



CB₁ and LPA₁ Receptors Relationship in the Mouse Central Nervous System

Estíbaliz González de San Román¹, Iván Manuel¹, Catherine Ledent², Jerold Chun³, Fernando Rodríguez de Fonseca^{4,5}, Guillermo Estivill-Torrús^{4,6}, Luis Javier Santín^{4,7} and Rafael Rodríguez Puertas^{1,8*}

¹ Department of Pharmacology, Faculty of Medicine and Nursing, University of the Basque Country (UPV/EHU), Leioa, Spain, ² Institut de Recherche Interdisciplinaire en Biologie Humaine et Moléculaire, Université Libre de Bruxelles, Brussels, Belgium, ³ Sanford Burnham Prebys Medical Discovery Institute, La Jolla, CA, United States, ⁴ Instituto de Investigación Biomédica de Málaga-IBIMA, Málaga, Spain, ⁵ Unidad de Gestión Clínica de Salud Mental, Málaga, Spain, ⁶ Unidad de Gestión Clínica de Neurociencias, Hospital Regional Universitario de Málaga, Málaga, Spain, ⁷ Departamento de Psicobiología y Metodología de las Ciencias del Comportamiento, Universidad de Málaga, Málaga, Spain, ⁸ Neurodegenerative Diseases, Biocruces Bizkaia Health Research Institute, Barakaldo, Spain

OPEN ACCESS

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*Correspondence:

Rafael Rodríguez Puertas
rafael.rodriguez@ehu.es

Received: 11 December 2018

Accepted: 03 September 2019

Published: 19 September 2019

Citation:

González de San Román E,
Manuel I, Ledent C, Chun J,
Rodríguez de Fonseca F,
Estivill-Torrús G, Santín LJ and
Puertas RR (2019) CB₁ and LPA₁
Receptors Relationship in the Mouse
Central Nervous System.
Front. Mol. Neurosci. 12:223.
doi: 10.3389/fnmol.2019.00223

Neurolipids are a class of bioactive lipids that are produced locally through specific biosynthetic pathways in response to extracellular stimuli. Neurolipids are important endogenous regulators of neural cell proliferation, differentiation, oxidative stress, inflammation and apoptosis. Endocannabinoids (eCBs) and lysophosphatidic acid (LPA) are examples of this type of molecule and are involved in neuroprotection. The present study analyzes a possible relationship of the main receptor subtypes for both neurolipid systems that are present in the central nervous system, the CB₁ and LPA₁ receptors, by using brain slices from CB₁ KO mice and LPA₁-null mice. Receptor-mediated G protein activation and glycerophospholipid regulation of potential precursors of their endogenous neurotransmitters were measured by two different *in vitro* imaging techniques, functional autoradiography and imaging mass spectrometry (IMS), respectively. Possible crosstalk between CB₁ and LPA₁ receptors was identified in specific areas of the brain, such as the amygdala, where LPA₁ receptor activity is upregulated in CB₁ KO mice. More evidence of an interaction between both systems was that the CB₁-mediated activity was clearly increased in the prefrontal cortex and cerebellum of LPA₁-null mice. The eCB system was specifically over-activated in regions where LPA₁ has an important signaling role during embryonic development. The modifications on phospholipids (PLs) observed in these genetically modified mice by using the IMS technique indicated the regulation of some of the PL precursors of both LPA and eCBs in specific brain areas. For example, phosphatidylcholine (PC) (36:1) was detected as a potential LPA precursor, and phosphatidylethanolamine (PE) (40:6) and PE (p18:0/22:6) as potential eCB precursors. The absence of the main cerebral receptors for LPA or eCB systems is able to induce modulation on the other at the levels of both signaling and synthesis of endogenous neurotransmitters, indicating adaptive responses between both systems during prenatal and/or postnatal development.

Keywords: neurolipids, lysophosphatidic acid, cannabinoids, GPCR, autoradiography, imaging mass spectrometry, brain

INTRODUCTION

During past decades, lipid molecules present in the CNS were considered components of cell membranes and organelles, intermediary metabolites, or constituents of the energy reservoirs. Currently, it is known that neurolipids are bioactive molecules that can act as neurotransmitters with neuromodulatory properties. Studies analyzing lipid molecules related to signaling systems are clarifying the complex integration of different lipid-metabolic pathways with other physiological functions mediated by lipids. The involvement of lipids in physiological and pathological processes can now also be analyzed by the development of new and potent analytical tools and instruments that enable rapid, high-throughput lipidomic analyses of rodent and human brain tissue sections at anatomical resolution, such as IMS (Gonzalez de San Roman et al., 2017; Martinez-Gardeazabal et al., 2017).

Lipid mediators, synthesized from glycerophospholipids, are a class of bioactive lipids that are produced locally through specific biosynthetic pathways in response to extracellular stimuli. These lipid molecules, which hereafter we will call neurolipids, mediate neurotransmission as important endogenous regulators of multiple cerebral processes related to neuroprotective actions, such as neural cell proliferation, differentiation, response to oxidative stress, inflammation and apoptosis. Neurolipids are transported to extracellular compartments (by non-well-defined mechanisms), usually bind to specific GPCRs to trigger intracellular signaling and responses in target cells, and then are sequestered rapidly through enzymatic or non-enzymatic processes (Murakami, 2011). Representative members of this class of neurolipids are eCBs and the LP, LPA.

The first CB receptor cDNA was cloned in 1990 as the first GPCR for lipid mediators (Matsuda et al., 1990). Two CB subtypes have been cloned: CB₁, the most abundant CB receptor subtype in the CNS, and CB₂, which is more restricted to glial cells. However, the CB₂ receptor appears to be expressed by some neurons, particularly under certain pathological conditions (Van Sickle et al., 2005; Viscomi et al., 2009; Garcia-Gutierrez and Manzanares, 2011; Navarrete et al., 2012). Moreover, there is evidence for other possible G protein-coupled CBs in the brain (Jarai et al., 1999; Di Marzo et al., 2000; Breivogel et al., 2001). Concerning the other above-mentioned LPs, the first high-affinity cognate cell surface receptor for LPA that was identified as the most abundant in the CNS was LPA₁, but two additional receptors have been identified (LPA₂ and LPA₃). More recently, another three LPA receptors were identified, which were somewhat divergent receptors (LPA₄, LPA₅, LPA₆) (reviewed in Choi et al., 2010; Yung et al., 2014). These two families of GPCRs, the CB and the LPA GPCRs, are phylogenetically

related. CBs share 18–20% identity of the amino acid sequence with LPA receptors, in particular with LPA₁, LPA₂, and LPA₃ (Chun et al., 1999).

Both LPA and eCBs are synthesized mainly by the cleavage of phospholipids (PLs), probably at the cell membrane. The distribution pattern of CB₁ and CB₂ receptors in the developing and adult brain is highly correlated with the expression of the DAGL α/β enzymes, responsible for 2-AG synthesis, suggesting that PL precursors would also be closely localized (Bisogno et al., 2003; Yoshida et al., 2006; Oudin et al., 2011). However, little is known about the specific lipid species that constitute the eCB precursors and particularly, about their specific localization in the brain (Lu and Mackie, 2016). Therefore, one of the aims of the present study is to identify these potential precursors through MALDI-IMS assays. This technique has enriched lipidomic studies due to the new dimensions added by IMS, i.e., the anatomical mapping of the molecules in tissue sections, a key piece of information to understand the physiological roles played by lipids present in the tissue (Caprioli et al., 1997; Jackson et al., 2005; Skraskova et al., 2015; Mohammadi et al., 2016).

Supporting the relationship between the eCB and LPA systems, it is relevant that the endogenous ligands for these systems are closely related, e.g., 2-AG can be metabolized to 2-arachidonoyl-LPA through the action of a monoacylglycerol kinase (Kanoh et al., 1986; Shim et al., 1989). The opposite direction of this phosphorylation reaction, i.e., dephosphorylation, also seems to be possible (Hiroyama and Takenawa, 1998; Nakane et al., 2002). Thus, it appears that 2-arachidonoyl-LPA and 2-AG could be mutually interconverted within a cell, and the direction of the reaction may even differ among the subcellular compartments within the cells and could be modified depending on the availability of substrates, such as ATP (Zhao and Abood, 2013). However, 2-arachidonoyl LPA would not directly interact with the cannabinoid CB₁ receptor, and 2-AG, in turn, would not display affinity for the LPA₁ receptor (Nakane et al., 2002). Moreover, structural analyses of the crystal structure of antagonist-bound LPA₁ receptor predict a functional crosstalk with CB₁ receptors (Chrencik et al., 2015).

During the last decade, the roles of the eCB and LPA systems in the regulation of neuronal progenitor proliferation and differentiation have been described, involving both systems in neurogenesis at the subventricular zone (Birgbauer and Chun, 2006; Galve-Roperh et al., 2006). However, LPA, through binding to the LPA₁ receptor, acts only during the prenatal development of the brain (Hecht et al., 1996). In the meantime, eCBs, through binding to CB₁ and CB₂ receptors, regulate the migration of subventricular zone-derived neuroblasts in the postnatal brain (Oudin et al., 2011). Nevertheless, the eCB system may also control embryonic neuronal development and maturation (Diaz-Alonso et al., 2012).

In addition, both systems display relevant roles in the limbic brain areas and pathways that control emotional processes, such as the amygdala connections, where both systems are involved in the extinction of fear-conditioned responses (Marsicano et al., 2002; Tan et al., 2010; Pedraza et al., 2014). Furthermore, both systems seem to be involved in the control of cognitive processes linked to the hippocampus, such as spatial memory.

Abbreviations: 2-AG, 2-arachidonoyl glycerol; AEA, anandamide; cb WM, cerebellum white matter; CB, cannabinoid receptor; cc, corpus callosum; Cx layer VI, frontal cortex layer VI; eCB, endocannabinoid; GlcCer, glucosylceramide; GPCR, G protein-coupled receptor; ic, internal capsule; LP, lysophospholipid; LPA, lysophosphatidic acid; MALDI-IMS, matrix-assisted laser desorption/ionization imaging mass spectrometry; PA, phosphatidic acid; PC, phosphatidylcholine; PE, phosphatidylethanolamine; ROI, region of interest; TIC, total ion current; VZ, ventricular zone.

maLPA₁-null mice showed, through the LPA₁ receptor-signaling pathway, long-term spatial memory impairment, but not short-term memory impairment (Castilla-Ortega et al., 2010).

On the other hand, direct hippocampal CB₁ activation by high doses of exogenous or endogenous cannabinoid compounds induce characteristic long-term memory impairment (Puighermanal et al., 2009). In the same way, the genetic deletion of CB₁ receptor induces neuronal loss in CA1 and CA3 areas of the hippocampus, which triggers a decline in cognitive functions (Bilkei-Gorzo et al., 2005).

In summary, both neurolipid systems are implicated in cortical development in the prenatal brain, in the extinction of fear-conditioned behavior in the amygdala, and in the modulation of long-term memory in the hippocampus, suggesting a convergence in the control of similar physiological functions in the CNS. In the present study we analyze the adaptive changes that are probably produced during mouse prenatal and postnatal development in the eCB and LPA neurolipid systems using both maLPA₁-null and CB₁ KO mice, to analyze the interactions and crosstalk between the CB₁ and LPA₁ mediated-activities and to identify the anatomical localization of the possible precursors of the endogenous ligands for both signaling systems. Technically, the study combines functional [³⁵S]GTPγS autoradiography with MALDI-IMS to analyze consecutive brain slices.

MATERIALS AND METHODS

Chemicals

[³⁵S]GTPγS (initial specific activity 1250 Ci/mmol) was purchased from Perkin Elmer (Boston, MA, United States). WIN55212-2 was purchased from Tocris (Bristol, United Kingdom). Oleoyl-L-α-lysophosphatidic acid sodium salt (LPA), 2-mercaptobenzothiazole (MBT), DL-dithiothreitol (DTT), guanosine-5'-diphosphate (GDP), guanosine-5'-o-3-triphosphate and β-radiation sensitive Kodak Biomax MR films were acquired from Sigma-Aldrich (St. Louis, MO, United States). The [¹⁴C]-microscales used as standards in the autoradiographic experiments were purchased from Amersham Biosciences (Buckinghamshire, United Kingdom) and American Radiolabeled Chemicals (ARC, St. Louis, MO, United States). Finally, for the preparation of the different buffers, the treatment of slides, re-crystallization of the matrix and film development, several additional compounds supplied from different laboratories were used. All the compounds were of the highest commercially available quality for the necessity of the neurochemical studies.

Animals and Tissue Preparation

maLPA₁-null homozygous ($n = 8$) and wild-type 3-month-old males ($n = 8$) (on a mixed background C57Bl/6 × 129SW) were obtained from Hospital Carlos Haya, Málaga, Spain, as a result of a collaboration with Dr. Estivill-Torrús's research group. The maLPA₁-null (from Málaga variant of LPA₁-null) mouse colony arose spontaneously from the initially reported LPA₁-null mouse line (Contos et al., 2000) while crossing heterozygous

foundational parents within their original mixed background since phenotypic variations have been described in almost complete perinatal viability and show a reduced VZ, altered neuronal markers, and increased cortical cell death that results in a loss of cortical layer cellularity in adults (Estivill-Torrús et al., 2008; Matas-Rico et al., 2008).

CB₁-knockout mice are a strain maintained at the University of the Basque Country and were provided by C. Ledent of the University of Brussels (Belgium). For this study, 9 week-old male CB₁-knockout ($n = 5$) and wild-type mice ($n = 5$) were used. The generation of mice lacking CB₁ CBs was described previously (Ledent et al., 1999). To homogenize the genetic background of the mice, the first generation of heterozygous mice was bred for 30 generations on a CD1 background, with selection for the mutant CB₁ gene at each generation. Mice were housed in a temperature (22°C) and humidity-controlled (65%) room with a 12:12-h light/dark cycle (light between 08:00 and 20:00 h), with food and water *ad libitum*. All procedures were performed in accordance with European animal research laws (European Communities Council Directives 86/609/EEC, 98/81/CEE and 2003/65/CE; Commission Recommendation 2007/526/EC) and the Spanish National Guidelines for Animal Experimentation and the Use of Genetically Modified Organisms (Real Decreto 1205/2005 and 178/2004; Ley 32/2007 and 9/2003). All the experimental protocols were approved by the Local Ethics Committee for Animal Research at the University of the Basque Country (CEIAB/21/2010/Rodríguez Puertas).

Mouse brains were quickly removed under anesthesia. Then, tissues were frozen on dry ice and kept at −80°C. The brains were cut on a Microm HM550 cryostat (Thermo, Germany) to obtain 20 μm sections that were mounted onto gelatin-coated slides, and these were stored at −20°C until use.

[³⁵S]GTPγS Binding Assay

The tissue sections were air-dried for 15 min then washed in HEPES-based buffer (50 mM HEPES, 100 mM NaCl, 3 mM MgCl₂, and 0.2 mM EGTA, pH 7.4) for 30 min at 30°C in a water bath. The preincubation was repeated in new buffer. In a second step, the slides were incubated for 2 h at 30°C supplemented with 2 mM GDP, 1 mM DTT, adenosine deaminase (3 μ/l) and 0.04 nM [³⁵S]GTPγS. The agonist-stimulated binding was measured under the same conditions in the presence of the specific GPCR agonists oleoyl-L-α-lysophosphatidic acid sodium salt; LPA (10^{−5} M) and WIN55212-2 (10^{−5} M). Non-specific binding was determined in the presence of 10 μM non-labeled GTPγS. Sections were washed twice in an ice-cold (4°C) HEPES buffer (50 mM, pH 7.4), dipped in distilled water, and air-dried. Sections were exposed to autoradiography film (Kodak Biomax MR) together with ¹⁴C standards for 48 h at 4°C in hermetically closed cassettes.

Quantitative Image Analysis of Autoradiograms

Films were scanned and quantified by transforming the optical densities into nCi/g of tissue equivalent (nCi/g t.e.) using ImageJ software (NIH-IMAGE, Bethesda, MA, United States)

(developed at the U.S. National Institutes of Health and freely available on <https://imagej.nih.gov/ij/>). The [¹⁴C] radioactive standards that were co-exposed with the tissue slides were used to calibrate the optical densities with the level of radioactivity labeled to the sections. Experimental data were analyzed by using the computer programs GraphPad Prism (v. 5.0, GraphPad) and Microsoft Excel. Data are expressed as the mean values ± SEM. The basal binding was calculated as nCi/g tissue equivalent, using the values provided in the ¹⁴C microscales. The agonist stimulation of [³⁵S]GTPγS binding is expressed by the percentage of stimulation over the basal (%) in the presence of the different agonists, calculated as: $(([\text{³⁵S]GTP}\gamma\text{S agonist-stimulated binding}) \times 100 / ([\text{³⁵S]GTP}\gamma\text{S basal binding})) - 100$. The regions of interest (ROI) were defined from the scanned film in the case of the GTPγS autoradiography and directly from the image obtained from MALDI-IMS, using counter stained consecutive sections and a mouse brain atlas, without knowing the genotype of the mice and without taking into account the intensities of the rest of the animals. Differences between regions for each mouse genotype (wild type vs. transgenic) were analyzed by the unpaired two-tailed Student's *t* test.

Sample Preparation for MALDI-IMS

The original lipid composition and anatomical characteristics of the tissue must be well-preserved throughout the sample-preparation process (Schwartz et al., 2003). The fresh-frozen brains of the mice were cut on a Microm HM550 cryostat (Thermo, Germany) to obtain 20 μm sections and stored at −20°C until the moment of use.

Once the initial tissue preparation steps were completed, the matrix was deposited on the tissue surface prior to analysis by a sublimation process using the protocol described by Gonzalez de San Roman et al. (2017). For tissue sections mounted on glass slides, sublimation was performed using 300 mg of MBT, which was used as a chemical matrix, to control the deposition time and temperature (30 min, 140°C). Therefore, it was possible to control the thickness of the matrix layer and optimize the S/N ratio of the mass spectra, avoiding lipid migration on the tissue slice thanks to the lack of solvents using this sublimation procedure.

Mass Spectrometer

A MALDI LTQ-XL-Orbitrap (Thermo Fisher, San Jose, CA) equipped with a nitrogen laser ($\lambda = 337$ nm, rep. rate = 60 Hz, spot size = 80 × 120 μm) was used for mass analysis. Thermo's ImageQuest and Xcaliber software were used for MALDI-IMS data acquisition. The images were acquired in both negative and positive ion modes. The positive ion range was 500–1000 Da, with 10 laser shots per pixel at a laser fluence of 15 μJ. The negative ion range was 400–1100 Da, with 10 laser shots per pixel at a laser fluence of 15 μJ. The target plate stepping distance was set to 150 μm for both the *x*- and *y*-axes by the MSI image acquisition software. The mass resolution was approximately 100,000 laser shots in both positive and negative ion modes. The data were normalized using the TIC values to avoid potential displacement in the masses along the tissue that may be induced by experimental factors, including irregularities of the surface.

Image and Spectral Analysis for MALDI-IMS

The MALDI-IMS technique was applied to localize and semi-quantitatively analyze the different lipid species present in WT and maLPA₁-null mice in positive and negative ion detection modes. We employed optimized experimental conditions for lipid detection previously set up by our research group and others, including selection of the MBT chemical matrix and deposition mode by sublimation procedures (Astigarraga et al., 2008; Yang and Caprioli, 2011). First, IMS of sagittal mouse brain sections was performed using the positive ion detection mode, and approximately 300 mass peaks were detected in the mass range from 500 to 900 *m/z*. Then, the same slices of tissue were analyzed in negative ion detection mode using a mass range from 400 to 1100 *m/z*. A complete mass spectrum was obtained from each pixel along all the surface of each brain tissue slice, obtaining the slice images as a composition of the intensity color of each peak (molecule or *m/z*) at each pixel. Specifically, an ion of interest can be extracted from the spectra, and an image of that particular ion distribution in the tissue can be visualized. Once we had analyzed at least five sagittal brain slices samples from five different animals of WT and another five samples of maLPA₁-null mice, we selected different ROIs, such as hippocampus, cortex, cerebellum, cc, and striatum. The spectrum normalization was calculated using the TIC for each mass to exclude a number of noise spectra. Next, we compared WT and maLPA₁-null using Origin[®]8 software.

In summary, the MALDI images were generated using ImageQuest software (Thermo Scientific). Each of the *m/z* values was plotted for signal intensity per pixel (mass spectrum) across a given area (tissue section). The *m/z* range of interest was normalized using the ratio of the TIC for each mass spectrum. The intensity reached by each mass spectrum (intensity of each peak, *m/z* value or molecule) was further calculated as a ratio of the peak with the highest intensity, and the average spectrum was calculated with OriginPro 8 software (Northampton, MA, United States). The most intense peak was considered 100%. Then, the two-tailed unpaired *t* test was performed for the comparison of two groups. The results were considered significant if $p \leq 0.05$.

Peak Assignment

Analysis of the lipid composition at CNS tissue samples from mice included in the present study was complex. A large number of different possible lipid species were detected, and some of them shared similar masses and were not detected and/or assigned to a specific lipid molecule by previous studies. Nevertheless, the assignment of lipid species was facilitated by the use of the Lipid MAPS database¹ and different previous reports (Berry et al., 2011; Martinez-Gardeazabal et al., 2017), using a 5 ppm mass accuracy as the tolerance window for the assignment. The numbers (*x*:*y*) following the glycerolipid species denote the total length and the number of double bonds of the acyl chains, respectively, while the GlcCer species numbers correspond to the length and number

¹<http://www.lipidmaps.org/>

of double bonds of the acyl chain added to those of the attached sphing-4-enine (d18:1) or sphinganine (d18:0) base.

RESULTS

[³⁵S]GTPγS Binding Assay of maLPA₁-Null Mouse Brain Sections

The [³⁵S]GTPγS binding stimulated by WIN55212-2 was measured in brain slices of maLPA₁-null and WT mice to localize and quantify the activity of CB₁ CBs. The aim was to observe, in adult mice was the possible modulation of cannabinoid signaling that was induced by the lack of the LPA receptor subtype, LPA₁, during the animal's previous development. The basal activity (in the absence of agonist) of the G_{i/o}-coupled GPCR in maLPA₁-null mice was already shown in Gonzalez de San Roman et al. (2015). The G_{i/o}-coupled CB₁ receptor activity induced by the CB₁ agonist WIN55212-2 was increased at the prefrontal cortex layers I–III (WT 212 ± 19% vs. maLPA₁-null 369 ± 49%, $p \leq 0.05$) and in layer VI (WT 284 ± 14% vs. maLPA₁-null 396 ± 22%, $p \leq 0.05$). The increase in the CB₁ activity was also significant in the cerebellum gray matter (cb GM) of maLPA₁-null mice compared to WT (WT 23 ± 15% vs. maLPA₁-null 107 ± 13%, $p \leq 0.05$) and cb WM (WT 678 ± 149% vs. maLPA₁-null 1377 ± 207%, $p \leq 0.05$). The globus pallidus, a nucleus with a high density of CB₁ receptors in mice, also showed an increase in the activity of these receptors in maLPA₁-null mice (WT 1705 ± 151% vs. maLPA₁-null 2037 ± 82%), but this change was not statistically significant (Table 1 and Figure 1). The [³⁵S]GTPγS binding stimulated by oleoyl-L-α-lysophosphatidic acid sodium salt (LPA) showed no stimulations in any brain area of the maLPA₁-null mice, demonstrating the specificity of the experimental binding procedure and the right phenotype of the animals (Gonzalez de San Roman et al., 2015).

[³⁵S]GTPγS Binding Assay in CB₁ KO Mouse Brain Sections

We compared the [³⁵S]GTPγS binding stimulated by LPA in CB₁ KO and WT mice to observe the consequences of the developmental absence of the main eCB receptor on the signaling through cerebral GPCRs for the LPA₁ receptors. There were statistically significant changes that were restricted to the amygdala and showed increased [³⁵S]GTPγS binding induced by LPA (WT -20 ± 4.3% vs. CB₁ KO 32 ± 6.3%, $p \leq 0.05$). The LPA₁ receptor activity of CB₁ KO mice was comparable to WT mice in all the other brain areas that were analyzed (Table 2 and Figure 2). The [³⁵S]GTPγS binding stimulated by WIN55212-2 showed no stimulation in any brain area of the CB₁ KO mice, demonstrating the specificity of the experimental binding procedure and the right phenotype of the animals (data not shown).

MALDI-IMS in maLPA₁-Null Mouse Brain Sections

Some lipid species showed changes in positive ion detection mode in maLPA₁-null mice compared to WT mice. Three lipid

species, GlcCer (d18:1/14:0) + K⁺ in cortex (WT 14.5 ± 0.8% vs. maLPA₁-null 9.3 ± 1.5%, $p < 0.05$) and striatum (WT 22.0 ± 1.3% vs. maLPA₁-null 15.2 ± 2.3%, $p \leq 0.05$), PA (16:0/18:1) + K⁺ in hippocampus (WT 46.5 ± 2.0% vs. maLPA₁-null 37.2 ± 3.4%, not significant) and cortex (WT 47.5 ± 2.0% vs. maLPA₁-null 37.3 ± 3.5%, $p \leq 0.05$), and PC(32:0)⁺ in hippocampus (WT 27.3 ± 3.6% vs. maLPA₁-null 17.9 ± 0.5%, $p \leq 0.05$), were present at lower levels in maLPA₁-null mice. By contrast, the intensity of the peaks for PC(36:1) + K⁺ in hippocampus (WT 16.3 ± 0.8% vs. maLPA₁-null 20.4 ± 0.5%, $p < 0.05$) and cortex (WT 15.8 ± 0.7% vs. maLPA₁-null 19.6 ± 1.5%, $p \leq 0.05$), PC(38:4) + K⁺ in hippocampus (WT 8.4 ± 0.4% vs. maLPA₁-null 11.3 ± 1.0%, $p \leq 0.05$) and cortex (WT 10.3 ± 0.7% vs. maLPA₁-null 13.5 ± 1.1%, $p \leq 0.05$) and PC(38:6) + K⁺ in hippocampus (WT 12.0 ± 0.6% vs. maLPA₁-null 15.7 ± 0.9%, $p \leq 0.05$) was higher in the KO mice (Table 3 and Figure 3. See “*p*” values in table of Supplementary Material).

MALDI-IMS in CB₁ KO Mouse Brain Sections

The results of the MALDI-IMS experiments using CNS slices from WT and CB₁ KO mice were also performed in positive and negative ion detection modes. As has been described, we used an optimized protocol for the lipid detection. The analysis of IMS on sagittal mouse brain slices was performed in positive ion detection mode in a mass range from 500 to 1000 m/z and in negative ion detection mode from 400 to 1100 m/z. We selected the ROI and followed the steps described in the “Materials and Methods” section. The results indicated

TABLE 1 | [³⁵S]GTPγS binding induced by WIN55212-2 (10 μM) in different areas of WT and maLPA₁-null mice, calculated as percentage over the basal value.

Brain region	Stimulation by WIN55212-2 (%)		
	WT	maLPA ₁ -null	<i>p</i> -value
Amygdala	362 ± 50	232 ± 22	0.06
Cerebellum			
White matter	2.3 ± 15	107 ± 13*	0.001
Gray matter	679 ± 149	1377 ± 207*	0.04
Corpus callosum	108 ± 20	150 ± 11	0.18
Striatum	254 ± 18	255 ± 23	0.75
Frontal cortex			
Layer I–III	212 ± 19	369 ± 49*	0.05
Layer IV	188 ± 33	236 ± 14	0.27
Layer V	223 ± 25	282 ± 12	0.07
Layer VI	284 ± 14	396 ± 22*	0.02
Hippocampus			
Dorsal CA1 radiata	371 ± 51	341 ± 38	0.69
Ventral CA3 radiata	288 ± 23	266 ± 12	0.51
Internal capsule	53 ± 16	33 ± 14	0.28
Globus pallidus	1705 ± 151	2037 ± 82	0.21

Data are mean ± SEM values, in percentage of stimulation over the basal (%). The *p*-values were calculated by the unpaired two-tailed Student's *t* test. * $p \leq 0.05$. WT ($n = 8$) and maLPA₁ null ($n = 8$).

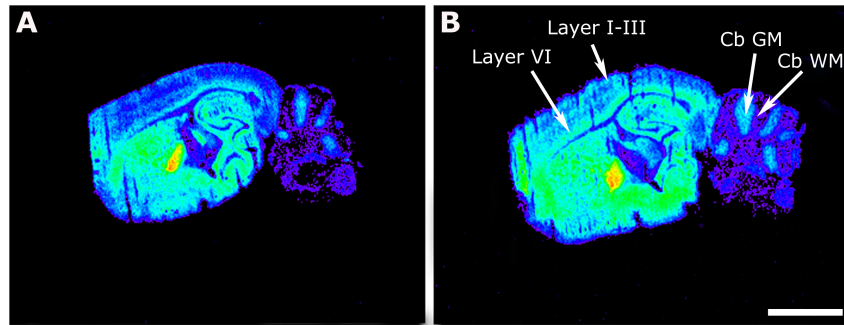


FIGURE 1 | Representative autoradiograms of WT **(A)** and maLPA₁-null mice **(B)** in sagittal sections that show [³⁵S]GTP_γS binding stimulated by WIN55212-2 (10⁻⁵ M). Note the increase in the binding in maLPA₁-null mice at different cortical layers (Layer I-III and Layer VI) and at the cerebellar gray matter (cb GM) and white matter (cb WM). Scale bar = 3 mm.

that some lipid species were modified in the brain of CB₁ KO mice in both positive and negative ion detection modes. Some lipid species were present at a higher intensity than in WT mouse brain. These lipid species included PC(32:0)⁺ in hippocampus (WT 37.6 ± 3.6% vs. CB₁ KO 65.3 ± 3.1%, $p < 0.01$) and cortex (WT 33.2 ± 3.7% vs. CB₁ KO 54.7 ± 6.5%, $p < 0.05$) and PC(34:1)⁺ also in hippocampus (WT 48.6 ± 5.0% vs. CB₁ KO 67.7 ± 3.5%, $p < 0.05$) and cortex (WT 51.2 ± 4.8% vs. CB₁ KO 69.5 ± 4.5%, $p < 0.05$). Both PC molecules were increased in the frontal cortex, hippocampus and striatum but were not modified in the cerebellum of the CB₁ KO mice. In contrast, the relative intensities of other lipid species were lower in CB₁ KO mice

than in WT mice in the hippocampus, frontal cortex and cerebellum but not modified in the striatum. These lipid species included PE(p18:0/22:6) in hippocampus (WT 3.4 ± 0.2% vs. CB₁ KO 1.1 ± 0.6%, $p < 0.05$) and cortex (WT 3.7 ± 0.1% vs. CB₁ KO 1.0 ± 0.6%, $p < 0.05$), PE(18:0/22:6)⁻ in hippocampus (WT 8.5 ± 0.3% vs. CB₁ KO 4.4 ± 1.9%, $p < 0.01$), and phosphatidylserine (PS) (18:0/22:6)⁻ in cortex (WT 73.3 ± 9.5% vs. CB₁ KO 46.9 ± 4.7%, $p < 0.01$) and striatum (WT 57.9 ± 4.8% vs. CB₁ KO 40 ± 2.7%, $p < 0.05$) (**Table 4** and **Figure 4**. See “ p ” values in table of **Supplementary Material**).

DISCUSSION

The present study shows specific anatomical alterations of a few lipid species that are potential PL precursors of LPA or eCBs, analyzing simultaneously in the same animals the regulation of the signaling by their specific CB₁ and LPA₁ receptors in KO mice for each of these receptors, which are the respective predominant subtypes present in the CNS. The analyzed regions were selected attending to previously described brain areas showing high densities of LPA₁ or CB₁ receptors.

The analysis of the activity of CB₁ receptors in maLPA₁-null mice allowed us to detect a regulation mechanism in both in the frontal cortex and in the cerebellum. The absence of LPA₁ in maLPA₁-null mice results in a reduction of neuronal cells in layers II/III, V, and VI, increased apoptosis, alterations in the formation of the cerebral cortex and premature expression of neuronal markers (Estivill-Torrus et al., 2008). The eCB system is a critical component of frontal cortex physiology. The CB₁ receptor is mainly expressed in layers II/III and V/VI (Lafourcade et al., 2007), same areas where there is a depletion of neurons in maLPA₁-null mice. Therefore, the increased functional activity of CB₁ receptors suggests a compensatory effect of the eCB system to balance the neuronal reduction. Furthermore, the cerebellum is another brain area where we detected an increase in CB₁ receptor activity in maLPA₁-null mice. Cannabinoids modulate the proliferation of cerebellar neuronal precursors via the CB₁ receptor (Trazzi et al., 2010). Hence, the lack of the

TABLE 2 | [³⁵S]GTP_γS binding induced by LPA (10 μM) in different areas of WT and CB₁ KO mouse brains, calculated as stimulation percentage over basal.

Brain region	Stimulation by LPA (%)		
	WT	CB ₁ KO	p -value
Amygdala	-20 ± 4.3	32 ± 6.3*	0.0008
Cerebellum			
White matter	229 ± 56	124 ± 46	0.2
Gray matter	50 ± 6.5	51 ± 27	0.96
Corpus callosum	343 ± 72	325 ± 59	0.84
Striatum	21 ± 9.3	24 ± 5.5	0.8
Frontal cortex			
Layer I-III	60 ± 19	46 ± 21	0.6
Layer IV	53 ± 14	57 ± 27	0.62
Layer V	50 ± 11	64 ± 26	0.64
Layer VI	48 ± 15	62 ± 28	0.57
Hippocampus			
Dorsal CA1 radiata	42 ± 11	18 ± 23	0.38
Ventral CA3 radiata	1.4 ± 13	14 ± 5	0.44
Internal capsule	203 ± 41	210 ± 44	0.91
Globus pallidus	2.2 ± 11	62 ± 42	0.16

Data are mean ± SEM values, in percentage of stimulation over basal (%). SEM values, in percentage of stimulation over basal (%). The p -values were calculated by the unpaired two-tailed Student's t test. * $p \leq 0.05$. WT ($n = 5$) and CB₁ KO ($n = 5$).

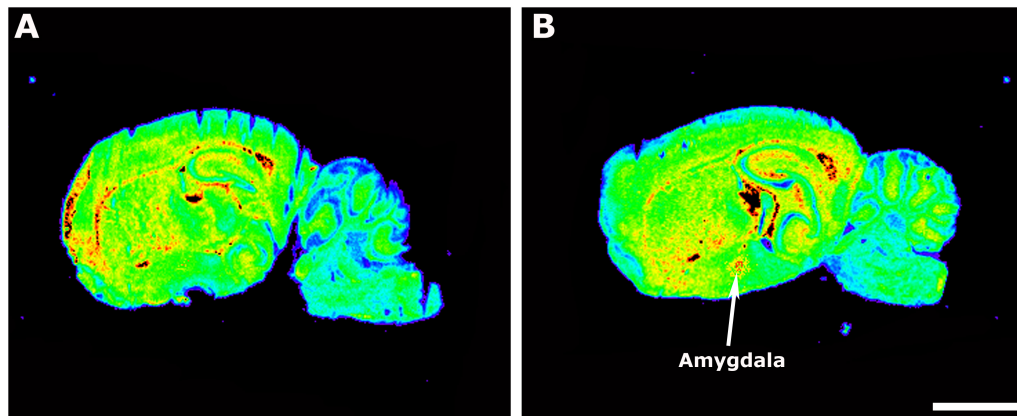


FIGURE 2 | Autoradiographic images of sagittal sections from WT **(A)** and CB₁ KO mice **(B)** showing [³⁵S]GTPγS binding stimulated by LPA (10⁻⁵ M). Note the increase in the binding at the amygdala in CB₁ KO mice. Scale bar = 3 mm.

TABLE 3 | MALDI-IMS intensities (expressed as % of the most abundant peak) of molecular species of PC and PA that were found modified in positive ion detection mode in sagittal brain sections from WT (*n* = 5) compared to the maLPA₁-null (*n* = 5).

Assignment	m/z	Cortex		Hippocampus		Striatum		Corpus callosum		Cerebellum	
		WT	LPA ₁ -null	WT	LPA ₁ -null	WT	LPA ₁ -null	WT	LPA ₁ -null	WT	LPA ₁ -null
GlcCer(d18:1/14:0) + K ⁺	710.4899	14.5 ± 0.8	9.3 ± 1.5**	22.6 ± 1.0	19.1 ± 2.4	22.0 ± 1.3	15.2 ± 2.3*	14 ± 0.9	11.1 ± 1.7	21.3 ± 2.3	21.1 ± 3.5
PA(16:0/18:1) + K ⁺	713.4535	47.6 ± 2.0	37.3 ± 3.5*	46.5 ± 2.0	37.2 ± 3.4*	45.1 ± 2.2	35.3 ± 3.3*	34.6 ± 2.9	28.9 ± 2.9	34.5 ± 1.1	32.2 ± 4.3
PC(32:0) ⁺	734.5700	20.2 ± 3.2	25.3 ± 7.1	27.1 ± 3.6	17.9 ± 1.7*	28.1 ± 3.3	26.7 ± 6.1	19.5 ± 3.0	20.9 ± 4.3	21.4 ± 2.2	22.7 ± 4.4
PC(36:1) + K ⁺	826.5733	15.8 ± 0.7	19.6 ± 1.5*	16.3 ± 0.8	20.4 ± 0.5*	22.2 ± 1	26.2 ± 0.9*	37.7 ± 1.1	42.0 ± 3.6	28.1 ± 0.8	28.2 ± 0.9
PC(38:6) + K ⁺	844.5270	10.3 ± 0.7	13.5 ± 1.1*	8.4 ± 0.4	11.3 ± 1.0*	8.3 ± 0.6	10.3 ± 1.2	6.5 ± 0.5	8.5 ± 1.6	12.9 ± 1.1	16.1 ± 0.6*
PC(38:4) + K ⁺	848.5572	8.1 ± 0.9	8.7 ± 1.1	12 ± 0.6	15.7 ± 0.9*	11.1 ± 0.6	13.2 ± 1.0	8.9 ± 0.4	11.1 ± 1.1	5.3 ± 0.2	6.4 ± 0.4*

Data are mean ± SEM values. The *p*-values were calculated by the unpaired two-tailed Student's *t* test **p* < 0.05, ***p* < 0.01.

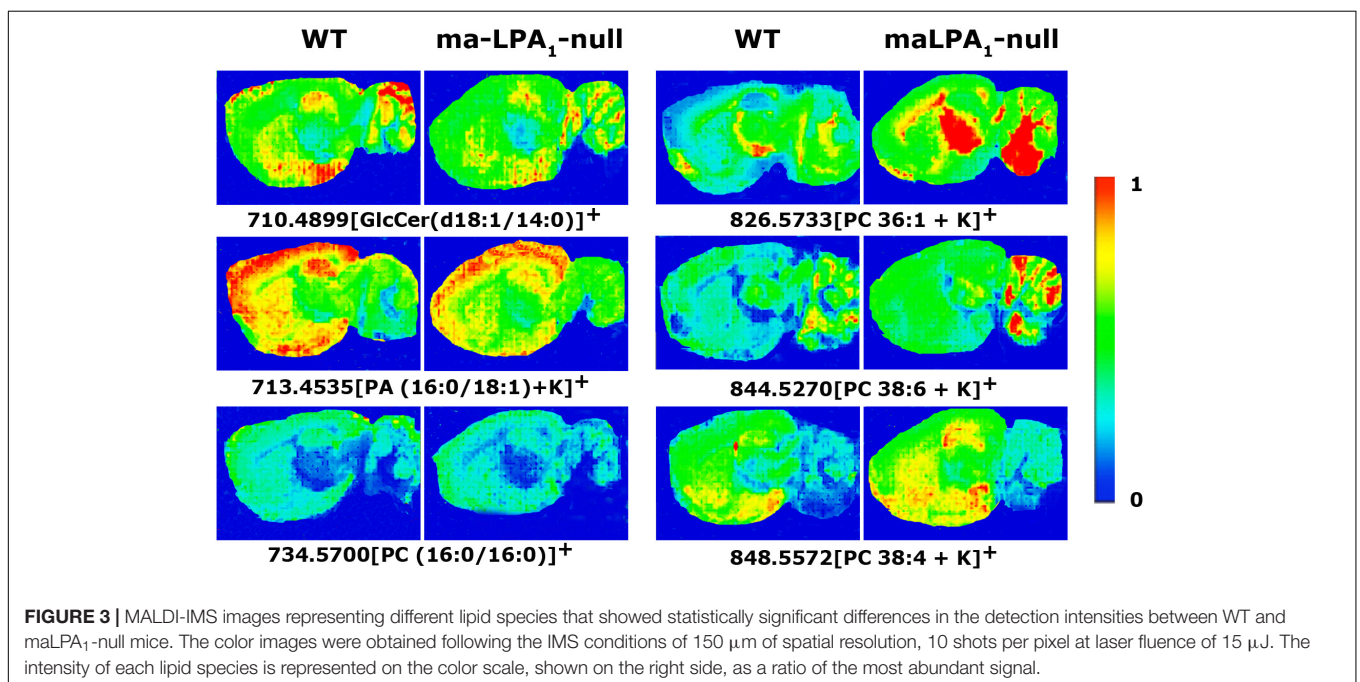


FIGURE 3 | MALDI-IMS images representing different lipid species that showed statistically significant differences in the detection intensities between WT and maLPA₁-null mice. The color images were obtained following the IMS conditions of 150 μm of spatial resolution, 10 shots per pixel at laser fluence of 15 μJ. The intensity of each lipid species is represented on the color scale, shown on the right side, as a ratio of the most abundant signal.

TABLE 4 | MALDI-IMS intensities (expressed as % of the most abundant peak) of molecular species of PC, PE, and PS in positive and negative ion detection modes that were modified in sagittal brain sections from WT (*n* = 5) compared to CB₁ KO mice (*n* = 5).

Assignment	Exp(m/z)	Cortex		Hippocampus		Striatum		Cerebellum	
		WT	CB ₁ KO	WT	CB ₁ KO	WT	CB ₁ KO	WT	CB ₁ KO
PC(32:0) ⁺	736.5654	33.2 ± 3.7	54.7 ± 6.5*	37.6 ± 3.6	65.4 ± 3.1**	31.4 ± 4.1	49.3 ± 6*	42.3 ± 7.5	51.4 ± 4
PC(34:1) ⁺	760.5856	51.2 ± 4.8	69.5 ± 4.5*	48.6 ± 5.0	67.7 ± 3.5*	51.7 ± 5.2	67.7 ± 5.1*	65.2 ± 7.9	72.3 ± 4.2
PE(p18:0/22:6) ⁻	774.5432	3.7 ± 0.1	1 ± 0.6**	3.4 ± 0.2	1.1 ± 0.6*	1.4 ± 0.2	0.9 ± 0.2	4.1 ± 1.2	1.5 ± 0.5
PE(18:0/22:6) ⁻	790.5381	12.6 ± 0.7	10 ± 2.9	8.5 ± 0.3	4.4 ± 1.9**	9.5 ± 1.2	6 ± 0.9	10.6 ± 2	5.6 ± 0.9*
PS(18:0/22:6) ⁻	834.5252	73.3 ± 9.5	46.9 ± 4.7**	53.9 ± 4.5	44.9 ± 4.3	57.9 ± 4.8	40 ± 2.7*	41.1 ± 7.7	32.6 ± 2.4

Data are mean ± SEM values. The *p*-values were calculated by the unpaired two-tailed Student's *t* test **p* ≤ 0.05, ***p* ≤ 0.01.

LPA₁ receptor could lead to an adaptive regulation in CB₁-mediated activity.

On the other hand, when the activity of LPA₁ receptors was analyzed in CB₁ KO mice, the LPA₁ receptor activity was increased only in the amygdala compared with WT mice. The CB₁ receptor plays an important role in processes mediated by the amygdala, such as emotional responses (Azad et al., 2004; Laviolette and Grace, 2006; Roche et al., 2007; Tan et al., 2010). The eCB system in the amygdala has also been implicated in pain modulation (Manning et al., 2003), fear conditioning (Marsicano et al., 2002), anxiety (Imperatore et al., 2015) and fear-conditioned learning (Llorente-Ovejero et al., 2017). The LPA₁ receptor plays a crucial role in the extinction of fear conditioning (Pedraza et al., 2014) and has been associated with the mixed depressive-anxiety phenotype (Moreno-Fernandez et al., 2017). Our results suggest that the lack of the CB₁ receptor leads to an increased LPA₁ receptor activity in the amygdala, as a compensatory effect exerted by LPA signaling in this limbic area. Considering the present results, it is difficult to hypothesize why no other brain regions have been regulated in CB₁ KO mice, this regional exclusivity to the amygdala emphasizes the already reported role of LPA₁ receptors in fear extinction, that might be indicating a close physiological control in anxiety behavior and fear-conditioned learning together with CB₁ receptors. However, other functions modulated by the eCB system, such as pain or movement control, are possibly not being compensated by LPA₁ signaling.

The lack of LPA₁ receptor expression during mouse development led to an increase in the activity of the CB₁ receptor in the cortical area and cerebellum, and the lack of the CB₁ receptor led to an increase in LPA₁ receptor activity in the amygdala. Therefore, the absence of neurotransmissions mediated by CB₁ or LPA₁ receptors in each strain of knockout mice converged to a common compensatory mechanism between both systems in some specific brain areas (cortex, cerebellum and amygdala). The reported compensation would affect receptors coupled to other types of G proteins, however, as previously mentioned, we were only able to analyze those coupled to the G_{i/o} subtype. It is improbable that CB₁ receptors play a role since previous results reported a similar distribution regarding the CB₁ receptor autoradiographic densities compared to functional autoradiography stimulated by specific agonists such as the WIN55212-2 (Llorente-Ovejero et al., 2018). However, it has not been yet possible to get the distribution of LPA₁ receptors.

Moreover, the co-regulation of eCBs and LPA must be yielded during the pre- and postnatal development of both strains of mice.

The mechanisms underlying the observed modulation of CB₁ receptors in LPA₁-null mice may involve an increase in the expression of CB₁ receptors mediated by another subtype of LPA receptors coupled to G_{i/o} proteins (see **Supplementary Material**).

The metabolic precursors of the endogenous agonists for both neurolipid systems, eCB and LPA, are PLs present at the cellular membranes. The metabolism of PLs such as PC, PS and PE is thought to be responsible for the synthesis of LPA and the eCBs AEA and 2-AG. Therefore, we also hypothesized that the identification of specific PL modifications in the brain of CB₁- and LPA₁-KO mice would help us to understand the molecular neuroscience of the interactions between both systems. Thus, the PL precursor localization was an important step to clarify the synthesis of these lipid mediators. The application of the MALDI-IMS technique to maLPA₁-null and CB₁ KO mice allowed us to determine the anatomical localization of each lipid species in brain tissue slices. Unlike classical neurotransmitters, eCBs and LPA are not stored in specific compartments of the cells, such as vesicles, but instead are produced mainly “on demand” by stimulus-dependent cleavage of membrane PL precursors (Schmid et al., 1990; Di Marzo et al., 1994; Sugiura et al., 1995; Aoki, 2004). However, little is known about which are the specific lipid species for the synthesis of the endogenous agonists LPA, AEA, and 2-AG, or about their anatomical localization within the brain.

The results obtained with the MALDI-IMS assay in maLPA₁-null and WT mice showed differences in the intensity of some lipid species, mainly in the positive ion detection mode. The affected species were PA(16:0/18:1) + K⁺ and four different PCs, including PC(32:0), PC(36:1) + K⁺, PC(38:6) + K⁺, and PC(38:4) + K⁺, whose more probable acyl chains were assigned based on previous studies and were identified as 16:0, 18:0, 18:1, 20:4, and 22:6 (Sugiura et al., 2009; Berry et al., 2011; Martinez-Gardeazabal et al., 2017). Although much has been learned about the physiological roles of LPA through the analyses of LPA receptors, the mechanism by which LPA is produced remains unclear. At least two pathways have been postulated. In the first pathway, LPA would be produced from PL by the autotaxin enzyme. In the second pathway, PA would be generated from PL or diacylglycerol and then deacylated by different phospholipases,

Commission Recommendation 2007/526/EC) and the Spanish National Guidelines for Animal Experimentation and the Use of Genetically Modified Organisms (Real Decreto 1205/2005 and 178/2004; Ley 32/2007 and 9/2003). All the experimental protocols were approved by the Local Ethics Committee for Animal Research at the University of the Basque Country (CEIAB/21/2010/Rodriguez Puertas).

AUTHOR CONTRIBUTIONS

EG, IM, and RP contributed to the conception, design, and experiments of the study, performed the statistical analysis, and wrote the manuscript. CL provided and characterized the CB₁ KO mice. JC, FR, GE-T, and LS provided and characterized the LPA₁ null mice. GE-T contributed to the discussion of the manuscript. All authors contributed to the manuscript revision, read, and approved the submitted version.

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FUNDING

This work was supported by the Departments of Industry and Education from the Basque Government KK-2017/14 Elkartek and IT975-16 Consolidated Research Group Grants. Technical and human support provided by the General Research Services SGIker [University of the Basque Country (UPV/EHU), Ministry of Economy and Competitiveness (MINECO), Basque Government, European Regional Development Fund (ERDF) and European Social Fund (ESF)] is gratefully acknowledged.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fnmol.2019.00223/full#supplementary-material>

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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