception is an increasing focus of investigation related to Pain Medicine [131] [132] [133] [134] [135].

The neuroprotective effects of pregnenolone (**Figure 3**) and role of progesterone in neurogenesis within the nociceptive system have been well described [136] [137] [138]. The effect of dehydroepiandrosterone (DHEA) on peripheral and central receptors has also been well described [139]. This 5-alpha

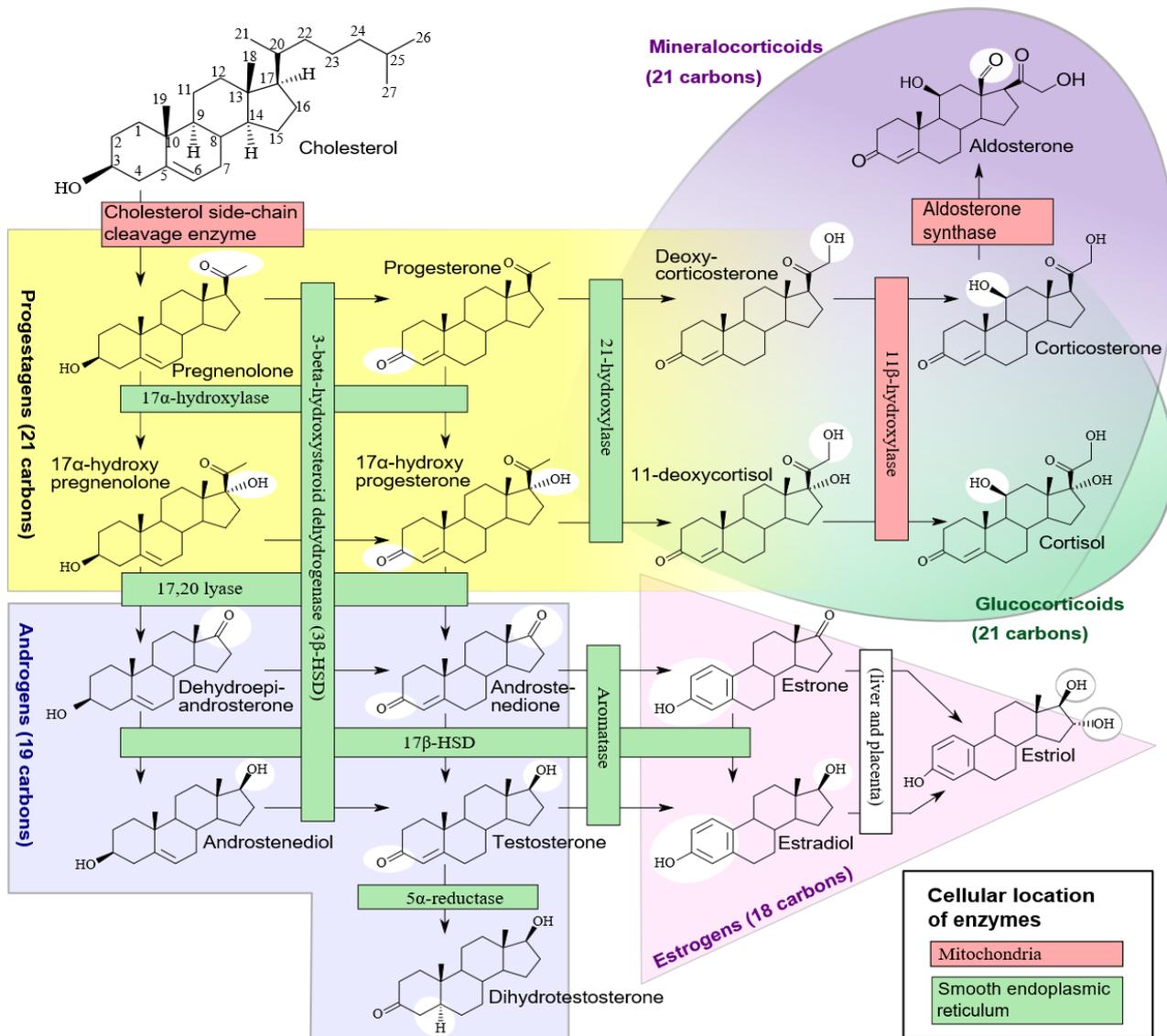


Figure 3. Steroidogenesis

(https://en.wikiversity.org/wiki/WikiJournal_of_Medicine/Diagram_of_the_pathways_of_human_steroidogenesis)

(<https://doi.org/10.15347/wjm/2014.005>).

reduced neurosteroid is produced in the neuron. At the present time it is apparent from the mammalian models that inflammatory pain upregulates GABA mediated inhibition of nociceptive transmission by signaling an increase in endogenous neurosteroid production [140].

Neurosteroid production within the nociceptive system can be either typical or nongenomic (epigenetic). These steroids rapidly modulate neurons within the nociceptive pathway through ionotropic (specific and nonspecific cation channel) receptors and by coupled G-protein, metabotropic neurosteroid receptors in peripheral nociceptor cell membrane [141] [142] [143] [144].

The gonadal and secosteroid hormones vitamin D and testosterone, most particularly vitamin D3, have wide ranging implications in health and disease [145].

Their function in multiple body systems is increasingly well understood. There is evidence from both clinical and foundational studies that they may also play a role as “pseudo-neurosteroids” within the nociceptive system, affecting transduction, transmission and modulation of pain signaling, either directly or through the regulation of calcium binding proteins [146] [147].

Steroid hormones, including vitamin D and testosterone, are cholesterol derivatives. The genes/enzymes responsible for regulation of the vitamin D hormone include several cytochrome P450 related enzymes, specifically CYP2R1, CYP27B1 and vitamin D 25 hydroxylase and hydroxyl vitamin D3 1- α -hydroxylase [148] [149] [150]. In the case of testosterone, regulatory genes/enzymes include CYP11A (mitochondrial cytochrome P450 oxidase), CYP 17A (a related oxidase in the endoplasmic reticulum), 3- β hydroxysteroid dehydrogenase and 17- β hydroxysteroid dehydrogenase [151].

3. Vitamin D

Vitamin D3 is a prohormone produced in skin through ultraviolet irradiation of 7-dehydrocholesterol. It is biologically inert and must be metabolized to 25-hydroxy vitamin D3 in the liver and then to 1 α , 25-hydroxyvitamin D3 in the kidney before it becomes active [152] (Figure 4).

The hormonal form of vitamin D3, *i.e.*, 1 α , 25-hydroxyvitamin D3, acts through a nuclear receptor to carry out its many functions, including calcium absorption, phosphate absorption in the intestine, calcium mobilization in bone, and calcium reabsorption in the kidney [153] [154]. It also has several noncalcemic functions in the body.

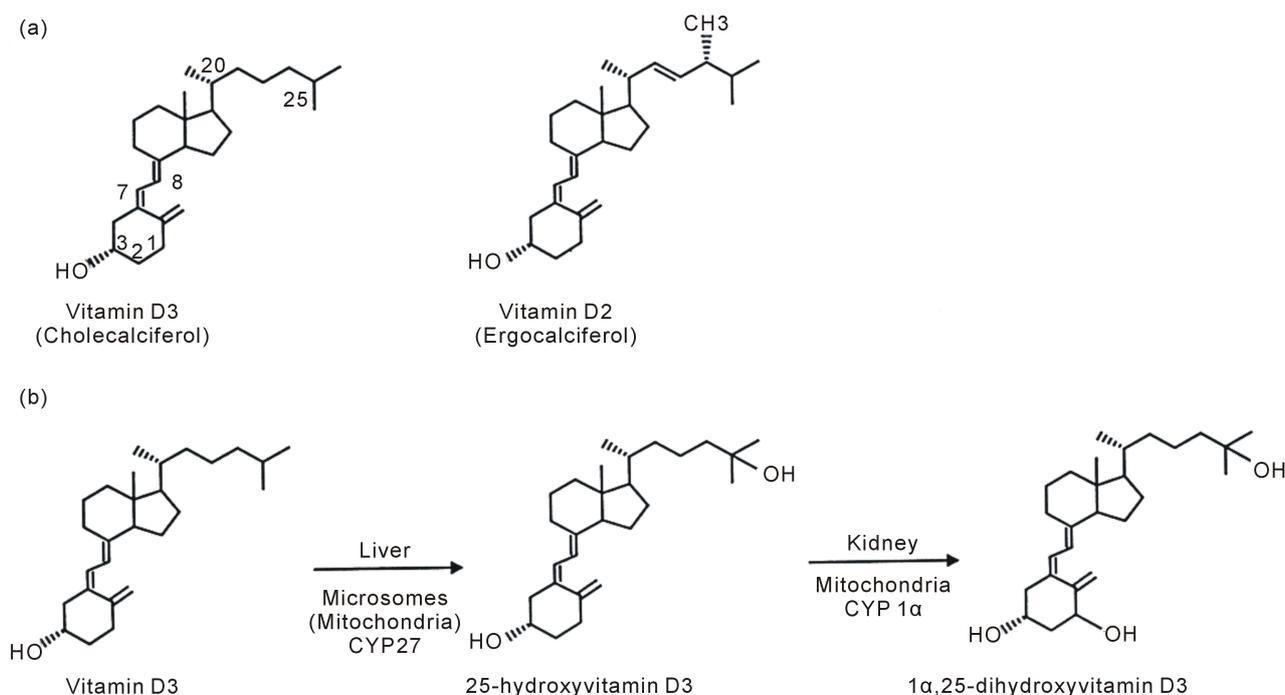


Figure 4. (From <http://physrev.physiology.org/content/78/4/1193.figures-only>).

The critical role of vitamin D in human physiologic systems is increasingly recognized as a key determinant in the homeostasis involved in health maintenance. This secosteroid has been identified as a key element in the normal development and operation of wide ranging metabolic pathways that impact, among others, the musculoskeletal and neurologic systems.

Vitamin D exists in several forms. The two predominant forms are vitamin D2 (ergocalciferol), and vitamin D3 (cholecalciferol) (**Figure 4**), known together as calciferol. All forms are fat-soluble lipids derived from cholesterol that function as hormones [155] [156]. The forms of vitamin D are secosteroids (steroids in which one of the bonds in the steroid rings is broken) [157]. The difference in structure and function between vitamin D forms relates to their respective side chains.

Vitamin D3 and vitamin D2 can be ingested. Vitamin D3 can also be synthesized from cholesterol by ultraviolet irradiated skin. In the epidermal basal and spinosum strata large quantities of vitamin D3, 7-Dehydrocholesterol can be produced rapidly by optimal ultraviolet light exposure, at wavelengths between 295 and 300 nm [158].

Activation of calciferol occurs through two separate hydroxylation stages. The first, conversion to calcidiol (25-hydroxyvitamin D3) occurs in the liver and the second, conversion of 25-hydroxyvitamin D3 to the active hormone calcitriol (1,25 dihydroxyvitamin D3 or 1,25(OH)₂D3) occurs in the kidney. These conversions are mediated by several cytochrome P450-related enzymes including CYP2R1 and CYP27B1 [159] [160].

Ingested or endogenously produced, cholecalciferol is hydroxylated in the liver at position 25 to form calcidiol by hepatocyte produced vitamin D 25 hydroxylase. There are two enzymes thought to be involved in the 25-hydroxylation step. They are most active in the liver but can be seen elsewhere in the body [161].

In the proximal renal tubules calcidiol is hydroxylated by 25-hydroxyvitamin D3 1- α -hydroxylase at the 1- α position to perform calcitriol.

In addition to renal hydroxylation, calcitriol is synthesized in the immune system by monocytes. Dihydroxyvitamin D3 in this instance acts not as a hormone, but rather as a cytokine, stimulating the innate immune system [162] [163].

Once made, the product is released into the plasma, where it is bound to α -globulin, vitamin D binding protein. This protein transports calcitriol to its target organs. Calcitriol circulates as a hormone, regulating the serum calcium and phosphate concentration and related growth and remodeling of bone as well as more diverse neuromuscular and immune functions [164].

Once at its target, calcitriol binds with the vitamin D receptor (VDR) in the cell nucleus. The VDR C-domain which is a DNA-binding domain, a calcitriol-binding domain called the E-domain, as well as an F-domain, which is one of the activating domains. When calcitriol activates this nuclear pathway, the

VDR/ligand collectively determines the specific transcriptional response and downstream physiologic effect [165].

Calcitriol can also activate calcium channels in the plasma membrane, in a signal transduction pathway [166].

The VDR modulates the gene expression of calcium and phosphorus transport proteins (including calbindin) [167]. The VDR is a cell nuclear receptor that can facilitate either the activation or suppression of its target genes [168]. The receptor acts via vitamin D-responsive elements (VDREs) which are located near the target gene. When the VDR binds with calcitriol, the receptor changes its confirmation. It concomitantly binds multiple protein coactivators when facilitating active transcription. In this instance the stereotactic change allows phosphorylation of serine-205 and transcription is either suppressed or initiated, depending on the gene [169] [170]. There are multiple coactivators which might provide a highly variable dynamic phenotypic and transcriptional response in many different body systems [171].

This wide array of dynamic response is probably intimately related to calcitriol's role in both health and disease. It allows for homeostasis in multiple systems and escape from this homeostasis may have notable genomic plastic effects such as tumorigenesis [172] [173] [174].

Both an excess and a deficiency in vitamin D appear to cause abnormal functioning and premature aging [175] [176] [177]. The relationship between serum calcidiol level and all-cause mortality is parabolic [178].

Through activation of the VDR, calcitriol activates osteoblasts to secrete receptor activator nuclear factor- κ B ligand (RANKL) [179] [180]. Osteoclastogenesis and bone resorption are activated by RANKL. Activated VDRs promote bone mineralization but also stimulate osteoclastic elevation of serum calcium and phosphorus concentrations. They regulate parathyroid hormone production and affect the function of pancreatic islet cells [181] [182] [183] [184]. VDRs are also present in monocytes and activated T and B cells and are important in immune system function [185] [186].

VDRs regulate expression of tyrosine hydroxylation via gene activation in the adrenal medullary cells. They are also involved in the biosynthesis of nitric oxide synthase [187] [188]. It is reasonable to thus propose a role for vitamin D receptors participating in, and possibly linking, the physiologic responses to both stress and pain.

3.1. Vitamin D Hormonal Homeostasis

The synthesis of cholecalciferol is generally adequate to maintain serum concentrations and toxicity is prevented through a negative feedback loop.

Cytochrome enzymes are agents of vitamin D homeostasis, as well as participants in the highly differential response of nuclear targets. They possibly provide a window through which a link between vitamin D/steroid hormone and nociceptive function can be seen under both homeostatic and plastic conditions.

1,25-dihydroxyvitamin D₃ is degraded by mitochondrial enzymes in the target cells CYP24A1 facilitates a series of catabolic steps that begins with 24 hydroxylation of 1,25(OH)₂D₃ and ends with the production of calcitroic acid. Feedback regulation of both production in the kidney and degradation at peripheral targets maintains homeostasis of the active metabolite (1,25(OH)₂D₃).

Transmembrane serum calcium-sensing proteins in the parathyroid gland bind to G proteins when calcium concentrations fall. This stimulates the release of parathyroid hormone (PTH). Parathyroid hormone then stimulates proximal convoluted tubule cells and osteoblasts. Notably, PTH elevates 1 α -hydroxylase concentrations in the convoluted tubule cells. This favors hydroxylation of calcidiol to calcitriol [189] [190].

Subsequently vitamin D signals cells to promote kidney reabsorption of calcium. When blood calcium levels exceed the threshold of the system, either through mobilization from bone, gastrointestinal absorption or kidney reabsorption, the cascade of events induced by the parathyroid gland will be inhibited. When serum calcium concentrations are excessively elevated, thyroid glands C-cells secrete calcitonin, which blocks bone calcium mobilization. CYP27B1 is also down-regulated by calcitriol itself, which then negatively signals CYP27B1 transcription, thus curbing vitamin D synthesis [191].

Calcitonin also stimulates the renal 1 α -hydroxylation that provides vitamin D hormone for non-calceic needs under normal calcium conditions [192]. Such non-calceic needs are just beginning to be identified, but the potential impact of vitamin D, the VDR and VDREs are likely to prove to be immense.

One example of this is vitamin D hormone induction of 24-hydroxylase (CYP24). CYP24 is not only involved in the control of vitamin D production itself. It is also involved in the processing of nociceptive signals in the DRG (dorsal root ganglion), as well as testosterone production in the Leydig cells [193].

3.2. Epigenetics of Vitamin D

Epigenetic mechanisms are intrinsic to vitamin D signaling pathways. The effects are mediated both upstream at the activating or inactivating gene/enzymes CYP27A1, CYP27B1 or CYP24 as well as at the VDR [194]. Activity of VDRs can be modulated epigenetically by histone acetylation [195].

Calcitriol is an active participant in predetermined epigenetics. The effect of vitamin D on fetal programming and gene regulation are reflected in the normal operation of many physiologic systems throughout life. Another nongenomic, probabilistic, way in which vitamin D might enhance the ability of human systems to respond to stimuli likely exists.

A signal transduction mechanism that is VDR/VDRE dependent may operate in either the typical gene transcription pathway or through a signal transduction pathway that involves calcium channels located on the plasma membrane [196] [197] [198]. There is evidence that the nuclear VDR/VDREs ligand mediating genomic effects is different from the membrane VDR/VDREs that initiate the

nongenomic transduction pathway effects [199] [200] [201].

Vitamin D also has a more fundamental role in the epigenetic regulation-plastic or homeostatic physiological systems. Epigenetic regulation by calcitriol stimulates the expression of the JMJD3 gene which codes for a histone demethylase [201]. To date there have been relatively few reliably documented instances where this mechanism is active. Nonetheless vitamin D signaling might have a multisystem applicability through its regulatory action on the expression of genes coding for histone demethylases of the Jumonji C (JmjC) domain and lysine-specific demethylase (LSD) families, and subsequently on gene transcription and cell phenotype [202] [203].

3.3. Testosterone

Testosterone is a steroid hormone, and androgen rather than a secosteroid. It is synthesized by the Leydig cells in the testes, to a lesser extent in the ovaries, and minimally in the zona reticularis of the adrenal cortex and skin [204]. In the serum it is transported to target tissues by the sex-hormone-binding-globulin protein.

In men, testosterone is a determining epigenetic factor for reproductive tissue and secondary sexual characteristic development. It promotes increased muscle and bone mass through increased protein synthesis in these testosterone receptor-dense tissues [205].

The serum concentration of testosterone is 7 - 8 times greater in the adult male than in the adult female. Testosterone sensitivity is greater in the female. The daily production and consumption of testosterone is greater in the male.

The anabolic effects of testosterone include augmentation of muscle mass, bone density, linear growth, bone maturation and sex organ maturation [206] [207]. To do this it likely interacts at a molecular level with the vitamin D hormone system of signaling as previously described.

A developmental epigenetic effect of the hormone first occurs with gender formation during the second trimester, with feminization or masculinization of the fetus. Animal studies point to aromatase (an enzyme that converts testosterone into estradiol) as being responsible for male sexual differentiation of the cerebrum [208]. Serum levels of testosterone during this key developmental period are a better predictor of sex typed behavior than adult levels [209] [210].

Testosterone is a physiologic regulator of the hypothalamic-pituitary-adrenal axis and plays a role in both cognition and general health/physical energy [211]. It determines the density of thromboxane A2 receptors on platelets and megakaryocytes responsible for platelet aggregation [212] [213]. Testosterone levels decline gradually with age.

In addition to its well described positive trophic effects on skeletal and cardiac muscle and other organs, there is evidence that testosterone affects attention, memory and spatial orientation [214] [215] [216] [217].

A non-linear relationship between testosterone and its physiologic functions

is supported by the literature. There is a curvilinear relationship which exists between spatial performance and circulating testosterone. Both deficiency and excess of circulating hormone have a negative effect on cognition [218].

3.4. Testosterone Homeostasis

The amount of testosterone synthesized is regulated by the hypothalamic-pituitary-gonadal axis (**Figure 5**) through gonadotropin-releasing hormone produced in the hypothalamus. This stimulates the release of luteinizing and follicle stimulating hormones from the pituitary. These hormones stimulate the production of testosterone. Testosterone acts through a negative feedback loop on the hypothalamus and pituitary to inhibit the release of stimulatory hormones [219].

There are multiple extrinsic factors that can affect testosterone production. These include weight loss (increased synthesis as fat cell production of aromatase increases testosterone conversion into estradiol, lowering baseline serum testosterone levels and this signaling increased testosterone production), zinc deficiency (decreased synthesis), sleep (production increases during REM sleep), exercise and protein ingestion (increased production). Notably, there is a positive correlation between vitamin D and testosterone levels [220] [221] [222].

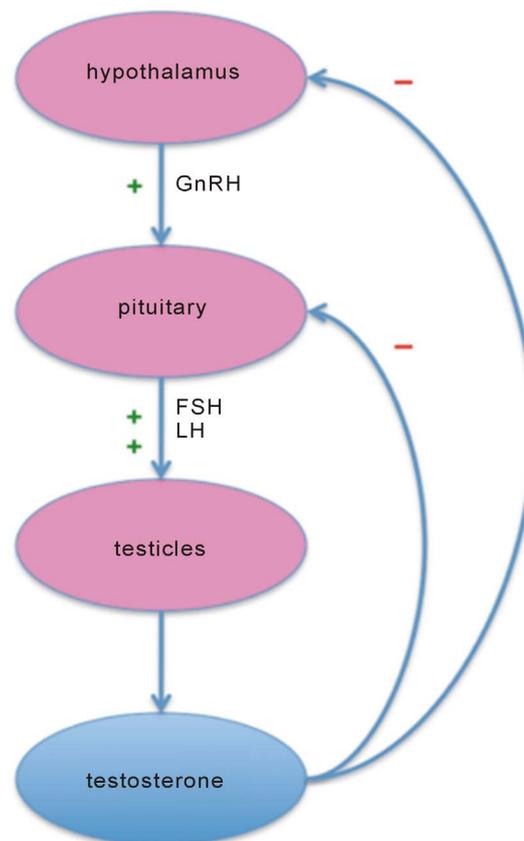


Figure 5. Hypothalamic-pituitary-testicular axis (http://www.wikilectures.eu/w/Hypothalamic-pituitary-gonadal_axis).

Free Testosterone is transported into the target cell cytoplasm where both the hormone and its reduced derivative 5-alpha dihydrotestosterone (via 5-alpha reductase) bind to the androgen receptor. This complex then enters the cell nucleus and binds nucleotide sequences of chromosomal DNA [223]. As with vitamin D, the mechanism involves hormone activity elements which can impact transcriptional activity thereby causing androgen effects.

3.5. Testosterone and Vitamin D

There is an association with vitamin D and testosterone levels. Some of the evidence is conflicting regarding vitamin D supplementation as a means to increase the production of testosterone in men [224] [225] [226]. It is unclear whether the response of testosterone to D3 supplementation is dependent upon serum levels of vitamin D. The association between calcitriol and total and free testosterone is linear at typical calcitriol concentrations and achieves a plateau at higher levels [227].

3.6. Testosterone and Epigenetics

Beyond its clear role in predetermined epigenetics, testosterone likely also plays a part in probabilistic epigenetic mechanics. The small amounts of testosterone produced in the adrenal glands may have implications for the nociceptive system.

Testosterone produced by the adrenal cortex participates with aldosterone and cortisol in the modulation of the stress response [228]. Testosterone and its estradiol derivative can also be considered as secondary neurosteroids that impact nociception [229] [230]. Adrenal testosterone and its derivatives are produced in the Zona Reticularis, the inner most cortical layer, along with androstenediones and the estrogen-precursor, dehydroepiandrosterone (DHEA) and its derivatives. There is evidence that stress related testosterone production is epigenetically modifiable through gene targets of several miRNAs [231]. It is reasonable to consider pain as a stressor that alters testosterone production that in turn modifies nociceptive processing. This thought is consistent with evidence that negatively correlate pain perception and certain chronic pain states with testosterone levels [232] [233] [234].

Testosterone mediated epigenetic change in the nervous system is well documented in motor pathways [235] [236] [237]. Its role in regulating the coupling mechanisms between calcium channels Ca (v2.2) and transmitter release at neuromuscular junctions has been demonstrated [238]. It seems that testosterone is one of the steroid hormones which produce both genomic and non-genomic effects in not just motor, but also possibly sensory, nervous system signaling [239] [240]. The non-genomic effects may operate through modulation of the plasma membrane proteins, including voltage- and ligand-operated ion channels or G-protein-coupled receptors [241] [242]. Seventeen beta-estradiol, testosterone, pregnenolone sulfate and dehydroepiandrosterone sulfate increase the hydrolytic

activity of plasma membrane Ca^{2+} -ATPase in a dose dependent manner. They decrease the stimulatory effect of the calcium pump activator, calmodulin [243].

The activity of both calcium channels and calmodulin has been amply demonstrated in the nociceptive system [244] [245]. This represents a possible epigenetic interface between testosterone and nociception.

3.7. Participating Gene/Enzymes, Signaling Proteins and Receptors

There are several genes/enzymes, signaling proteins and receptors that play a prominent role at the interface between vitamin D and testosterone hormone signaling, epigenetic mechanisms and the nociceptive systems. These elements are located within the nociceptive framework—sometimes discretely (such as in the brainstem, dorsal laminae or root ganglia) and at times diffusely. Included in this list are the enzymes Jumonji domain-containing 3 (Jmjd3) histone demethylase, CYP24A1 (25-hydroxyvitamin D_3 -24-hydroxylase), CYP17A1 (steroid 17-alpha-monooxygenase, or 17 α -hydroxylase/17, 20 lyase/17,20 desmolase), and CYP27B1 (25-hydroxyvitamin D_3 1-alpha hydroxylase).

Proteins, such as calbindin-D28K, multiple bone morphogenetic proteins (BMPs) and the Homer/Homer 1 protein, have identifiable functions that intersect domains, as do various receptors such as the VDR receptor, the chemokine CC motif receptor 2 (CXCR2) and GABA, glutamate and G-protein receptors.

3.8. Jumonji Domain-Containing 3 (Jmjd3)

Jumonji domain-containing 3 (Jmjd3) is a histone demethylase present in the cell nucleus that specifically catalyzes the removal of trimethylation of histone H3 at lysine 27 (H3K27me3) [246]. Its role in cell differentiation and predetermined epigenetics has been well described. For example, it regulates the expressions of Bone sialoprotein BSP and Osteocalcin OCN via transcription factors Runx2 and Osterix and drives osteoblast differentiation [247]. It also is a notable epigenetic agent within the nervous system [248] [249]. Speculatively, it might prove to link such diverse processes as inflammation, nociception and cell differentiation [250].

Vitamin D induces the expression of the Jmjd3 gene via VDR signaling [251] [252]. There is also transcriptional regulation of Jmjd3 from the cell cytoplasm via the signal transducers and activators of transcription (STAT) proteins STAT1 and STAT3, and this is a crucial link between a painful stimulus and nociceptive response, in this case by inducing inflammation in microglia [253] [254]. Cytotoxic and inflammatory factors (particularly cytokines) are associated with microglial activation and signaling within the nociceptive system [255] [256].

The cytokines activate STAT proteins by binding with Janus kinase. This enzyme then phosphorylates the STAT protein which is subsequently transported into the cell nucleus. The STAT protein binds to the target gene and activates

transcription [257] [258]. In the instance of pain, it is reasonable to assume that this would include multiple activating and inhibitory or silencing nociceptive factors. Such relevance of STAT proteins, and Jmjd3, to the nociceptive system has been recently recognized [259].

Further evidence suggests that Jmjd3 may also serve an epigenetic regulatory function within the nociceptive system in non-inflammatory pain states, such as chronic bladder pain/interstitial cystitis, although the evidence for this is less compelling [260].

3.9. CYP24A1, 25-Hydroxyvitamin D₃-24-Hydroxylase

CYP24A1, 25-hydroxyvitamin D₃-24-hydroxylase, is a mitochondrial enzyme that degrades the hormonal form of the vitamin (calcitriol). A homeostatic balance exists wherein calcitriol rapidly induces CYP24A1 expression and is thus the primary regulator of CYP24A1.

CYP24A1 expression is up-regulated by 1,25-dihydroxyvitamin D(3) via a vitamin D receptor (VDR)/retinoid X receptor (RXR) heterodimer that binds to two vitamin D response elements (VDREs) located near the proximal promoter. Along with calcitriol, co-regulators are responsible for an increase in RNA polymerase II and histone H4 acetylation, further enhancing the CYP24A1 up-regulation [261] [262].

The enzyme's primary function is to limit the extent and duration of vitamin D responsive target transcription by affecting the hormone's circulating levels in both normal physiological or pathological states, specific to an individual cell type/tissue [263].

The baseline level of CYP24A1 expression is determined in a cell type-specific manner by various factors including glucocorticoids, estrogens, testosterone, retinoid ligands and local growth factors [264] [265] [266].

3.10. CYP17A1

CYP17A1 is found in the zona reticularis of the adrenal cortex. It catalyzes synthesis of certain lipids, including cholesterol and its neurosteroid derivatives [267]. It has both 17 α -hydroxylase and 17,20-lyase activities, and is a key enzyme for the downstream production of neurosteroids, including testosterone [268] [269] [270].

Single nucleotide polymorphisms (SNPs) in CYP17A1 and VDR genes appear to be significantly associated with arthralgia. Interactions between CYP27B1 and both CYP17A1 and VDR SNPs may produce an additive effect on pain intensity. [271].

CYP27B1 and CYP24 expression in unmyelinated sensory neurons controls vitamin D metabolite concentrations [272]. Unmyelinated CGRP-positive neurons seem to have a separate and distinct vitamin D phenotype with hormonally-regulated ligand and receptor levels [273].

Within a neural cell population that is mainly nociceptive, these findings sug-

gest that vitamin D signaling may play a specialized role. The implication is, through nuclear or extranuclear signaling pathways, calcitriol may affect sensory neurons thereby affecting sensory processes including pain and proprioception.

3.11. Calcium Binding Proteins

Among the various calcium binding proteins, Calbindin D28K and Calretinin are present in sensorineural pathways [274]. Calbindin-D28K functions in the intestine, kidney and neuroendocrine cells. Animal studies have demonstrated its activity in laminae I and II of the dorsal horn and in spinal ganglia, in a distribution similar to that of substance P-containing primary afferent neurons [275].

This would suggest that calbindin has a regulatory role in pain transmission, likely through its binding of free calcium [276] [277]. Animal studies demonstrate that a lack of calbindin D28K is associated with deficient GABAergic neurotransmission and dysfunctional sensory processing of nociceptive stimuli [278]. This also supports the idea that the protein plays an active role in nociceptive sensory transmission.

Calbindin is encoded in humans by the CALB1 gene [279]. The protein is transcribed by this VDR regulated gene, although this vitamin D dependence may have exceptions, as perhaps in its synthesis in the brain [280] [281].

Calbindin thus provides a link between vitamin D and nociceptive systems. It might also provide a link to other steroid hormones such as testosterone. There is evidence that androgen hormones facilitate renal calcium transport which leads to a compensatory decrease in Calbindin-D28K expression [282]. Admittedly speculative, an indirect pathway for testosterone directed, homeostatic, regulation of Calbindin-D28K expression might exist.

Calbindin may play a significant role in central processing of nociceptive signals [283] [284]. The evidence for this being a Vitamin D dependent process is not clear.

Animal studies indicate that chronic deafferentation of skin and peripheral tissues that induce central pain states are associated with plasticity of nociceptive pathways. More specifically, central pain states are associated with an increase in activity of Calbindin cells at spinal, brainstem, and thalamic levels, specifically Calbindin-D28K regulation of gamma-aminobutyric acid type A receptors [285].

3.12. Bone Morphogenetic Protein-2 (BMP2)

Bone morphogenetic protein-2 (BMP2) is an important component of multiple signaling pathways. These pathways include the hedgehog pathway (note participation of the protein in predetermined epigenetics in this instance) and the transforming growth factor beta (TGFB) pathway [286].

BMP2 stimulates osteoblastic differentiation in concert with vitamin D (activated VDRs) and is itself epigenetically down-regulated by vitamin D through calcitriol induced transcriptional repression by DNA methylation and histone

modification [287].

BMPs, possibly including BMP2, might also play a signaling role in the developing nociceptive system [288]. It is unclear at this time whether BMP2 might act in adult neurosensory modulation, but seems to participate indirectly in the expression of ligands that direct sensory neuronal differentiation [289].

3.13. Interleukin-8 Receptor, Beta, or Chemokine CC Motif Receptor 2

Interleukin-8 receptor, beta, or chemokine cc motif receptor 2, or CXCR2 is a member of the G protein-coupled receptors. The ligand is interleukin-8, which it binds with high affinity, and transduces the signal through a G-protein activated second messenger system (G-coupled) [290] [291].

CXCR2 is a pro-inflammatory receptor that is active in processing (induction and sensitization) both neuropathic and inflammatory pain [292] [293] [294]. It is epigenetically regulated by histone modification as evidenced in animal studies [295], although its regulation is poorly understood and likely complex. In other systems where they coexist, VDR/vitamin D elements down-regulate CXCR2 expression [296].

3.14. Structural Proteins and the Metabotropic Glutamate Receptors

The neuronal protein Homer1 is encoded by the HOMER1 gene. It is a post-synaptic scaffold protein that is widely expressed in the central nervous system as well as in peripheral tissues, the list of which notably includes the kidney and ovary [297] [298].

The expression of Homer1 is induced by neuronal activity. Thus Homer1 expression increases after periods of activity or stress, injury, or other challenge. It binds several targets that affect both indirectly via G proteins (metabotropic glutamate receptor) and directly via the inositol triphosphate, IP₃Rs receptor [299] [300].

Homer1 is associated with the Shank scaffold protein and there is evidence that the interaction between the 2 scaffold proteins may be epigenetically modifiable and thus alter the response of the system [301] [302].

The Metabotropic glutamate receptor 5 regulates neuronal excitability in the spinal dorsal horn, promoting nociceptive transmission. Thus metabotropic glutamate (mGluR) receptors play important roles in the modulation of nociception [303].

Pain transmission is inhibited by stimulation of metabotropic glutamate 2 (mGlu2) receptors in the posterior horn of the spinal cord [304]. mGluRs can also be seen in pain regulatory centers of the brainstem, forebrain and in peripheral nociceptors [305] [306] [307]. mGlu2 receptor regulation occurs via the acetylation-promoted activation of the p65/RelA transcription factor [308] [309].

Homer1 binds receptors with the net effect of uncoupling glutamate receptors

from the excitatory pathway [310]. It also contracts the dendritic spine. It allows the CNS to self-down-regulate under conditions of excessive stimulation (CNS homeostatic plasticity) [311] [312] [313] [314].

Homer proteins also influence the function of their binding partners. Binding to Homer1 alters the function of cation non-specific (TRPC1) and calcium specific (IP3R) channels [315]. In this way, Homer proteins regulate localization of binding partners and affect neuronal signaling. While this mechanism is best described in the brain, the constituent elements of this hemostatic/plastic mechanism are present in the nociceptive system as well.

In short, metabotropic glutamate receptors (mGluRs) and Homer proteins play critical roles in neuronal functions including plasticity and nociception. Homer proteins regulate mGluR function by facilitating coupling to effectors such as the inositol triphosphate receptor as noted above. This modulation occurs postsynaptically. Thus, alteration of mGluR signaling by changes in Homer protein expression may confer sensitivity to the neuronal response to stimulation, such as a nociceptive stimulus.

The postsynaptic structural effect of the protein on the dendritic spine contains the rise in calcium ions released from intracellular stores, damping excessive stimulation [316] [317]. Along with the change in dendritic spine confirmation, the protein scaffold (including Homer1) undergoes translocation along with the intracellular Ca^{2+} channel inositol triphosphate receptor (IP3R) and endoplasmic reticulum (ER) proteins that are vitamin D dependent (Calreticulin and Calbindin) [318]. The induced change might have consequences for local Ca^{2+} homeostasis as well as overall neuronal signaling.

3.15. Inhibitory Neurosignaling by Gamma-Aminobutyric Acid (GABA) and G Proteins

Ubiquitous in central nervous system, GABA (**Figure 6**) regulates neuronal excitability. This includes nociceptive pathways [319]. GABA acts pre-and post synaptically. Its direct action occurs by binding to an ionotropic (direct) receptor—the GABA A receptor (a ligand-gated chloride ion channel receptor). It also acts indirectly through a metabotropic receptor—the GABA B receptor [320]. In this instance it regulates intermediary, coupled G proteins which open or close ion channels including calcium channels.

Voltage gated calcium channels modulate the function of peripheral and central pain pathways by influencing fast synaptic transmission and neuronal excitability [321]. Both the various subtypes of high voltage activated type Ca^{2+} channels and the low voltage activated or transient (T)-type Ca^{2+} channels (T-channels) participate in the modulation of nociception [322].

G proteins may also play an additional role in the processing of pain signals by modulating endogenous opioid supraspinal antinociception [323] [324]. Animal studies of thermal induced nociception suggest that they also function at a spinal level as regulators of opioid antinociceptive pathways [325].

Within DRG neurons, G protein coupled proton-sensing receptors have been

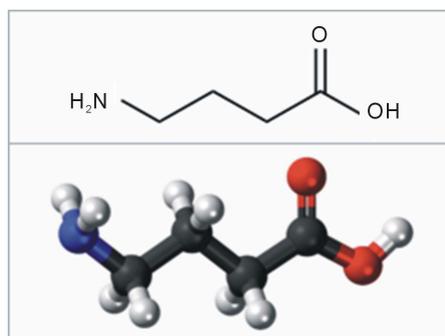


Figure 6. γ -Aminobutyric acid or GABA

(https://commons.wikimedia.org/wiki/File:Gamma-Aminobutters%C3%A4ure_-_gamma-aminobutyric_acid.svg) (https://commons.wikimedia.org/wiki/File:GABA_3D_ball.png).

identified [326]. Such GABA-G-protein coupled receptors might have a role in epigenetic regulation of pain related to insults that produce local tissue acidosis, such as is seen with mechanical trauma, inflammation and ischemia.

Neurons that produce GABA as their output (GABAergic neurons) have mainly inhibitory action [327]. Loading of GABA and glycine into synaptic vesicles via the vesicular GABA transporter (VGAT) is an essential step in inhibitory neurotransmission [328] [329].

Alteration of GABAergic and/or glycinergic neurotransmission is linked to sensory processing in various pain disorders [330]. GABA, once released from vesicles, rapidly activates GABA type A receptors. This gives rise to an inhibitory, small and brief postsynaptic current, the phasic response [331]. Neurosteroids released from close proximity neurons or glia prolong the decay of this current. This enhances synaptic inhibition.

Neurons may also contain extrasynaptic receptors that are activated by low levels of ambient GABA, producing a tonic response—a background current that might influence neuronal firing [332]. Neurosteroids can also enhance this response, even at concentrations that have little effect on the phasic response. $3\alpha5\alpha$ -THPROG, 5α -pregnan- 3α -ol-20-one; 5α -DHPROG, 5α -dihydroprogesterone have demonstrated this effect in animal studies [333].

Epigenetic modulation, through the phosphorylation of protein, can affect the sensitivity of GABA (A)-receptors to neurosteroids [334] [335].

4. Neurosteroids and Gaba Mediated Nociception

Neurosteroids represent a class of endogenous steroids that are synthesized in the brain, the adrenals and the gonads. They have potent and selective effects on the GABA A-receptor [336].

Neurosteroids act at an interface of homeostatic and epigenetic modulation of the nociceptive system and might be influenced through vitamin D dependent systems. In a non-genomic manner, reduced metabolites of testosterone, deoxycorticosterone and progesterone are positive modulators of GABA A-receptor.

5α -androstane- 3α , $3\alpha5\alpha$ -tetrahydrodeoxycorticosterone ($3\alpha5\alpha$ -THDOC), Al-

lopregnanolone (3 α -OH-5 α -pregnan-20-one) and 17 α -diol(Adiol) augment the GABA-mediated Cl⁻ currents acting on a site(s) through a pathway which is currently unidentified. This does not involve the GABA receptor [337] therefore further enhancing inhibition.

Other neurosteroids may decrease inhibitory neurosignaling. For example, acting as GABA A-receptor antagonists are 3 β -OH pregnane steroids and pregnenolone sulfate(PS). This process, already identified in areas of the CNS which subserve cognition, memory and mood, almost certainly is altered in chronic pain states, and might be active in nociceptive anatomic substrates as well. This most likely would occur for inhibitory synaptic transmission in lamina II of the spinal cord.

Endogenous 5 alpha-reduced neurosteroids are produced locally in lamina II and modulate GABA A-receptor function during inflammatory pain [338]. The production of 5 alpha-reduced neurosteroids is controlled by the endogenous activation of the peripheral benzodiazepine receptor (PBR), which initiates the first step of neurosteroidogenesis by stimulating the translocation of cholesterol across the inner mitochondrial membrane.

Stimulation of the PBR prolongs GABAergic signaling, at least during inflammatory pain [339], perhaps indicating that neurosteroidogenesis plays a regulatory role in nociception at the spinal cord level.

The amount of inhibition caused by GABA A-receptors can be varied by tetrahydro-deoxycorticosterone, endogenous neurosteroids, and allopregnanolone.

5. Clinical Considerations

The above information, largely abstracted from animal studies, is of unclear meaning in a clinical context. The heterogeneity of studies in design, intent and quality limit the ability to accurately assess them for significance and size effect.

Epidemiological studies consistently demonstrate that gender differences, often correlated with hormonal modulation, in the incidence, prevalence and modulation of deep tissue and inflammatory pain [340] [341]. Gonadal hormones are thought to play a modulatory role at the level of the primary afferent, dorsal horn and supraspinal sites, and descending inhibitory pain pathways. Their function appears, at least in part, to depend upon the balance between estradiol and testosterone.

Multiple meta analysis of the use of vitamin D for the treatment of chronic pain yield contradictory conclusions [342] [343]. In the chronic pain literature, results are inconsistent. In vitamin D deficient patient's, pain threshold and tolerance, particularly in instances of acute pain, appear to be lower. In such cases there is moderate evidence supporting the use of vitamin D3 to reduce pain. There is evidence that vitamin D may provide improved pain control in patients undergoing treatment for rheumatoid arthritis, osteoporosis, and sickle cell disease [344] [345] [346]. There is currently an ongoing, large cohort, well-designed study exploring pain severity and cartilage integrity as affected by vitamin D

status and patients with osteoarthritis [347].

In part the action of vitamin D may be etiology dependent, being expressed differentially following mechanical as opposed to biochemical (trauma with tissue acidosis, inflammatory, ischemic) insults [348]. It may also depend upon overall health status [349].

6. Concluding Thoughts

The above review is based upon information currently available. The relative explosion in pertinent research across diverse disciplines that encompasses genetics, physiology and clinical sciences is adding to our understanding on an almost daily basis. The link between mechanisms that provide homeostatic balance and plasticity within the nociceptive system is concurrently becoming clear.

Neuronal signaling is mediated by mechanical means, neurotransmitters or a vast array of proteins, many of which have been described in detail. The wide variety of signaling elements are often common to both steroid, and specifically vitamin D, dependent systems and the nociceptive system. These particularly include the signaling mechanisms, the neurotransmitters and receptors that effect nociceptive function through transcription of proteins that function not just physiologically, but also in a homeostatic or plastic manner.

Cytokines, protein kinases, various receptors that are stimulated directly (VDR, ionotropic receptors as examples) or through secondary messaging (G protein coupled metabotropic receptors), neurosteroid/steroid hormone, cholinergic, dopaminergic, serotonergic, GABA, glutamate and other signaling systems, and structural proteins and neurotrophic factors all play an apparent role.

The operational mechanics are inconclusive of the epigenetic pathways utilized by many systems to respond to signaling. The speculation that steroid dependent sub-systems within the nociceptive system, under certain conditions, might be signaled by vitamin D3, and possibly in specific cases by testosterone, is a reasonable one given the current evidence base.

Viewing homeostasis within the framework of epigenetics allows reasoned speculation as to how various human systems interact to maintain integrity and function, while responding in a plastic manner to external stimuli. This holds promise in the clinical application of information in order to provide more evidence based, specific and targeting intervention in the management of human pain.

While this understanding of complex systems is in its infancy, it suggests potentially fruitful areas for both foundational and clinical research. It might be a seed for the future development of a concept of epigenetics, plasticity and homeostasis, and the role of vitamin D3, in the nociceptive system.

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