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Valence coding in amygdala circuits

Michele Pignatelli1, **Anna Beyeler**²

¹Picower Institute for Learning and Memory, Department of Brain and Cognitive Sciences, Massachusetts Institute of Technology, Cambridge, 02139 MA, USA

²Neurocentre Magendie, INSERM 1215, Université de Bordeaux, 146 Rue Léo Saignat, 33000 Bordeaux, France

Abstract

The neural mechanisms underlying emotional valence are at the interface between perception and action, integrating inputs from the external environment with past experiences to guide the behavior of an organism. Depending on the positive or negative valence assigned to an environmental stimulus, the organism will approach or avoid the source of the stimulus. Multiple convergent studies have demonstrated that the amygdala complex is a critical node of the circuits assigning valence. Here we examine the current progress in identifying valence coding properties of neural populations in different nuclei of the amygdala, based on their activity, connectivity, and gene expression profile.

Neural substrate of valence

The concept of valence

Across the animal kingdom, environmental stimuli can elicit a repertoire of behavioral responses ranging from approach to avoidance. Valence is the *subjective value* assigned to sensory stimuli which determines subsequent behavior. Positive valence leads to approach and consummatory behaviors while negative valence leads to defensive and avoidance behaviors [1,2]. For many sensory stimuli the assigned valence is innate, however, valence is weighted by the internal state of the organism and by its previous experiences [3,4] (Box 1). A simple example of state-dependence of valence is the value assigned to food, which strongly depends on the homeostatic needs of the animal [5]. Another internal state regulating valence assignment is basal anxiety. Indeed, high anxiety levels can induces a bias towards negative valence, even for stimuli that are normally rewarding [6].

Despite the fundamental role of valence on animal survival and well-being, the underlying neurobiological substrate remains partially understood. One of the main working hypothesis postulates that specific neural circuits assign valence to stimuli in order to activate defined motor patterns and ensure an adaptive behavioral response [3,7]. In line with this hypothesis, human brain imaging has identified divergent networks activated in response to stimuli of

Corresponding author: Beyeler, Anna (anna.beyeler@inserm.fr). Conflict of interest statement Nothing declared.

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positive or negative valence [8–10]. Multiple animal models including non-human primates [11], rodents $[12^{\bullet\bullet}]$, drosophila [13] and bees [14] have been used to decipher how neuronal populations composing these networks encode valence.

Defining valence circuits – role of the amygdala

A vast body of literature reporting gain and loss of function experiments, as well as correlative measures of neuronal activity, has identified the amygdala complex as a central node to drive specific motor patterns in response to external stimuli [4,15–17]. The amygdala complex includes three main groups of nuclei: the basolateral amygdala (BLA), the central amygdala (CeA) and the medial amygdala (MeA) (Figure 1). Developmentally, the CeA and MeA arise from the same cell lineage, presenting a striatal-like organization compared to the BLA which originates from a different lineage and presents a cortical-like organization [18,19] (Figure 1a–b). Thus, the CeA is composed almost exclusively of inhibitory neurons, and the MeA is mainly composed of GABAergic neurons but contains one third of glutamatergic cells [20]. In contrast, the BLA is mainly composed of excitatory projection neurons $(-85%)$ and of a small proportion of local inhibitory interneurons $(-15%)$ [18,19]. Together with fast amino acid neurotransmitters, neurons of amygdala nuclei also produce numerous neuropeptides and express several neuromodulator receptors (Figure 1c). Despite increasing knowledge of anatomical and molecular properties of amygdala neurons, we are just starting to unravel their contribution to valence.

Neural coding of valence

The role of neuronal populations in assigning valence has been studied using gain and loss of function experiments, and through analysis of neural activity recorded during tasks of opposite valences. Valence coding has been defined in terms of neural firing in response to at least two conditioned stimuli (CS), one of positive and one of negative valence $[12\bullet 21]$ 23]. Depending on their changes in firing rate in response to both CSs, neurons can be classified into nine coding populations $[12\bullet 24]$ (Figure 2a). Among these nine classes, two include neurons responding similarly to cues of both positive and negative valence which could in principle support an arousal response. In addition, valence can also be defined as the differential response to positive and negative stimuli $[21,25^{\bullet},26,27^{\bullet}]$ (Figure 2b). In this case, neurons excited (or inhibited) by both positive and negative stimuli may still encode valence as they display a stronger response for one specific stimulus. In this framework, valence coding is rather defined by a coding preference or bias, than by an on/off coding pattern.

Recent advances in neurotechnologies allow us to analyze valence coding properties of single neurons in specific populations defined by other features including connectivity (inputs and outputs) and gene expression. This expands the experimental possibilities from local recordings within single brain regions, to circuit dissection at synaptic and molecular scales (Figure 3). The scope of this review is to synthesize the latest findings and future directions in identifying hallmarks of amygdala populations depending on their valence coding properties.

Valence coding in populations of the central amygdala (CeA)

The CeA is the main output of the amygdala and has primarily been studied in the context of fear-related behaviors [28]. However, the CeA has also repeatedly been reported to promote appetitive behaviors $[29\bullet 30,31]$. Although contradictory, these results could be supported by divergent activity of distinct neural populations. Extensive research has been dedicated to identify the function of gene-defined and projection-defined populations within the capsular, lateral, and medial areas of the CeA (CeC, CeL and CeM, Figure 1). Pharmacological inhibition of CeL as well as optogenetic activation of CeM both induce unconditioned freezing suggesting that these different subregions differentially encode valence [32]. Subregions of CeA express selective genetic markers such as protein kinase-Cδ (PKCδ), somatostatin (SOM), corticotropin-releasing factor (CRF), tachykinin 2 (Tac2), neurotensin (Nts) or serotonin 2A receptor (5-HT2_A, Figure 1c) [29^{\bullet},33^{\bullet},34], and a complex microcircuit connectivity characterizes the interaction among these cells $[35,36^{\circ}]$.

PKCδ ⁺ cells represent a prominent subpopulation in both CeC and CeL. Optogenetic inhibition of this population can suppress defensive behavior $[29\bullet 37]$. Nevertheless, while optogenetic activation of PKC δ^+ cells in CeC can drive defensive behaviors, activation of CeL PKCδ ⁺ cells does not drive valence-related behaviors and their suppression does not inhibit defensive behavior, but instead enhances drinking behavior [29●●] (Table 1). Consistently, it has been reported that neurons inhibited by a cue predicting a footshock $(CeL_{OFF} neurons)$ [32] largely overlap with PKC δ^+ cells [35]. However, optogenetic activation of PKCδ⁺ cells in CeL can increase fear-cue generalization and can be anxiogenic [38]. Lastly, optogenetic activation of PKC δ^+ cells in CeL suppresses food intake [39] whereas activation of $5HT2_a⁺$ cells, a marker for PKC δ^- cells in CeL, promotes food intake $[33]$.

As the PKC δ^+ population, the SOM⁺ population represents about 40% of the neurons in CeL and the two populations interact through mutual inhibition [36●]. Optogenetic activation of SOM⁺ neurons in CeL and in CeM can drive appetitive behaviors $[29\bullet\bullet]$, and their inhibition in CeL promotes defensive behaviors [40]. Consistent with this finding, activation of SOM+ neurons can decrease conditioned flight responses [41] but can also initiate passive freezing $[41,42]$. Finally, CRF⁺ cells are necessary for defensive behaviors [43], can increase conditioned flight responses, and the balance between conditioned flight and freezing behaviors is regulated by local inhibitory connections between CRF+ or activation of SOM⁺ neurons [41]. Altogether, activation of PKC_δ⁺ and SOM⁺ neurons are able to drive both appetitive and defensive behaviors depending on the experimental conditions (Table 1).

This discrepancy might stem from divergent connectivity of genetically defined populations, including synaptic inputs and outputs. For example, PKC₆+ cells of CeC receive direct inputs from neurons of the parabrachial nucleus expressing calcitonin gene-related peptide (PBN_{cgRP}) [44], and optogenetic activation of those inputs suppresses appetite and drives defensive responses [45,46]. On the other hand, inhibition of inputs from the paraventricular nucleus of the thalamus (PVT), which mainly targets $SOM⁺$ cells in CeL, strongly reduces fear conditioning [47]. Furthermore, inputs from the intermediate insular cortex (i.e. bitter

gustatory cortex) in CeA promote avoidance behaviors [48]; however, the genetic identity of the CeA target population remains unknown. Further, projection neurons of CeL and CeM targeting the ventrolateral periaqueductal grey (vlPAG) strongly drive hunting behavior [49●]. Finally, a recent functional mapping study has shown that inhibitory projection form CeA suppresses activity of vlPAG local interneurons disinhibiting the excitatory cells, which in turn project to the cholinergic cells of the magnocellular nucleus of the medulla driving a defensive response [50●●]. Overall, despite in depth knowledge of genetic populations of the CeA, few studies have analyzed their single-unit activity in response to both positive and negative valence, leaving their valence coding properties elusive (Table 1).

Valence coding in populations of the basolateral amygdala (BLA)

Multiple studies have performed single-unit recordings in the BLA during stimuli of both positive and negative valence. Although direct optogenetic stimulation of the lateral amygdala (LA) can elicit a defensive response in a naïve mouse [51], recordings of BLA neurons in monkeys, rats and mice have shown that around 50% of the units respond to predictive cues of positive or negative valence $[12^{\bullet}\bullet, 21, 27^{\bullet}]$, with an overrepresentation of neurons responding to positive valence in monkeys [21] and mice $[12\bullet$, and an even distribution of neuron responding to both valences in rats $[27\bullet]$. Additionally, pioneering work has shown that some BLA neurons track the value of a sensory stimulus during reversal of the CS-US association [21,22] emphasizing the critical role of the BLA in valence coding. Finally, a recent study has also identified that even if relatively few cells in the BLA cells encode valence, the valence assigned to a stimulus can be decoded at the population level of neural activity [27●].

As the BLA is mainly composed of glutamatergic projection neurons, the search for neuronal features defining the polarity of valence has been predominantly focused on postsynaptic targets (Table 1). Optogenetic activation has shown that projections to CeA (BLA-CeA) [52], medial prefrontal cortex (BLA-mPFC) [53–55] and ventral hippocampus (BLAvHPC) [56] can drive defensive behaviors. On the contrary, optogenetic activation of projections to the nucleus accumbens (BLA-NAc) has repeatedly been shown to support reinforcement [52,57,58] (Figure 3a). This accumulation of results reporting regulation of valence-related behavior by BLA projections supports the hypothesis that anatomically divergent populations of the BLA differentially encode valence. Moreover, recordings combined with optogenetic photoidentification of specific neural subpopulations have shown that BLA-NAc units are preferentially excited by a positive CS and BLA-CeA units are preferentially excited by a negative one [12●●]. Further, synaptic inputs on BLA-NAc and BLA-CeA neurons are regulated in an opposite manner after learning associations of positive and negative valence [52]. Importantly, in vivo recordings have also revealed heterogeneity of single neuron activity within projection-defined populations $[12^{\bullet\bullet}, 53, 59]$. This supports a model where valence coding of a projector population can be inferred from the projection target of its neurons, but the projection target of a single neuron is not sufficient to infer its valence coding properties (Figure 2).

BLA projection neurons are segregated in large neurons in the anterior part (magnocellular) and smaller neurons in the posterior part (parvocellular) [60]. Activity-dependent profiling

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combined with extensive gene screening $[61,62^{\bullet\bullet}]$ has shown that the magno-cellular and parvocellular populations are defined by the expression of the $Rspo2$ and $Ppp1r1b$ genes, respectively. Interestingly, optogenetic stimulation of Rspo2⁺ cells elicits a defensive response in naive mice whereas stimulation of $Ppp1r1b⁺$ cells promotes an appetitive response $[62^{\bullet}\bullet]$. Both populations send projections to the NAc and CeA, Rspo2⁺ cells monosynaptically contacting PKC δ^+ cells of the CeC whereas Ppp1r1b⁺ cells innervate the other cellular subtypes of the CeM and CeL (Figure 3b) [29●●]. The anteroposterior topography of the Rspo2 and Ppp1r1b gene markers does not overlap with the distribution of BLA-NAc and BLA-CeA populations which are intermingled with mediolateral and dorsoventral gradients [25●]. The ability of genetically defined and anatomically defined populations to drive polarized behaviors combined with the coding heterogeneity recorded in BLA projectors raises the interesting possibility that defining populations using a combination of anatomical and genetic approaches may be instrumental in selecting populations sharply tuned to a specific valence.

Populations of local inhibitory interneurons of the BLA expressing SOM or parvalbumine (PV) have been shown to differentially drive behavioral responses to aversive cues [63]. However, their role in positive valence coding remains unexplored. Similarly, oscillatory activity, which is generated by local inhibitory interneurons [64], is known to causally regulate behaviors driven by negative valence [65●], but has not been investigated with positive valence (Box 2). In addition, the BLA receives inputs from a vast array of regions also involved in valence, including the mPFC, anterior cingulate cortex (ACC), auditory cortex and multiple nuclei of the thalamus — all of which have been almost exclusively analyzed during aversive states [55,66–69]. Albeit essential to understand the functional role of local interneurons and inputs to the BLA in fear and defensive behaviors, the studies leave their implication in reward processing uncharted.

Valence in other amygdala nuclei

Most studies analyze the origin of valence in the CeA and BLA but surrounding amygdaloid nuclei also regulate valence. For example, direct optogenetic activation of the basomedial amygdala (BMA, Figure 1) is anxiogenic, as the optogenetic activation of the vmPFC inputs to this nucleus [70]. Interestingly, the BMA directly projects to the ventromedial hypothalamus (VMH) which regulates defensive and social behaviors [71].

Neurons in the medial amygdala (MeA, Figure 1) have repeatedly been shown to regulate social behaviors [20,72] and GABAergic neurons of the posterodorsal MeA promote social behaviors of both negative (e.g. aggression) and positive valence (e.g. mating and social grooming) [73]. Neurons in the MeA can be genetically identified by the unique marker laminin β 3 [74] and express numerous receptors including oxytocin receptors [72], estrogen receptors and the CRF receptor 2 [75]. MeA cells expressing CRF-2 receptor mRNA are active during a social experience of negative valence (social defeat stress) [76]. In addition, a subpopulation of MeA neurons expressing kisspeptin protein modulates anxiety and sexual partner preference in male mice [77], whereas neurons expressing the alpha-estrogen receptor controls body weight [78]. When analyzed independently of projection or gene markers, neurons of the cortical amygdala (CoA, Figure 1) represent odor objects of both

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valences using distributive population codes [79]. Optogenetic inhibition of CoA reduces innate responses to odors of both positive and negative valence [80]. Interestingly, neurons activated by odors of positive or neutral valence are mainly recruited in the posterior section of the CoA, compared to neurons activated by an odor of negative valence which are equally distributed in the antero-posterior axis [80].

Importantly, the intercalated cells (ITC), which are clusters of GABAergic interneurons (Figure 1), were shown to relay negative valence to the BLA, including fear and pain information [81–84].

Moving forward to crack the valence code

Gain and loss of function experiments have demonstrated that neuronal subpopulations of the amygdala defined by their projection targets or gene expression can drive behaviors of opposite valence (Figure 3). Activity-dependent markers and electrophysiological recordings have revealed that average activity of a population is generally consistent with the driven behaviors (Figure 3c). Yet, recordings revealing single-unit heterogeneity in valence coding within populations $[12^{\bullet}\bullet, 53]$ suggest the presence of functional subpopulations. Increasing the level of specificity by integrating multiple cell features, such as genetic identity and anatomical connectivity, could promote the identification of more uniform populations selectively encoding one valence $[85\bullet]$ (Figure 2c-d).

Anatomical complexity

Although the activity of BLA projection-defined populations can predict valence, these cells send collaterals to multiple brain regions [12●●]. The distribution of collaterals at a single cell level and its correlation with valence coding properties remains unexplored (Figure 3b). Projection collaterals, topography, and post-synaptic cell identity in the downstream region represent critical points that could reconcile conflicting results. For example, the NAc and the CeA both contain neurons expressing both dopamine D1 and D2 receptors, which have been shown to induce behaviors of opposite valence in the dorsal striatum [86]. Moreover it was shown that depending on the dorsal-to-ventral axis, optogenetic stimulation of NAc neurons induces preference or avoidance respectively [87]. To circumvent these limitations, systematic mapping of projection-defined, activity-defined or genetically defined populations in whole brain samples [88] will provide a greater level of understanding of the anatomo-functional organization of the amygdala. Micro-circuit connectivity including feedforward, feedback, and mutual inhibition also appears as a mechanism of population selection. For instance, optogenetic activation of the BLA-CeA population induces a stronger inhibition of neighboring neurons than activation of other projector populations $[25\bullet, 89]$. Moreover, mutual inhibition was described between functionally divergent populations such as PKC δ^+ and SOM⁺ neurons in CeA [35], as well as Rspo2 and Ppp1rb1 neurons in BLA $[62^{\bullet}\bullet]$.

Genetic complexity

Unique transcriptional signatures of multiple immediate early genes have been identified in the amygdala after experiences of positive and negative valence [90]. Similarly, neurons with

an increased expression of cyclic adenosine monophosphate response element-binding protein (CREB) in the LA are preferentially recruited to encode a memory of negative valence compared to neurons with a lower expression of CREB [91]. These studies highlight that beyond stable gene markers, dynamic gene expression is also a defining feature of neural populations encoding valence. Importantly, genetic identification of multiple genes is now possible in 'intact' fixed samples using new technologies such as MERFISH [92] or STARmap [93]. Interestingly, these techniques might also allow to identify the contribution of glial cells in valence coding which has so far only been described in CeM, for negative valence [94]. We expect the combination of these approaches with anatomical tracing and mapping of cellular activation to potentiate the progress of our understanding of valence coding in amygdala nuclei.

Conclusions

Over the last decade, the study of valence coding in the amygdala has made unprecedented progress by revealing elaborate genetic and anatomical circuits differentially involved in positive and negative valence (Figure 3). This exceptional leap forward is the fruit of technological advancements combined with the spread of systematic behavioral testing of both positive and negative valence in the same experiment. Beyond this experimental prerequisite, recent studies have even started to combine recordings in response to both positive and negative valence with recordings during anxiety-related behaviors [95], providing crucial data to understand the role of valence circuits in state anxiety. Future investigations into valence coding in animal models of neuropsychiatric disorders, might further advance our understanding of valence circuit dysregulations in the physiopathology of diseases including post-traumatic stress disorders, anxiety, depression, and addiction.

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Box 1 Innate versus learned valence in the amygdala.

Innate valence is attributed without requirement of learning and guides innate behavioral responses which have been selected during species evolution [5]. A clear example of innate valence is the unconditioned approach and avoidance exhibited by mice in presence of odorants of peanut oil and trimethylthiazoline (TMT), respectively. Neural ensembles in the BLA active during stimuli of positive or negative valence, also named 'engrams' [91,99], can drive behavioral responses such as approach for a 'positive engram' or avoidance for a *'negative engram'* [99,100]. In the dentate gyrus of the hippocampus, the valence of a 'positive engram' (neurons in a male mouse activated during interaction with a female) can be reversed by reactivating this *'engram'* during exposure to an experience of negative valence (electric footshock) [99]. Interestingly, the engram cells of the BLA do not exhibit such behavioral plasticity [99]. Nevertheless, pairing the activation of an innate *positive or negative engram* in the BLA with an olfactory stimulus can support learning and drive conditioned behaviors to the stimulus, even though it has not been paired with an aversive or rewarding experience [100]. This observation suggests that learned valence can be encoded by the same populations encoding innate valence. However, studies in projection-defined populations suggest that BLA-vHPC neurons specifically encode innate negative valence and not learned valence [12●●,56]. Similarly, in the CeA, direct electrophysiological recordings from neurons expressing the 5HT2A-R indicate that their activity is suppressed during innate fear but not during learned-fear, and that their inactivation upregulates innate-freezing response while downregulating learned-freezing response [101].

Box 2 Oscillatory synchronization.

Cortical regions of the mammalian brain generate patterns of rhythmic oscillations of the local field potential (LFP) covering frequencies from 0.05 to 500 Hz [64]. Selective frequency bands are associated with different brain states and behaviors. Originally described in the neocortex and hippocampus, oscillations have also been observed in the rodent BLA [102], where changes in power of specific LFP frequencies have been correlated with learning of associations of negative valence [103,104]. Interestingly, it was shown that local oscillations can have different impact on neurons depending on their downstream target [103]. Consistent with the existence of distributed brain states, synchronous oscillations in the theta $(7-12 \text{ Hz})$ and gamma $(40-120 \text{ Hz})$ bands between the BLA and interconnected regions occur during consolidation and retrieval of emotional memories [104–106]. For example during retrieval of a fear memory, the hippocampus and amygdala are synchronized in the theta band [107], whereas prefrontalamygdala circuits display synchronized 4-Hz oscillations [65●]. Interneurons are powerful regulators of this synchronized activity and are tightly controlled by several neuromodulators providing a gating mechanism for synaptic plasticity [108]. Whether oscillations of different frequencies, including gamma and theta display valence specific modulation remains unknown.

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Figure 1.

The amygdala complex and genetically identified populations. (**a**) Atlas of horizontal and coronal sections of the adult mouse brain highlighting the different nuclei of the amygdala. (**b**) Schematic of the different amygdala nuclei and identified genetic markers.

Figure 2.

Valence coding and population biases. (**a**) Definition of nine classes of neurons depending on their response to stimuli of positive and negative valence $[12\bullet$. In this classification neurons responding to both stimuli in a similar way (excitation or inhibition to both stimuli) do not encode valence. (**b**) Alternative classification of units including the amplitude of the response. In this case, neurons responding to both stimuli in a similar way also encode valence as they exhibit a stronger response to one valence [12●●,21]. (**c**) Multidimensional definition of neurons encoding valence. (**d**) Each line represents a neuronal population and every dot corresponds to a single neuron. A single feature defines populations with valence coding biases, and combining multiple features could potentially reveal valence selective populations.

Figure 3.

Circuit diagram illustrating valence biases in BLA and CeA. (**a**) Optogenetic activation of three projection-defined BLA populations induces defensive behaviors [52,53,56] and activation of the last population induces appetitive behaviors [52,57,58] (**b**) Intra-amygdala circuit diagram of genetic populations in the anterior (a) and posterior (p) BLA, and CeA. Anterior BLA Rspo2+ and posterior BLA Ppp1r1b+ neurons drive opposite behavioral responses and reciprocally inhibit each other [62●●]. Rspo2+ neurons innervate CeC PKCδ ⁺ neurons driving a defensive response. CeC PKC6⁺ neurons inhibit CeL PKC6⁺ neurons and Tac2+ CeM neurons, which mediate appetitive responses. Ppp1r1b+ neurons innervate all CeA neurons driving appetitive responses. CeC and CeL $PKC\delta^+$ neurons antagonize each other [29●●] (**c**) Recordings of BLA neurons defined by their projection have revealed coding biases for learned positive and negative valence. Although collateralization has been described at a population level, the relationship between collateralization pattern and valence coding at a single neuron level remains unknown.

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Studies manipulating and recording neural activity in gene-defined, input-defined and projection-defined populations. Studies manipulating and recording neural activity in gene-defined, input-defined and projection-defined populations.

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study reporting bidirectional manipulation of the tested behavior/s *: study reporting bidirectional manipulation of the tested behavior/s

'x': not tested, RTPP/A: real time place preference/avoidance, CPA: conditioned place avoidance, PL: prelimbic, IL: infralimbic, adBNST: anterodorsal part of the bed nucleus of the stria terminalis 'x': not tested, RTPP/A: real time place preference/avoidance, CPA: conditioned place avoidance, PL: prelimbic, IL: infralimbic, adBNST: anterodorsal part of the bed nucleus of the stria terminalis ,63,66,85 • ,96–98,102] $52 - 54,56 - 59,62$ • ,35,38–42,45–48,49 $\ddot{3}$.
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