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Epigenetics, estradiol, and hippocampal memory consolidation

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Abstract

Epigenetic alterations of histone proteins and DNA are essential for hippocampal synaptic plasticity and cognitive function, and contribute to the etiology of psychiatric disorders and neurodegenerative diseases. Hippocampal memory formation depends on histone alterations and DNA methylation, and increasing evidence suggests that regulation of these epigenetic processes by modulatory factors such as environmental enrichment, stress, and hormones substantially influences memory function. Recent work from our laboratory suggests that the ability of the sex-steroid hormone 17 β -estradiol (E₂) to enhance novel object recognition memory consolidation in young adult female mice is dependent on histone H3 acetylation and DNA methylation in the dorsal hippocampus. Our data also suggest that enzymes mediating DNA methylation and histone acetylation work in concert to regulate the effects of E₂ on memory consolidation. These findings shed light on the epigenetic mechanisms that influence hormonal modulation of cognitive function, and may have important implications for understanding how hormones influence cognition in adulthood and aging. This review will provide a brief overview of the literature on epigenetics and memory, describe in detail our findings demonstrating that epigenetic alterations regulate E₂-induced memory enhancement in female mice, and discuss future directions for research on the epigenetic regulation of E₂-induced memory enhancement.

Keywords

histone acetylation; DNA methylation; hippocampus; novel object recognition; estrogen

Introduction

Gene expression is necessary for long-term alterations in central nervous system structure and function. In recent years, it has become increasingly clear that epigenetic mechanisms, which regulate transcriptional access to DNA, play a significant role in the etiology of age-related memory decline, depression, drug addiction, and alcoholism, as well as the pathophysiology of neurodevelopmental (e.g., Rett's syndrome, Fragile X syndrome), psychiatric (e.g., schizophrenia, post-traumatic stress disorder), and neurodegenerative (e.g., Alzheimer's disease) disorders (1-11). Epigenetic alterations do not change the genetic code, but rather regulate the transcription of existing genes by methylating specific cytosine residues on the DNA or modifying the histone proteins around which DNA is supercoiled. In addition to their contributions to disease onset and risk, epigenetic alterations are critically important to controlling the gene expression associated with normal learning, memory, and environmental experience (5, 12-16). As will be discussed below, histone modifications (e.g., acetylation, phosphorylation, methylation) and DNA methylation are necessary for both basic long-term memory formation and the modulatory influences of hormones on memory. Most research on the epigenetics of learning and memory has

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focused on the hippocampus, largely because deficits in the types of memory subserved by this structure are characteristic of many neuropsychiatric and neurodegenerative diseases. However, recent data support the importance of epigenetic modifications to memory mediated by other brain regions including the amygdala and prefrontal cortex (17-19). Nevertheless, this review will focus on the role of epigenetic alterations in the hippocampus because this brain region has been the focus of the few studies examining the role of epigenetic mechanisms in mediating effects of 17β -estradiol (E_2) on memory.

Why is it important to study how epigenetics might influence hormonal regulation of cognition? From a clinical standpoint, drugs that inhibit histone deacetylation have shown promise as potential treatments for cognitive dysfunction a myriad of animal models of neurodegenerative and psychiatric diseases, including Alzheimer's disease, Parkinson's disease, schizophrenia, depression, and traumatic brain injury (5). The prevalence of serious mental illness, including depression, anxiety disorders, schizophrenia, and dementia is nearly double in women compared to men (20-23), suggesting that organizational or activational effects of sex steroid hormones contribute to sex differences in the etiology and/or symptomatology of these illnesses. Because hippocampal dysfunction and cognitive deficits, including memory loss, are common to these mental illnesses (24), pinpointing the contribution of epigenetic alterations to hormonal regulation of cognition is important to the development of novel drugs for disorders in which sex steroid hormones are thought to increase risk. Further, because hormone treatment can elevate the risk of side effects that are harmful (e.g., breast cancer, heart disease) or undesirable (e.g., gynecomastia in men), targeting the epigenetic mechanisms through which hormones influence cognition could lead to safer and more acceptable treatment options for patients.

Many outstanding comprehensive reviews have detailed the epigenetic mechanisms involved in the neurobiology of learning and memory (e.g., (4, 12, 13, 15, 25-27)), and therefore, this literature will be only briefly summarized here. Instead, this review will focus largely on data showing that epigenetic alterations are critical for E_2 to enhance hippocampal-dependent novel object recognition memory. These studies from my own laboratory are, thus far, the only research to investigate the roles of epigenetic alterations in hormone-induced memory enhancement. Therefore, this work will be described in some detail. Because the study of epigenetic influences on hormonal regulation of cognition is clearly in its infancy, this review will conclude by considering future directions for this research in the hope of inspiring others to begin studying this important issue.

The epigenetics of hippocampal memory

Within chromosomes, DNA is tightly supercoiled around histone octamers containing two copies each of histones H2A, H2B, H3, and H4 (28) (Fig. 1). Each of these histone proteins has an amino acid tail that can be altered by post-translational modifications including acetylation, phosphorylation, methylation, ubiquitination, and sumoylation. Many of these modifications relax the bonds between histones and DNA, thereby allowing transcription factors access to the DNA. Hippocampal learning, such as contextual fear conditioning, increases the acetylation, phosphorylation, and methylation of histone H3 in the hippocampus (29-31). Of the four core histones, H3 appears to be the most consistently altered by learning and E_2 in the hippocampus (29, 32, 33).

Histone acetylation is the most well studied chromatin modification associated with hippocampal learning and memory. Histone acetylation is regulated by histone acetyltransferases (HATs), which add acetyl groups to specific lysine residues, and histone deacetylases (HDACs), which remove these acetyl groups (34) (Fig. 1). The dependence of hippocampal memory and plasticity on HAT activity is supported by reports that mutations of the HATs p300/CBP and PCAF (p300/CBP-associated factor) impair hippocampal long-

term potentiation (LTP) and hippocampal-dependent spatial, contextual fear, and novel object recognition memory (35-41). Pharmacological inhibition of HAT activity in the dorsal hippocampus also blocked novel object recognition memory consolidation in wild-type mice (32), providing converging evidence for a role of histone acetylation in memory formation. In contrast to HATs, certain HDACs, like HDAC2 and HDAC3, are potent negative regulators of hippocampal synaptic plasticity and memory formation (42, 43). For example, overexpression of HDAC2 impairs contextual and cued fear conditioning and spatial memory, reduces hippocampal spinogenesis and LTP, and suppresses the expression of proteins necessary for synaptic plasticity including CREB, CaMKIIA, NR2A, NR2B, and β -catenin (42). Such deficits are reversed by HDAC2 knockout or treatment with an HDAC inhibitor (42). HDAC2 knockout also enhances LTP magnitude, accelerates extinction of conditioned fear and taste aversion, and improves prefrontal cortex-dependent attentional set-shifting (44). Further, deletion of HDAC3 in the dorsal hippocampus enhances long-term novel object recognition and object placement memory in mice (43). Systemic or intracranial administration of HDAC inhibitor drugs, such as trichostatin-A (TSA), sodium butyrate (NaB), suberoylanilide hydroxamic acid (SAHA), and RGFP136 also support an essential role for histone acetylation in hippocampal learning and memory. In wild-type rodents, these HDAC inhibitors increase hippocampal histone H3 and H4 acetylation, facilitate LTP, and enhance several forms of hippocampal memory, including contextual fear conditioning, spatial memory, and novel object recognition (33, 42, 43, 45, 46). Moreover, HDAC inhibitors reverse hippocampal memory deficits in mouse models of aging (47) and Alzheimer's disease (8, 48), supporting their possible use for treating cognitive dysfunction associated with aging and neurodegenerative disease. Another potentially promising approach to reducing cognitive dysfunction comes from a recent study showing that an activator of p300/CBP HATs promotes hippocampal neurogenesis and enhances spatial memory in the Morris water maze (49).

In addition to histone modifications, DNA methylation also plays a major role in regulating hippocampal memory consolidation (26, 27, 50-52). DNA methylation generally decreases transcriptional access to DNA, although the functional effects of this gene silencing depend on the genes altered. DNA methylation is catalyzed by DNA (cytosine-5') methyltransferases (DNMTs) that methylate cytosine residues in CpG islands on DNA (Fig. 1). This methylation serves to reduce transcriptional access to DNA. DNMT1 is a maintenance methyltransferase that transfers established methylation marks from one strand of DNA to the other (53). DNMT3A and DNMT3B are *de novo* methyltransferases that add new methyl marks to previously unmethylated cytosines (27, 53). The *de novo* methyltransferases appear to be more involved in hippocampal learning, as illustrated by findings indicating that the expression of DNMT3A and DNMT3B, but not DNMT1, mRNA is increased in the hippocampus by contextual fear learning (51). Contextual fear conditioning also increases the methylation of memory suppressor genes like protein phosphatase 1 (*PPI*), but decreases the methylation of memory promoting genes like *reelin* (51). Supporting the importance of DNA methylation in memory formation are recent data showing that genetic deletion of the protein Growth arrest and DNA damage-inducible 45b (*Gadd45b*), which regulates gene-specific demethylation, enhances late-phase hippocampal LTP, contextual fear memory, and spatial memory (54). Moreover, DNMT inhibitors like 5-aza-2-deoxycytidine (5-AZA) and zebularine prevent induction of hippocampal LTP and contextual fear memory consolidation (50, 51, 55). Interestingly, these effects are blocked by HDAC inhibitors, and the ability of contextual fear conditioning to increase H3 acetylation is blocked by DNMT inhibition (50). These data suggest an important synergy between histone acetylation and DNA methylation in regulating hippocampal memory formation.

E₂ and hippocampal memory

E₂ has emerged in recent decades as a pivotal modulator of hippocampal function and hippocampal memory. Many extensive reviews on this subject are available (e.g., (56-65)), so I will provide only a succinct description of this work here. The hippocampus is exceptionally sensitive to E₂, as demonstrated by seminal work showing that E₂ increases CA1 dendritic spine density in naturally cycling or ovariectomized female rats within 24 hours of exposure (66, 67). E₂ also promotes neurogenesis in the dentate gyrus of the hippocampus (see (68) for a recent review), suggesting that it regulates multiple aspects of hippocampal morphology essential for long-term memory formation. Moreover, E₂ regulates forms of synaptic plasticity thought to underlie learning and memory, including LTP (69-71). Although a positive correlation between high levels of E₂ and hippocampal memory formation has been reported in many studies, this association is not universally observed. The relationship between naturally cycling E₂ and memory has been somewhat difficult to test due to rapidly changing levels of gonadal hormones in circulation. Some evidence suggests that high levels of E₂ during proestrus are associated with enhanced spatial memory and spatial strategy use (72-74), whereas other studies report no effects of cyclic hormone fluctuations on spatial memory, social recognition, or novel object recognition (75-80). The contribution of hippocampally-synthesized E₂ to learning and memory is currently unknown, but will be important to assess in future work. Because of the challenges associated with assessing memory within the context of the natural estrous cycle, the vast majority of studies in animal models have been conducted using ovariectomized female rats and mice administered acute or chronic E₂ either systemically or directly into the dorsal hippocampus. Generally, exogenous E₂ administered to ovariectomized young adult rodents enhances several types of hippocampal-dependent memory, including spatial memory, novel object recognition, social recognition, inhibitory avoidance, and trace eyeblink conditioning (see (57, 63, 81, 82) for reviews). However, not all studies report an E₂-induced enhancement in hippocampal memory (e.g. (83, 84)), and comparisons across studies suggest that the beneficial effects of E₂ depend on numerous elements of the experimental design, including dose, age at treatment, duration and type of treatment, duration of hormone loss prior to treatment, timing of treatment relative to testing, type of memory tested, and task difficulty (see (57) for a discussion of these issues).

The past few years has seen a proliferation of studies examining acute effects of E₂ administered immediately after training to examine effects of E₂ on memory consolidation. These studies are quite consistent in showing that E₂, and agonists of ER α and ER β , enhance the consolidation of spatial memory measured in the Morris water maze, spatial memory measured in an object placement task, and novel object recognition memory (33, 80, 85-94). Unlike pre-training treatments, immediate post-training E₂ treatments allow effects of E₂ on memory consolidation to be pinpointed in the absence of potentially confounding effects on motivation and anxiety. E₂ given two or three hours after training does not affect spatial memory or object recognition (87, 93, 94), indicating that E₂ influences memory consolidation fairly rapidly after training. Because effects of E₂ can be attributed specifically to the memory consolidation phase of memory formation, this design permits more causal links between E₂-induced memory enhancement and specific cellular and molecular changes within the hippocampus.

The rapid effects on hippocampal memory consolidation are likely mediated by some combination of estrogen receptors (ERs) and other plasma membrane receptors. ERs of both the classical (ER α and ER β) and non-classical types (e.g., GPER, Gq-mER) are thought to mediate the effects of E₂ in the hippocampus. ER α and ER β are located throughout the hippocampus in the nuclei, dendritic spines, and axon terminals of pyramidal neurons and interneurons (95-97). ER α and ER β may mediate the epigenetic effects of E₂ in several ways. In their classical mechanism of action, these ERs dimerize upon estrogen binding, and

then the hormone-ER complex binds to estrogen response elements (EREs) on DNA to facilitate gene transcription (Fig. 2). ERE-mediated transcription requires coregulator proteins. Many coactivators function as HATs or interact with HATs, whereas some corepressors exhibit HDAC activity (98-100). Therefore, histone acetylation is intricately involved in ERE-mediated gene transcription. However, ER α and ER β may also exert epigenetic effects by regulating cell-signaling pathways that initiate processes like histone acetylation. In this non-classical mechanism, the ERs translocate to the plasma membrane after binding E₂ (101, 102), where they interact with integral membrane proteins like metabotropic glutamate receptors (mGluRs) to rapidly initiate extracellular signal-regulated/mitogen activated protein kinase (ERK/MAPK) signaling and stimulate phosphorylation of the transcription factor cAMP response element-binding protein (CREB) (103, 104) (Fig. 2). This E₂/mGluR signaling is essential for E₂ and agonists of ER α and ER β to enhance novel object recognition and object placement memory consolidation (105). Other data support the involvement of putative membrane-bound ERs, including GPER (a.k.a., GPR30, GPER1), in mediating the effects of E₂ on ERK signaling and hippocampal memory (87, 106-108) (Fig. 2). Although it is not yet clear which ERs mediate specific cell signaling events, it has become increasingly well accepted that both classical and non-classical ERs facilitate the rapid effects of E₂ (109).

The rapid effects of E₂ on memory consolidation fit well with data showing that E₂ can activate hippocampal cell signaling within minutes. For example, E₂ activates numerous cell signaling cascades in the dorsal hippocampus within 5 minutes, including the ERK/MAPK and phosphatidylinositol-3/Akt (PI3K/Akt) pathways (87, 89, 110-114), which play critical roles in hippocampal long-term memory formation (115, 116). Our own work has shown that the ability of E₂ to enhance novel object recognition memory consolidation in young and middle-aged ovariectomized mice is dependent on activation of PI3K and ERK in the dorsal hippocampus (87, 89). We have also shown that the E₂-induced activation of the p42 isoform of ERK is dependent on initial activation of the upstream kinases PI3K and PKA in the dorsal hippocampus (88-90), suggesting that p42 ERK functions as something of a final common signaling molecule leading to the activation of transcription factors such as CREB (Fig. 2). ERK activation is necessary for other kinases (e.g., PKC) to increase histone H3 acetylation (29), suggesting that ERK can also influence gene transcription by altering chromatin structure. As such, ERK appears to not only activate transcription factors, but also to regulate transcriptional access to DNA via histone acetylation. Given the importance of ERK activation to E₂-induced memory enhancement, we reasoned that epigenetic processes influenced by ERK, such as histone acetylation, might be involved in the estrogenic modulation of memory.

E₂, epigenetics, and hippocampal memory

Histone acetylation—We first tested whether our novel object recognition task was sensitive to epigenetic alterations. Mice first accumulated 30 seconds exploring two identical objects in an open arena (117) (Fig. 3A). Immediately after training, mice were infused with vehicle or the HDAC inhibitor TSA into the dorsal hippocampus. Forty-eight hours later, mice were allowed to explore one novel and one familiar object. Because mice are inherently drawn to novelty, mice who remember the familiar object will spend significantly more time than chance (15 seconds) exploring the novel object (117). As in our previous work (87, 118), vehicle-treated females exhibited intact object recognition memory 24 hours after training, but not 48 hours after training (33) (Fig. 3B). However, mice infused with the HDAC inhibitor TSA into the dorsal hippocampus displayed intact novel object recognition memory 48 hours later (Fig. 3B), suggesting that HDAC inhibition rendered this memory more persistent than normal. This finding is consistent with similar data from male mice (45). Importantly, the effects of HDAC inhibition were limited to a specific window of

time after training during which memory consolidation occurs, as indicated by the fact that infusion of TSA delayed three hours after training had no effect on memory consolidation (33) (Fig. 3B).

We next examined the effects of E₂ or TSA on histone H3 and H4 acetylation 30 minutes after infusion into the dorsal hippocampus. As would be expected from an HDAC inhibitor, TSA significantly increased acetylation of both H3 and H4 (33) (Fig. 4A). However, the effects of E₂ were more specific; like contextual fear conditioning (29), E₂ increased acetylation of histone H3 (Fig. 4A), but not histone H4 (33). We have replicated this specificity in several studies, and have subsequently shown no effect of E₂ on histone H2B in young females (32) and on histones H2A and H2B in middle-aged females (unpublished observations), suggesting that genes associated with histone H3 are particularly important for the functional effects of E₂ in the dorsal hippocampus.

Given that p42 ERK activation in the dorsal hippocampus is necessary for E₂ to enhance novel object recognition memory consolidation (87, 89), we next examined whether ERK activation was also necessary for E₂ to increase histone H3 acetylation. Mice were given a single intracerebroventricular (ICV) infusion of vehicle or E₂ immediately following a bilateral dorsal hippocampal infusion of vehicle or the ERK pathway inhibitor U0126. The rationale for this triple infusion procedure was to allow us to administer E₂ to the brain and specifically inhibit signaling in the dorsal hippocampus without having to infuse twice into the dorsal hippocampus in rapid succession and risk damaging hippocampal tissue. U0126 blocked the E₂-induced increase in histone H3 acetylation (Fig. 4B), whereas histone H4 acetylation remained unchanged by either drug (33). These data demonstrate that ERK activation in the dorsal hippocampus is necessary for E₂ to enhance both memory and histone H3 acetylation.

But is histone H3 acetylation necessary for E₂ to enhance novel object recognition memory consolidation? This question was addressed in a subsequent study designed to test whether a HAT inhibitor could prevent E₂ from influencing memory and histone acetylation. We used the potent HAT inhibitor garcinol, which had not previously been used *in vivo* to study the effects of histone acetylation on biological functions. Garcinol is derived from the rind of the *Garcinia indica* fruit, and is highly permeable to cultured cells (119, 120). We first established a dose of garcinol that did not impair memory on its own using a shorter 24-hour delay between training (33, 118) to ensure that any effects on memory at a longer 48-hour delay were due to a specific interaction between E₂ and garcinol, rather than a garcinol-induced blockade of general memory formation. Immediately after novel object recognition training, mice were infused with vehicle or one of four doses of garcinol into the dorsal hippocampus. All but the 0.001 μg dose impaired novel object recognition (Fig. 4C) (32). However, this dose prevented E₂ from facilitating novel object recognition memory consolidation (Fig. 4D) (32), suggesting that histone acetylation is necessary for E₂-induced memory enhancement. Further, garcinol prevented E₂ from increasing histone H3 acetylation, but had no effect on H2B or H4 acetylation (32). Together, these data suggest that acetylation of H3 in the dorsal hippocampus is essential for the beneficial effects of E₂ on memory.

E₂ can also influence the expression of HDAC proteins in the dorsal hippocampus. As described above, HDAC2 and HDAC3 are detrimental for hippocampal memory formation (42, 43). Consistent with the role of HDAC2 as a negative modulator of memory, E₂ significantly decreased levels of HDAC2 protein in the dorsal hippocampus four hours after infusion (Fig. 4E) (32, 33). E₂ induced similar reductions of HDAC3 protein in middle-aged females (unpublished observations). In contrast, HDAC1 protein levels in the dorsal hippocampus were not affected by E₂ (32, 33), which is consistent with previous work

showing a minimal role of HDAC1 in hippocampal memory (42). Interestingly, garcinol completely blocked the E₂-induced reduction of HDAC2 protein in the dorsal hippocampus four hours after infusion (Fig. 4F), while having no effects on HDAC1 or HDAC2 on its own (32). These findings suggest that histone acetylation regulates levels of HDAC2 protein in the dorsal hippocampus.

DNA methylation—Because learning-induced histone H3 acetylation is blocked by DNMT inhibition (50), we next wondered whether DNA methylation could also regulate the ability of E₂ to enhance hippocampal memory. We first examined the effects of E₂ on expression of the three DNMT enzymes. mRNA for DNMT3A and DNMT3B, but not DNMT1, in the dorsal hippocampus was increased 45 min after infusion of E₂ into the dorsal hippocampus (33). However, only DNMT3B protein was significantly affected by E₂, and levels of this *de novo* methyltransferase were increased by E₂ four hours after dorsal hippocampal infusion (Fig. 5A) (32, 33). This result suggests that E₂ may preferentially increase DNA methylation at previously unmethylated cytosine residues. Interestingly, the increase in DNMT3B protein was blocked by garcinol (Fig. 5A) (32), suggesting that histone acetylation is necessary for E₂ to increase DNMT3B levels.

We next examined the role of DNA methylation in mediating the effects of E₂ on memory. As with histone acetylation, we first tested whether novel object recognition is sensitive to pharmacological manipulations of DNA methylation. Immediately after training, ovariectomized females were infused with vehicle or the DNMT inhibitor 5-AZA into the dorsal hippocampus. 5-AZA significantly enhanced novel object recognition memory consolidation (Fig. 5B) (33), suggesting that DNMTs regulate novel object recognition independent of E₂. As with the HDAC inhibitor TSA, the effects of 5-AZA were limited to a brief window of time after training, as an infusion delayed three hours after training had no effect on memory (Fig. 5B) (33). We next found that 5-AZA prevented E₂ from facilitating novel object recognition memory (Fig. 5B) (33), suggesting that activation of DNMTs is necessary for E₂ to enhance novel object recognition memory consolidation. Although this finding suggests that DNA methylation regulates E₂-induced memory enhancement, more definitive conclusions await direct measurement of specific E₂-induced changes in DNA methylation.

In summary, our data show that E₂-induced increases in dorsal hippocampal histone acetylation are specific to histone H3 and are dependent on ERK activation in the dorsal hippocampus. E₂ also decreases levels of HDAC2, and possibly HDAC3, protein in the dorsal hippocampus four hours after infusion, and this effect depends on histone acetylation. Further, novel object recognition itself is enhanced by HDAC inhibition and impaired by HAT inhibition, demonstrating that histone acetylation is essential for novel object recognition memory consolidation in ovariectomized females. These findings indicate that ERK-driven histone H3 acetylation in the dorsal hippocampus is necessary for E₂ to enhance novel object recognition memory consolidation, possibly through decreased expression of the memory-repressing HDAC2. Our data also suggest that an increase in *de novo* DNA methylation may be essential for E₂ to enhance novel object recognition memory consolidation. The most likely targets of this putative methylation are genes whose expression is detrimental for memory, such as *Hdac2*, *Hdac3*, or *PPI1*. The fact that the HAT inhibitor garcinol prevented E₂ from increasing DNMT3B levels suggests that histone acetylation may regulate DNA methylation by influencing levels of DNMT enzymes. As such, our data support the notion that the enzymes regulating DNA methylation and histone acetylation work in concert to mediate effects of E₂ on the expression of genes that mediate hippocampal memory consolidation. Ongoing work in our laboratory is aimed at identifying these genes.

Future directions

To date, our studies of the epigenetic processes that regulate E₂-induced memory enhancement provide a tantalizing glimpse into the complex epigenetic mechanisms through which E₂ influences memory. This work has only begun to reveal the countless ways in which chromatin modifications may influence the hormonal regulation of cognition. For example, it is difficult to know at this point whether E₂ influences epigenetic mechanisms in a fundamentally different manner from learning itself, or rather enhances the mechanisms already triggered by learning. In the case of post-training treatments, the answer may be the latter, unless learning triggers locally-synthesized E₂ that substantively alters how learning influences epigenetic processes during the learning event. Indeed, E₂ present during learning (whether locally-synthesized or exogenous) may play a permissive role in facilitating epigenetic alterations during learning that are not possible without E₂. This issue will need to be addressed in future studies using aromatase inhibitors to block local E₂ synthesis in ovariectomized females. Other future directions for this research are discussed below.

Epigenetics, estradiol, and aging—The loss of estrogens and progestins at menopause significantly increases the risk of memory decline and Alzheimer's disease (AD) in middle-aged women relative to men (23, 121). Although estrogens can enhance hippocampal memory in menopausal women and aging female rodents (57, 122), it has become widely recognized that estrogen treatment must be started during a critical period in middle age to benefit cognitive function in both women and rodent models (123). Indeed, duration of hormone loss has emerged as a critical regulator of the mnemonic response to E₂ in middle-aged rats, with delays of five months or more between ovariectomy and treatment preventing E₂ from enhancing spatial working memory in tasks such as the radial arm maze and T-maze (124-127). The precise mechanisms underlying this loss of responsiveness are unclear, but are likely due to alterations in the hippocampus. In middle-aged female rats, extended hormone loss prevents E₂ from enhancing hippocampal synaptic physiology (128), increasing hippocampal levels of choline acetyltransferase (129), and up-regulating ER α (130). Age-related reductions in ER α and ER β levels could contribute to this reduced hippocampal responsiveness, as levels of both receptors are significantly decreased in the middle-aged and aged female hippocampus (130-133). One proposed mechanism that may contribute to the etiology of the critical period and, more specifically, the loss of hippocampal ER α and ER β , is the increased ubiquitination and degradation of ER α and ER β that occurs in the CA1 region of aged female rat hippocampus (133).

Another mechanism that might contribute to the age-related reduction of classical ERs is increased methylation of ER α and ER β . The expression of ER α is highly regulated by methylation in specific promoters during early development. For example, methylation of ER α 5' Exon A is increased on post-natal day 10 in male mice, which coincides with a significant reduction in ER α 5' Exon A mRNA expression at this age (134). In support of this potential mechanism, ER β promoter methylation was increased in the neocortex of middle-aged (9-12 months old), but not young (3-4 months old), female rats, which corresponded with an age-related reduction in ER β mRNA (135). However, our own preliminary data from female mice indicates that epigenetic processes remain responsive to E₂ into middle-age (15-16 months old), where we find that dorsal hippocampal infusion of E₂ can still increase histone H3 acetylation, decrease HDAC2 and HDAC3 protein, and increase DNMT3B protein in the dorsal hippocampus (unpublished observations). E₂ also enhances object recognition memory in middle-aged female mice (89), so perhaps the mouse hippocampus remains responsive to E₂ further into old age than the rat hippocampus. Future studies in aged mice may resolve this issue, as E₂ no longer enhances object recognition or activates ERK or PI3K in aged (21 months old) female mice (89). Therefore, methylation changes similar to those observed in middle-aged rats may occur in aged female mice.

Regardless of the age of onset, epigenetic alterations are likely to play a major role in the closing of the critical period in females. As such, future research that pinpoints how age-related alterations in chromatin modifications influence the mnemonic response to E₂ could be used to develop treatments that reverse these changes, thereby significantly extending the critical period and enhancing the effectiveness of estrogen therapies.

Epigenetics and sex differences—Because all of our own work to date on epigenetics, estrogen, and memory was conducted in females, it will also be necessary to determine if similar epigenetic alterations occur in males in response to estradiol or testosterone. It is also important to note that the research reviewed above on the epigenetics of learning and memory has been historically conducted in males. Therefore, research detailing the modulatory influences of ovarian hormones on the epigenetics of learning and memory would add greatly to a literature that has studied epigenetic mechanisms primarily in males. Indeed, it is unknown if the epigenetic response to learning or hormones differs in the male and female hippocampus, so potential sex differences should be examined in future work. Several lines of evidence support the possible existence of such sex differences. For example, the masculinization of brain regions like the bed nucleus of the stria terminalis is regulated by testosterone-induced histone acetylation (136). In adulthood, contextual fear learning increases ERK activation in the ventral hippocampus more in male rats than in gonadally intact females, so epigenetic events downstream from ERK activation, like histone H3 acetylation, may be increased more in males than in females. Consistent with this notion are data showing that histone H3 acetylation in the hippocampus and cortex is higher in male mice than in females on embryonic day 18 and post-natal day 0 (137). In these same brain regions, males also exhibited higher levels of histone H3 methylation than females on post-natal days 0 and 6 (137). DNA methylation may also be sexually dimorphic, given numerous sex differences reported in the patterns of DNA methylation in the neonatal rodent brain (138). Given the dearth of studies examining the epigenetics of sex differences in the adult brain, this topic is ripe for investigation.

Other future directions—In addition to histone acetylation, other histone modifications, such as phosphorylation and methylation, play important roles in regulating memory formation (30, 31, 139). Therefore, the effects of E₂ on these processes should be examined in future studies. Much more work will also be needed to identify which promoter regions on key memory genes are altered by epigenetic processes in order to gain a more precise understanding of how gene expression in the hippocampus is altered by E₂. Future research should also investigate the roles that epigenetic alterations play in regulating the effects of E₂ and related hormones on other forms of hippocampal memory (e.g., spatial and contextual memories), and on other cognitive processes mediated elsewhere in the brain (e.g., the prefrontal cortex and amygdala).

Conclusions

Emerging data on epigenetic mechanisms have already revolutionized the study of cognition and mental illness. Understanding how modulatory factors, such as hormones, regulate the epigenetic code is essential to uncovering the molecular mechanisms that govern psychological processes in both females and males. Such discoveries will open the door to exciting new avenues of research that may lead to novel treatments to reduce the incidence and severity of neurodegenerative and psychiatric disorders.

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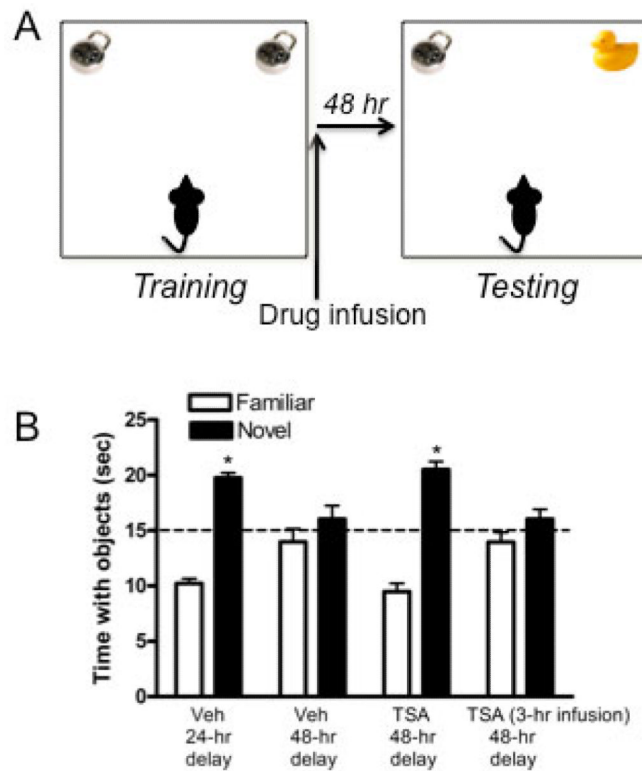


Figure 1.

Representation of the histone octamer illustrating the processes of histone acetylation and DNA methylation. Histone acetylation is regulated by histone acetyltransferases (HATs) that add acetyl groups (Ac) to lysine residues (K) on histone tails, and histone deacetylases (HDACs) that remove acetyl groups from lysine residues. During DNA methylation, DNA methyltransferases (DNMTs) add methyl groups to cytosine residues within CpG islands on DNA. Adapted with permission from (58).

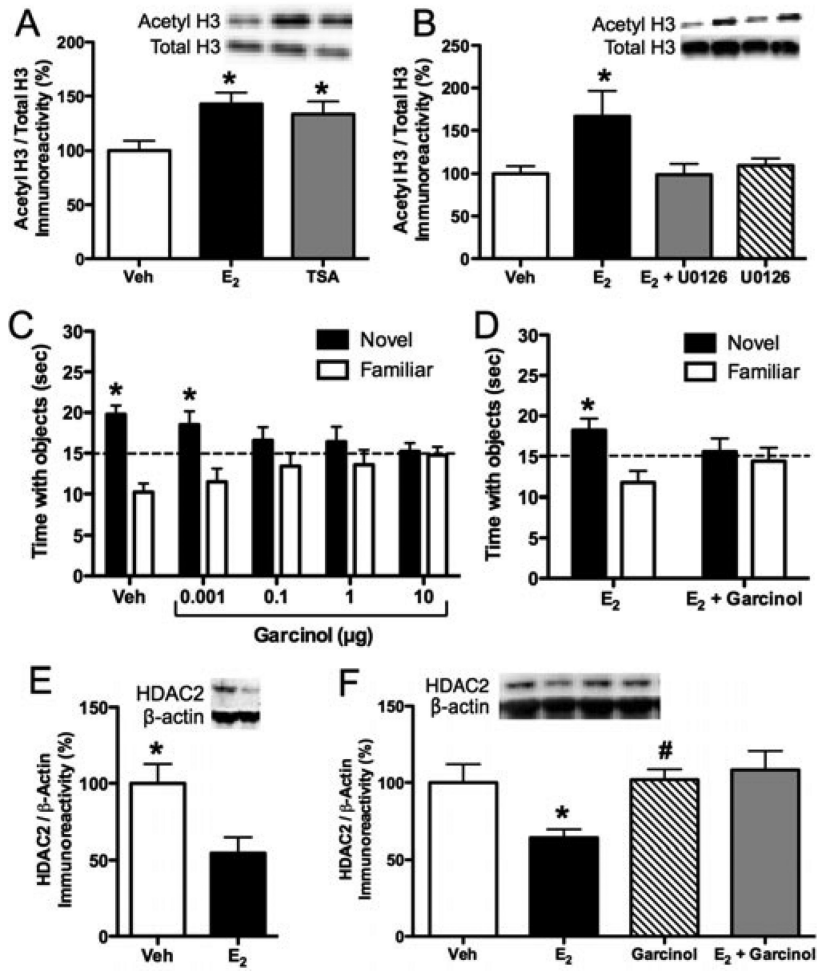


Figure 2. Our current working model of the molecular mechanisms mediating the rapid effects of E₂ on memory consolidation. ERα and ERβ could influence memory by binding to coregulators, including HATs, and stimulating estrogen response element (ERE)-mediated gene transcription. Alternatively, E₂ may rapidly enhance memory consolidation by triggering interactions between ERs and metabotropic glutamate receptors (mGluRs), NMDA receptor activation, and/or membrane ER activation, all of which can activate ERK and mammalian target of rapamycin (mTOR) signaling in dorsal hippocampal neurons. Activation of ERK then leads to histone H3 acetylation, and potentially the methylation of memory repressor genes like *Hdac2*, *Hdac3*, or *reelin*, causing increased expression of genes that facilitate protein synthesis and memory consolidation. This model is based on my laboratory's findings (32, 33, 87-90, 105), some of which are discussed in more detail in the main text.

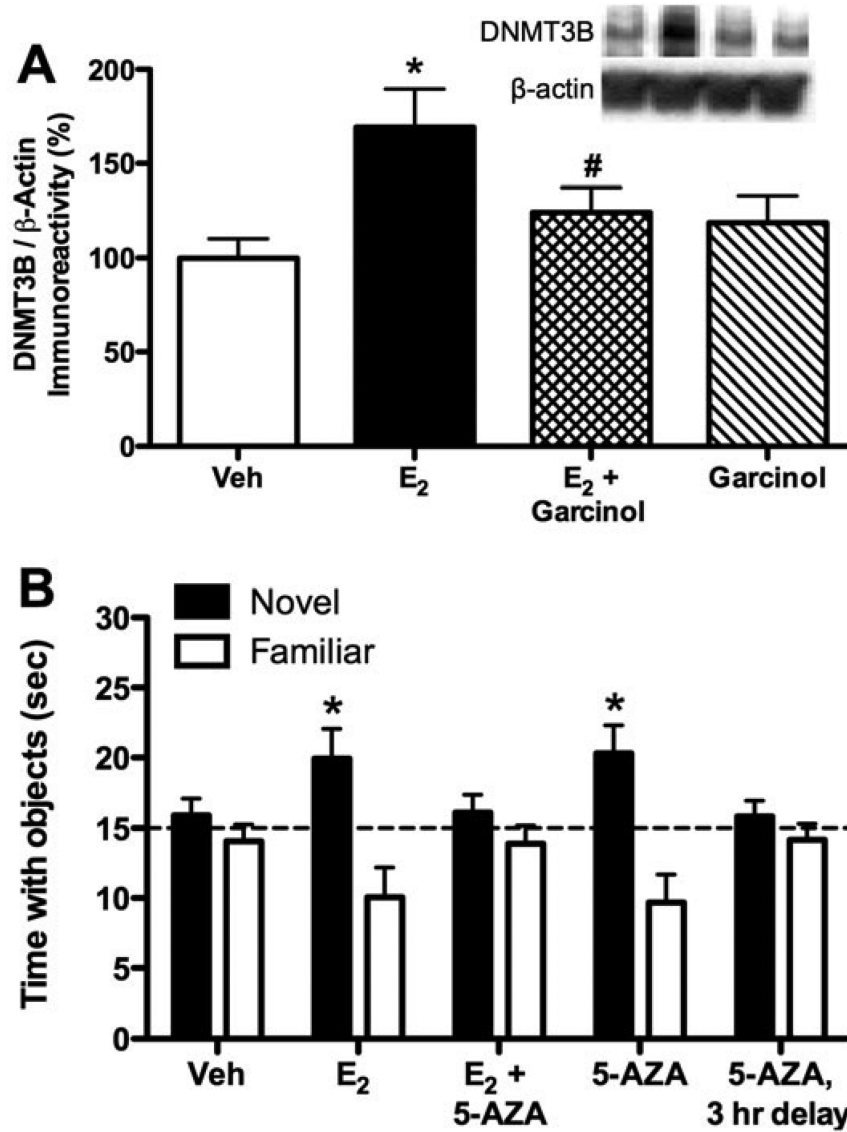


Figure 3. (A) Schematic of the novel object recognition testing protocol. Mice accumulate 30 seconds exploring two identical objects in an open arena. Immediately post-training, mice are infused and then returned to their home cage. Retention is tested 24 or 48 hours later by presenting mice with one novel and one familiar object. Mice who remember the familiar object spend more time than chance (15 sec) exploring the novel object. (B) The HDAC inhibitor TSA enhances novel object recognition memory consolidation. Ovariectomized female mice given bilateral infusions of vehicle into the dorsal hippocampus immediately after training spent significantly more time than chance (dashed line at 15 sec; $*p < 0.05$ relative to chance) with the novel object 24 hours after infusion, but not 48 hours after infusion, suggesting that they did not remember the familiar object for 48 hours. In contrast, mice given bilateral infusions of TSA (16.5 mM/hemisphere) into the dorsal hippocampus immediately after training did spend significantly more time than chance ($*p < 0.05$) with the novel object 48 hours later. However, this memory enhancement was not observed if TSA infusion was delayed for three hours. These data suggest that histone acetylation

enhances novel object memory consolidation. Bars represent the mean \pm SEM for each object. Panel B reprinted with permission from (33).

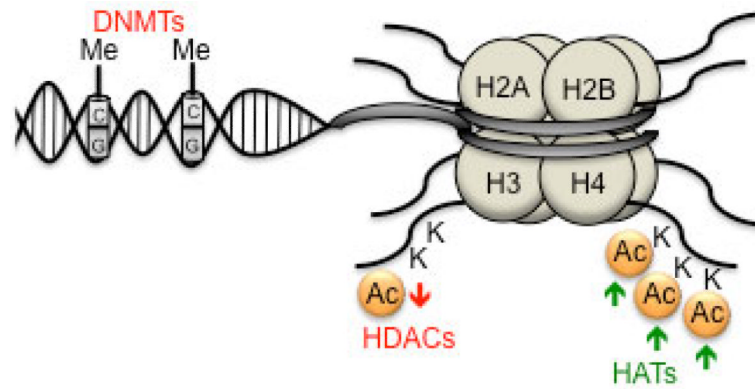


Figure 4.

ERK-driven histone H3 acetylation is necessary for E_2 to enhance novel object recognition memory consolidation. (A) Bilateral infusion of β -cyclodextrin encapsulated E_2 ($5 \mu\text{g}/\text{hemisphere}$) or TSA ($16.5 \text{ mM}/\text{hemisphere}$) into the dorsal hippocampus significantly increased histone H3 acetylation in the dorsal hippocampus relative to vehicle 30 minutes after infusion ($*p < 0.05$). (B) Infusion of E_2 ($10 \mu\text{g}$) into the dorsal third ventricle significantly increased histone H3 acetylation in the dorsal hippocampus relative to vehicle 30 minutes after infusion ($*p < 0.05$). Infusion of the ERK pathway inhibitor U0126 ($0.5 \mu\text{g}/\text{hemisphere}$) into the dorsal hippocampus blocked this increase, but had no effect on H3 acetylation on its own. (C) Mice were given bilateral infusions of vehicle or one of four doses of the HAT inhibitor garcinol into the dorsal hippocampus immediately after novel object recognition training. Mice infused with 0.1 , 1 , or $10 \mu\text{g}/\text{hemisphere}$ spent no more time than chance with the novel object. In contrast, mice infused with vehicle or $0.001 \mu\text{g}$ garcinol exhibited a significant preference for the novel object ($*p < 0.05$ relative to chance), suggesting that all but the lowest dose of garcinol impaired novel object recognition memory consolidation. (D) When this lowest dose ($0.001 \mu\text{g}$) of garcinol was infused into the dorsal hippocampus with E_2 , it blocked the effects of E_2 on memory, demonstrating that histone acetylation is necessary for E_2 to enhance novel object recognition memory consolidation. (E) Bilateral infusion of E_2 into the dorsal hippocampus significantly reduced levels of HDAC2 protein in the dorsal hippocampus four hours after infusion ($*p < 0.05$ relative to vehicle). (F) The E_2 -induced decrease in HDAC2 protein was blocked by $0.001 \mu\text{g}$ garcinol, indicating that histone acetylation is necessary for E_2 to reduce HDAC2 levels. Bars in all panels represent the mean \pm SEM. Insets in panels A, B, E, and F illustrate representative Western blot images. Acetylated H3 protein was normalized to total H3, and HDAC2 protein was normalized to β -actin. Reprinted with permission from (32, 33).

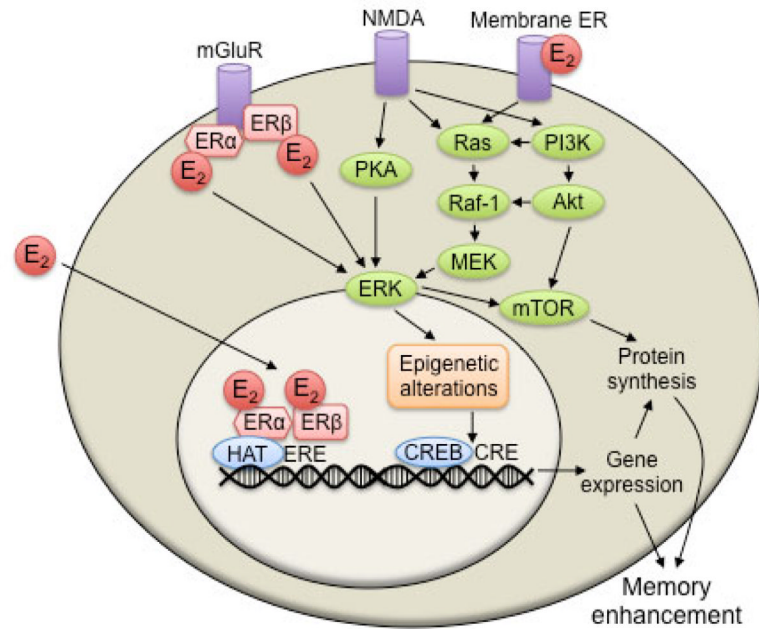


Figure 5.

DNA methyltransferase enzymes are involved E₂-induced memory enhancement. (A) Bilateral infusion of E₂ (5 μg/hemisphere) into the dorsal hippocampus significantly increased levels of DNMT3B protein in the dorsal hippocampus relative to vehicle four hours after infusion ($*p < 0.05$). This increase was blocked by concurrent infusion of garcinol ($\#p < 0.05$ relative to the E₂ group), suggesting that histone acetylation is necessary for E₂ to increase DNMT3B levels in the dorsal hippocampus. Garcinol alone had no effect on DNMT3B levels. Inset illustrates representative Western blot images. DNMT3B protein was normalized to β-actin. Reprinted with permission from (32). (B) Bilateral infusion of 5-AZA (100 μg/hemisphere) into the dorsal hippocampus administered immediately, but not three hours, after training significantly increased the time spent with the novel object relative to chance ($*p < 0.05$), suggesting that DNA methyltransferase enzymes regulate novel object recognition within a three-hour time window after training. 5-AZA blocked the memory enhancing effect of E₂, indicating that DNMT enzymes regulate the memory-enhancing effects of E₂. Reprinted with permission from (33). Bars in both panels represent the mean ± SEM.