

PKC δ is an activator of neuronal mitochondrial metabolism that mediates the spacing effect on memory consolidation

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Abstract

Relevance-based selectivity and high energy cost are two distinct features of long-term memory (LTM) formation that warrant its default inhibition. Spaced repetition of learning is a highly conserved cognitive mechanism that can lift this inhibition. Here, we questioned how the spacing effect integrates experience selection and energy efficiency at the cellular and molecular levels. We showed in *Drosophila* that spaced training triggers LTM formation by extending over several hours an increased mitochondrial metabolic activity in neurons of the associative memory center, the mushroom bodies (MBs). We found that this effect is mediated by PKC δ , a member of the so-called ‘novel PKC’ family of enzymes, which uncovers the critical function of PKC δ in neurons as a regulator of mitochondrial metabolism for LTM. Additionally, PKC δ activation and translocation to mitochondria result from LTM-specific dopamine signaling on MB neurons. By bridging experience-dependent neuronal circuit activity with metabolic modulation of memory-encoding neurons, PKC δ signaling binds the cognitive and metabolic constraints underlying LTM formation into a unified gating mechanism.

eLife assessment

This **fundamental** work substantially advances our understanding of the molecular basis of long-term memory formation. The study identifies PKC δ as a major molecular player in long-term memory formation and describes its translocation to mitochondria to promote pyruvate metabolism, specifically after spaced training. The evidence supporting the conclusions is **compelling** and the work will be of broad interest to neuroscience and medicine.

Introduction

Long-term memory (LTM) is a fundamental cognitive process that allows organisms to efficiently retain and retrieve information over extended (and sometimes lifelong) periods of time. Since the long-term retention of fortuitous or poorly relevant associations can drive maladaptive behavior, the triage of learning experiences and routing to LTM has to be tightly gatekept. As a result of this cognitive constraint, brains have evolved mechanisms for the default inhibition of LTM formation (Abel et al., 1998 [\[1\]](#); Scheunemann et al., 2018 [\[2\]](#)). Under certain circumstances, LTM inhibition is lifted in a process known as LTM gating. Defective gating in either direction is expected to cause memorization deficits or (on the contrary) hypermnnesia, with both conditions leading to a severe deterioration in the quality of life. It is therefore crucial to decipher the underlying mechanisms behind this precisely regulated process. One of the most conserved conditions known to potentially lift the default inhibition of LTM formation is the spaced repetition of learning (Abel et al., 1998 [\[1\]](#); Shaughnessy, 1977 [\[3\]](#)), which has been reported in a number of species from *Aplysia* (Sutton et al., 2002 [\[4\]](#)), *C. elegans* (Nishijima and Maruyama, 2017 [\[5\]](#)) and *Drosophila* (Tully et al., 1994 [\[6\]](#)) to mice (Glas et al., 2021 [\[7\]](#)) and humans (Shaughnessy, 1977 [\[3\]](#)). This phenomenon is called the spacing effect, in contrast with intensive learning (or cramming), in which massed presentation of information leads to the formation of a less persistent form of consolidated memory (Shaughnessy, 1977 [\[3\]](#)). Studies in animal models, in particular in fruit flies using an associative aversive olfactory paradigm, demonstrated that LTM formation following spaced training exerts a significant energetic burden on organisms (Mery and Kawecki, 2005 [\[8\]](#); Padamsey and Rochefort, 2023 [\[9\]](#); Plaçais et al., 2017 [\[10\]](#); Plaçais and Preat, 2013 [\[11\]](#)). Following the paired delivery of an odorant with electric shocks, flies show learned avoidance of this odorant for a couple hours (Quinn et al., 1974 [\[12\]](#)). Whereas spaced repetition of odor/shock pairing allows sustained retention (up to one week) (Bouzaiane et al., 2015 [\[13\]](#); Heisenberg, 2003 [\[14\]](#)), massed training results in the rapid decline (1-2 days) of the formed memory, which provides a powerful, experimentally tractable way to model the spacing effect versus cramming. Strikingly, in the hours following spaced training in fruit flies, their sucrose intake is observed to increase by over twofold (Plaçais et al., 2017 [\[10\]](#)), which does not occur after massed training. In addition, spaced, but not massed, training decreases the survival duration of flies under conditions of limited resources (Plaçais and Preat, 2013 [\[11\]](#)). These observations reveal a major impact of LTM formation on the energy balance of the whole organism, with this metabolic constraint being an additional incentive for the default inhibition of LTM formation. Interestingly, the recent finding that cellular energy fluxes are involved in the control of LTM formation (Plaçais et al., 2017 [\[10\]](#)) suggests that both cognitive and metabolic constraints linked with LTM formation may be merged in a unitary, cost-effective gating process. Indeed, we previously showed that the upregulation of mitochondrial metabolic activity in neurons of the mushroom bodies (MB), the insect brain's memory center, in the first hours following spaced training is critical to initiating LTM formation (Plaçais et al., 2017 [\[10\]](#)). This upregulation of mitochondrial metabolism depends on post-learning dopamine signaling from a specific pair of MB-afferent neurons, called MP1 neurons (or PPL1-γ1pedc neurons (Aso et al., 2014 [\[15\]](#))), which show sustained calcium rhythmic activity in the same time windows encompassing the first hours after spaced training (Plaçais et al., 2012 [\[16\]](#)). MP1 activates MB mitochondrial activity via the DAMB receptor (also named Dop1R2) (Plaçais et al., 2017 [\[10\]](#)). The putative interdependence of cognitive and metabolic constraints, two sides of the same coin, therefore calls for the identification of the neuronal molecular gatekeeper at the core of the spacing effect, linking neuronal network activity and mitochondrial energy metabolism.

The G-protein-coupled receptor DAMB preferentially engages with Gq (Cassar et al., 2015 [\[17\]](#); Himmelreich et al., 2017 [\[18\]](#)), which signals via the second messengers DAG (Mizuno and Itoh, 2009 [\[19\]](#)) and calcium, two canonical activators of the broad family of PKC enzymes. One particular PKC isoform, PKCδ, that belongs to the 'novel' PKC class (Duquesnes et al., 2011 [\[20\]](#)) exclusively regulated by DAG but not calcium (Duquesnes et al., 2011 [\[20\]](#)), shows unique properties that make it a candidate of particular interest. In non-neuronal mammalian cells, it was shown that PKCδ can translocate to mitochondria upon its activation (Wu-zhang et al., 2012 [\[21\]](#)), where it specifically

localizes to the intermembrane space. There, PKC δ is able to activate oxidative metabolism by targeting the pyruvate dehydrogenase (PDH) complex (Acin-Perez et al., 2010; Kim and Hammerling, 2020), which catalyzes the first step of pyruvate metabolism for oxidative phosphorylation. Despite this evidence, the mechanisms underlying the regulation of PKC δ translocation to mitochondria upon activation, and how it interfaces with extracellular signals, remains poorly understood. Although PKC δ expression is commonly used to identify specific neurons in the mammalian brain (Cai et al., 2014; Cui et al., 2017; Dilly et al., 2022; Haubensak et al., 2010; Wang et al., 2020; Williford et al., 2023), the functional role of PKC δ in brain tissues has remained thus far largely unexplored. Nonetheless, the putative ability of PKC δ to act as the interface between Gq-mediated activation and metabolic activity control prompted us to study this kinase as the missing piece in the puzzle of LTM gating that could bridge dopaminergic activation and neuronal mitochondrial metabolism.

We first uncovered that PKC δ activation is required in MB neurons for LTM formation through behavior experiments involving targeted genetic inhibition of PKC δ and *in vivo* functional brain imaging using a specific sensor of PKC δ activity, δ CKAR (Kajimoto et al., 2010; Wu-zhang et al., 2012), which we introduced in *Drosophila*. We further showed that PKC δ is a downstream effector of DAMB and that its translocation to the mitochondria is triggered upon LTM formation by MP1/DAMB signaling. Employing *in vivo* imaging of cellular pyruvate consumption, we showed that PKC δ intervenes in LTM formation through its metabolic role as a mitochondrial activator, by releasing the pyruvate dehydrogenase (PDH) complex inhibition. We therefore revealed that a major effect of spaced training is to mobilize the DAMB/PKC δ signaling cascade in order to perpetuate for several hours a neuronal metabolic enhancement that only transiently occurs after a single learning session. Overall, our data establish PKC δ as an essential activator of neuronal pyruvate mitochondrial metabolism that mediates the spacing effect on memory consolidation.

Results

PKC δ is required in MB neurons for LTM formation

To investigate the role of PKC δ in memory, we downregulated PKC δ expression at the adult stage in the MB neurons (see schematic in **Figure 1A**) and assessed memory formed using different protocols of aversive olfactory conditioning. These different protocols include the single association between an odor and shocks (1x conditioning), which elicits a short-lived memory that will rapidly decay after a few hours; 5 spaced cycles of conditioning with 15 min of rest intervals (5x spaced), which induces LTM; and 5 massed presentations without pauses (5x massed), which leads to the formation of a less robust, cramming-like type of memory (Bouzaiane et al., 2015; Heisenberg, 2003; Tully et al., 1994). To spatially and temporally restrict PKC δ RNAi expression, we took advantage of the VT30559-Gal4 MB driver (Pla  ais et al., 2017) combined with the ubiquitously expressed thermosensitive Gal4 inhibitor tub-Gal80^{TS} (McGuire et al., 2003). This system allows inducing RNAi expression in the MBs of adult flies, by transferring them at 30°C two days before conditioning. This protocol successfully decreased the whole-head PKC δ mRNA level (**Figure 1B**), thereby revealing PKC δ expression in MB neurons. When PKC δ was knocked down in adult MB neurons, flies subjected to 5x spaced conditioning presented LTM impairment (**Figure 1C**). When flies of the same genotype were kept at 18°C prior to conditioning, i.e. without induction of RNAi expression, LTM was normal (**Figure 1C**). In addition, the sensitivity to shocks and odors was normal in induced flies (**Supplementary Table 1**). We then investigated if other types of aversive memory were also affected by PKC δ knockdown in adult MB neurons. No defect was detected when memory was measured 24 h after 5x massed conditioning (**Figure 1C**), and memory was not affected when tested 3 h after single-cycle training (**Figure 1C**). All of these results were replicated with a second non-overlapping RNAi against PKC δ (**Figure 1 – figure supplement 1A**), which downregulates PKC δ expression

with similar efficiency (**Figure 1 – figure supplement 1B** [↗](#)). Altogether, these series of experiments demonstrate that PKC δ is specifically required for LTM in adult MB neurons, fulfilling the first condition for a molecular effector of the spacing effect.

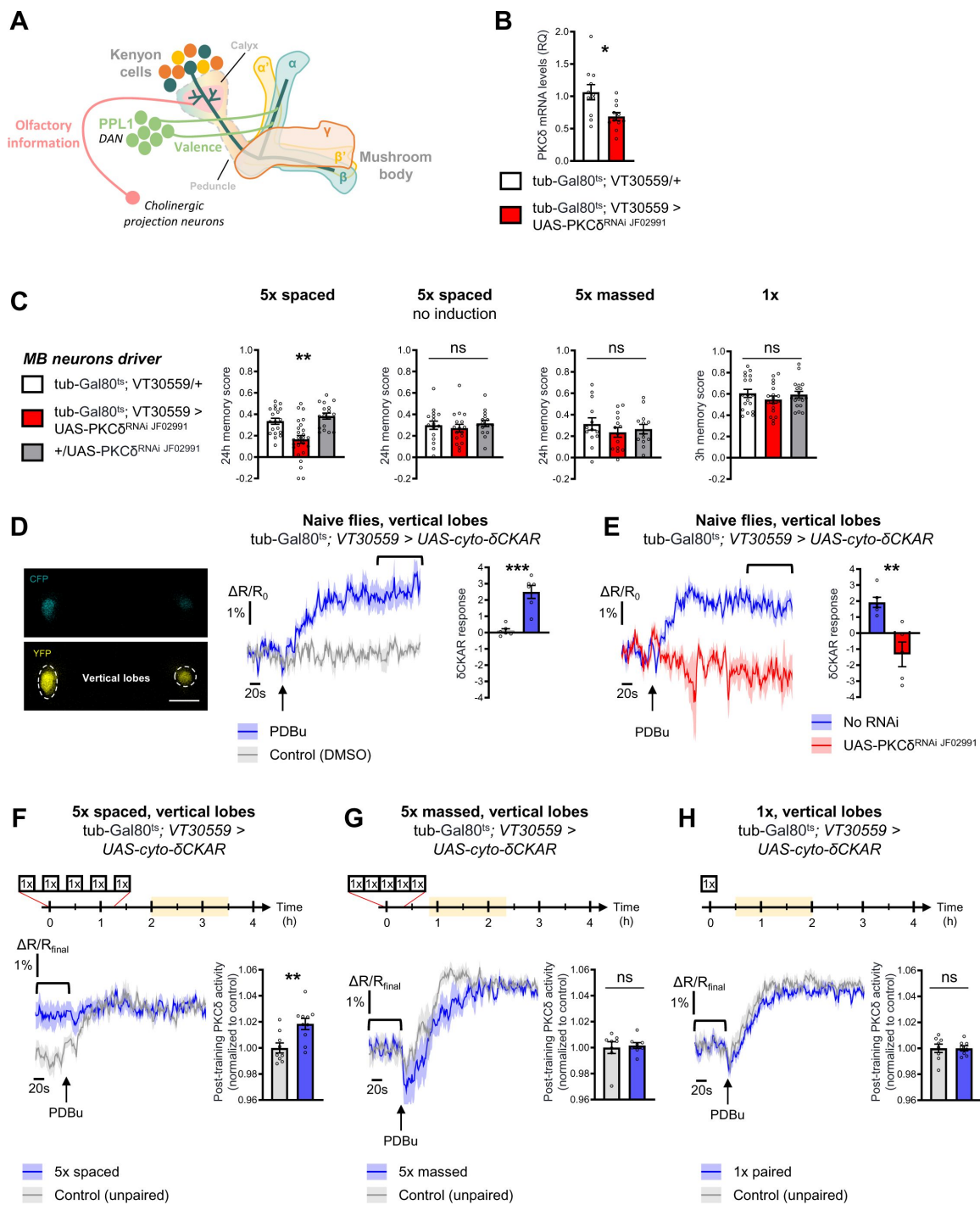


Figure 1.

PKC δ is required in MB neurons for LTM formation.

(A) Schematic representation of *Drosophila* MB. The MB includes ~2,000 intrinsic neurons per brain hemisphere. Their cell bodies are located in the dorsal posterior part of the brain. MB neurons each send a single neurite into the neuropil, which first traverses the calyx, a dendritic region where MB neurons receive olfactory input from projections neurons, and then extends into a long axonal branch. The bundled axons of MB neurons form a fascicle called the peduncle, which traverses the brain to the anterior part, where axons branch to form horizontal and vertical lobes according to three major branching patterns – α/β , α'/β' and γ (Aso et al., 2014) – that define as many neuronal categories. The MB lobes receive input from dopaminergic neurons (the DANs), which signal stimuli of positive and negative valences in a region-specific manner (Aso et al., 2014). During associative learning, dopamine release on coincidentally odorant-activated MB output synapses modulates the synaptic drive to the network of MB output neurons, which bias subsequent odor-driven behavior (Heisenberg, 2003; Hige, 2018). Aversive LTM induced by spaced training is more specifically encoded within the α/β neurons (Pascual and Pr  at, 2001; S  journ   et al., 2011; Yu et al., 2006), and we previously showed that LTM retrieval involves the depression of an attraction-mediated pathway efferent from the MB vertical lobes (Aso et al., 2014; Bouzaiane et al., 2015; Dolan et al., 2018; S  journ   et al., 2011). However, according to another recent study, LTM retrieval mobilizes in parallel another MB output circuit efferent from the medial lobes (Jacob and Waddell, 2020). **(B)** Expression of PKC δ RNAi in adult MB neurons induced a significant reduction in the mRNA level of PKC δ measured by RT-qPCR in fly heads. Relative Quantification (RQ) was performed, indicating the foldchange of mRNA levels relative to the control genotype ($n=11$, $t_{20}=2.826$, $p=0.0104$). **(C)** PKC δ knockdown in adult MB neurons impaired memory after 5x spaced conditioning ($n=17-25$, $F_{2,58}=12.59$, $p<0.0001$). Without the induction of PKC δ RNAi expression, memory formed after 5x spaced conditioning was normal ($n=15-17$, $F_{2,45}=0.4100$, $p=0.6661$). Memory formed after 5x massed training ($n=13-14$, $F_{2,37}=0.6511$, $p=0.5273$) and 1x training ($n=18$, $F_{2,51}=0.8135$, $p=0.4490$) was normal in flies knocked down for PKC δ in adult MB neurons. **(D)** The cyto- δ CKAR sensor was expressed in adult MB neurons and visualized in the CFP and YFP channels. Cytosolic PKC δ activity levels are recorded within the vertical lobes of the MBs (indicated with dashed line). Scale bar=50 μ m. In naive flies, application of 250 μ M of PDBu (black arrow), a pharmacological activator of PKC δ , resulted in the increase of the cyto- δ CKAR response, reaching a plateau, as compared to the DMSO control ($n=6$, $t_{10}=5.658$, $p=0.0002$). Quantification of the mean cyto- δ CKAR response was performed 280 s after PDBu application on a time window of 560 s (black line). **(E)** In naive flies, application of 250 μ M of PDBu (black arrow) resulted in an increase in the cyto- δ CKAR response that is abolished when PKC δ is knocked down in adult MB neurons ($n=5-6$, $t_9=4.182$, $p=0.0024$). Quantification of the mean cyto- δ CKAR response was performed 280 s after PDBu application on a time window of 560 s (black line). **(F)** To compare post-conditioning cytosolic PKC δ activities (between 30 min and 1 h 30 min post-conditioning, in yellow on the imaging time frame), cyto- δ CKAR traces were normalized to the plateau value reached after addition of PDBu (saturation of the sensor), thus the activity level of cytosolic PKC δ is estimated as the cyto- δ CKAR signal value before PDBu application. Cytosolic PKC δ activity is increased in the vertical lobes after 5x spaced associative paired conditioning as compared to a non-associative spaced conditioning (unpaired) protocol ($n=9-10$, $t_{17}=3.178$, $p=0.0055$). Quantification of the mean post-training PKC δ activity was performed on a time window of 120 s before PDBu application (black line). **(G)** After 5x massed paired conditioning, cytosolic PKC δ activity was not changed as compared to 5x massed unpaired conditioning ($n=8$, $t_{14}=0.3282$, $p=0.7476$). **(H)** Similarly, after 1x paired conditioning, cytosolic PKC δ activity was not changed as compared to 1x unpaired conditioning ($n=8$, $t_{14}=0.004121$, $p=0.9968$). Data are expressed as mean $\pm$ SEM with dots as individual values, and were analyzed by one-way ANOVA with post hoc testing by the Tukey pairwise comparisons test (C) or by unpaired two-sided t-test (B, D-H). Asterisks refer to the least significant P-value of post hoc comparison between the genotype of interest and the genotypic controls (C), or to the P-value of the unpaired t-test comparison (B, D-H) using the following nomenclature: * $p<0.05$, ** $p<0.01$, *** $p<0.001$, ns: not significant, $p>0.05$. See also **Figure 1 – supplement 1** and **Supplementary Table 1**.

Next, we investigated whether PKC δ was activated in MB neurons following spaced training. We took advantage of the existence of a genetically encoded FRET-based fluorescent reporter of PKC δ -specific activity, δ CKAR (Kajimoto et al., 2010; Wu-zhang et al., 2012), and generated

Drosophila lines carrying this sensor under UAS control. Expression of the δ CKAR sensor in the adult MB neurons was achieved using the tub-Gal80^{ts};VT30559-Gal4 driver as for the behavior experiments. To assess the efficacy of the δ CKAR sensor in *Drosophila* neurons, we first used two-photon *in vivo* imaging in the MB vertical lobes of naïve flies to monitor the response of the δ CKAR sensor to pharmacological activation of PKC δ , using PDBu (Wu-zhang et al., 2012). PDBu application induced a robust response of the sensor as compared to solvent alone (Figure 1D). Because PDBu can activate other PKCs than PKC δ (Alzamora et al., 2007; Wu-zhang et al., 2012), we ascertained the specificity of this response by performing the same experiment in flies expressing PKC δ RNAi in the MB at the adult stage, where PDBu failed to elicit a δ CKAR response as compared to flies that do not carry PKC δ RNAi (Figure 1E). Notably, the order of magnitude of the maximum δ CKAR response (2-3%) is consistent with what was previously measured *in cellulo* (Wu-zhang et al., 2012).

Having established the responsiveness and the specificity of the δ CKAR sensor, we sought to use this tool to measure the PKC δ activity level after conditioning in the MB vertical lobes, which are privileged sites of LTM encoding (Pascual and Pr  at, 2001; S  journ   et al., 2011; Yu et al., 2006). To compare post-conditioning PKC δ activity between different protocols, δ CKAR traces were normalized to the plateau value reached after saturation of the sensor by addition of PDBu, so that the activity level of PKC δ in each individual fly could be estimated as a δ CKAR signal value before PDBu application (Figure 1F). Measurements were performed in a time window of 30 min to 1 h 30 min after the end of training, when increased mitochondrial metabolism in MB vertical lobes after 5x spaced was previously reported (Pla  ais et al., 2017; Rabah et al., 2022). Using this procedure, we observed that the PKC δ activity level was increased following spaced training, as compared to control flies that were submitted to a non-associative unpaired spaced protocol (Figure 1F). Importantly, the PKC substrate-uncompetitive inhibitor Bis IV (Wu-zhang et al., 2012) (Figure 1 – figure supplement 1C) was still able to induce a decrease in PKC δ activity after spaced training (Figure 1 – figure supplement 1D), ruling out the alternative hypothesis that lack of a PDBu-induced δ CKAR response following spaced training might stem from an inhibition of PKC δ expression or a decrease of its activity below the detection threshold of the δ CKAR sensor. Therefore, we conclude from our results that 5x spaced conditioning actually induced a marked enhancement of PKC δ activity in MB neurons. In addition, neither massed nor 1x training elicited such an increase in PKC δ activity levels (Figure 1G-H), which supports the specific effect of spaced conditioning on PKC δ activation and is consistent with the outcome of our behavioral experiments.

The specific requirement of PKC δ in LTM formation prompted us to investigate whether it was more particularly required in α/β neurons of the MB, one of the three anatomical categories of MB neurons and a subpopulation known to be pivotal in LTM encoding (Pascual and Pr  at, 2001; S  journ   et al., 2011; Yu et al., 2006). We therefore restricted PKC δ RNAi expression to the α/β neurons exclusively at the adult stage, by means of the tub-Gal80^{ts};c739-Gal4 inducible driver (Turrel et al., 2018). This strongly impaired LTM performance after spaced training (Figure 2A). When RNAi expression was not induced, LTM was normal (Figure 2A). Na  ve odor and shock avoidance were unaffected by PKC δ knockdown in adult α/β neurons (Supplementary Table 1). Neither 3-h memory after 1x training (Figure 2A) nor memory after massed training were impaired (Figure 2 – figure supplement 1A). Hence, we show that PKC δ is more specifically required in α/β neurons for LTM formation. We then investigated PKC δ activity after spaced conditioning more specifically in α/β MB neurons using the δ CKAR sensor. Consistent with the requirement of PKC δ specifically for LTM in the α/β neurons, we observed an increase in PKC δ post-training activity after spaced conditioning (Figure 2B), an activation that was not elicited by a single-cycle of training (Figure 2C).

Altogether, we demonstrate here that PKC δ is specifically activated after spaced training and is required for LTM formation in MB α/β neurons, placing it as a key player of the spacing effect.

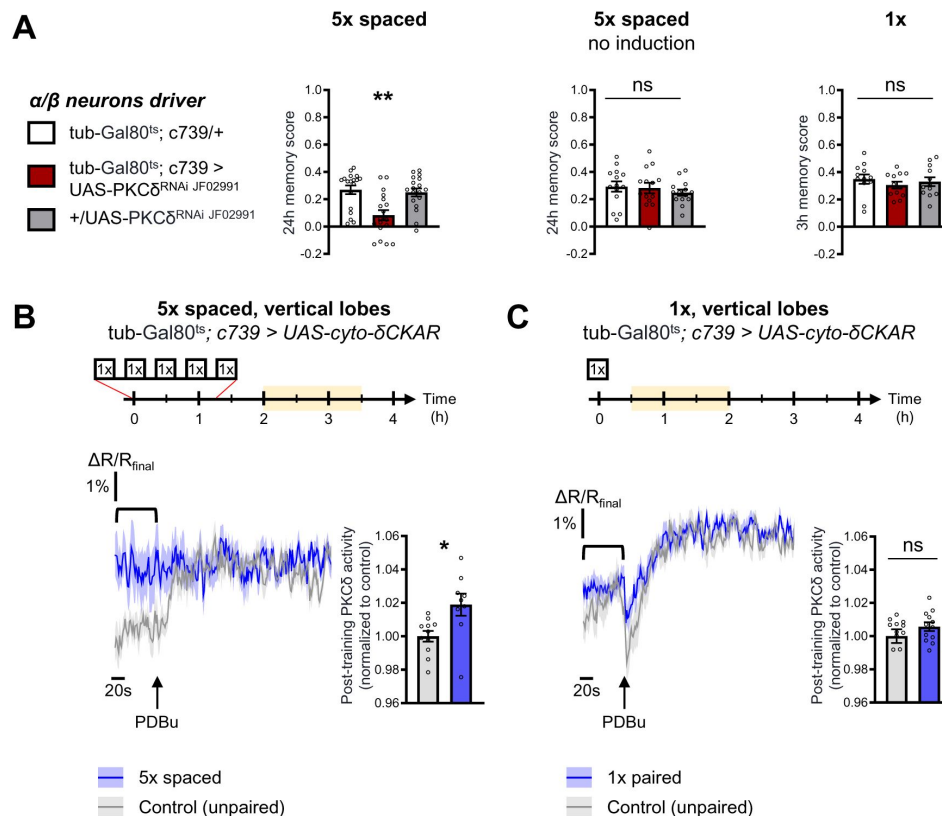


Figure 2.

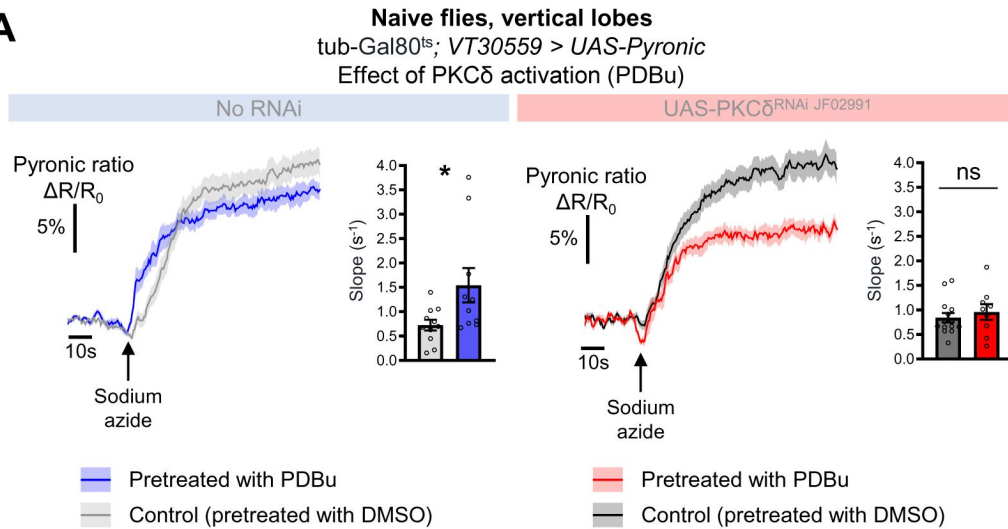
PKCδ is required in α/β neurons for LTM formation.

(A) When PKCδ was knocked down specifically in the α/β neurons of MBs, memory after 5x spaced conditioning was impaired ($n=18$, $F_{2,51}=9.521$, $p=0.0003$). Without PKCδ RNAi induction, memory after 5x spaced conditioning was normal ($n=14$, $F_{2,39}=0.4673$, $p=0.6301$). Memory was also normal after 5x massed training ($n=18$, $F_{2,51}=1.771$, $p=0.1805$) and 1x training ($n=12$, $F_{2,33}=0.5069$, $p=0.6070$) in flies expressing PKCδ RNAi in adult α/β MB neurons. (B) Using the same approach as detailed in Figure 1F, the post-training activity of cytosolic PKCδ was measured specifically in the α/β neurons, between 30 min and 1 h 30 min post-conditioning (in yellow on the imaging time frame). After 5x spaced paired conditioning, cytosolic PKCδ activity was increased in the α lobes as compared to unpaired conditioning ($n=9-11$, $t_{18}=2.723$, $p=0.0140$). (C) After 1x paired conditioning, cytosolic PKCδ activity was not changed as compared to unpaired conditioning ($n=12$, $t_{22}=1.159$, $p=0.2590$). Data are expressed as mean ± SEM with dots as individual values, and were analyzed by one-way ANOVA with post hoc testing by the Tukey pairwise comparisons test (A) or by unpaired two-sided t-test (B-C). Asterisks refer to the least significant P-value of a post hoc comparison between the genotype of interest and the genotypic controls (A) or to the P-value of the unpaired t-test comparison (B-C) using the following nomenclature: * $p<0.05$, ** $p<0.01$, ns: not significant, $p>0.05$. See also Figure 2 – figure supplement 1 and Supplementary Table 1.

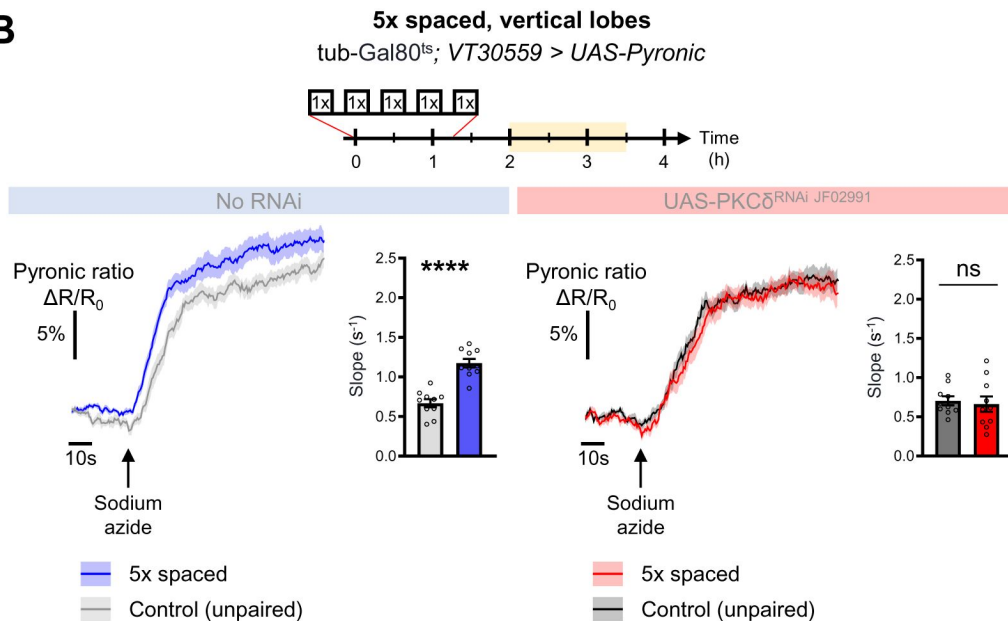
PKC δ regulates mitochondrial pyruvate metabolism for LTM

We have shown that PKC δ activation occurs after spaced training concomitantly to the increased mitochondrial metabolic activity that is known to be critical for the initiation of LTM formation (Plaçais et al., 2017 [↗](#)). As PKC δ can modulate mitochondrial metabolism in other tissues (Acin-Perez et al., 2010 [↗](#); Kim and Hammerling, 2020 [↗](#)), we wondered whether PKC δ activation in neurons was involved in this process. To address this question, we first asked whether pharmacological PKC δ activation using PDBu in a naïve context could be sufficient to upregulate the mitochondrial pyruvate flux in MB neurons. To this end, we used *in vivo* two-photon imaging of the genetically encoded pyruvate sensor Pyronic (San Martín et al., 2014) expressed in all MB neurons. We employed a previously characterized protocol (Plaçais et al., 2017 [↗](#)) to obtain a dynamic measurement of the pyruvate flux to mitochondria, by measuring the slope of pyruvate accumulation following the injection of sodium azide, a potent inhibitor of the mitochondrial respiratory chain (complex IV) (**Figure 3 – figure supplement 1A** [↗](#)). In the brains of naïve flies, activation of PKC δ through PDBu application resulted in an upregulated pyruvate flux to the mitochondria of the MB vertical lobes (**Figures 3A** [↗](#) and **Figure 3 – figure supplement 1B** [↗](#)). This upregulation did not occur when PKC δ was knocked down in adult MB neurons (**Figures 3A** [↗](#) and **Figure 3 – figure supplement 1B** [↗](#)), indicating that the increased pyruvate consumption relies on PKC δ activation by PDBu. These results reveal that in naïve flies, PKC δ activation is sufficient to increase the pyruvate flux to mitochondria in MB neurons.

A



B



C

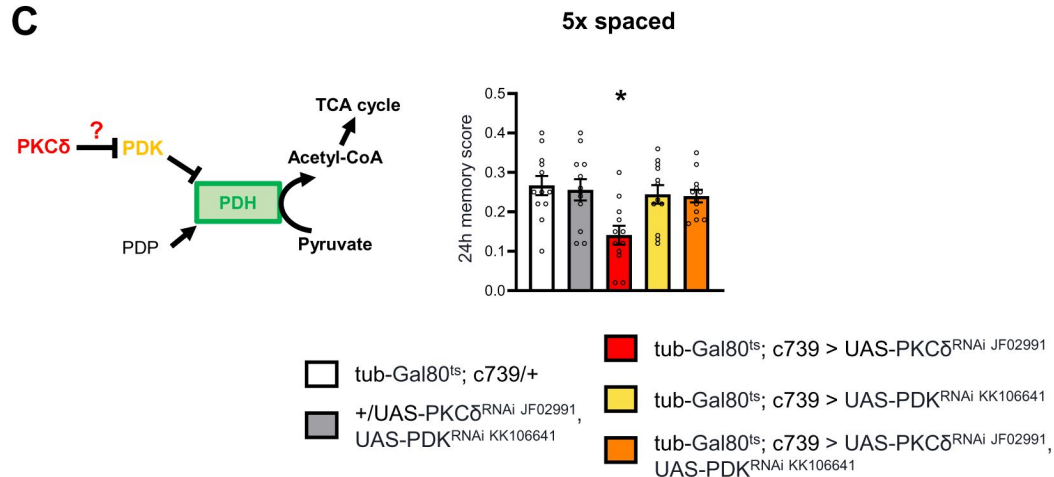


Figure 3.

PKC δ regulates mitochondrial pyruvate metabolism upon LTM formation.

(A) The pyruvate sensor Pyronic was expressed in adult MB neurons and the pyruvate FRET signal was quantified in the vertical lobes. In naïve control flies (tub-Gal80^{TS}; VT30559, UAS-Pyronic), PDBu pretreatment (250 μ M, 3 min) elicited a faster pyruvate accumulation following sodium azide application (5 mM, black arrows) as compared to flies pretreated with the DMSO solvent alone (left panel, slope measurement $n=10-11$, $t_{19}=2.311$, $p=0.0322$). This PDBu pretreatment induced increase in pyruvate accumulation is abolished when PKC δ is knocked down in MB neurons as compared to DMSO pretreatment (right panel, slope measurement $n=9-14$, $t_{21}=0.6734$, $p=0.5080$). Notably, the plateaus of the pyruvate accumulation kinetics are lower when PDBu is injected onto the brains as compared to the DMSO controls. Indeed, PDBu injection is followed by a slight increase in the measured Pyronic ratio that is not sensitive to PKC δ knockdown, indicating a PDBu indirect effect independent of PKC δ on pyruvate neuronal levels (**Figure 3 – figure supplement 1B**). **(B)** In control flies (tub-Gal80^{TS}; VT30559, UAS-Pyronic), spaced training elicited a faster pyruvate accumulation in axons of MB neurons after sodium azide application (5 mM; black arrow) as compared to non-associative unpaired training (left panel, slope measurement $n=10$, $t_{18}=6.751$, $p<0.0001$). PKC δ knockdown in adult MB neurons (tub-Gal80^{TS}; VT30559, UAS-Pyronic, UAS-PKC δ RNAi) impaired the spaced training induced increase in pyruvate accumulation in axons of MB neurons following sodium azide application (right panel, slope measurement $n=10$, $t_{18}=0.3794$, $p=0.7089$). As for **Figures 1** and **2**, imaging was performed between 30 min and 1 h 30 min post-conditioning, represented in yellow on the imaging time frame. **(C)** Left panel: schema of the regulation of the pyruvate dehydrogenase (PDH) complex. In mitochondria, PDHC catalyzes the conversion of pyruvate to acetyl-CoA, which enters the tricarboxylic acid cycle (TCA). PDH can be inactivated through phosphorylation by PDK. In contrast, PDP can activate a phosphorylated PDH. In our model, PKC δ regulates PDH activity via PDK inhibition. Right panel: after 5x spaced conditioning, flies coexpressing the PDK and PKC δ RNAi in the α/β MB neurons at the adult stage (tub-Gal80^{TS}; c739>UAS-PKC δ RNAi, UAS-PDK RNAi) exhibited normal memory formation as compared to genotypic controls (tub-Gal80^{TS}; c739/+ and +/-UAS-PKC δ RNAi, UAS-PDK RNAi). Flies solely expressing the PKC δ RNAi in α/β neurons at the adult stage (tub-Gal80^{TS}; c739>UAS-PKC δ RNAi) exhibited the reported LTM defect, whereas flies that were only knocked down for PDK in adult α/β neurons (tub-Gal80^{TS}; c739>UAS-PDK RNAi) formed normal memory ($n=12$, $F_{4,55}=4.746$, $p=0.0023$). Data are expressed as mean $\pm$ SEM with dots as individual values, and were analyzed by unpaired two-sided t-test (A-B) or by one-way ANOVA with post hoc testing by the Tukey pairwise comparisons test (C). Asterisks refer to the P-value of the unpaired t-test comparison or to the least significant P-value of post hoc comparison between the genotype of interest and the genotypic controls using the following nomenclature: * $p<0.05$, **** $p<0.0001$, ns: not significant, $p>0.05$. See also **Figure 3 – figure supplement 1C**.

We then investigated whether PKC δ mediates metabolic upregulation after spaced training. As previously reported (Plaçais et al., 2017), we observed an increased pyruvate flux in MB vertical lobes following spaced conditioning (**Figure 3B**) during the same time frame as for PKC δ activation. Remarkably, this effect was abolished by PKC δ knockdown in adult MB (**Figure 3B**). Therefore, we conclude that a critical role of PKC δ in LTM formation is to upregulate mitochondrial pyruvate metabolism for LTM gating.

Next, we examined how PKC δ could regulate mitochondrial pyruvate consumption. We previously showed that the upregulation of the pyruvate flux critical for LTM formation is directly related to the level of pyruvate dehydrogenase (PDH) activity (Plaçais et al., 2017). PDH activity is regulated by its level of phosphorylation: the PDH kinase (PDK) inhibits PDH, whereas PDH phosphatase (PDP) activates it (Lavington et al., 2014) (**Figure 3C**). Furthermore, in non-neuronal cells, PKC δ has been described as an inhibitor of PDK (Acin-Perez et al., 2010; Kim and Hammerling, 2020). Therefore, we hypothesized that a similar mechanism – i.e. PDK inhibition resulting in PDH activation – may occur in neurons in the context of LTM formation. To test this hypothesis, we reasoned that genetic inhibition of PDK may alleviate the LTM defect elicited by PKC δ knockdown (as described in **Figure 1C**). Indeed, we observed that coexpression of PDK

and PKC δ RNAis in adult α/β MB neurons did not induce a memory impairment, whereas expression of the PKC δ RNAi alone induced an LTM defect as expected (**Figure 3C**). Thus, inhibiting PDK is sufficient to fully rescue the memory defect induced by loss of PKC δ , showing that upregulating pyruvate flux is the critical function of PKC δ in LTM formation.

MP1 neurons activate PKC δ in the mitochondria of MB neurons via DAMB signaling

As detailed in the introduction, the metabolic upregulation induced by spaced training has been shown to be triggered by early post-learning activity of MP1 dopamine neurons, through the Gq-coupled DAMB receptor (Plaça et al., 2017). We therefore asked if MP1 neuronal dopamine signaling through the DAMB receptor could activate PKC δ and induce its mitochondrial translocation, which would be detected as an increase in PKC δ activity specifically at the level of the mitochondria. For this, we expressed a mitochondria-addressed δ CKAR sensor, mito- δ CKAR (**Figure 4 – figure supplement 1**), in MB neurons, and monitored PKC δ activity while artificially activating MP1 neurons in naïve flies using dTrpA1, a heat-sensitive cation channel that allows to induce neuronal firing through acute temperature increase (Hamada et al., 2008; Plaça et al., 2012). At the level of the peduncle, where MP1 neurons project on to the α/β MB neurons (Aso et al., 2014) (**Figure 4A**), flies subjected to the activation of MP1 neurons showed an increased PKC δ mitochondrial activity as compared to flies that received a similar thermal treatment but did not express dTrpA1 (**Figure 4B**). Strikingly, in flies that were additionally knocked down for the DAMB receptor in the MBs, MP1 neuron activation failed to increase PKC δ mitochondrial activity (**Figure 4B**). Interestingly, we found that PKC δ mitochondrial activity could also be increased in the vertical lobes of the MB in response to MP1 activation (**Figure 4C**). Altogether, these data show that DAMB signaling from MP1 neurons triggers increased PKC δ mitochondrial activity, reflecting its translocation to mitochondria in MB neurons.

To explore whether PKC δ mitochondrial activation and translocation occur upon 5x spaced conditioning for LTM formation, we expressed the mito- δ CKAR sensor in α/β neurons and measured PKC δ activity after 5x spaced training, using the same method as in **Figure 1F-H**. At the level of the peduncle, we found that 5x spaced training elicited a marked increase in PKC δ mitochondrial activity, as compared to the corresponding unpaired protocol (**Figure 5A**). Remarkably, DAMB knockdown in adult α/β neurons hampered PKC δ activation in mitochondria after 5x spaced training (**Figure 5A**). We observed a similar DAMB-dependent effect at the level of the vertical lobes (**Figure 5B**). Altogether, our data show that MP1-DAMB signaling induced by spaced conditioning results in PKC δ activation at the level of the mitochondria, where it upregulates the PDH complex to gate LTM formation through increased pyruvate flux.

Spaced training prolongs learning-induced metabolic enhancement

The results obtained thus far uncover a DAMB/PKC δ cascade that mediates an increase in pyruvate consumption by MB neuronal mitochondria. As previously reported (Rabah et al., 2022), single-cycle training also induces a metabolic upregulation of similar magnitude, typically observed 1-2 h after training. However, we observed that the metabolic enhancement induced by single-cycle training (**Figure 6A**) faded away rapidly, as it was no longer detectable 3 hours after 1x training (**Figure 6B**). Moreover, the metabolic upregulation occurring after 1x training was not dependent on DAMB signaling (**Figure 6C**), nor did it require PKC δ activity in MB neurons (**Figure 6D**), contrary to what was observed after spaced training (see Plaça et al., 2017 for DAMB and **Figure 3B** for PKC δ). This led us to hypothesize that the role of this DAMB/PKC δ cascade after spaced training is to extend the duration of the metabolic enhancement in MB neurons. Indeed, measurements performed 3-4 hours as well as 8-9 hours after the last cycle of spaced training (i.e. respectively 5-6 hours and 10-11 hours after the end of the first training

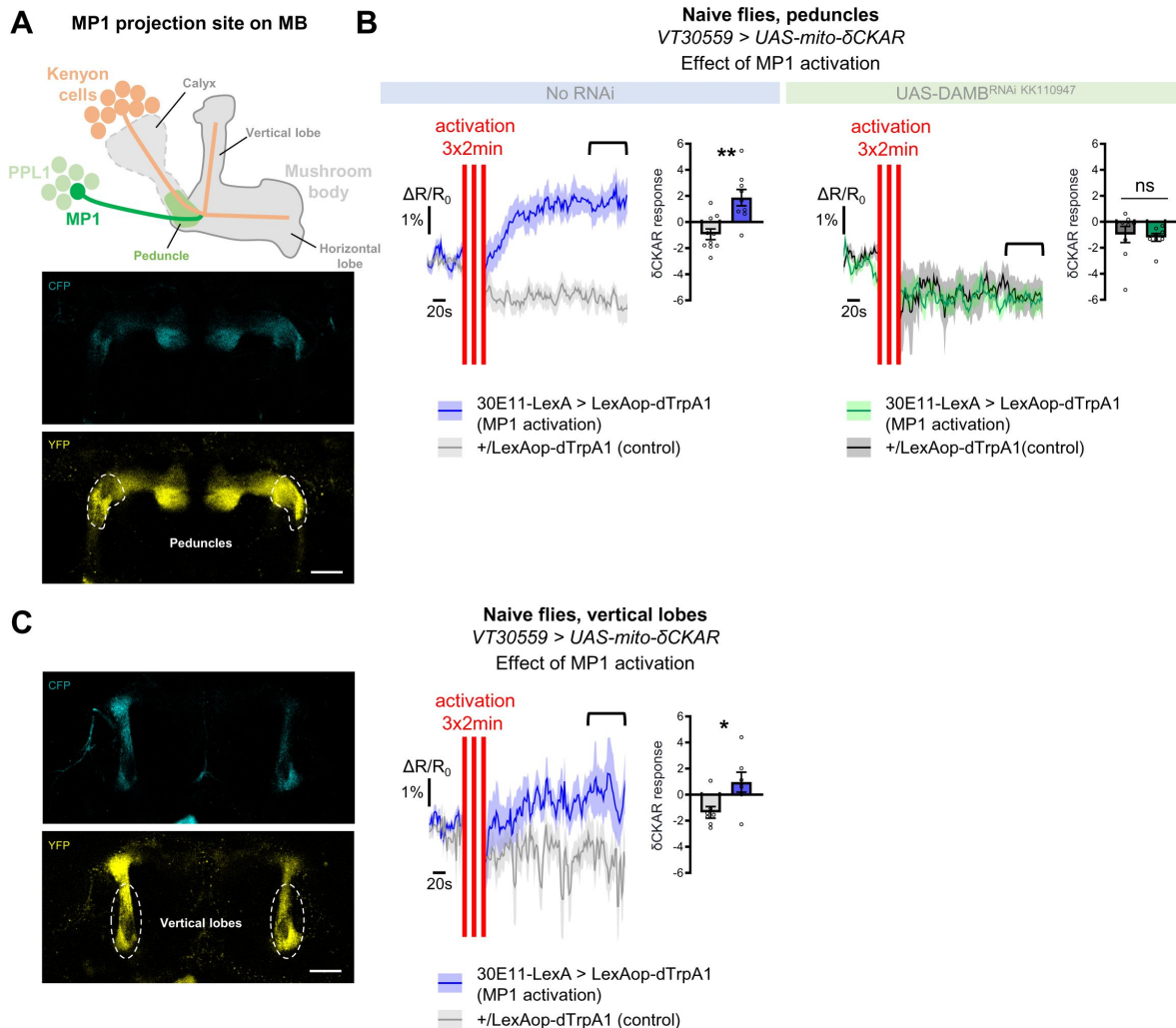


Figure 4.

MP1 neurons control PKC δ activity in the MB neurons via DAMB signaling.

(A) Top panel: Schema of the MB structure and its afferent MP1 neuron. The dopaminergic neuron MP1 (depicted in green) in the PPL1 cluster projects onto the peduncle area of the MBs. Lower panel: The mito- δ CKAR sensor was expressed in adult MB neurons and visualized in the CFP and YFP channels. The region of recording for panel B is at the level of the MB peduncles (dashed line). (B) Naïve flies expressing the mito- δ CKAR sensor in MB neurons together with the dTrpA1 (a heat-sensitive cation channel) in MP1 neurons (30E11-LexA driver) were subjected to a thermal treatment consisting of three 2-min periods at 30°C separated by 2 min (red vertical lines); control flies expressed the mito- δ CKAR in MB neurons but not the dTrpA1 channel (no 30E11-LexA driver). Mitochondrial PKC δ activity was recorded before (baseline) and immediately after the activation periods. Quantification of the mean mito- δ CKAR response was performed 120 s after the last cycle of thermal activation on a time window of 480 s (black line). In naïve flies expressing the dTrpA1 channel in MP1 neurons (30E11-LexA; *VT30559 > UAS-mito- δ CKAR*, *LexAop-dTrpA1*), activation of MP1 increased mitochondrial PKC δ activity as compared to control flies (*VT30559 > UAS-mito- δ CKAR*, *LexAop-dTrpA1*) ($n=9-10$, $t_{17}=3.830$, $p=0.0013$). When DAMB was knocked down in MB neurons (30E11-LexA; *VT30559 > UAS-mito- δ CKAR*, *UAS-DAMB RNAi*, *LexAop-dTrpA1*), MP1 activation failed to increase mitochondrial PKC δ activity as compared to control flies (*VT30559 > UAS-mito- δ CKAR*, *UAS-DAMB RNAi*, *LexAop-dTrpA1*) ($n=8-9$, $t_{15}=0.3148$, $p=0.7572$). (C) The mito- δ CKAR sensor was expressed in adult MB neurons and mitochondrial PKC δ activity was recorded in the vertical lobes (dashed line). As in the peduncle region, in naïve flies expressing the dTrpA1 channel in MP1 neurons (30E11-LexA; *VT30559 > UAS-mito- δ CKAR*, *LexAop-dTrpA1*), activation of MP1 increased mitochondrial PKC δ activity in the vertical lobes as compared to control flies (*VT30559 > UAS-mito- δ CKAR*, *LexAop-dTrpA1*) ($n=7$, $t_{12}=2.622$, $p=0.0223$). Data are expressed as mean $\pm$ SEM with dots as individual values and were analyzed by unpaired two-sided t-test. Asterisks refer to the P-value of the unpaired t-test comparison using the following nomenclature: * $p<0.05$, ** $p<0.01$, ns: not significant, $p>0.05$. Scale bar=30 μ m. See also **Figure 4 – figure supplement 1**.

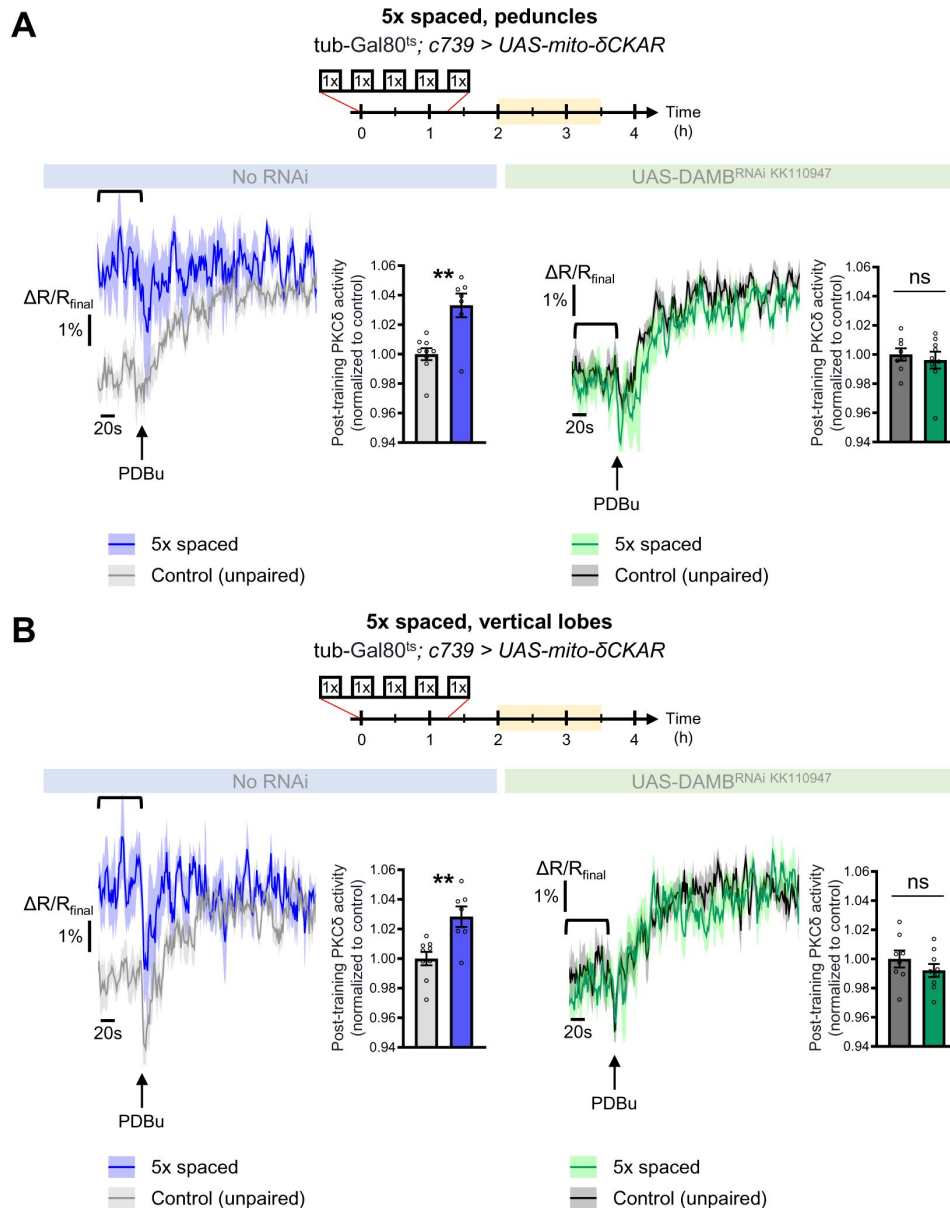


Figure 5.

PKC δ translocates to the mitochondria of α/β neurons upon LTM formation.

The mito- δ CKAR sensor was expressed in adult α/β neurons and the post-training activity of mito-PKC δ was measured in the peduncle (**A**) or vertical lobes (**B**), between 30 min and 1 h 30 min post-conditioning (in yellow on the imaging time frame). The same approach was used as in **Figure 1F-H** with PDBu application to reach saturation level of the sensor and quantification of the mean post-training PKC δ activity performed on a time-window of 120 s before PDBu application (black line). (**A**) After 5x spaced paired conditioning, mitochondrial PKC δ activity in the peduncle was increased as compared to unpaired conditioning (left panel, $n=7-9$, $t_{14}=3.555$, $p=0.0032$). When DAMB was knocked down in adult α/β neurons, mitochondrial PKC δ activity was not changed after 5x spaced paired conditioning as compared to unpaired conditioning (right panel, $n=8-9$, $t_{15}=1.089$, $p=0.2934$). (**B**) At the level of the vertical lobes, after 5x spaced paired conditioning, mitochondrial PKC δ activity was increased as compared to unpaired conditioning (left panel $n=7-9$, $t_{14}=3.932$, $p=0.0015$). When DAMB was knocked down in adult α/β neurons, mitochondrial PKC δ activity was not changed after 5x spaced paired conditioning, as compared to unpaired conditioning (right panel $n=8-9$, $t_{15}=0.5247$, $p=0.6075$). Data are expressed as mean $\pm$ SEM with dots as individual values, and were analyzed by unpaired two-sided t-test. Asterisks refer to the P-value of the unpaired t-test comparison using the following nomenclature: ** $p<0.01$, ns: not significant, $p>0.05$.

cycles) revealed that increased metabolic activity was still occurring (**Figure 6E-F** [↗](#)). In contrast, measurements performed 24 hours after spaced training showed that the metabolic enhancement had stopped by that time point (**Figure 6G** [↗](#)). Altogether, our results demonstrate that spaced training specifically recruits dopamine/DAMB/PKC8 signaling to perpetuate the metabolic activation in MB neurons, which is critical for initiating LTM formation (**Figure 7** [↗](#)).

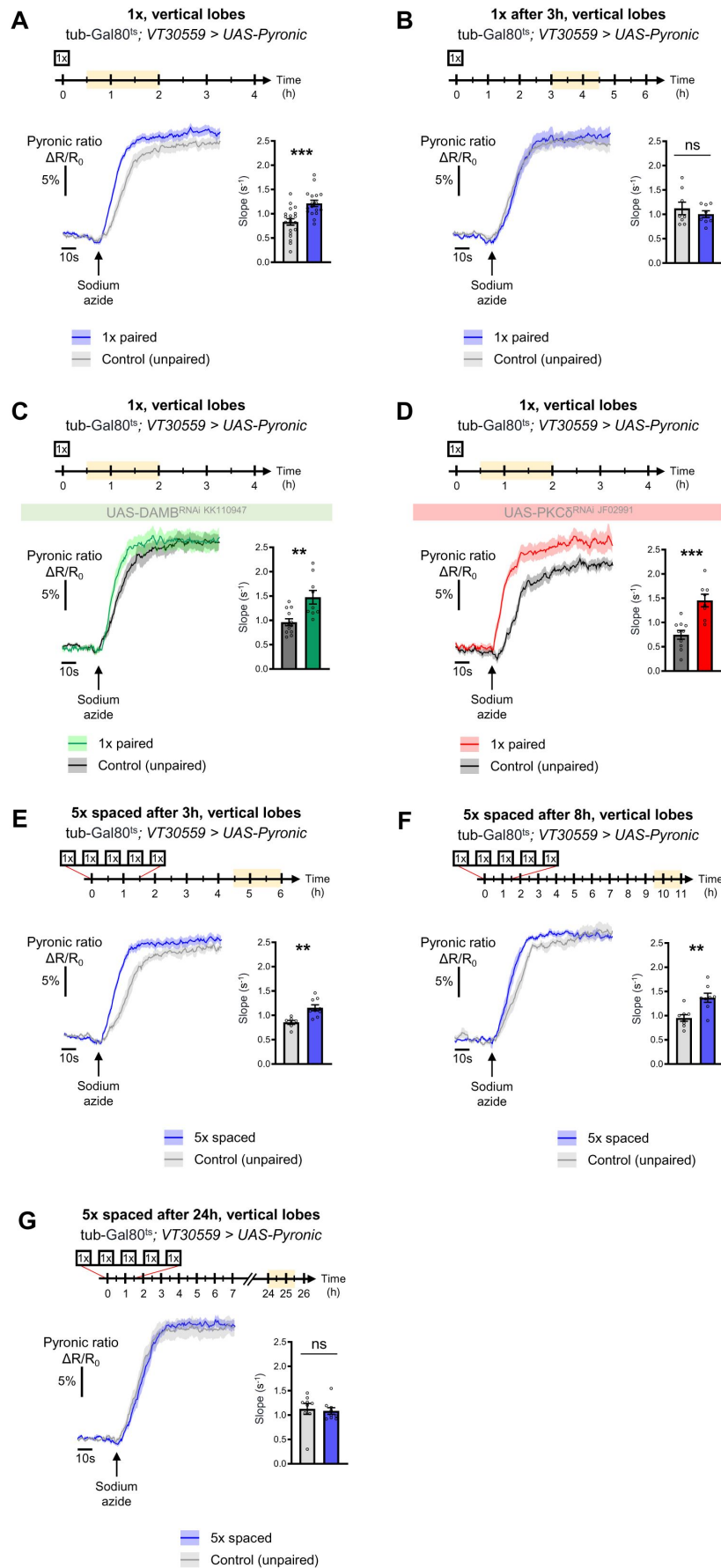


Figure 6.

The DAMB/PKC δ axis is specific to LTM formation.

The pyruvate sensor Pyronic was expressed in adult MB neurons and pyruvate accumulation was measured after conditioning in the vertical lobes. For each panel, the period of imaging after conditioning is indicated in yellow on the imaging time frame. **(A)** 30 min to 1 h 30 min after 1x paired conditioning, an increased pyruvate flux was measured in control flies (tub-Gal80^{TS};VT30559, UAS-Pyronic) as compared to non-associative unpaired 1x training (slope measurement $n=17-20$, $t_{35}=4.075$, $p=0.0003$). Here, we pooled the data obtained from control flies acquired in parallel to DAMB and PKC δ knockdown flies (panels C and D). **(B)** 3 h to 4 h 30 min after 1x paired conditioning of control flies (tub-Gal80^{TS};VT30559, UAS-Pyronic), the rate of pyruvate accumulation was similar as compared to unpaired conditioning (slope measurement $n=8$, $t_{14}=0.8022$, $p=0.4359$). **(C)** 30 min to 1 h 30 min after 1x paired conditioning, the pyruvate flux was still increased when DAMB was knocked down in the MBs at the adult stage (tub-Gal80^{TS};VT30559, UAS-Pyronic, UAS-DAMB RNAi) (slope measurement $n=9-12$, $t_{19}=3.528$, $p=0.0022$). **(D)** Similarly, PKC δ knockdown in adult MB neurons (tub-Gal80^{TS}; VT30559, UAS-Pyronic, UAS-PKC δ RNAi) did not impair the 1x conditioning induced increase in pyruvate accumulation in MB neuron axons (slope measurement $n=8-10$, $t_{16}=4.568$, $p=0.0003$). **(E)** 3 h to 4 h 30 min after the last cycle of 5x spaced conditioning of control flies (tub-Gal80^{TS};VT30559, UAS-Pyronic), the pyruvate flux was increased as compared to 5x spaced unpaired conditioning (slope measurement $n=9-7$, $t_{14}=3.889$, $p=0.0016$). **(F)** 8 h to 9 h 30 min after the last cycle of 5x spaced conditioning of control flies (tub-Gal80^{TS};VT30559, UAS-Pyronic), the pyruvate flux was still increased as compared to 5x spaced unpaired conditioning (slope measurement $n=8$, $t_{14}=3.628$, $p=0.0027$). **(G)** 24 h after the last cycle of 5x spaced conditioning of control flies (tub-Gal80^{TS};VT30559, UAS-Pyronic), the pyruvate flux was similar as compared to 5x spaced unpaired conditioning (slope measurement $n=9$, $t_{16}=0.3256$, $p=0.7489$). Data are expressed as mean $\pm$ SEM with dots as individual values, and were analyzed by unpaired two-sided t-test. Asterisks refer to the P-value of the unpaired t-test comparison using the following nomenclature: ** $p<0.01$, *** $p<0.001$, ns: not significant, $p>0.05$.

Discussion

In this study, we unveiled a detailed molecular mechanism underlying the spacing effect on memory consolidation. We established that PKC δ , a known regulator of mitochondrial pyruvate metabolism in several peripheral tissues, is a critical player in LTM formation in α/β MB neurons, while being dispensable for less stable forms of aversive memory. Additionally, we imported in *Drosophila* a genetically-encoded FRET sensor for PKC δ (Kajimoto et al., 2010; Wu-zhang et al., 2012), which allowed observing the PKC δ activity level *in vivo*. Thus, we reported a specific activation and mitochondrial translocation of PKC δ following spaced training, but not 1x or massed training. We established that specific dopaminergic neurons (MP1 neurons), which are required early after spaced training for LTM formation (Plaçaïs et al., 2017, 2012), activate PKC δ translocation to mitochondria, through a specific Gq-coupled dopamine receptor, DAMB. Consistent with the role of this dopamine signaling that we previously reported (Plaçaïs et al., 2017), we showed here that activated PKC δ persistently upregulates pyruvate metabolism, thereby allowing LTM formation. Altogether, our data demonstrate that PKC δ , acting as an activator of mitochondrial metabolism, is a neuronal gatekeeper of LTM formation. More generally, our findings provide a detailed mechanistic description of how dopamine signaling orchestrates memory consolidation through sustained modulation of neuronal energy fluxes, thereby resolving within a single gating mechanism the cognitive and metabolic constraints linked to LTM formation.

Although PKCs have been widely implicated in learning and memory in a large variety of model organisms (Van Der Zee and Douma, 1997), the precise contribution of PKC δ in memory formation and consolidation in mammals remains largely unknown. Nevertheless, PKC δ is highly expressed

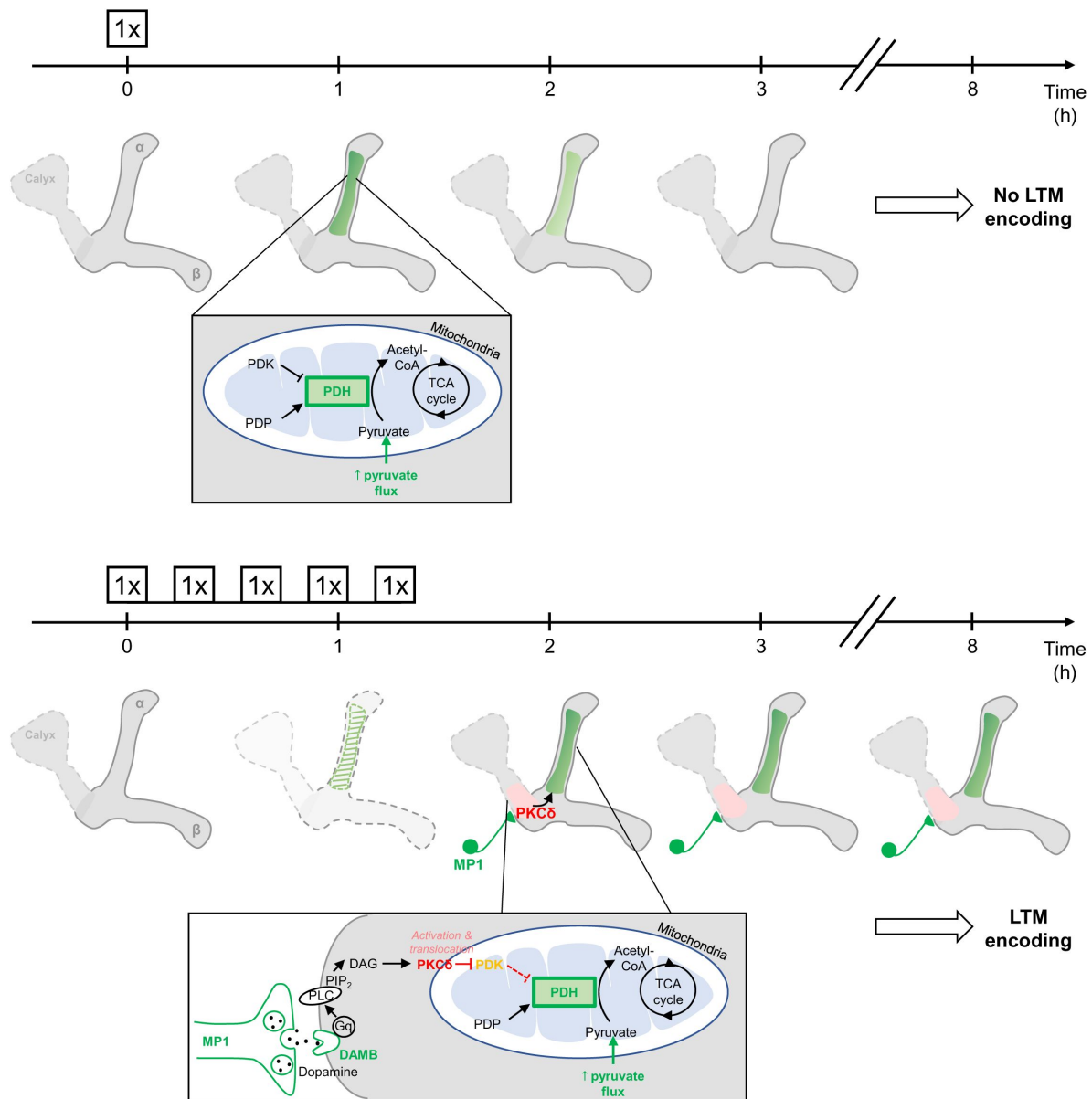


Figure 7.

Schema of the energy-based gating of LTM, illustrating the role of PKC δ downstream of the DAMB signaling cascade.

After 1x training, the pyruvate flux to the mitochondria in the vertical lobes of MB neurons is increased (Rabah et al., 2022). This increased energy state is not maintained but is progressively turned off, and after 3 h, the MBs are back to their basal energy state. Upon spaced training, in addition to the mechanism occurring after 1x training, the enhanced oscillatory activity of MP1 neurons activates DAMB signaling in the efferent α/β MB neurons. The DAMB receptor preferentially couples with Gq and the produced DAG activates PKC δ , which results in its translocation to mitochondria. There, PKC δ can activate the PDH, by releasing the inhibition exerted by PDK. The enhanced PDH activity promotes an increase in mitochondrial pyruvate flux, and this enhanced energy state gates memory consolidation, thereby enabling LTM formation. After 3 and even 8 hours, the lasting effect of PKC δ on mitochondrial metabolism maintains the high energy state of the MBs needed to support LTM formation.

in brain regions associated with learning, and more specifically aversive learning and memory (Zafiri and Duvarci, 2022). In particular, it is found in the CA3 layer of the hippocampus, as well as in a specific region of the central nucleus of the amygdala (CeA) called CE1 (Haubensak et al., 2010) (see also <http://mouse.brain-map.org>). There, PKC δ marks about 50% of CE1 GABAergic neurons (Haubensak et al., 2010). Strikingly, it was shown that CeA is implicated in learning and consolidation of Pavlovian fear conditioning (Steinberg et al., 2020; Wilensky et al., 2006), and more specifically that PKC δ + neurons of the CeA projecting to the substantia innominata (SI) bidirectionally modulate negative reinforcement learning (Cui et al., 2017). However, no link between the function of PKC δ itself and memory consolidation or metabolism has been established yet, as the PKC δ -expressing feature of these neurons was only used as a means to genetically target them in the aforementioned studies. Our work thus sketches a possibly conserved role of neuronal PKC δ in the context of memory formation and consolidation in mammals, which nevertheless remains to be investigated. A possible role of PKC δ in plasticity mechanisms in mice was substantiated by the recent observation, in CA1 pyramidal neurons from mice organotypic slices, that stimulation-induced DAG production downstream of NMDA receptors (Colgan et al., 2018) can activate PKC δ in spines for local plasticity, and, at a longer timescale, its translocation to the nucleus for plasticity-induced transcription upon LTP formation (Colgan et al., 2023).

How is post-learning dopamine signaling coupled with PKC δ activation? DAMB is a dopamine receptor that has the ability to activate Gq with great efficiency and dopamine sensitivity (Himmelreich et al., 2017), which results in the production of DAG, a canonical activator of the majority of PKC enzymes. Once activated by DAG, the local hydrophobic patch generated by DAG fixation is thought to guide PKCs to various membranes (Hurley and Grobler, 1997), and notably to mitochondria in the case of PKC δ where it localizes to the intermembrane space (Acin-Perez et al., 2010; Kim and Hammerling, 2020). In addition, PKC δ is specific among PKCs in that it does not require activation loop phosphorylation for catalytic competence (Duquesnes et al., 2011). This direct link between DAG and PKC δ (and the absence of any requirement for PKC δ phosphorylation) may explain its physiological role as an efficient relay between extracellular cues sensed by receptors and intracellular metabolism at the level of the mitochondria. DAMB/Gq can also activate calcium signaling (Cassar et al., 2015; Himmelreich et al., 2017), the other canonical second-messenger pathway downstream of Gq. Since increases in mitochondrial calcium flux are another way to enhance PDH complex activity (Denton et al., 1972; Glancy and Balaban, 2012), one cannot exclude that mitochondrial calcium signaling may also play a role in the gating mechanism for LTM formation.

Gq/PKC signaling has also been shown to play a major role in memory in rodents. Mutation in the phosphosite of TrkB that binds phospholipase C (PLC) to produce DAG and activate PKC signaling impaired expression and maintenance of synaptic long-term potentiation in the hippocampus, and overall reduced learning in mice (Gruart et al., 2007; Minichiello et al., 2002). Thus, the Gq-DAG mechanism of PKC δ activation for memory consolidation could be conserved in mammals. While DAMB has no direct homology with mammalian dopaminergic receptors (instead belonging to an “invertebrate type” class of receptors as demonstrated by sequence comparison (Mustard et al., 2005)), it should be noted that several mammalian dopamine receptors are also known to mobilize Gq signaling, such as the D1-D2 and the D5-D2 dopamine receptor heteromers (So et al., 2009; Young and Thomas, 2014). D1-like receptor can also directly engage with Gq/11 and therefore PLC (Rashid et al., 2007). In mammals, this non-canonical D1-like receptor/Gq coupling was notably found in the hippocampus and amygdala (Jin et al., 2001; Ming et al., 2006), two brain areas that are enriched in PKC δ + neurons (Haubensak et al., 2010; Zafiri and Duvarci, 2022). Anatomical studies demonstrate that both D1 and D2 receptors are expressed in the CeA, a region of the brain enriched in PKC δ + neurons (Zafiri and Duvarci, 2022). Periaqueductal gray/dorsal raphe (PAG/DR) afferent dopaminergic neurons exhibit phasic activation in response to an aversive unconditioned stimulus (US) and to a conditioned stimulus (CS) associated with the aversive US (Groessl et al., 2018; Zafiri and Duvarci, 2022), which could preferentially activate

the D1 receptor-expressing CeA neurons during aversive learning (Zafiri and Duvarci, 2022 [↗](#)). It would be of particular interest to explore the involvement of PKC δ neurons in this process, and to study whether PKC δ could be mobilized downstream of D1/Gq signaling in the context of aversive memory in mammals. Aside from dopaminergic receptors, a wide variety of memory-relevant receptors have been reported to activate Gq signaling, with adrenergic receptors being the most commonly cited kind. In physiological conditions, α -adrenergic receptors are considered to be the principal activators of Gq signaling (Duquesnes et al., 2011 [↗](#)). β -adrenoreceptor subtypes are expressed in the hippocampus and amygdala; these regions receive noradrenergic afferences from the locus coeruleus, which plays a critical role in regulating behavioral memory in rodents, and are key for the processing of memories (Sara, 2009 [↗](#)), and more specifically for their consolidation (Sara, 2009 [↗](#); Souza-Braga et al., 2018 [↗](#)).

Here, we propose a model in which a state of high energy consumption in MB neuron axons necessary for LTM gating is prolonged by PKC δ , which boosts the PDH complex activity in MB mitochondria. Such a role is consistent with previous descriptions in non-neuronal mammalian cells. It is indeed known that PKC δ can regulate the PDH complex (Acin-Perez et al., 2010 [↗](#); Kim and Hammerling, 2020 [↗](#)): activation of PKC δ leads to the phosphorylation of a putative PDK phosphatase, thereby enhancing its activity and promoting dephosphorylation of PDK, which inhibits it and thereby releases the inhibition it exerts on the PDH complex (Acin-Perez et al., 2010 [↗](#); Kim and Hammerling, 2020 [↗](#)). As PDK knockdown rescued the LTM defect induced by PKC δ knockdown in our study, we propose that PKC δ boosts the PDH complex activity via this mechanism of PDK-Pase activation, resulting in PDK inhibition in MB neuronal mitochondria. This lasting effect of PKC δ on mitochondrial metabolism thus maintains the pyruvate flux upregulated in MB vertical lobe mitochondria, which unlocks memory consolidation to form LTM.

While our work uncovers a molecular switch controlling the metabolic upregulation of the MB neurons, the role for this enhanced pyruvate flux to mitochondria has not yet been unveiled. Several hypotheses could be considered, which are not mutually exclusive. First, increased pyruvate incorporation into the TCA cycle could lead to acceleration of oxidative phosphorylation and subsequent enhanced ATP production, in support of sustained neuronal activity or of the substantial energy cost of *de novo* protein synthesis on which LTM formation depends at later stages (Davis and Squire, 1984 [↗](#); Helmstetter et al., 2008 [↗](#); Jarome and Helmstetter, 2014 [↗](#)). Second, acceleration of the TCA cycle and oxidative phosphorylation can also be accompanied by increased ROS production (Rosato et al., 2014 [↗](#)), both of which are increasingly recognized as neuronal signaling molecules (Sinenko et al., 2021 [↗](#); Zhang et al., 2016 [↗](#)). Third, acceleration of the TCA cycle alone, decoupled from oxidative phosphorylation, could produce acetylcholine, the neurotransmitter used by MB neurons, and/or acyl groups that are crucial for subsequent epigenetic modifications. This non-canonical TCA cycle has recently been reported in a model of mammalian stem cells (Arnold et al., 2022 [↗](#)). Finally, TCA cycle intermediates could be used for amino acid synthesis to fulfill the need for *de novo* protein synthesis, which is a hallmark of LTM.

Our study extends to the context of memory formation in neurons the beneficial role of PKC δ in the modulation of mitochondrial metabolism, whereas it was first extensively described in the mouse embryonic fibroblast (Acin-Perez et al., 2010 [↗](#)). There, PKC δ serves as an indispensable supervisor of mitochondrial energy production: by sensing the cytochrome c redox state as a proxy of the respiratory chain workload, it adjusts mitochondrial metabolism within safe margins (that can be overpassed when fuel flux surpasses the capacity of the electron-transport chain, causing detrimental ROS release) (Acin-Perez et al., 2010 [↗](#); Kim and Hammerling, 2020 [↗](#)). Strikingly, PKC δ was also widely described as detrimental to cells in pathological conditions, with a well-characterized role in cardiac (Inagaki et al., 2003 [↗](#); Zaja et al., 2014 [↗](#)) and neuronal (Bright et al., 2004 [↗](#); Dave et al., 2011 [↗](#); Phan et al., 2002 [↗](#)) cell death upon ischemic incidents. In this model, PKC δ takes part in apoptotic events through a caspase-induced signaling cascade in mitochondria, notably via cleavage by caspase-3 at the PKC δ caspase-dependent cleavage site, which releases a 40 kDa active fragment. Furthermore, transient episodes of ischemia can also

activate PKC δ through ROS-dependent mechanisms, leading to its phosphorylation and subsequent activation. PKC δ can then bind and phosphorylate Drp1, a major mitochondrial fission protein, thereby increasing its activity. This mechanism was described in cardiomyocytes during anoxia-reoxygenation injury (Zaja et al., 2014 [DOI](#)), and in neurons under oxidative stress *in cellulo*, as well as *in vivo* in the context of hypertension-induced encephalopathy (Qi et al., 2011 [DOI](#)). Finally, PKC δ has been implicated in neurodegenerative diseases such as Alzheimer's disease (AD) (Du et al., 2018 [DOI](#)) and Parkinson's disease (PD) (Kaul et al., 2005 [DOI](#); Yang et al., 2004 [DOI](#); Zhang et al., 2007 [DOI](#)). However, a number of these studies should be considered carefully, as some of their results are based on PKC δ inhibition by rottlerin, which has been found to be an inappropriate and ineffective PKC δ pharmacological inhibitor (Soltoff, 2007 [DOI](#)). Nevertheless, various pieces of evidence show increased expression of PKC δ in AD patients (Du et al., 2018 [DOI](#)), pointing towards the fact that PKC δ inhibition plays an important protective role in brain aging (Conboy et al., 2009 [DOI](#)), ischemia (Bright et al., 2004 [DOI](#); Dave et al., 2011 [DOI](#); Phan et al., 2002 [DOI](#)), and neurodegenerative disease (Du et al., 2018 [DOI](#); Kaul et al., 2005 [DOI](#); Yang et al., 2004 [DOI](#); Zhang et al., 2007 [DOI](#)).

Altogether, it is now emerging that PKC δ is functionally ambivalent: while its role in metabolism regulation maintains essential physiological functions such as LTM gating in the brain as demonstrated in this study, stress conditions unveil negative effects mediated by this kinase that derail the system equilibrium. The interplay between the two modes of activation of PKC δ by DAG and oxidative stress is probably at the heart of its contrasting duality. Expanding upon our work, it could be of particular interest to explore whether competition between PKC δ activation via these two modes, DAG and oxidative stress, occurs upon aging and/or pathology.

Material and Methods

Resource availability

Materials availability

Materials generated in this study are available from the corresponding authors without restriction.

Data and code availability

All data needed to evaluate the conclusions are present in the manuscript and/or the Supplementary Information. Data reported in this manuscript will be shared by the corresponding authors upon request. Any additional information required to reanalyze the data reported in this manuscript is available from the corresponding authors upon request.

Key resources table

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Chemicals, peptides, and recombinant proteins		
3-octanol (99%)	Sigma-Aldrich	Cat. #153095
4-methylcyclohexanol (98%)	Sigma-Aldrich	Cat. #218405
Paraffine GPR Rectapur	VWR	Cat. #24679.360

NaCl	Sigma-Aldrich	Cat. #S9625
KCl	Sigma-Aldrich	Cat. #P3911
MgCl ₂	Sigma-Aldrich	Cat. #M9272
CaCl ₂	Sigma-Aldrich	Cat. #C3881
D-trehalose	Sigma-Aldrich	Cat. #9531
Sucrose	Sigma-Aldrich	Cat. #S9378
HEPES-NaOH	Sigma-Aldrich	Cat. #H7637
Phorbol 12,13-dibutyrate (PdBu)	Tocris	Cat. #4153
Bisindolylmaleimide IV (Bis IV)	Sigma-Aldrich	Cat. #B3306
Sodium Azide	Sigma-Aldrich	Cat. #71289
Critical commercial assays		
RNeasy Plant Mini Kit	QIAGEN	Cat. #74904
RNA MinElute Cleanup Kit	QIAGEN	Cat. #74204
SuperScript III First-Strand Kit	ThermoFisher Invitrogen	Cat. #18080-051
SYBR Green I Master mix	Roche	Cat. # 04729692001
Experimental models: Organisms/strains		
tubulin-Gal80 ^{ts} ;VT30559-Gal4	Plaça et al., 2017	
tubulin-Gal80 ^{ts} ;c739-Gal4	Turrel et al., 2018	
tubulin-Gal80 ^{ts} ;elav-Gal4	Silva et al., 2022	
30E11-LexA	BDSC	#54209
UAS-PKC ^Δ RNAi JF02991	BDSC	#28355
UAS-PKC ^Δ RNAi KK109117	VDRC	#101421
UAS-DAMB ^Δ RNAi KK110947	VDRC	#105324
UAS-PDK ^Δ RNAi KK106641	VDRC	#106641
LexAop-dTrpA1	Liu et al., 2012	N/A
tubulin-Gal80 ^{ts} ;VT30559-Gal4, UAS-Pyronic	Plaça et al., 2017	N/A
30E11-LexA;VT30559-Gal4	Plaça et al., 2017	N/A
UAS-cyto-δCKAR;UAS-PKC ^Δ RNAi JF01991	This paper	N/A
UAS-mito-δCKAR;UAS-DAMB ^Δ RNAi KK110947	This paper	N/A
UAS-mito-δCKAR;UAS-DAMB ^Δ RNAi KK110947;LexAop-dTrpA1	This paper	N/A
UAS-PDK ^Δ RNAi KK106641;UAS-PKC ^Δ RNAi JF02991	This paper	N/A
UAS-mtDsRed	BDSC	#93056
Oligonucleotides		
Primer PKC ^Δ forward: 5'-GGCACCAAACACCCGTATCT-3'	This paper, DRSC Fly Primer Bank	Primer Pair PP14953
Primer PKC ^Δ reverse: 5'-CCCATAGAATCTGGCTCGCT-3'	This paper, DRSC Fly Primer Bank	Primer Pair PP14953
Primer tub forward: 5'-TTGTCGCGTGTGAAACACTTC-3'	Turrel et al., 2018	N/A
Primer tub reverse: 5'-CTGGACACCAGCCTGACCAAC-3'	Turrel et al., 2018	N/A
Recombinant DNA		
pcDNA3-deltaCKAR	Addgene	#31526
pJRFC-MUH	Addgene	#26213
pJRFC-MUH-UAS-deltaCKAR	This paper	
pJRFC-MUH-UAS-delta mitoCKAR	This paper	

Experimental model and subject details

D. melanogaster flies were maintained on standard cornmeal-yeast-agar medium. Stocks were kept at 18°C and 60% humidity under a 12-hour light:12-hour dark cycle. Genetic crosses were performed at 18°C for behavior experiments or at 23°C for imaging experiments (except when indicated otherwise). Both male and female flies were used for behavior experiments. Female flies were used for imaging experiments due to their larger size. Flies from the Vienna Drosophila Resource Center (VDRC) collection were outcrossed for 5 generations to a reference strain carrying the w¹¹¹⁸ mutation in an otherwise Canton Special (Canton S) genetic background. Since TRiP RNAi transgenes do not carry a mini-white marker but are labeled with a y⁺ marker, flies from the TRiP RNAi collection were outcrossed to a y⁺w^{67c23} strain in an otherwise Canton S background. The Canton S strain was used as the wild type strain.

To target MB neurons, the VT30559-Gal4 line was used in combination with the thermosensitive TARGET system tubulin-Gal80^{ts} to generate the tub-Gal80^{ts};VT30559-Gal4 inducible driver line (Plaçaïs et al., 2017 [DOI](#)), so as to temporally control the expression of the desired transgene. Gal4 activity was released by transferring 0- to 2-day-old adult flies to 30°C for 2-3 days. Likewise, the c739-Gal4 line was used to specifically target α/β neurons, and the tubulin-Gal80^{ts};c739-Gal4 construct line previously generated in the laboratory and described in Turrel et al., 2018 [DOI](#) allowed temporal control of the Gal4 activity. As described in Silva et al., 2022 [DOI](#), the tubulin-Gal80^{ts};elav-Gal4 system was used for time-controlled pan-neuronal knockdown. To target MP1 neurons independently of the Gal4 system, the 30E11-LexA driver was used (Plaçaïs et al., 2017 [DOI](#)). The tub-Gal80^{ts}; VT30559-Gal4, UAS-Pyronic line was previously generated in our research group and described in Plaçaïs et al., 2017 [DOI](#). The UAS-cyto- δ CKAR and UAS-mito- δ CKAR lines were generated for this study (see ‘Generation of transgenic flies’ section below). The following genetic constructs were generated in this study by combining the appropriate UAS-RNAi line (listed in the key resources table) and FRET sensor transgenes: i) UAS-cyto- δ CKAR;UAS-PKC δ ^{RNAi} JF01991, ii) UAS-mito- δ CKAR;UAS-DAMB^{RNAi} KK110947, iii) UAS-mito- δ CKAR;UAS-DAMB^{RNAi} KK110947;LexAop-dTrpA1, and iv) UAS-PDK^{RNAi} KK106641; UAS-PKC δ ^{RNAi} JF02991. All other fly lines used in this study are listed in the key resources table and either come from the VDRC collection or TRiP RNAi collection, or were previously published.

Method details

Aversive olfactory conditioning and memory test

The behavioral experiments, including sample sizes, were conducted similarly to previous studies from our research group (Plaçaïs et al., 2017 [DOI](#); Scheunemann et al., 2018 [DOI](#)). For all experiments, training and testing were performed in a sound- and odor-proof room at 25°C and 80% humidity. Experimental flies (male and female) were transferred to fresh bottles containing standard medium on the day before conditioning for the non-induced condition. For the induced condition, flies were transferred 2 days before the experiment at 30.5°C to allow RNAi expression.

Conditioning

Flies were conditioned by exposure to one odor paired with electric shocks and subsequent exposure to a second odor in the absence of shock. A barrel-type machine was used for simultaneous automated conditioning of six groups of 40–50 flies each. Throughout the conditioning protocol, each barrel was attached to a constant air flow at 2 L.min⁻¹. The odorants 3-octanol (odor O) and 4-methylcyclohexanol (odor M), diluted in paraffin oil at 0.360 and 0.325 mM respectively, were alternately used as conditioned stimuli (CS). For a single cycle of associative training, flies were first exposed to an odorant (the CS+) for 1 min while 12 pulses of 5 s-long, 60 V electric shocks were delivered; flies were then exposed 45 s later to a second odorant without shocks (the CS-) for 1 min. Here, the groups of flies were subjected to one of the following olfactory conditioning protocols: 1 cycle training (1x), five consecutive associative training cycles (5x massed training), or five associative cycles spaced by 15-min inter-trial intervals (5x spaced conditioning). Non-associative control protocols (unpaired protocols) were also employed for *in vivo* imaging experiments. During unpaired conditionings, the odor and shock stimuli were delivered separately in time, with shocks occurring 3 min before the first odorant. After training and until memory testing, flies were kept on regular food at 25°C (for 3 h-memory test) or at 18°C (for 24 h memory test).

Memory test

The memory test was performed either 3 h after 1x conditioning or 24 h after 5x conditioning in a T-maze apparatus comprising a central elevator to transfer the flies to the center of the maze arms. During the test, flies were exposed simultaneously to both odors (the same concentration as during conditioning) in the T-maze. After 1 min of odorant exposure in the dark, flies were

trapped in either T-maze arm, retrieved and counted. A memory score was calculated as the number of flies avoiding the conditioned odor minus the number of flies preferring the conditioned odor, divided by the total number of flies. A single memory score value is the average of two scores obtained from two groups of genotypically identical flies conditioned in two reciprocal experiments, using either odorant (3-octanol or 4-methylcyclohexanol) as the CS+. The indicated 'n' is the number of independent memory score values for each genotype.

Odor perception test

The olfactory acuity of flies was tested after conditioning with the CS+, since electric shocks modify their olfactory perceptions. Flies were then immediately tested in a T-maze, where they had to choose between the CS- or its solvent (paraffin oil). Odor concentrations used in this assay were the same as for the memory assays. At these concentrations, both odorants are innately repulsive. The odor-interlaced side was alternated for successively tested groups. After 1 minute, flies were counted, and naïve odor avoidance was calculated as for the memory test.

Electric shock perception test

During the test, flies must choose between two barrels: one delivering the electric shocks, and one that is neutral. The compartment where the electric shocks are delivered was alternated between two consecutive groups. After 1 minute, flies were counted, and shock avoidance was calculated as for the memory test.

In vivo imaging

Crosses for imaging experiments were raised at 23°C and fly progeny were induced for three days at 30.5°C to drive sufficient expression of the probe (and the desired RNAi) for use in imaging, except for MP1 activation experiments involving the thermosensitive LexAop-dTrpA1 transgene in which flies were always kept at 18°C. As in all previous imaging work from our laboratory, all *in vivo* imaging was performed on female flies, which are preferred since their larger size facilitates surgery. Naïve (not trained) or conditioned flies (1x, 5x spaced or 5x massed and their corresponding unpaired controls) were gently handled by aspiration without anesthesia and glued on their dorsal side to a plastic coverslip coated with a thin transparent plastic sheet. The coverslip was then placed on a recording chamber. Surgery was performed to obtain an imaging window on the fly head by removing the cuticle, trachea and fat bodies, thereby exposing the underlying MB neurons. During the procedure, the head capsule is bathed in a drop of artificial hemolymph: NaCl 130 mM (Sigma cat. # S9625), KCl 5 mM (Sigma cat. # P3911), MgCl₂ 2 mM (Sigma cat. # M9272), CaCl₂ 2 mM (Sigma cat. # C3881), D-trehalose 5 mM (Sigma cat. # 9531), sucrose 30 mM (Sigma cat. # S9378), and HEPES hemisodium salt 5 mM (Sigma cat. # H7637). At the end of the procedure, any remaining solution was absorbed and a fresh 90-μL droplet was applied on the preparation. When performed on flies that underwent olfactory conditioning, the imaging experiments were performed within the time period after conditioning indicated on each figure panel.

FRET δCKAR imaging

Imaging was performed using a SP8 DIVE Leica 2-photon microscope equipped with a 25x, 1.0 NA water immersion objective. Two-photon excitation of CFP was achieved using an Insight X3 Spectra Physics laser tuned to 840 nm. 512x250 images were acquired at the rate of one image every two seconds, with two z plans imaged in parallel (vertical lobes and peduncle). Typically, the images comprised the structures of both brain hemispheres, although only one hemisphere was visible in some preparations. Two spectrally tunable hybrid detectors were adjusted to detect 440-490 nm CFP emission and 510-550 nm YFP emission. Two minutes after the beginning of image acquisition, 10 μL of a 2.5 mM phorbol 12,13-dibutyrate (PDBu, Tocris cat. # 4153) solution (25 mM PDBu stock solution in DMSO dissolved at 1/10 in artificial hemolymph) were injected into the 90 μL-droplet bathing the fly's brain, bringing PDBu to a final concentration of 250 μM (DMSO: 1/100). In control experiments, PDBu injection was replaced by the injection of DMSO alone (final

concentration: 1/100). To inhibit PKC δ , two minutes after the beginning of image acquisition, 10 μ L of a 50 μ M bisindolylmaleimide IV (Bis IV, Sigma cat. # B3306) solution (500 μ M stock solution in DMSO dissolved at 1/10 in artificial hemolymph), bringing Bis IV to a final concentration of 5 μ M. In control experiments, Bis IV injection was replaced by the injection of DMSO alone (final concentration: 1/100). Drug application during the recording could give rise to artifactual perturbation of the signal at the time of injection, with variability from one experiment to another. In **Figure 1F**, a section of the presented traces corresponding to the 15 seconds following the injection was smoothed using a running average procedure (with a time window of 30 s) to remove injection artefacts that were especially large in this initial series of experiments. The injection technique was subsequently improved so that no smoothing was applied on any of the other presented experiments (including in particular **Figure 2B**, which reports a similar phenomenon as **Figure 1F**).

For image analysis, regions of interest (ROI) were delimited by hand around each visible vertical lobe or peduncle region, and the average intensity of both CFP and YFP channels over each ROI were calculated over time after background subtraction; the background was evaluated as the mean intensity over a region of interest placed in a nonfluorescent part of the brain. The δ CKAR sensor was designed so that FRET from CFP to YFP decreases when PKC δ phosphorylating activity increases. The inverse FRET ratio, ΔR (CFP/YFP), was computed to obtain a signal that positively correlates with PKC δ phosphorylating activity. To measure the δ CKAR response (**Figure 1D-E**, **Figure 1 – figure supplement 1C-D**, **Figure 4**), the ΔR ratio was normalized by a baseline value calculated over the 2 min preceding drug injection (PDBu or Bis IV). To measure PKC δ post-training activity (**Figure 1F-H**, **Figure 2B-C**, **Figure 5**), the ΔR ratio was normalized by a plateau value calculated from 6 min 40 s to the end of the recording, and the controls were normalized to 1.

For the MP1 activation experiments in which PKC δ response activity was assayed (**Figure 4**), flies were prepared as previously reported and placed on a custom-made device equipped with a Peltier cell to allow precise control of the temperature under the microscope. Flies were recorded for 2 min at 18°C to establish a baseline and then received thermal treatment for MP1 activation, consisting of three consecutive periods of 2 min at 30°C followed by 2 min at 18°C. The recording was continued for 10 min after the last activation period. To measure PKC δ response activity, the ΔR was normalized by the baseline value calculated over the 2 min preceding thermal treatment, and the controls were normalized to 1.

The indicated ‘n’ is the number of animals that were assayed in each condition.

FRET imaging of pyruvate flux

Two-photon imaging was performed using a Leica TCS-SP5 upright microscope equipped with a 25x, 0.95 NA water immersion objective. Two-photon excitation was achieved using a Mai Tai DeepSee laser tuned to 825 nm. The frame rate was two images per second. 512x150 images were acquired at a rate of two images per second. The emission channels for mTFP and Venus were the same as described in [Gervasi et al., 2010](#). Measurements of pyruvate consumption were performed according to a previously well-characterized protocol ([Plaçais et al., 2017](#)). After 1 min of baseline acquisition, 10 μ L of a 50 mM sodium azide solution (Sigma cat. #71289; prepared in the same artificial hemolymph solution) were injected into the 90 μ L-droplet bathing the fly's brain, bringing sodium azide to a final concentration of 5 mM. In experiments involving pretreatment of the brains (**Figure 3A**), 250 μ M of PDBu or 1/100 DMSO (final concentrations) were injected into the hemolymph droplet 3 minutes prior to sodium azide injection. Image analysis was performed as previously described ([Plaçais et al., 2017](#)). ROI were delimited by hand around each visible MB vertical lobe, and the average intensity of the mTFP and Venus channels over each ROI was calculated over time after background subtraction. The Pyronic sensor was designed so that FRET from mTFP to Venus decreases when the pyruvate concentration increases. To obtain a signal that positively correlates with pyruvate concentration, the inverse

FRET ratio was computed as mTFP intensity divided by Venus intensity. This ratio was normalized by a baseline value calculated over the 1 min preceding drug injection. The slope was calculated between 10 and 70% of the plateau. The indicated 'n' is the number of animals that were assayed in each condition.

RT-qPCR analyses

To assess the efficiency of the PKC δ RNAi used in this study, female flies carrying the tubulin-Gal80^{ts};elav-Gal4 pan-neuronal inducible driver were either crossed with UAS-PKC δ RNAi JF02991 or UAS-PKC δ KK109117 males, or with CS males for controls (please note that crosses of these RNAi lines with the constitutive elav-Gal4 driver were lethal for the progeny). To assess PKC δ presence in the MB neurons, female flies carrying the tubulin-Gal80^{ts};VT30559-Gal4 MB neuron driver were either crossed with UAS-PKC δ RNAi JF02991 males, or with CS males for controls. Fly progeny were raised at 23°C throughout their development. Newly hatched flies were transferred to fresh food vials at 30.5°C for 4 days of induction before RNA extraction, as previously reported (Silva et al., 2022 [\[1\]](#)). RNA extraction and cDNA synthesis were performed using the RNeasy Plant Mini Kit (Qiagen), RNA MinElute Cleanup Kit (Qiagen), oligo(dT)20 primers and the SuperScript III First-Strand kit (Thermo Fisher Invitrogen). Amplification was performed using a LightCycler 480 (Roche) and the SYBR Green I Master mix (Roche). Specific primers used for PKC δ cDNA and the reference α -Tub84B (Tub, CG1913) cDNA are specified in the key resources table. The level of PKC δ cDNA was compared against the level of the α -Tub84B reference cDNA. Each reaction was performed in triplicate. The specificity and size of amplification products were assessed by melting curve analyses. Expression relative to the reference was presented as the foldchange compared to the calibrator (relative quantification $RQ = 2^{-\Delta\Delta C_t}$, where C_t is the cycle threshold).

Generation of transgenic flies

To generate the UAS-cyto- δ CKAR line, the pcDNA3-deltaCKAR plasmid (Addgene #31526) was digested by HindIII and XbaI. The resulting fragment was purified by electrophoresis and cloned into a pJFRC-MUH plasmid (Addgene #26213) in the XbaI/NotI subcloning site. The resulting construct was verified by restriction analysis and sequenced by PCR. This subcloning was outsourced to RDBiotech (France). The UAS-mito- δ CKAR line was generated using the plasmid mito- δ CKAR generated in Wu-zhang et al., 2012 [\[2\]](#) by subcloning the mito- δ CKAR fragment (HindIII/XbaI) into the pJFRC-MUH plasmid. The generation of the transgenic fly strains via the embryonic injection of the two vectors was outsourced to Rainbow Transgenic Flies, Inc (CA, USA).

Quantification and statistical analysis

Statistical parameters including the definitions and exact value of n, deviations and P values are reported in the figures and corresponding legends. Data are expressed as the mean $\pm$ SEM with dots as individual values corresponding to either a group of 40–50 flies analyzed together in a behavioral assay, or the response of a single recorded fly for imaging. Statistical analysis and graphs were made using Prism 8 (GraphPad software, v8.4.3). Comparisons between 2 groups were performed using a two-tailed unpaired t-test; results are provided as the value t_x of the t distribution with x degrees of freedom obtained from the data. Comparisons between multiple groups were performed using one-way ANOVA followed by Tukey's post hoc test for pairwise comparisons. ANOVA results are given as the value of the Fisher distribution $F_{x,y}$ obtained from the data, where x is the numerator degrees of freedom and y is the denominator degrees of freedom. Asterisks denote the smallest significant difference between the relevant group and its controls with the post hoc comparisons (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$, ns: not significant).

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Author contributions

Conceptualization: all authors

Methodology: T.C., A.P., P.-Y.P.

Investigation: T.C.

Writing—original draft: T.C., A.P., P.-Y.P.

Writing—review & editing: all authors

Funding: T.P., P.-Y.P.

Competing interests

The authors declare no competing interests.

Supplemental information

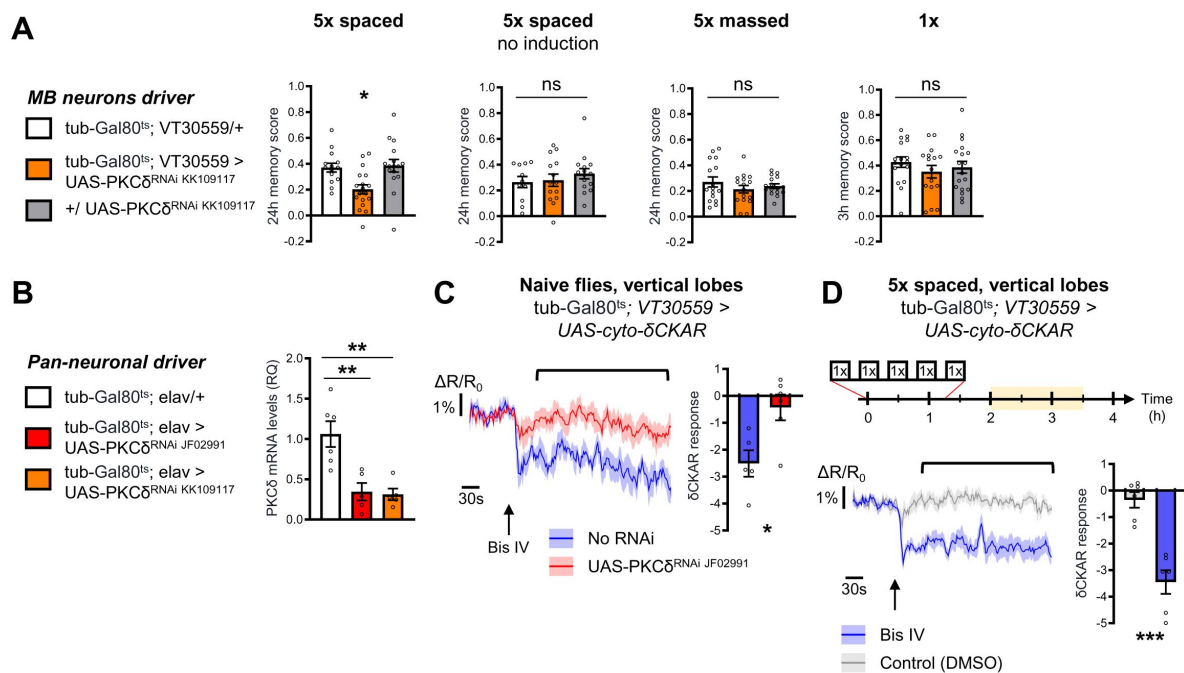


Figure 1 – figure supplement 1.

Control experiments for behavior analysis and δCKAR imaging experiments.

(A) Behavior analysis with a second PKCδ RNAi: 24-h memory after 5x spaced conditioning was also specifically impaired after induction of the PKCδ RNAi expression in adult MB ($n=14-18$, $F_{2,45}=6.764$, $p=0.027$), and it was not impacted without induction ($n=11-15$, $F_{2,37}=0.6226$, $p=0.5421$). No memory defect was found after 5x massed training ($n=16$, $F_{2,45}=0.8968$, $p=0.4151$) or 1x training ($n=17-18$, $F_{2,48}=0.6592$, $p=0.5219$) in flies knocked down for PKCδ in adult MB. (B) Pan-neuronal expression of either PKCδ RNAi at the adult stage significantly reduced PKCδ mRNA levels. Relative Quantification (RQ) was performed, indicating the foldchange of mRNA levels relative to the control genotype ($n=5-6$, $F_{2,13}=11.85$, $p=0.0012$). (C) In naïve flies, application of 5 μM of Bis IV (black arrow), a PKC inhibitor, resulted in a decrease in the cyto-δCKAR response, and this response was abolished when PKCδ was knocked down ($n=5-6$, $t_9=3.007$, $p=0.0148$). Quantification of the mean cyto-δCKAR response was performed 20 s after Bis IV application on a time window of 250 s (black line). (D) After 5x spaced training, Bis IV injection also decreased the cyto-δCKAR response as compared to the DMSO control ($n=6$, $t_{10}=4.825$, $p=0.0007$). Data are expressed as mean ± SEM with dots as individual values, and were analyzed either by one-way ANOVA with post hoc testing by the Tukey pairwise comparisons test (A-B), or by an unpaired two-sided t-test (C-D). Asterisks refer to the least significant P-value of post hoc comparison between the genotype of interest and the genotypic controls (A-B) or to the P-value of the unpaired t-test comparison (C-D) using the following nomenclature: * $p<0.05$, ** $p<0.01$, *** $p<0.001$, ns: not significant, $p>0.05$.

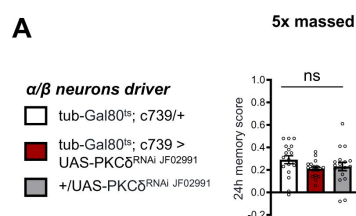


Figure 2 – figure supplement 1.

Control analysis of 24-h memory formed after massed training upon PKCδ knockdown in α/β neurons.

(A) 24-h memory after 5x massed training was normal when PKCδ RNAi was expressed in the α/β neurons at the adult stage as compared to its genotypic controls ($n=18$, $F_{2,51}=1.771$, $p=0.1805$). Data are expressed as mean ± SEM with dots as individual values, and were analyzed by one-way ANOVA with post hoc testing by the Tukey pairwise comparisons test. ns: not significant, $p>0.05$.

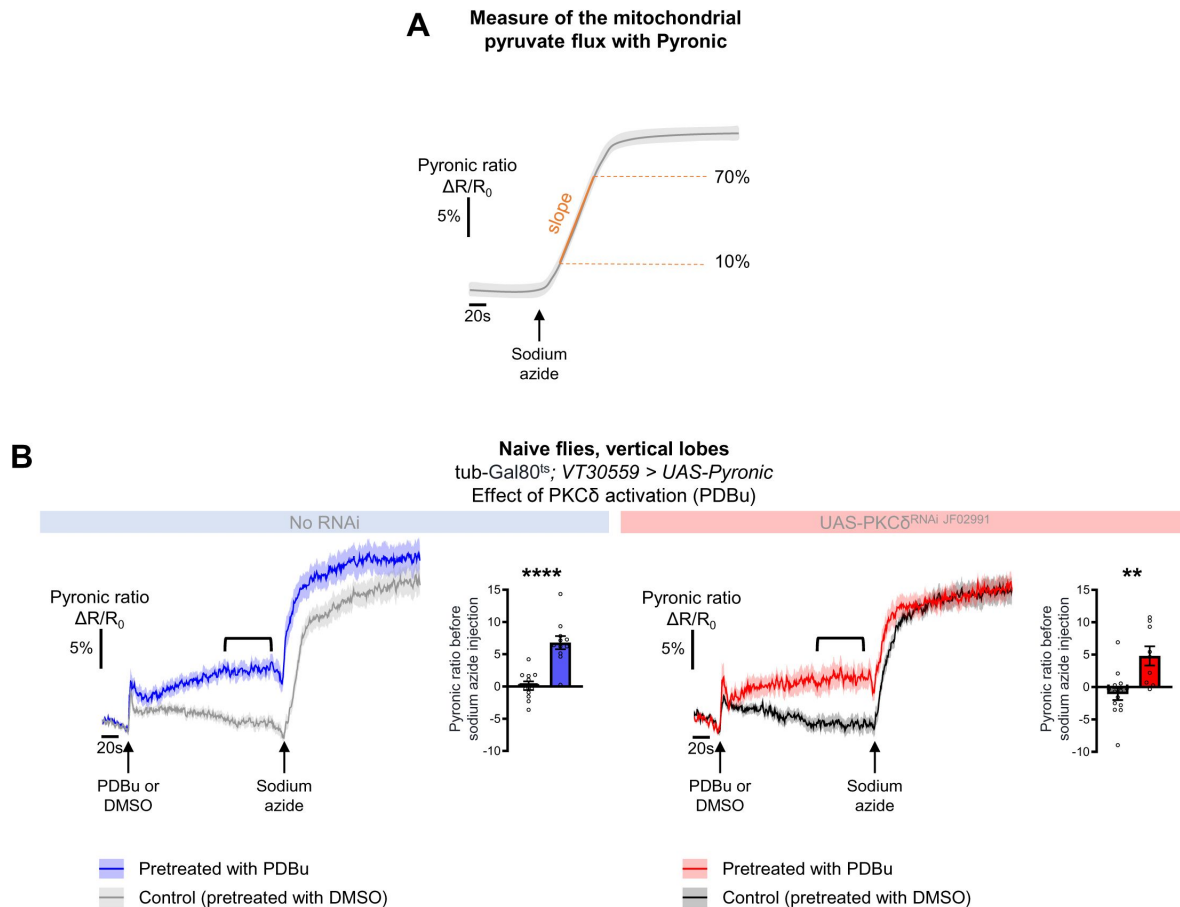


Figure 3 – figure supplement 1.

Additional information on pyruvate flux measurement using the Pyronic sensor.

(A) Schema representing the measure of the mitochondrial pyruvate flux using the pyruvate FRET sensor Pyronic. Here, mitochondrial respiration is blocked by sodium azide at the beginning of the recording, thereby stopping pyruvate mitochondrial uptake. The expected kinetic of pyruvate accumulation following the azide treatment is represented in grey, showing that pyruvate accumulates from the arrest of its mitochondrial uptake until saturation of the sensor. The rate of pyruvate accumulation (i.e. the slope of the measured kinetic, measured between 10 and 70% of the plateau) reflects the rate at which pyruvate was consumed by mitochondria for energy production before their blockade. **(B)** Complete recording of pyruvate imaging data shown in [Figure 3A](#). In control flies (*tub-Gal80^{ts};VT30559, UAS-Pyronic*), PDBu injection is followed by a progressive increase in the measured Pyronic ratio (black line) as compared to DMSO injection ($n=11$, $t_{20}=5.437$, $p<0.0001$). This effect is not sensitive to PKCδ knockdown (*tub-Gal80^{ts};VT30559, UAS-Pyronic, UAS-PKCδ RNAi* flies, $n=9-14$, $t_{21}=3.542$, $p=0.0019$). As PDBu is known to activate other PKCs (Wu-zhang et al., 2012), this observation likely reflects a PDBu off-target effect independent of PKCδ on pyruvate neuronal levels. This effect explains why, when normalized just before azide injection (as in [Figure 3A](#)), the pyruvate accumulation plateaus appear lower when PDBu is injected onto the brains as compared to the DMSO controls. Data are expressed as mean $\pm$ SEM with dots as individual values, and were analyzed by unpaired two-sided t-test. Asterisks refer to the P-value of the unpaired t-test comparison using the following nomenclature: ** $p<0.01$, **** $p<0.0001$.

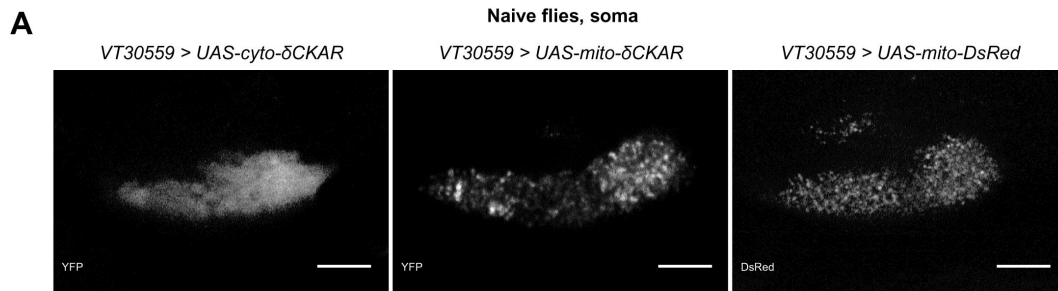


Figure 4 – figure supplement 1.

Subcellular addressing of the cyto- δ CKAR and mito- δ CKAR probes.

(A) Comparison of fluorescence sub localization in the soma of MB neurons in flies expressing either cyto- δ CKAR, mito- δ CKAR or mito-DsRed (DsRed is addressed to mitochondria using the COX8 targeting sequence (Lutas et al., 2012)) under the control of the VT30559 driver. Mito- δ CKAR punctate signal, similar to what is observed for mito-DsRed signal, indicates mitochondrial localization of the probe, in contrast to the diffuse signal observed with cyto- δ CKAR. This comparison was done in the soma area because it is the only MB region where the density of mitochondria allows their discrimination by conventional microscopy. Images were acquired by 2-photon microscopy, cyto-and mito- δ CKAR sensors were visualized through the YFP channel, and the mito-DsRed signal was acquired by 750 nm excitation and 580-610 nm detection. Scale bar=20 μ m.

Genotypes	Shock Avoidance		Naive odor avoidance			
			Octanol		Methylcyclohexanol	
	Mean $\pm$ s.e.m.	Statistics	Mean $\pm$ s.e.m.	Statistics	Mean $\pm$ s.e.m.	Statistics
tubGal80 ^{ts} ;VT30559/+	0.63 $\pm$ 0.057	F _{2,33} =2.60 p=0.090 n=12	0.74 $\pm$ 0.053	F _{2,27} =5.60 p=0.0092** n=9-11	0.72 $\pm$ 0.069	F _{2,27} =1.27 p=0.30 n=9-11
tubGal80 ^{ts} ;VT30559>UAS-PKC δ RNAi JF02991	0.76 $\pm$ 0.033		0.53 $\pm$ 0.070		0.60 $\pm$ 0.082	
UAS-PKC δ RNAi JF02991/+	0.64 $\pm$ 0.039		0.44 $\pm$ 0.073		0.56 $\pm$ 0.069	
tubGal80 ^{ts} ;VT30559/+	0.47 $\pm$ 0.052	F _{2,33} =0.38 p=0.69 n=12	0.63 $\pm$ 0.040	F _{2,33} =2.76 p=0.078 n=12	0.66 $\pm$ 0.046	F _{2,33} =0.64 p=0.53 n=12
tubGal80 ^{ts} ;VT30559>UAS-PKC δ RNAi KK109117	0.42 $\pm$ 0.039		0.70 $\pm$ 0.033		0.67 $\pm$ 0.034	
UAS-PKC δ RNAi KK109117/+	0.43 $\pm$ 0.047		0.57 $\pm$ 0.047		0.61 $\pm$ 0.050	
tubGal80 ^{ts} ;c739/+	0.45 $\pm$ 0.060	F _{2,39} =0.61 p=0.55 n=14	0.58 $\pm$ 0.050	F _{2,33} =2.48 p=0.099 n=12	0.46 $\pm$ 0.044	F _{2,33} =0.94 p=0.40 n=12
tubGal80 ^{ts} ;c739>UAS-PKC δ RNAi JF02991	0.40 $\pm$ 0.053		0.45 $\pm$ 0.036		0.47 $\pm$ 0.051	
UAS-PKC δ RNAi JF02991/+	0.49 $\pm$ 0.059		0.48 $\pm$ 0.045		0.54 $\pm$ 0.048	

Supplementary Table 1.

Sensory acuity controls, related to Figure 1.

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Editors

Reviewing Editor

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Reviewer #1 (Public Review):

Summary:

This is a detailed description of the role of PKC δ in *Drosophila* learning and memory. The work is based on a previous study (Plaçais et al. 2017) that has already shown that for the establishment of long-term memory, the repetitive activity of MP1 dopaminergic neurons via the dopamine receptor DAMB is essential to increase mitochondrial energy flux in the mushroom body.

In this paper, the role of PKC δ is now introduced. PKC δ is a molecular link between the dopaminergic system and the mitochondrial pyruvate metabolism of mushroom body Kenyon cells. For this purpose, the authors establish a genetically encoded FRET-based fluorescent reporter of PKC δ -specific activity, δ CKAR.

Strengths:

This is a thorough study of the long-term memory of *Drosophila*. The work is based on the extensive, high-quality experience of the senior authors. This is particularly evident in the convincing use of behavioral assays and imaging techniques to differentiate and explore various memory phases in *Drosophila*. The study also establishes a new reporter to measure the activity of PKC δ - the focus of this study - in behaving animals. The authors also elucidate how recurrent spaced training sessions initiate a molecular gating mechanism, linking a dopaminergic punishment signal with the regulation of mitochondrial pyruvate metabolism. This advancement will enable a more precise molecular distinction of various memory phases and a deeper comprehension of their formation in the future.

Weaknesses:

Apart from a few minor technical issues, such as the not entirely convincing visualisation of the localisation of a PKC δ reporter in the mitochondria, there are no major weaknesses. Likewise, the scientific classification of the results seems appropriate, although a somewhat more extensive discussion in relation to *Drosophila* would have been desirable.

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Reviewer #2 (Public Review):

Summary

This study deepens the former authors' investigations of the mechanisms involved in gating the long-term consolidation of an associative memory (LTM) in *Drosophila melanogaster*. After having previously found that LTM consolidation 1. costs energy (Plaçais and Pr  at, Science 2013) provided through pyruvate metabolism (Plaçais et al., Nature Comm 2017) and 2. is gated by the increased tonic activity in a type of dopaminergic neurons ('MP1 neurons') following only training protocol relevant for LTM, i.e. interspaced in time (Plaçais et al., Nature Neuro 2012), they here dig into the intra-cell signalling triggered by dopamine input and eventually responsible for the increased mitochondria activity in Kenyon Cells. They identify a particular PKC, PKC δ , as a major molecular interface in this process and describe

its translocation to mitochondria to promote pyruvate metabolism, specifically after spaced training.

Methodological approach

To that end, they use RNA interference against the isozyme PKC δ , in a time-controlled way and in the whole Kenyon cell populations or in the subpopulation forming the α/β lobe. This knock-down decreased the total PKC δ mRNA level in the brain by ca. 30%, and is enough to observe decreased in flies performances for LTM consolidation. Using Pyronic, a sensor for pyruvate for in vivo imaging, and pharmacological disruption of mitochondrial function, the authors then show that PKC δ knock-down prevents a high level of pyruvate from accumulating in the Kenyon cells at the time of LTM consolidation, pointing towards a role of PKC δ in promoting pyruvate metabolism. They further identify the PDH kinase PDK as a likely target for PKC δ since knocking down both PKC δ and PDK led to normal LTM performances, likely counterbalancing PKC δ knock-down alone.

To understand the timeline of PKC δ activation and to visualise its mitochondrial translocation in a subpart of Mushroom body lobes they imported in fruitfly the genetically-encoded FRET reporters of PKC δ , δ CKAR, and mitochondria- δ CKAR (Kajimoto et al 2010). They show that PKC δ is activated to the sensor's saturation only after spaced training, and not other types of training that are 'irrelevant' for LTM. Further, adding thermogenetic activation of dopaminergic neurons and RNA interference against Gq-coupled dopamine receptor to FRET imaging, they identify that a dopamine-triggered cascade is sufficient for the elevated PKC δ -activation.

Strengths and weaknesses

The authors use a combination of new fluorescent sensors and behavioral, imaging, and pharmacological protocols they already established to successfully identify the molecular players that bridge the requirement for spaced training/dopaminergic neurons MP1 oscillatory activity and the increased metabolic activity observed during long-term memory consolidation.

The study is dense in new exciting findings and each methodological step is carefully designed. Almost all possible experiments one could think of to make this link have been done in this study, with a few exceptions that do not prevent the essential conclusions from being drawn.

The discussion is well conducted, with interesting parallels with mammals, where the possibility that this process takes place as well is yet unknown.

Impact

Their findings should interest a large audience:

They discover and investigate a new function for PKC δ in regulating memory processes in neurons in conjunction with other physiological functions, making this molecule a potentially valid target for neuropathological conditions. They also provide new tools in drosophila to measure PKC δ activation in cells. They identify the major players for lifting the energetic limitations preventing the formation of a long-term memory.

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