

## Epigenetic Mechanisms Mediate Nicotine-Induced Reward and Behaviour in Zebrafish



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**Abstract:** Nicotine induces long-term changes in the neural activity of the mesocorticolimbic reward pathway structures. The mechanisms involved in this process have not been fully characterized. The hypothesis discussed here proposed that epigenetic regulation participates in the installation of persistent adaptations and long-lasting synaptic plasticity generated by nicotine action on the mesolimbic dopamine neurons of zebrafish. The epigenetic mechanisms induced by nicotine entail histone and DNA chemical modifications, which have been described to lead to changes in gene expression. Among the enzymes that catalyze epigenetic chemical modifications, histone deacetylases (HDACs) remove acetyl groups from histones, thereby facilitating DNA relaxation and making DNA more accessible to gene transcription. DNA methylation, which is dependent on DNA methyltransferase (DNMTs) activity, inhibits gene expression by recruiting several methyl binding proteins that prevent RNA polymerase binding to DNA. In zebrafish, phenylbutyrate (PhB), an HDAC inhibitor, abolishes nicotine rewarding properties together with a series of typical reward-associated behaviors. Furthermore, PhB and nicotine alter long- and short-term object recognition memory in zebrafish, respectively. Regarding DNA methylation effects, a methyl group donor L-methionine (L-met) was found to dramatically reduce nicotine-induced conditioned place preference (CPP) in zebrafish. Simultaneous treatment with DNMT inhibitor 5-aza-2'-deoxycytidine (AZA) was found to reverse the L-met effect on nicotine-induced CPP as well as nicotine reward-specific effects on genetic expression in zebrafish. Therefore, pharmacological interventions that modulate epigenetic regulation of gene expression should be considered as a potential therapeutic method to treat nicotine addiction.

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### 1. INTRODUCTION

Tobacco consumption has gradually decreased in developing countries (CDC, 2008; [http://www.cdc.gov/tobacco/data\\_statistics/tables/trends/cig\\_smoking](http://www.cdc.gov/tobacco/data_statistics/tables/trends/cig_smoking)). Recent data indicate that about 63% of the international population is protected by at least one tobacco consumption control measure. Nevertheless, up-to-date research suggests approximately 7.2 million people around the world continue to prematurely die annually due to illnesses caused by smoking tobacco cigarettes [1, 2]. Tobacco abusers primarily die from cancer and cardiovascular and pulmonary disease [3]. Another crucial problem with tobacco smoking is related to a well-defined sequence of drug usage and abuse that affects people in western societies. In this sequence, frequent use of non-illegal drugs, such as tobacco and/or alcohol, precedes

the use of cocaine and other illicit drugs [4-6]. Nonetheless, cellular and molecular mechanisms underlying substance use shift remain virtually unknown [5].

The principal alkaloid present in tobacco is nicotine, which binds to nicotinic acetylcholine receptors (nAChR) expressed in different tissues of the body of many vertebrate and invertebrate animals. NACHRs are ligand-gated cation channels that are widely distributed throughout the central and peripheral nervous system, skeletal muscles, and immune system [7]. NACHRs are expressed in nearly every region of the brain, both at pre- and postsynaptic sites [8, 9]. NACHRs expressed in neurons of the mesolimbic dopamine circuit and interrelated structures, such as the amygdala, hippocampus, and habenula (Hb), are critical mediators of reinforced behaviour and rewarding properties of nicotine [10]. The rewarding effects of nicotine on the brain are principally mediated by  $\alpha 4$ ,  $\beta 2$ ,  $\alpha 6$  and  $\alpha 7$  nAChR subunits [11]. However, more recently, experimental evidence has convincingly demonstrated that  $\alpha 5$ ,  $\alpha 3$ , and  $\beta 4$  nAChR subunits are also strongly associated with nicotine addiction [12].

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Interactions among the environment, exteroceptive and visceral sensitivity, and gene expression regulate animal behaviour. Slight differences in the interaction among genes, interoception and the environment may be responsible for generating either vulnerability or resilience to the compulsive seeking of drugs [13-15]. At the molecular level, epigenetic mechanisms integrate interoceptive and exteroceptive sensitivity by controlling gene transcription and RNA splicing to maintain homeostasis and regulate the adaptive behaviour of cells and organisms that is why unregulated epigenetic mechanisms can lead to disease and maladaptation, such as neurodegenerative disorders, cancer and drug addiction [16-22]. Regarding addiction, chromatin structure and gene expression are epigenetically reconfigured in neurons of the reward mesolimbic pathway by repeated exposure to drugs [5, 23, 24]. Epigenetic regulation of gene induction or silencing generates persistent alterations in neuronal circuitry functioning that may result in long-lasting drug-seeking compulsive behaviours [25, 26]. Unfortunately, this maladapted plasticity of the reward circuitry occurs in spite of the adverse consequences of drug consumption for homeostasis and the psychophysical well-being of consumers.

Epigenetics is defined as heritable chemical modifications to DNA and histones, which are able to control the transcription of genes without altering the coding sequence of DNA [27-29]. Every epigenetic enduring change could be heritable and reversible. Epigenetic modifications of DNA molecules and histones induce the remodeling/repositioning of nucleosomes and reorganization of the chromatin structure, making DNA more or less accessible to transcriptional machinery components [30].

Different types of chemical modifications are involved in the epigenetic control of gene expression by altering the chromatin condensation status and binding of the transcriptome components (Fig. 1). Among epigenetic mechanisms, DNA methylation has been associated with long-term chemical modifications that generate silencing of genes. Epigenetic post-translational modifications of histones, depending on the particular chemical group modified in these proteins, can activate or inactivate gene expression. Other important epigenetic mechanisms involve non-coding RNA gene silencing, RNA-editing, non-coding DNA regulatory sequences, prion-based epigenetic inheritance and Polycomb group proteins. The latter are a set of transcription repressors involved in developmental morphogenesis, chromosome X inactivation, and haematopoiesis. Other functions controlled by epigenetic mechanisms include protection against the viral genome and retrotransposon insertion, DNA replication and cell proliferation, DNA repair and maintenance of genomic stability, and aging [22, 31, 32].

DNA methylation is catalyzed by DNA methyltransferases (DNMTs) and occurs in cytosines within CpG islands. It has been more recently demonstrated that guanine and adenine can also be methylated [33-36]. DNA methylation is a reversible epigenetic mechanism because methyl groups can be removed from DNA bases by the coordinated action of demethylases with DNA repair protein complexes [37-40].

Histones are post-translationally modified by several mechanisms, including acetylation, methylation, phosphorylation, ADP ribosylation, ubiquitylation, and sumoylation,

among other more recently described chemical modifications of histone tails [41, 42]. Histone tail acetylation is regulated by histone acetyltransferases (HATs), which have been associated with short- and long-term epigenetic modifications [20, 43, 44]. On the other hand, histones are deacetylated by histone deacetylases (HDACs), which are a target of pharmacological treatments for several diseases [45, 46]. Generally, acetylated histones induce an "open" state of the chromatin structure [47], which enables access to transcription factors and RNA pol II to DNA. Histone acetylation and deacetylation must be maintained under homeostatic equilibrium since their deregulation results in different pathological conditions [22, 48]. Furthermore, histones can be methylated by histone methyltransferases (HMTs), and this kind of epigenetic modification can be either repressive or permissive for gene transcription [49]. For instance, methyltransferase activity of Polycomb group proteins catalyzes lysine 27 methylation of histone H3, causing gene repression [50].

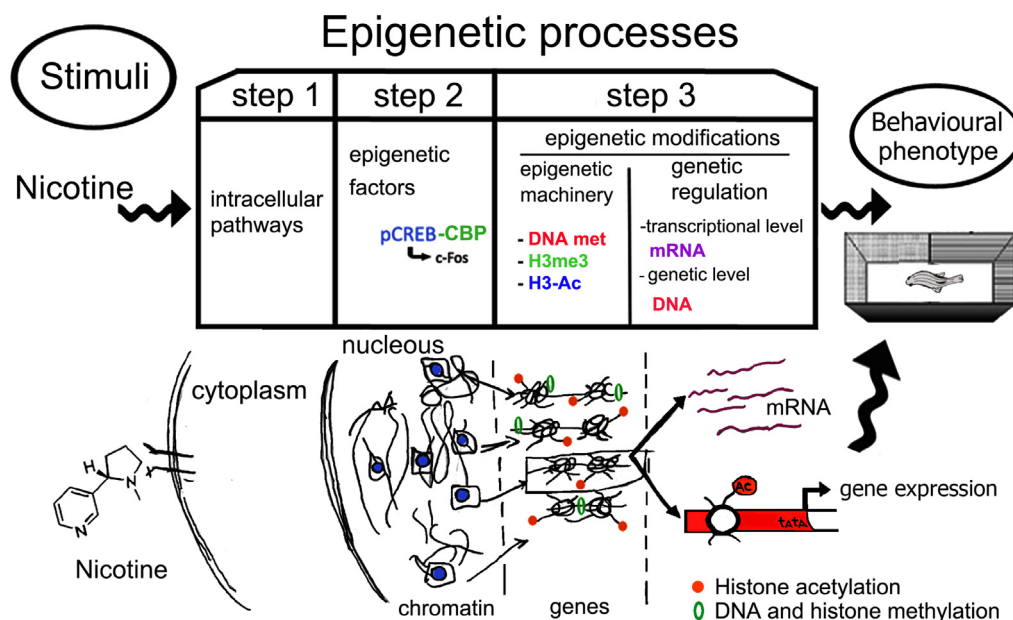
It has been suggested that the homeostatic balance of enzymes that catalyze post-translational modifications of histones and DNA methylation, as well as expression of factors that work as acetyl- and methyl-readers, is disrupted in neurons of the reward dopamine circuitry in addicted people and animal models of addiction [13, 51, 52]. For example, histone H3 and H4 acetylation increases in the main structures of the reward pathway as a consequence of acute or chronic exposure to psychostimulant drugs, such as nicotine, opiates and alcohol. Drug-stimulus induces unbalance between HAT and HDAC activity generating a high degree of histone tail acetylation in neurons of the nucleus accumbens (NAcc) [5, 23, 46, 53-55].

Furthermore, epigenetic regulatory interaction between histone and DNA methylation has been described to regulate the integration of environmental and interoceptive stimuli at the transcriptional level [18, 56]. In this regard, DNMT activity is recruited to chromatin by heterochromatin protein 1 (HP1), which binds to histone H3 trimethylated in lysine 9 (H3K9me3) [57]. Moreover, DNMT3a recruitment and maintenance of DNA methylation at intergenic regions require the presence of histone H3 dimethylated in lysine 36 (H3K36me2) in the nucleosome [58, 59].

It has also been suggested that DNA methylation may work in concert with histone tail modifications to dynamically regulate memory formation by remodelling chromatin structure in the adult nervous system [60, 61]. There are, however, some controversial findings regarding cause-effect mechanisms since it has been observed that DNA methylation patterns can guide histone modifications, whereas other studies suggest that histone tail chemical modifications guide DNA methylation status and gene expression silencing [48, 62].

## 2. NICOTINE REWARD

Nicotine modulates synaptic inputs to brain mesolimbic structures in an acute and long-lasting manner [63, 64]. Chronic nicotine exposure modifies the synaptic activity of diverse brain neuronal circuits, including mesolimbic dopamine pathway structures, and induces upregulation of nA-ChRs causing long-term addictive behaviors [7, 8]. Repeated nicotine exposure induces synaptic circuitry plasticity, such



**Fig. (1).** Scheme and drawing depicting some of the epigenetic processes involved in nicotine reward in the zebrafish brain. The epigenetic mechanisms principally studied in our laboratory and described in this review are histone H3 acetylation (H3-Ac) and methylation (H3me3), as well as DNA methylation. Acetylation was assessed by using the HDAC inhibitor phenylbutyrate and immunocytochemistry of some H3-acetylated. Methylation was studied by means of treatments with a methyl donor (L-methionine) to promote and enhance methylation of histones and DNA and a DNA methyltransferase activity inhibitor (5-Aza-2'-deoxycytidine). The permissive state of gene transcription allowed by histone acetylation in specific gene promoters is depicted in the cartoon. In contrast, DNA methylation is generally repressive for transcription. (A higher resolution/colour version of this figure is available in the electronic copy of the article).

as enhancement of glutamatergic input from cortical prefrontal areas onto dopamine terminals, projection neurons coming from the ventral tegmental area (VTA), and intrinsic neurons of the NAcc [65-71]. In nicotine addiction, different nAChR subtypes appear to differentially mediate somatic *vs.* affective components of withdrawal [72, 73]. The Hb, a small bilateral nucleus in the midbrain, is highly conserved among vertebrate species and has been implicated in nicotine addiction and negative reward among other physiological functions, including stress responses, learning and mood disorders [74, 75]. The Hb is highly interconnected with the interpeduncular nucleus (IPN), a singular structure in the midbrain tegmentum, forming a neuronal axis. The Hb-IPN axis is special considering nicotine reward because it densely expresses virtually all neuronal subtypes of nAChR [76, 77].

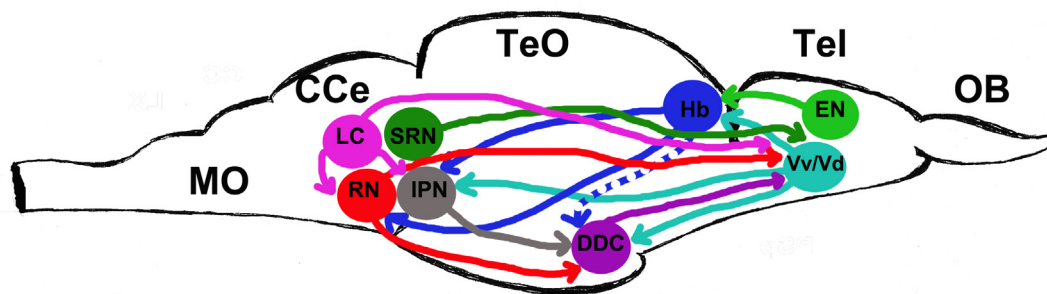
It has become very clear that exposure to psychostimulant drugs in combination with environmental and interoceptive factors affect DNA methylation and covalent histone tail modifications in neurons of brain structures activated by drug reward [54, 78-80]. Nicotine action on the mesocorticolimbic circuitry provokes long-lasting modifications at the molecular level, including epigenetic regulation of gene expression [5, 81]. The rewarding properties of nicotine, as well as other drugs of abuse, are studied in vertebrate animal models using self-administration and the conditioned place preference (CPP) task.

Regarding animal models to study drug reward, zebrafish (*Danio rerio*) are vertebrates of small size that have diurnal habits, including locomotor activity and feeding behaviour. This species of teleost fish is relatively easy to reproduce and maintain in laboratory conditions and possesses diverse advantages to study locomotor and exploratory behaviour as

well as many other physiological parameters of a diurnal animal. It has been conclusively demonstrated that zebrafish is an excellent experimental animal model to study addictive properties of drugs of abuse and addiction genetics [82].

Concerning the rewarding properties of nicotine, this species has been used to evaluate biochemical, genetic and epigenetic processes occurring in its brain mesolimbic circuitry (Fig. 2) after applying different nicotine treatments. Furthermore, a variety of behavioural tests have also been specifically developed for zebrafish to better characterize drug reinforcing properties. Recently, interesting studies have further highlighted zebrafish relevance as a translational model to identify genes involved in nicotine addiction and smoking behaviour in humans. Authors have discovered a crucial role for *slit3* by using a zebrafish mutant defective for this gene that is unable to develop nicotine preference. It has been demonstrated that this gene is also fundamental for nicotine addiction in humans [83]. Importantly, mutational and screening methodologies have been designed for describing new genes that might be involved in drug addiction [82, 83].

CPP remains so far the most studied behavioral task adequate to evaluate drugs of abuse reward in zebrafish. On the contrary, self-administration of drugs, widely used with rodents, has not been extensively developed for studies dealing with drug reward in zebrafish. There is only one compelling study that suggests that zebrafish can be effectively used to investigate drug addiction by self-administration [84]. CPP is a classical conditioning task in which an animal is taught to associate two *a priori* unrelated stimuli, that is, an environment with a rewarding drug. After repeated exposures to a drug in a particular environment, a single exposure to the



**Fig. (2).** Schematic sagittal view of the zebrafish brain depicting nuclei and pathways of the mesolimbic reward circuitry in zebrafish. The main structures of the zebrafish brain are also labelled. Different neurotransmitter pathways of the reward circuitry are colour-coded; 1) acetylcholine: dark green, 2) dopamine: purple & cyan, 3) glutamate: blue, 4) GABA: gray & light green, 5) norepinephrine: pink, and 6) serotonin: red; Dotted lines represent presumed connectivity.

**Abbreviations:** DDC: dopaminergic diencephalic cluster, EN: entopeduncular nucleus, IPN: interpeduncular nucleus, Hb: habenula, LC: locus coeruleus, RN: raphe nucleus, SRN: superior reticular nucleus, Vd: dorsal nucleus of the ventral telencephalic area, Vv: ventral nucleus of ventral telencephalic area; Zebrafish brain main areas: MO: medulla oblongata, CCe: corpus cerebelli, TeO: tectum opticum, Tel: telencephalon, OB: olfactory bulb; The drawing was based and modified from a study [149]. (A higher resolution/colour version of this figure is available in the electronic copy of the article).

environment without the drug generates an animal's response of drug-seeking [85-88].

CPP to nicotine has been well characterized in zebrafish, which have demonstrated higher CPP scores than the ones observed in rodents [89-93]. It has been reported that the CPP task can be studied in zebrafish as a translational research model for predicting human behaviour regarding drug abuse [88, 91]. Moreover, zebrafish offer the possibility of dissolving drugs of abuse such as nicotine, caffeine and opiates in the fish tank water. This experimental approach reduces stress and animal manipulation to a minimum by avoiding drug injections. Moreover, in the case of studying nicotine preference, in contrast to rodents, zebrafish can be tested with a broader range of doses without causing aversive effects [90, 92, 94, 95].

### 3. EPIGENETIC CHANGES INDUCED BY NICOTINE EXPOSURE

A growing number of studies suggest that epigenetics, that is, the processes controlling the accessibility of regulatory proteins to DNA, is key to understand how addiction develops and perhaps how it can be treated. In fact, HDAC inhibitors (HDACi) are currently under eager investigation because of their potential applicability in treating cancer and several neurological and psychiatric disorders.

### 4. NICOTINE EFFECTS ON THE BRAIN REWARD CIRCUITRY VIA HISTONE POST-TRANSLATIONAL MODIFICATIONS

Nicotine causes long-term changes in the mesolimbic reward circuitry [96, 97]; however, molecular, cellular and circuitry mechanisms that involve nicotine preference remain virtually unknown. Exposure to nicotine induces long-term neuronal changes in gene expression controlled by epigenetic mechanisms, such as histone acetylation regulated by HATs and HDACs [5, 81, 96-99]. It has been reported that nicotine has the capacity of facilitating histone H3 and H4 acetylation status by inhibiting HDAC activity in the striatum of mice

[5]. According to these studies, the nicotine effect may lead to a hyperacetylated state of histones that favours gene expression. On the other hand, it has also been reported that long-term nicotine exposure decreases H3K14 acetylation at the *brain-derived neurotrophic factor (bdnf)* Exon IV promoter region in rats. This effect was prevented by treatment with the HDACi sodium butyrate suggesting that specific HDAC activity can be induced by nicotine self-administration [99]. These findings suggest that nicotine reward also promotes a repressive chromatin structure silencing specific gene transcription.

Eighteen isoforms of HDACs classified in four classes (I, IIa and b, III, and IV) have been identified in mammals [100]. HDAC1 and HDAC2 proteins share more than 80% identity and act together in repressive complexes [101]. We have found that whereas nicotine induces CPP, the HDACi phenylbutyrate (PhB), selective for class I and IIa HDAC isoforms, abrogates nicotine-CPP consolidation in rats. Nicotine-CPP induces HDAC2 expression in the dorsal striatum and NAcc, the main nucleus of the mesolimbic reward pathway of the rat. This effect of nicotine-CPP correlates with the findings dealing with a nicotine-induced decrease in acetylation of the *bdnf* promoter described above [99]. Moreover, inhibiting HDAC activity with PhB causes a reduction of nicotine-seeking behaviours and HDAC2 expression [98]. The HDACi PhB inhibits preference but not aversion for nicotine. Therefore, HDAC inhibition primarily affects the motivational component of nicotine reward but not learning or mnemonic components because it did not affect nicotine aversion examined *via* a classical associative learning task [79]. It has been observed that self-administration of cocaine but not of sucrose is affected by inhibiting HDACs, suggesting that HDAC inhibition does not induce a common effect on the reward pathway in rats [102]. On the other hand, nicotine-conditioned rat brains show significant increases of H3K9 acetylation (H3K9ac), suggesting an effect of nicotine reward favouring transcription of specific genes [98].

We have evaluated for the first time HDACi disruptive effect on nicotine-environmental cue associative learning consolidation by using a five-choice conditioned place preference task in zebrafish. To this end, we have used a fish tank radial maze (FTRM) consisting of five arms of different colours [95]. By using this task, nicotine-CPP was robustly induced and consolidated even after testing nicotine-seeking behaviours during three consecutive days with distracting stimuli, such as the opening of novel arms- during testing sessions. As it was later found with a conventional CPP tank of two compartments [93], treatment with PhB during conditioning causes a disruptive effect on the reinforcing properties of nicotine. Nicotine reward in adult zebrafish, examined *via* CPP tasks, is dependent on HDAC activity in neurons of the mesolimbic pathway structures. Relative levels of HDAC1 mRNA (only one paralogue gene for *hdac1* and *hdac2* exists in zebrafish) are increased in nicotine-place conditioned zebrafish. Class III HDAC SIRT1 transcriptional expression is also increased by intermittent day-night nicotine pre-exposure followed by the establishment of a very robust nicotine-induced CPP. In contrast, reduced levels of SIRT1 mRNA are observed when chronic pre-exposure to nicotine or treatment with PhB prevents nicotine-CPP induction in zebrafish [93].

Furthermore, we have observed that H3K9ac is significantly increased by nicotine-induced CPP in the posterior tuberal nucleus (PTN) and the dorsal and ventral nuclei of the ventral telencephalon or subpallium (Vd/Vv) of the adult zebrafish brain (Fig. 2). PTN and Vd/Vv are the mesolimbic structures considered homologous to the VTA and NAcc, respectively, in the reward pathway of mammals. Repetitive nicotine exposure also increases H3K9ac in the dorsal Hb (dHb) [92], which interconnects with the interpeduncular nucleus that negatively modulates the VTA and NAcc activity [75]. Therefore, our studies indicate that a widespread and static state of acetylation of histones, promoted by inhibiting class I and IIa HDAC activity, abrogates nicotine-induced place preference and associated nicotine-seeking behaviours in zebrafish and rats. Moreover, nicotine reward established via a classical conditioning task in zebrafish and rats can increase the expression of specific types of HDAC, likely causing gene repression. Therefore, nicotine-induced increase in H3K9ac, which promotes specific gene transcription, must be balanced by HDAC1/2 and SIRT1 activity in key nuclei of the reward pathway to promote nicotine-induced long-term neuronal plasticity in the mesolimbic circuitry.

We have also found in rats and zebrafish that cAMP-responsive element protein phosphorylation (pCREB) increases in structures of the reward pathway immediately after the establishment of nicotine-CPP. Therefore, pCREB could be critical to induce brain changes related to nicotine reward-environmental cue associations [93, 97, 98]. Treatment with PhB during conditioning has no effect on pCREB levels observed in the majority of the structures of the reward pathway, suggesting that the increment in pCREB is independent or upstream of the nicotine reward effect on histone acetylation. However, HDACi treatment reverses the effect of nicotine-CPP on pCREB levels in the IPN and dHb, suggesting that these two areas of the mesolimbic circuitry are relevant for the inhibitory effect of the HDACi PhB on nicotine reward in zebrafish [97].

The observed increase in pCREB induced by nicotine-CPP might suggest the recruitment of CREB binding protein (CBP) to form pCREB-CBP complexes that bind to cAMP response elements (CRE) in promoter regions. CBP is a HAT and acetylates N-terminal ends of nearby histones, such as H3K9, to promote euchromatin formation and transcription [103]. Intermittent day-night nicotine pre-treatment, which potentiates nicotine-CPP consolidation, promotes the transcriptional expression of CBP in the brain portions containing the reward circuit structures of zebrafish [97].

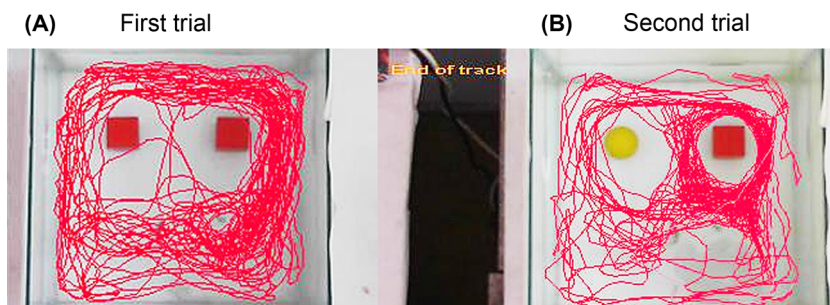
Mechanisms controlling HDAC activation have not yet been elucidated. Several Class II HDACs are activated *via* kinase phosphorylation, including  $\text{Ca}^{2+}$ /calmodulin-dependent protein kinase II (CaMKII) and cyclin-dependent protein kinase 5 (CDK5) [104, 105]. It is tempting to suggest that nicotine repetitive exposure provokes brain effects *via* nAChR that may involve kinase activation and phosphorylation of several targets, such as CREB protein and HDACs, in neurons of the mesolimbic pathway. Moreover, nicotine induction of CREB phosphorylation and CBP expression suggests pCREB-CBP complex formation, which in turn produces H3K9 acetylation promoting specific gene expression in cells of the reward nuclei of rat and zebrafish brains. In this regard, nicotine-activated nAChR induce the expression of transcription factors *via* CREB phosphorylation, such as the immediate early genes *c-fos* and *egr-1* regulating mechanisms of plasticity in neuronal circuits [106, 107].

Intermittent exposure to nicotine followed by short periods of abstinence in zebrafish significantly increases the reinforcing properties of nicotine. The persistence of nicotine effects on the reward circuit is likely mediated by changes in HDAC1 and SIRT1 expression, CREB phosphorylation and CBP transcriptional induction, regulating H3K9 acetylation and  $\alpha 6$  and  $\alpha 7$  nAChR subunit upregulation [93, 97]. Epigenetic mechanisms induced by nicotine preference also involve changes in the expression of the enzymes that regulate DNA methylation/demethylation and the induction of HDAC1-Sin3A-MeCP2 complex formation, which represses gene expression [108], as it has been observed in the reward circuit of rats [98]. Interestingly, treatment with the HDACi PhB abolishes nicotine-induced CPP and drug-seeking behaviours, whereas it completely abrogates HDAC1 and MeCP2 transcriptional expression in the zebrafish brain [97].

In conclusion, a bias in the acetylated state of various histone isoforms induced by a non-selective HDACi might disrupt a dynamic regulation of histone acetylation/deacetylation by specific signalling systems, such as the one mediated by nAChR in the dopamine mesolimbic circuitry, which is necessary to establishing nicotine-seeking behaviours and nicotine-induced priming for the dependence of other drugs of abuse [81].

## 5. NICOTINE AND HISTONE DEACETYLASE EFFECTS ON OBJECT PREFERENCE IN ZEBRAFISH

As it was previously described, zebrafish can learn to associate unconditioned and conditioned stimuli to produce a conditioned response reinforced by nicotine [90, 92-95]. The HDACi PhB prevents this association between stimuli and the locomotor response induced by nicotine during the CPP task in rats and zebrafish [90, 95, 97]. Therefore, taking into



**Fig. (3).** Picture representing the whole swimming trajectory (red tangle) of one zebrafish exploring for 5 minutes two objects submerged in the tank. (A) In the first trial and after three days of habituation to the tank, the zebrafish was placed back in the tank and explored for the first time two identical objects, in this case, red cubes. Before the second trial, one of the familiar objects was replaced by a novel object of different colours and shapes (in this case, a yellow ball was introduced in the tank). (B) After a short (90 min) or long (24 h) interval, the zebrafish was introduced in the tank and the locomotor activity of the zebrafish exploring the familiar and novel object was recorded. Zebrafish in different groups were treated with free-drug water, nicotine or/and the HDAC inhibitor phenylbutyrate (PhB) for 10 min immediately after the first trial was concluded. Zebrafish spent more time exploring the familiar red object, showing neophobia and preference for red over yellow objects of the same or different shapes. Nicotine in the short term and PhB in the long term significantly improved zebrafish awareness and recognition memory of familiar vs. novel objects [110]. (A higher resolution/colour version of this figure is available in the electronic copy of the article).

account zebrafish's ability for associative learning, zebrafish exploratory behaviour in an object preference task has been examined to analyze the effect of nicotine and HDACi on recognition memory consolidation (Fig. 3). Nicotine significantly enhances the exploration of a novel or familiar object by zebrafish when novel object preference was examined [109-111]. Size and colour are object features instrumental for zebrafish recognition memory. It has also been observed that acute administration of nicotine improves short-term but not long-term recognition memory for novel objects in zebrafish [110].

Memory consolidation in rodents is prevented by histone deacetylation regulated by HDAC activity [112, 113]. Taking into account that the HDACi sodium butyrate has been used to modify memory consolidation and potentiates long-term object recognition memory in rodents [114-116], we have assessed the effect of the HDACi PhB on recognition memory for novel objects in zebrafish [110]. Therefore, PhB effect on short- and long-term memory in the adult zebrafish was examined for the first time. It has been observed that the inhibition of HDACs with PhB enhanced long-term novel object recognition memory in zebrafish without affecting this type of memory when it was assessed in the short term. These findings, as in mice, support that epigenetic mechanisms involving a high degree of histone acetylation that promotes transcription are instrumental in consolidating and prolonging recognition memory for objects.

Another important consideration regarding findings dealing with nicotine and the HDACi PhB effects on object preference in zebrafish suggests that acute treatment with nicotine and PhB likely causes short- and long-term changes, respectively, in the activity of neuronal circuits in the brain involved in attention and recognition of visual cues. These neuronal activity changes induced by nicotine and an enhanced degree of histone acetylation might be accountable for improving spatial awareness and perception of colour, form and size of objects by zebrafish. Nicotine and HDACi in the brain significantly modify in the short and long term, respectively, locomotor activity and sensory interactions of

adult zebrafish with environmental cues. Therefore, apparently, nicotine and HDACi can stimulate attention and improve discrimination of the visual system helping for object and context recognition memory in zebrafish [110].

## 6. NICOTINE EFFECT ON HISTONE METHYLATION

Drugs of abuse can also directly regulate histone methylation. Histone methylation can induce or repress gene expression and methylation effects are context-dependent [117]. For example, histone H3 methylation at lysine 9 (H3K9me3) was found to be reduced in the NAcc after chronic cocaine administration [118]. This process is mediated by cocaine-induced downregulation of specific histone methyltransferases (HMT), G9a and GLP, which catalyze H3K9me3 formation [119]. Nicotine self-administration in rodents significantly decreases methylation at H3K27me3 and H3K9me2 sites in the promoter regions of *bdnf* and *cyclin-dependent kinase 5 (cdk-5)* [99, 120]. Acute treatment with nicotine reduces H3K9me2 levels and transcriptional expression of HMTs, and also decreases H3K9me2 specific binding to *bdnf* promoter in primary cultures of mouse cortical neurons and human lymphocytes [121]. Methylation of residues K27 and K9 of the H3 induces heterochromatin formation and represses gene expression [50, 57, 122]. Therefore, nicotine reward likely promotes transcription of these genes in the rodent brain.

L-methionine (L-met), which increases methionine availability, favours methylation of histones and DNA [123]. L-met supplementation was assessed on a nicotine-CPP task in zebrafish [124]. Three exposures to a low dose of L-met orally administered during conditioning are sufficient to abrogate nicotine reward effects on the zebrafish brain as well as several nicotine preference-associated locomotor behaviours. Interestingly, L-met treatment also causes an ansiolytic-like behaviour in zebrafish. DNA methylation effects are discussed in the next section, therefore, we focus herein on the effect of nicotine reward on histone methylation. Nicotine exposure during conditioning significantly decreases

H3K9me3 in the PTN and Vd/Vv (Fig. 2), which, as aforementioned, are two main structures in the reward pathway of zebrafish [124]. L-met supplementation blocks nicotine-induced CREB phosphorylation and significantly increases H3K9me3 in five key brain regions responsible for drug-seeking and reward in nicotine-place conditioned zebrafish. Moreover, relative expression levels of two HMT (G9a and SuV39H) mRNA are downregulated by nicotine preference in mesolimbic areas of the zebrafish brain. In opposition, treatment with L-met during nicotine conditioning increases the transcriptional expression of the two HMTs. Therefore, a decrease in histone methylation in the brain areas associated with drug reward associated areas might contribute addictive behaviours and underlie restatement [44].

## 7. NICOTINE AND DNA METHYLATION

DNA methylation simultaneously with post-translational modifications of histones is a key epigenetic mechanism involved in the control of gene expression. However, little is known concerning the regulation of addiction-like behaviors by DNA methylation.

DNMTs catalyze a reaction that adds a methyl group to the carbon-5 position of a cytosine (5mC), which is principally observed at CpG sites [28]. DNMT1 maintains methylated patterns in inherited strands of DNA through cell divisions, whereas DNMT3 catalyzes *de novo* DNA methylation. The presence of 5mC attracts methyl-CpG-binding domain proteins (MBD1-MBD4, MeCP2, and Kaiso among others), which recruit repressor complexes [28, 62, 125] and HDACs [126]. These methylated DNA binding proteins are known to be responsible for repressing gene transcription [127, 128].

Reversion of DNA methylation is regulated by a family of ten-eleven translocation (TET) methylcytosine dioxygenases that oxidize 5mC to 5-hydroxymethylcytosine (5hmC) [38]. In turn, TET enzymes can oxidize 5hmC to 5-formylcytosine (5fC) and 5-carboxylcytosine (5caC). 5fC and 5caC can be removed through a base excision repair mechanism of damaged DNA to produce plain cytosine [39, 129, 130]. Gadd45a regulates epigenetic gene activation by catalyzing repair-mediated DNA demethylation [131].

Looking for compounds that can reduce the rewarding properties of drugs of abuse, we and others focus attention on DNA methylation, hypothesizing that epigenetic regulation of gene transcription mediated by DNA methylation could be accountable for the neuronal changes induced by addictive drugs.

Cocaine induces global DNA hypomethylation and chronically administered L-met inhibits cocaine-CPP in mice [132]. It has also been observed that chronic exposure to L-met reduces the behavioural sensitization to cocaine and addictive-like behaviours *via* DNA methylation-dependent processes in rodents [133]. At the molecular level, methionine reverses hypomethylation induced by cocaine at CpG islands in the *c-fos* promoter. Repeated administration of nicotine for four days downregulates the expression of DNMT1 and prevents methionine-induced hypermethylation of glutamic acid decarboxylase 67 promoter, increasing its expression in GABAergic interneurons in the frontal cortex and hippocampus of mice [80].

It has been reported that brain levels and tissue distribution of 5mC and 5hmC are comparable between zebrafish and mammals. All DNMTs, as well as the majority of demethylation pathways, are highly conserved [134].

We have first observed, in zebrafish, that relative levels of DNMT1, DNMT3, TET1 and Gadd45 mRNA are significantly modified by chronic pre-exposure to nicotine for 14 days before nicotine-CPP in portions of the zebrafish brain containing the structures of the dopamine reward pathway [97]. The transcriptional expression of DNMT3 is increased, whereas levels of DNMT1 mRNA are reduced by chronic exposure to nicotine, which prevents nicotine-place preference consolidation. In opposition, DNMT1 transcriptional expression is significantly enhanced, whereas levels of DNMT3 mRNA are decreased in zebrafish treated with nicotine during daylight only, which mimics exposure intervals in smokers and induces strong consolidation of nicotine-place preference. Therefore, it seems that *de novo* DNA methylation mechanisms are inhibited, whereas maintenance methylation is intensified in zebrafish exposed to a day-night nicotine cycle that potentiates the rewarding properties of nicotine. Moreover, DNA demethylating enzymes TET1 and Gadd45 were highly expressed in zebrafish pre-exposed to chronic and intermittent day/night-nicotine. These pieces of evidence point out a dynamic process of DNA methylation maintenance by DNMT1 and demethylation regulated by TET1 and Gadd45. The findings suggest that nicotine reward consolidation also requires hypomethylated states, which are attained by inhibiting *de novo* methylation of DNA and promoting demethylation of specific genes.

Treatment with the HDACi PhB strongly induces the transcriptional expression of DNMT1, suggesting that a global state of histone acetylation causes DNMT1 gene expression induction. These findings also suggest that upregulation of DNMT1 expression is not sufficient for generating molecular changes in neurons of the mesolimbic circuit that lead to nicotine reward, but likely these molecular changes must be balanced by nicotine-induced regulation of HDAC activity. Treatment with PhB shows no effect on the transcriptional expression of TET1. Therefore, a further increase in DNMT1 transcriptional expression might be responsible for a high degree of gene methylation that, together with a high level of unregulated histone acetylation, prevents nicotine preference consolidation [97].

Furthermore, treatment for three days with a low dose of L-met completely abrogates nicotine-induced CPP and seeking behaviours associated with nicotine reward in zebrafish [124]. Nicotine-CPP inhibition caused by L-met correlates with transcriptional upregulation of DNMT1 and DNMT3. Moreover, L-met supplementation significantly reduces transcriptional expression of TET1 demethylase in the brain portions containing the structures of the reward circuitry of nicotine-conditioned zebrafish. Changes in mRNA levels of demethylases and methylases are accompanied by an increase in the percentage of cells immunopositive for 5mC and H3K9me3 in structures of the reward pathway.

Nicotine-CPP appears to have an opposite effect to treatment with L-met since nicotine-CPP consolidation correlates with a significant reduction of DNMT3 transcriptional expression, which catalyzes *de novo* methylation of DNA

strands, whereas the expression of TET1 demethylase increases. As aforementioned, nicotine-CPP correlates with HMT expression decrease.

Repeated administration of nicotine upregulates nAChR subunits [11, 135]. The upregulation of  $\alpha 6$  and  $\alpha 7$  but not  $\beta 2$  nAChR subunits is involved in nicotine-induced neuronal adaptations after nicotine-CPP in zebrafish [89, 90, 93, 124]. The HDACi PhB treatment during conditioning abolishes  $\alpha 6$  and  $\alpha 7$  nAChR subunit upregulation and nicotine-CPP.

Glutamatergic NMDAR1 is also upregulated after nicotine-CPP consolidation. Treatment with L-met during nicotine-place conditioning abrogates transcriptional upregulation of  $\alpha 6$  and  $\alpha 7$  nAChR subunits and NMDAR1. The disruptive effect on CPP given by L-met administration could be, at least in part, mediated by inhibiting  $\alpha 6$  and  $\alpha 7$  nAChR subunits and NMDAR1 upregulation.

Treatment with the DNMT inhibitor, decitabine, or 5-Aza-2'-deoxycytidine (AZA), during nicotine-place conditioning causes the opposite effect to L-met by increasing nicotine-CPP scores in zebrafish [124]. Similar findings have been described in rats using cocaine-induced CPP [136]. Moreover, treatment with AZA slightly potentiates the effect of nicotine-CPP on  $\alpha 6$  and  $\alpha 7$  nAChR subunit and NMDAR1 transcriptional expression. It has also been observed that AZA treatment reduces the transcriptional expression of enzymes related to the methylation of DNA and histones [124].

The observed findings indicate that an increase in global methylation is detrimental to the establishment of the nicotine rewarding properties in the mesolimbic circuitry of zebrafish. In contrast, global DNA hypomethylation by AZA facilitates nicotine reward.

By using the methylation-specific PCR technique (MSP) [137, 138], it has been found that nicotine-CPP in zebrafish induces hypomethylation in promoter regions of specific genes. Nicotine-CPP produces hypomethylation in the promoter region of the nAChR subunit and NMDAR1 genes [124]. This epigenetic mechanism likely underlies the upregulation of these neurotransmitter receptor mRNAs induced by nicotine-CPP in zebrafish reward circuitry nuclei.

In contrast, treatment with L-met increases the number of copies of the methylated (transcriptionally silenced) form of the  $\alpha 7$  nAChR subunit and NMDAR1 genes. Treatment with AZA in nicotine-conditioned zebrafish, as it has been observed with nicotine-conditioned animals in the absence of the DNMT inhibitor, increases the number of copies of the hypomethylated (transcriptionally permissive) form of these neurotransmitter receptor subunits, indicating that epigenetic regulation of expression of these genes plays a preponderant role in codifying the reinforcing properties of nicotine. Furthermore, L-met and AZA effects on the nicotine-CPP score are, at least in part, given by their ability to epigenetically regulate the expression of nAChR subunits and NMDAR1.

Methionine exposure reduces glutamate uptake and extracellular ATP catabolism in zebrafish telencephalon, dangerously increasing both neurotransmitters levels in the synaptic cleft [139]. Methionine was chronically administered to reduce cocaine-CPP in mice; however, it has been observed that long-term methionine exposure can provoke toxicity in humans and Alzheimer's disease-like memory deficiency in

mice [140-142]. Although it has been suggested that DNA methylation induces only long-term effects on gene expression [133], we have found that three days of L-met administration twenty minutes before conditioning are sufficient to abolish nicotine-induced CPP consolidation in zebrafish, suggesting that DNA methylation also triggers short-term neuroadaptations in the reward mesolimbic system of vertebrate [124].

## 8. EXPERIMENTAL AND CLINICAL TRIALS CARRIED OUT WITH SODIUM-4-PHENYLBUTYRATE, 5-AZA-2'-DEOXYCYTIDINE, AND L-METHIONINE

Several experimental studies in animal models of human disease as well as clinical trials indicate an important role for histone deacetylase inhibitors in treating human diseases. PhB has been approved by the US Food and Drug Administration (FDA) to treat urea cycle disorders. Clinical trials and experimental studies have indicated the potential benefit of using PhB for treating different types of cancer, cystic fibrosis, hemoglobinopathies, neurodegenerative and motor neuron disorders, such as Huntington's and Parkinson's disease and retinal and hepatic ischemia [56, 143]. Clinical trials have demonstrated significant amelioration of amyotrophic lateral sclerosis symptoms by using PhB in combination with other drugs [144]. Translational studies in mice have suggested a potential role of PhB for treating genetic myopathies and stroke [145]. DNA methylation and histone acetylation play a key role in the epigenetics of atherosclerosis [146]. Moreover, clinical trials have examined the combined and sequential action of demethylating agents, AZA and HDACi, for fighting HIV/AIDS [147]. Decitabine or AZA has also been approved by the FDA and is indicated as an antineoplastic agent for the treatment of patients with myelodysplastic syndromes (MDS) [148].

The effects of PhB are not only due to its function as an HDACi. PhB also plays a role as an ammonia sink and chemical chaperone [145]. Therefore, many more basic and translational studies need to be conducted to get insight into molecular mechanisms that mediate PhB, AZA and L-met effects on drug addiction [26, 46, 79, 98, 99, 124, 132, 149]. Regarding epigenetic effects, PhB and L-met likely act by inducing histone highly acetylated states and DNA and histone methylation, respectively, which completely abrogate nicotine-reward. It is likely that these compounds prevent gene expression regulation-driven, in nuclei of the reward circuitry, by drug of abuse repeated intake and drug-environment associations during habit acquisition for drug consumption. PhB is an approved pharmacological agent; it can exert potent metabolic and epigenetic actions on gene expression and stimulatory effects on long-term memory. A short treatment with L-met at low doses, avoiding toxicity issues, has also proved to prevent nicotine reinforcement. All of these features make them very interesting and powerful drugs to potentially treat drug addicts. This ultimate purpose will require conducting further experimental, and translational studies of drug reward and eventually clinical trials.

## CONCLUSION

The study of epigenetics involved in nicotine reward in the zebrafish model gives insight into the molecular mecha-



nisms that participate in establishing stimuli (drug)-environmental cues (exteroceptive sensitivity) associations during a learning experience (CPP). Our studies and studies of others have demonstrated a crucial role of histone acetylation/deacetylation and methylation/demethylation and DNA demethylation/hypomethylation occurring in neurons of the reward circuitry and interrelated structures when an individual becomes addicted to drugs.

Nicotine seeking is modulated by histone acetylation, since a class I and IIa HDAC inhibitor abolishes nicotine reward as well as nicotine-induced nAChR subunit upregulation, and is linked to changes in the expression of HDACs and HATs, together with increased CREB phosphorylation, in addition to other epigenetic factors that bind to DNA, allowing the transcription of specific genes. Nicotine induction of CREB phosphorylation, necessary to establish nicotine reward, is abrogated by global histone acetylation and methylation and DNA methylation. Treatment of zebrafish with HDAC inhibitors improves long-term but not short-term memory, suggesting a complex interaction between memory and generation and maintenance of drug addiction, probably mediated by histone acetylation. Moreover, nicotine effects and nicotine-CPP establishment are also associated to changes in HMT, DNMT and DNA-demethylase transcriptional expression. Nicotine reward is likely associated to demethylation of histone 3, which when highly methylated induces chromatin condensation and transcription blockade. Nicotine-induced changes in the brain structures of the reward pathway of zebrafish involve histone post-translational modifications that modulate specific transcription of genes. Some of these genes, such as nAChR and NMDAR subunits, are directly involved in nicotine effects on brain neural activity. A similar scenario was observed with DNA methylation in which administration of L-met and a DNMT inhibitor, respectively, decreases or increases the effectiveness of nicotine to induce seeking behaviours by modifying the expression of  $\alpha 6$  and  $\alpha 7$  nAChR and NMDA1R subunits.

Therefore, epigenetic mechanisms involving histone and DNA demethylation and histone deacetylation in the brain areas associated with nicotine reward might contribute to trigger and establish addictive behaviours and restatement. Epigenetic modulation that occurs in the brain during reward establishment can be pharmacologically interfered with to abrogate neuronal plastic changes induced by exteroceptive and interoceptive associations that lead to drug addiction.

#### CONSENT FOR PUBLICATION

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#### CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

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