Cooperative Interactions of LPPR/PRG Family Members in Membrane Localization and Alteration of Cellular Morphology

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ABSTRACT

The lipid phosphate phosphatase-related proteins (LPPRs), alternately known as Plasticity-Related Genes (PRGs), are classified as a novel brain-enriched subclass of the lipid phosphate phosphatase (LPP) superfamily. They induce membrane protrusions, neurite outgrowth or dendritic spine formation in cell lines and primary neurons. However, the exact roles of LPPRs and the underlying mechanisms are not certain. Here, we present the results of a large-scale proteome analysis to determine LPPR1-interacting proteins using co-immunoprecipitation coupled to mass spectrometry. We identified putative LPPR1 binding proteins involved in various biological processes. Most interestingly, we identified the interaction of LPPR1 with its family member LPPR3, LPPR4 and LPPR5. Their interactions were characterized by co-immunoprecipitation and co-localization analysis using confocal and super-resolution microscopy. Moreover, co-expressing two LPPR members mutually elevated their protein levels, facilitated their plasma membrane localization and resulted in an increased induction of membrane protrusions as well as the phosphorylation of S6 ribosomal protein. Together, we revealed a novel functional co-operation between LPPR family members and discovered for the first time that LPPRs likely exert their function through forming complex with its family members.

KEY WORDS: membrane protrusion, protein-protein interaction, filopodia, actin
INTRODUCTION

The lipid phosphate phosphatase-related proteins (LPPRs), alternately known as Plasticity-Related Genes (PRGs), are a family of six-transmembrane proteins enriched in brain, with five members (LPPR1-5) having been identified to date (Brauer and Nitsch, 2008; Brindley, 2004; Sigal et al., 2005; Strauss and Brauer, 2013). LPPRs are homologous to the lipid phosphate phosphatase (LPP) family proteins which are important enzymes that dephosphorylate bioactive lipids such as lysophosphatidic acid (LPA) (Brindley, 2004; Sigal et al., 2005). Although LPPRs show high homology to the LPPs, due to un-conservative substitutions of several crucial sites in the catalytic domains, they are unlikely to have a level of enzymatic activity equivalent to the typical LPPs. Therefore the LPPR proteins are designated as LPP-related proteins and comprise of a novel subfamily of the LPP superfamily (Brauer and Nitsch, 2008; Brindley, 2004; Sigal et al., 2005).

LPPR family members are all highly expressed in the central nervous system (CNS), specifically in neurons, with some differences in their spatial and temporal expression patterns. The first identified member, LPPR4, was originally named as Plasticity-Related Gene-1 (PRG-1) to reflect its regulated expression during brain development and in response to hippocampal lesions (Brauer et al., 2003). The expression of LPPR4 was increased both at the developmental stage characterized by active axon outgrowth and in regrowing axons following injury, and therefore LPPR4 was considered as a regulator of neuronal plasticity. The other four members, named PRG-2 to -5 (corresponding to LPPR3, LPPR1, LPPR2 and LPPR5, respectively), were found by in silico analysis (Brauer et al., 2003; Broggini et al., 2010; Savaskan et al., 2004).

LPPR family members show structural and sequence similarity in terms of their six-transmembrane domains, although each member has a very unique C-terminus. In particular, LPPR3 and LPPR4 have long (~400 aa) C-termini, while LPPR1, LPPR2 and LPPR5 have very short (~50aa) C-termini (Strauss and Brauer, 2013), implying that they may exert different functions in cells. LPPR4, being the most studied member, was found to be able to protect against LPA-induced neurite retraction (Brauer et al., 2003). LPPR4 also plays an important role in regulating excitatory neurotransmission, as knockout of LPPR4 leads to seizures and a change in excitatory synaptic efficacy (Trimbuch et al., 2009). LPPR4 has also been shown to inhibit LPA-induced vascular smooth muscle cell migration and proliferation (Gaaya et al., 2012).
Of the other four family members, LPPR1 and LPPR5 influence cell morphology while very little is known about LPPR2 and LPPR3. Overexpression of either LPPR1 or LPPR5 induces membrane protrusions in neuronal and non-neuronal cell lines (Broggini et al., 2010; Savaskan et al., 2004; Sigal et al., 2007). LPPR1 has been reported to promote neurite shaft protrusion in primary neurons (Velmans et al., 2013), while LPPR5 has been shown to induce neurite outgrowth (Broggini et al., 2010) and, more recently, to promote dendritic spine formation in hippocampal neurons (Coiro et al., 2014). The current findings suggest that LPPRs play putative roles in axonal outgrowth, regeneration or synaptic plasticity. However, whether the LPPR members have a redundant or distinct functions as well as their underlying mechanisms are still being explored.

In a recent phosphoproteomics screen, we demonstrated that the phosphorylation of LPPR1 was altered in response to chondroitin sulfate proteoglycans (CSPGs) (Yu et al., 2013), important regulators of axonal regeneration and neuronal plasticity. In this study, we aimed to gain more insights into the mechanism of action of LPPR1 by identifying the LPPR1-interacting proteins using affinity purification coupled to mass spectrometry (Berggard et al., 2007; Free et al., 2009). Surprisingly, we found that another three LPPR family members, LPPR3, LPPR4 and LPPR5, were associated with LPPR1. Their interactions were further confirmed by co-immunoprecipitation and co-localization analysis using confocal and super-resolution microscopy. More importantly, we revealed a novel functional co-operation between LPPRs, evidenced as enhanced protein levels and increased plasma membrane localization as well as increased induction of membrane protrusions. Our study thus reveals a novel functional interaction between LPPR family members, suggesting that these molecules may act as a complex in regulating cellular functions.

RESULTS

Importance of the C-terminus of LPPR1 in Plasma Membrane Localization and Membrane Protrusions Induction

Overexpression of LPPR1 produces membrane protrusions in several different cell types (Savaskan et al., 2004; Sigal et al., 2007). We therefore examined whether LPPR1 overexpression has a similar effect in Neuro2A cells. EGFP-LPPR1 was expressed in Neuro2A cells. Consistent with previous findings in other cell types (Sigal et al., 2007), LPPR1 protein was localized to both intracellular membrane structures and plasma
membranes of Neuro2A cells (Fig. 1A). Overexpression of a small C-terminal HA epitope
tagged LPPR1 showed an identical distribution pattern to EGFP-LPPR1 (Fig. 1B). Cells
expressing LPPR1 extended many thin, fragile membrane protrusions. Because many
protrusions were often destroyed during the staining process, to preserve better cell
morphology and also for live cell imaging purposes, we chose EGFP-tagged LPPR1 in most
of the experiments, although the LPPR1-HA construct was also used to make sure similar
results were obtained.

The C-terminus of each LPPR member is relatively unique, and a previous report
showed that the C-terminus of LPPR1 is important for filopodial induction (Sigal et al.,
2007). This is also the location of the change in phosphorylation by CSPGs (Yu et al.,
2013). Thus, to gain more information about the role of the C-terminus, we expressed full length
EGFP-LPPR1, the C-terminally truncated EGFP-LPPR1△C43, or just the C-terminal portion
EGFP-LPPR1CT in Neuro2A cells (Fig. S1A). Protein expression was confirmed by western
blot analysis with an anti-GFP antibody (Fig. S1B). The cellular distribution of these fusion
proteins was determined by confocal microscopy and a membrane targeting mCherry
construct was co-expressed to visualize the overall cell morphology. A large amount of
EGFP-LPPR1 protein was found in intracellular membrane structures such as endoplasmic
reticulum (ER), with some localized on the plasma membrane protrusions (Fig. S1C,D and
Fig. 1C). The distribution of EGFP-LPPR1 along the protrusions was discontinuous and often
showed a punctate pattern (Fig. 1C). In contrast, EGFP-LPPR1△C43 was exclusively
localized to intracellular membrane structures with very little on the plasma membrane (Fig. 1D,E).
This indicates an important role of the C-terminus of LPPR1 in facilitating protein
movement from the ER to the plasma membrane. Expressing the C-terminus itself (EGFP-
LPPR1CT) showed a diffuse cytoplasmic expression pattern similar to EGFP control (Fig. 1F,G).

To determine whether deletion of the C-terminus has an effect on the ability of
LPPR1 to induce membrane protrusions, we quantified the numbers of F-actin rich
protrusions in Neuro2A cells expressing full length or C-terminally truncated LPPR1.
Compared to cells expressing EGFP, cells expressing EGFP-LPPR1 extended many more
protrusions; this effect was significantly attenuated by deletion of the C-terminus (Fig. 1H,I).
However, overexpression of LPPR1△C43 still showed a slight but significant increase in
protrusion formation compared to EGFP alone, which indicates the presence of an additional
mechanism promoting protrusion formation independent of its plasma membrane
localization. Cells expressing only the C-terminus of LPPR1 (EGFP-LPPR1CT) showed no change in protrusion formation as compared to EGFP control (Fig. 1H,I). Similar results were found in other cell types, including human fibroblasts and Cos-7 cells. LPPR1 overexpression in Cos-7 cells also significantly induced the formation of membrane protrusions, and this effect was attenuated by deletion of its C-terminus (Fig. S1E).

Proteome-wide Identification of LPPR1- Interacting Proteins

The mechanism by which LPPR1 elicits protrusions is still an open question. Having characterized the localization pattern of LPPR1, we then sought to identify the interacting proteins of LPPR1 as a way to understand its function. Cell extracts were collected from Neuro2A cells expressing EGFP-LPPR1, EGFP-LPPR1ΔC43 or EGFP. GFP-Trap beads were added to co-immunoprecipitate EGFP tagged proteins and their binding partners. Because protein-protein interactions can be either weak or strong, considering both the coverage of binding protein identification and the binding specificity, we performed two independent co-immunoprecipitation experiments with varied stringency of the washing step. Consistent with previous reports (Sigal et al., 2007; Velmans et al., 2013), LPPR1 presents as a doublet visualized on PAGE gels after Coomassie Blue staining (Fig. 2A), likely due to post-translational modifications such as glycosylation or phosphorylation. The gel images also highlighted the differences among EGFP, EGFP-LPPR1 and EGFP-LPPR1ΔC43. By increasing both the detergent and the salt concentration in the washing buffer, fewer bands were seen in the second experiment as compared to the first experiment (Fig. 2A).

To determine which proteins are present in the complexes, in-gel digestion was performed and the resultant peptides were subjected to LC-MS/MS analysis. Supplementary Table S1 presents the unique peptides of LPPR1 identified from each sample. It is noteworthy that three peptides (aa281-295, aa296-304 and aa305-325) located at the C-terminus of LPPR1 were only found in full length EGFP-LPPR1 but not in the C-terminally truncated EGFP- LPPR1ΔC43 sample, and no LPPR1 peptides were present in the EGFP control group.

Overall, the raw data generated by the database search identified 910 proteins from the EGFP-LPPR1 sample and 813 proteins from the EGFP-LPPR1ΔC43 sample in Experiment-1, 531 proteins from the EGFP-LPPR1 sample, and 416 proteins from the EGFP-LPPR1ΔC43 sample in the higher-stringency Experiment-2 after subtraction of those also found in the EGFP control samples (Supplementary Table S2). Among them, 496 and 429
from the EGFP-LPPR1 and EGFP-LPPR1ΔC43 in Experiment-1, 306 and 236 from the EGFP-LPPR1 and EGFP-LPPR1ΔC43 in Experiment-2 are assigned based on only a single peptide matching. As proteins identified by one peptide match in proteomics are often found to be false positives (Carr et al., 2004), the data were filtered based on the following dual criteria: proteins were identified in both experiments and had 3 or more unique peptide matches in at least one of the two experiments. These criteria were met by 107 proteins (Supplementary Table S3). To gain insights into the various functions of the putative LPPR1 binding proteins, these proteins were subjected to Gene Ontology (GO) term annotation using DAVID. The significantly over-represented GO terms of Biological Process and KEGG Pathways are shown in Fig. 2B, showing that LPPR1 is associated with various biological processes such as protein localization, proteolysis and lipid biosynthesis. A number of proteins involved in lipid biosynthesis, including lysophosphatidylcholine acyltransferase 1, phosphatidylinositol synthase, sphingomyelin phosphodiesterase 4 and phosphatidate cytidylyltransferase 2, were enriched in the protein complexes, which indicated LPPR1 might play a role in regulating bioactive lipid signaling although LPPR1 itself does not possess lipid phosphatase activity.

Another interesting finding was that both mTOR and its upstream regulator PTEN were found associated with LPPR1. The mTOR peptides were found in both EGFP-LPPR1 and EGFP-LPPR1ΔC43 groups, but not in the EGFP control group. Moreover, it was found in both experiments with 4 and 2 unique peptides identified in Experiment-1 and the more stringent Experiment-2, respectively. For PTEN, only one unique peptide was present in both EGFP-LPPR1 and EGFP-LPPR1ΔC43 groups and it was identified in Experiment-1 but not in the high stringency Experiment-2. To validate the interaction of LPPR1 with mTOR and PTEN, we performed co-immunoprecipitation experiments. Our results showed that both mTOR and PTEN were co-precipitated with LPPR1. This interaction was not dependent on the C-terminus of LPPR1, as both LPPR1 and LPPR1ΔC43 were able to precipitate mTOR and PTEN (Fig. 2C).

Most intriguingly, another three LPPR1 family members: LPPR3, LPPR4 and LPPR5 were identified as binding partners of LPPR1. LPPR3 and LPPR4 seemed to bind both EGFP-LPPR1 and EGFP-LPPR1ΔC43: 7 and 6 unique peptides of LPPR4 were found in the EGFP-LPPR1 and the EGFP-LPPR1ΔC43 group, respectively; 9 and 4 unique peptides of LPPR3 were found in the EGFP-LPPR1 and the EGFP-LPPR1ΔC43 group, respectively; no peptides were found in the EGFP control group (Supplementary Table S1). This suggests
that the binding of LPPR3 and LPPR4 to LPPR1 is not through its C-terminus. LPPR5, which
shares the highest similarity with LPPR1 among all LPPR members, was also detected by
proteomics, although only one unique peptide was present in the EGFP-LPPR1 group.

**Interactions of LPPR family members**

The interaction of LPPR1 with LPPR3 and LPPR4 was validated by reciprocal co-
immunoprecipitation. When EGFP-LPPR1 was co-transfected with Flag-LPPR3 or Flag-
LPPR4, LPPR1 was co-precipitated with either Flag-LPPR3 or Flag-LPPR4 (Fig. 3A). Many
peptides were detected from LPPR3 and LPPR4, but only one peptide from LPPR5 was
found by proteomics. However, unlike LPPR3 and LPPR4, which have long C-termini, a
large portion of LPPR5 is comprised of hydrophobic transmembrane regions with very short
extramembrane regions; such proteins are very difficult to be detected by proteomics. We
therefore tested the interaction between LPPR1 and LPPR5 by reciprocal co-
immunoprecipitation. Flag-LPPR5 was co-expressed with EGFP-LPPR1 or a control EGFP
vector in Neuro2A cells; immunoprecipitation was performed using anti-Flag M2 agarose
affinity gel followed by immunoblotting with anti-GFP or anti-Flag antibody. We found that
EGFP-LPPR1, but not EGFP alone, was co-precipitated with Flag-LPPR5 (Fig. 3B). We also
excluded the effect of Flag on the binding as Flag itself was not able to precipitate EGFP-
LPPR1 (data not shown). To further identify whether the C-terminal portion of LPPR1 is
required for the interaction, the Flag-LPPR5 construct was co-expressed with EGFP, EGFP-
LPPR1, EGFP-LPPR1ΔC19 or EGFP-LPPR1ΔC43. GFP-Trap beads were used to
immunoprecipitate EGFP-tagged proteins. As shown in Fig. 3C, both full length LPPR1
(EGFP-LPPR1) and the C-terminally truncated forms of LPPR1 (EGFP-LPPR1ΔC19 and
EGFP-LPPR1ΔC43), but not EGFP alone, were able to interact with LPPR5. These results
confirmed the interaction between LPPR1 and LPPR5, and that the interaction is not through
the C-terminus of LPPR1. Similarly, LPPR5 was co-immunoprecipitated with LPPR3 and
LPPR4 (Fig. 3D). We also detected an interaction between EGFP-LPPR1 and LPPR1-HA, as
well as interaction between EGFP-LPPR5 and Flag-LPPR5, indicating that besides forming
heterodimers, LPPRs can also form homodimers (data not shown). It has been previously
demonstrated that LPPs (LPP1-LPP3) can form both homo- and hetero-oligomers (Long et
al., 2008). To determine whether LPPR1, which belongs to a distinct subfamily of the LPP
superfamily, can interact with LPPs, we performed co-immunoprecipitation experiments. No
interaction was detected between EGFP-LPPR1 and endogenous LPP1 or LPP2 (Fig. 3E).
Co-expression of LPPR members increases their protein level

One interesting phenomena we observed in the co-immunoprecipitate results was that, although we loaded the same amount of protein in the input, there was always a higher level of LPPRs in the samples obtained from co-expression of two LPPR members, as compared to the ones that are transfected with only one LPPR member together with an empty vector. To confirm this, we expressed various combinations of two LPPR members and detected the protein amount using western blotting. Indeed, we found that, when EGFP-LPPR1 was co-transfected with Flag-LPPR3, Flag-LPPR4 or Flag-LPPR5, the protein levels of EGFP-LPPR1, Flag-LPPR3, Flag-LPPR4 and Flag-LPPR5 were dramatically increased in the corresponding LPPR member co-expression groups, as compared to those expressing only a single LPPR member together with a control vector (Fig. 4A,B). Similarly, a concomitant elevation in the protein levels of LPPR5 and LPPR3, or LPPR5 and LPPR4 was also detected when LPPR5 was co-expressed with LPPR3 or LPPR4 (Fig. 4C). Interestingly, this was not seen when co-expressing LPPR3 with LPPR4 (Fig. 4D): the protein levels were not altered by each other. Co-expression of EGFP-LPPR1 with Flag-LPPR3, Flag-LPPR4 or Flag-LPPR5 also increased the protein phosphorylation of S6 ribosomal protein which correlates with an increase in protein synthesis (Fig. 4E). These results together indicate the LPPR members may be co-assembled and function as a complex in cells, which further supports the presence of functional cooperation between LPPR members.

Co-localization of LPPR Members at Plasma Membrane Protrusions

To further characterize the interaction between LPPR members, LPPR1 or LPPR1ΔC43 was co-expressed with LPPR5 and confocal microscopy was used to analyze the 3D distribution as well as co-localization. As demonstrated in Fig. 1, when LPPR1 alone was overexpressed in Neuro2A cells, it localized to both intracellular membranes and plasma membrane protrusions (Fig. 5A,A’). Deletion of the C-terminus of LPPR1 abolished its membrane localization: LPPR1ΔC43 protein was mainly found in intracellular membrane compartments (Fig. 5B,B’). In contrast to LPPR1, LPPR5 protein showed a more pronounced localization in plasma membrane protrusions (Fig. 5C). LPPR5 was also seen in some vesicle-like structures inside the cells (Fig. 5C’), but, compared to LPPR1, LPPR5 showed a more exclusive plasma membrane distribution pattern. In addition, unlike LPPR1, deletion of the C-terminal portion of LPPR5 showed little effect on its protein localization.
Similar to full length LPPR5, the LPPR5ΔC39 protein was also present predominantly in plasma membrane protrusions (Fig. 5D) with some located intracellularly (Fig. 5D’).

Surprisingly, when LPPR5 was co-expressed with LPPR1, the distribution of LPPR1 became very similar to LPPR5, i.e., a predominant localization to plasma membrane protrusions (Fig. 5E,G). This phenomenon was consistently observed after co-expressing EGFP-LPPR1 and Flag-LPPR5, LPPR1-HA and EGFP-LPPR5, or LPPR1-HA and Flag-LPPR5 in Neuro-2A cells (data not shown): all displayed a strong co-localization of LPPR1 with LPPR5 and a remarkable increase in membrane protrusions. Co-transfection of EGFP, HA or Flag control vector did not alter the overall distribution pattern of LPPR1 (data not shown). We next performed live cell imaging of EGFP-LPPR1 and Flag-LPPR5 co-transfected cells stained with CellMask Deep Red, and again the images showed an obvious overlap of EGFP-LPPR1 with CellMask plasma membrane staining (Fig. S2A-C). The same result was also obtained in LPPR1-HA and EGFP-LPPR5 co-transfected cells (data not shown). Confocal image analysis further demonstrated that the protrusions in Neuro2A cells co-expressing EGFP-LPPR1 and Flag-LPPR5 mainly projected from the ventral cell surface downwards onto the culture plate (Fig. S2). Fig. S2D and E are the top view (x-y) and side views (x-z; y-z) of a representative Z-stack of LPPR1 and LPPR5 co-transfected cells. Co-localization analysis using Imaris revealed that 88% of EGFP-LPPR1 co-localized with Flag-LPPR5 and 81% of Flag-LPPR5 co-localized with EGFP-LPPR1. From the 2D-fluorogram shown in Fig. S2F, the distribution of pairs of pixel intensities (corresponding to EGFP-LPPR1 and Flag-LPPR5) aligned to a diagonal with a Pearson's co-localization coefficient of 0.81. Z-projection of serial Z-stack images also revealed that the majority of the protrusions were located at the bottom of the cells towards the culture surface (Fig. S2G,H). A shift of localization was also found for LPPR1ΔC43 when co-expressed with LPPR5. Alone, LPPR1ΔC43 showed an intracellular retention pattern (Figs 1G, 5B); however, when co-expressed with LPPR5, a significant amount of LPPR1ΔC43 was found targeted to plasma membrane protrusions, although some still remained intracellularly (Figs 5F,H, S2I-L). Co-localization analysis showed that LPPR1ΔC43 was highly co-localized with LPPR5 with a Pearson's correlation coefficient of 0.85 (Fig. S2M,N). However, different from co-expression of full length LPPR1 and LPPR5, the distribution of which displayed a single cloud with diagonal alignment in the 2D-fluorogram (Fig. S2F), the distribution of pairs of pixel intensities for LPPR1ΔC43 and LPPR5 was separated into two clouds in the 2D-fluorogram (Fig. S2M). Interestingly, these two populations in the 2D-fluorogram correspond
to the signals derived from plasma membrane protrusions and from the intracellular portion, respectively (Fig. S2M,N). This indicates that LPPR5 could promote the trafficking of LPPR1\(\Delta C_{43}\) from the endomembrane system to plasma membrane protrusions. However, as a result of the C-terminal deletion of LPPR1, a small portion of LPPR5 was also retained intracellularly together with LPPR1\(\Delta C_{43}\).

The co-localization of LPPR1 and LPPR5 was further assessed by STED microscopy. A strong co-localization of EGFP- LPPR1 and Flag- LPPR5 was observed along the two opposed membranes of the filopodia (Fig. 5I-L). This data further suggests that LPPR1 and LPPR5 form complexes along the plasma membrane protrusions. The co-localization of LPPR1 with LPPR5 at membrane protrusions was also observed in human fibroblasts (Fig. S3A-D). In addition, this co-localization was not affected by C-terminal deletion of LPPR5. When LPPR1-HA was co-expressed with EGFP-LPPR5\(\Delta C_{39}\), they were still co-localized and present predominantly on membrane protrusions (Fig. S3E-H). Likewise, a similar distribution shift was also found with co-expression of LPPR5 with LPPR3 or LPPR4, and co-expression of LPPR1 with LPPR3 or LPPR4. Like LPPR1, LPPR3 or LPPR4 alone showed a more diffuse distribution pattern localized on both intracellular membranes and cell surface (Fig. S3I,K). However, when co-expressed with any two of above LPPR members, they all showed a strong co-localization on plasma membrane protrusions (Figs 6, S3J,L).

**LPPR5 Facilitates the Localization of LPPR1 to Plasma Membrane Protrusions Resulting in Enhanced Induction of Membrane Protrusions**

When Neuro2A cells are grown on uncoated surfaces, the protrusions induced by LPPRs extend in random directions mostly towards the cell periphery and downwards onto the culture plate, which makes them very difficult to count (Fig. S4A). In contrast, when plated onto Poly-L-Lysine (PLL) and laminin-coated surfaces, cells become flat and well-spread, and protrusions are now generated predominantly away from the cell periphery (Fig. S4B). This enabled us to separate the cell surface signal from the intracellular signal and also to more accurately count protrusions (Fig. 7). The majority of EGFP-LPPR1 was found inside the cells when expressed alone or with control vectors (Fig. 7A,C). However, when co-expressed with LPPR5, there was an increase in LPPR1 protein localized to the cell surface (Fig. 7B,D). The percentage of LPPR1 on the cell surface increased from 20% in control cells to 60% in cells that expressed both LPPR1 and LPPR5 (Fig. 7E).
Overexpression of either LPPR1 or LPPR5 alone has been reported to induce the formation of plasma membrane protrusions (Broggini et al., 2010; Sigal et al., 2007). We therefore evaluated whether the increased plasma membrane localization of LPPR1 as a result of co-expression with LPPR5 could further increase the formation of plasma membrane protrusions. While cells expressing either LPPR1 or LPPR5 generated more protrusions than control transfected cells, co-expression of LPPR1 and LPPR5 further increased the induction of protrusions as compared to cells expressing either alone (Fig. 7F). This reinforces the importance of cooperation between LPPR1 and LPPR5 in exerting their biological roles such as promoting cell protrusions.

**LPPRs induced actin-dependent plasma membrane protrusion**

A previous report showed that the protrusions induced by LPPRs are independent of the classic Cdc42-WASP-Arp2/3 pathway and do not require Ena/Vasp protein (Sigal et al., 2007), which made us wonder if the protrusions are driven by tubulin. However, we found that tubulin is almost absent in the LPPR-labeled protrusions (Fig. 8A). EB3-GFP was used to visualize microtubule assembly in live cells; we found that EB3 comets rarely moved into the LPPR-labeled protrusions (data not shown). In contrast, the actin-based motor protein myosin X was concentrated at the distal tip of almost every LPPR-labeled protrusion (Fig. 8B). Moreover, treatment of the cells with cytochalasin D resulted in rapid retraction of the membrane protrusions induced by LPPR1 and LPPR5 (Fig. 8C,D). SIM imaging allowed visualization with a higher resolution of F-actin filaments as well as the LPPR distribution along the protrusions, obtained from cells co-transfected with EGF-LPPR1 and Flag-LPPR5. Fig. 8E and F showed clearly that actin filaments in the protrusions were wrapped by LPPR1 and LPPR5 which were co-distributed along the two opposed membranes of the protrusions. These data indicate that the protrusions induced by LPPRs are actin-dependent.

As we found interaction of mTOR with LPPR1 and moreover an increase in phosphorylation of pS6 ribosomal protein by co-expression of LPPR proteins, we tested whether blockade of the mTOR pathway by rapamycin would alter the formation of protrusions induced by LPPR proteins. Treatment with rapamycin of LPPR1 and LPPR5 co-transfected cells had no obvious effect on LPPR protein distribution or protrusion formation, although the phosphorylation of pS6 ribosomal protein was significantly reduced (Fig. S4C,D), excluding mTOR as a signaling pathway for LPPR-induced protrusions. Thus, the
exact mechanism by which LPPRs induce membrane protrusions and potential roles of mTOR signaling downstream of LPPRs still requires further investigation.

DISCUSSION

In this study, with the aim of elucidating the function of LPPR1, we used affinity purification coupled to mass spectrometry to identify its interacting proteins. Analysis of the putative binding partners revealed that LPPR1 might be involved in multiple biological processes such as protein localization, protein catabolic process, transmembrane transport, lipid biosynthetic process and proteolysis. Although most LPPR members, including LPPR1 and LPPR5, show no phosphatase activity, some previous reports indicated that LPPRs may modulate LPA-induced signaling (Brauer et al., 2003; Broggini et al., 2010; Savaskan et al., 2004; Sigal et al., 2007). Our results showed that several important enzymes involved in phospholipid metabolism were present in the LPPR1 protein complexes, which might implicate a possible mechanism of LPPRs in regulating phospholipid signaling.

The most salient finding was that we identified interactions between LPPR1 and three other members of the LPPR family, LPPR3, LPPR4 and LPPR5. Co-expression of pairs of LPPR proteins provided further evidence of the strong binding and functional interaction between these LPPR members. The fact that the LPPR protein levels and their plasma membrane targeting are significantly increased when they are expressed in pairs is likely a result of increased protein stability through their interaction. This is reminiscent of the increased maturation and assembly of integrins when they are co-expressed (Heino et al., 1989). Further evidence for a functional consequence of these associations is that co-expression LPPR members increased the generation of membrane protrusions beyond that of any single LPPR family member. This is likely due to the higher level of protein expression as well as the increased protein translocation from intracellular compartments to the cell membrane. Overall, these data strongly support the idea that the LPPR proteins are acting as a complex.

Both LPPs and Drosophila LPP homologues have previously been reported to form oligomers. Although oligomerization seems to occur commonly in amongst LPP superfamily members, some specificity does exist. The Drosophila LPP homologue Wunen forms only homodimers, but not heterodimers, with Wunen-2 or human LPP1 and LPP3 (Burnett et al., 2004), while LPP1, LPP2 and LPP3 formed both homo- and hetero-oligomers (Long et al., 2008). The dimerization between Wunen monomers was prevented by point mutation of a
catalytic site and required the C-terminal portion (Burnett et al., 2004). In case of LPPRs, both homo- and hetero-oligomers exist and their interactions are independent of its C-terminal portion. Moreover, we detected no interaction between LPPR1 and LPPs either by proteomics or co-immunoprecipitation.

Among the five LPPR family members, LPPR3 and LPPR4 have a long C-terminus while LPPR1, -2 and -5 have a very short C-terminus. The hydrophilic C-terminus of each LPPR member positioned at the cytoplasmic side is quite unique and does not show significant sequence or domain similarity with each other (Brauer and Nitsch, 2008; Strauss and Brauer, 2013). The long C-terminal of LPPR4 is believed to play a role in intracellular interactions and signaling. The C-terminus of LPPR1 or LPPR5 has also been reported to be required for its biological function (Broggini et al., 2010; Sigal et al., 2007). Our results showed that the interactions of LPPR3, LPPR4 and LPPR5 with LPPR1 were independent of its C-terminus, as they bound to both full length and C-terminal truncated LPPR1. This implied that each LPPR protein, as a subunit of the LPPR complex, might exert distinct roles through its unique C-terminal portion. However, the role each LPPR member plays in the complex still needs further investigation.

The question arises as to whether these interactions take place between the endogenous proteins. Unfortunately, due to the lack of high-quality commercial antibodies for the LPPR family proteins, we could not determine their endogenous localization patterns and interactions. Spurious results can result from overexpression studies, and thus we designed our methods to prevent this possibility. First, we fused LPPR protein to different tags (i.e. EGFP, tdTomato, Flag or HA) in order to exclude the possible interference caused by these tags, and empty vector controls were used in every experiment. Second, we tested the interaction of LPPR members in different cell types such as Neuro-2A cells, Cos-7 cells and human fibroblasts as well as primary mouse cerebellar neurons (data not shown). Overall, we find very reproducible results using different tags or different cell types; the expression pattern of each LPPR fusion protein was also consistent with previous reports (Broggini et al., 2010; Sigal et al., 2007). Considering the strong interaction we detected in the overexpression system, and the association of endogenous LPPR members with recombinant LPPR1 detected by proteomics, we believe interactions between endogenous LPPR members would also occur within cells.

Our study identified mTOR as binding partner of LPPR1; we also detected an increase in phosphorylation of S6 ribosomal protein, a downstream target of mTOR, induced
by co-expression of LPPR proteins. However, we found blockade of the mTOR pathway with rapamycin had no effect on the generation of protrusions in response to LPPR expression, though phospho-S6 ribosomal protein was vastly reduced. Most recently, thin fragile actin-rich membrane protrusions (termed “cytonemes”) have been produced in cells in response to the overexpression of the 7-transmembrane domain molecules Lgr4 and Lgr5 (Snyder et al., 2015). Lgr-induced protrusions share many common features with those we describe here, including being dependent upon membrane localization, sensitivity to actin-depolymerization and being terminated by myosin X. Cytonemes have been identified as organizers of signaling molecules (Roy et al., 2014) and it may be that the activation of the mTOR pathway is a result of, rather than a cause of, protrusion formation.

In summary, this study suggested that, instead of playing separate or redundant roles in cells, the LPPR protein family members can also act together as a complex to exert their cellular function, which leads us in a new direct for exploring the exact molecular mechanisms of LPPR family proteins. While the exact functions of LPPR family members remain to be elucidated, our data suggest that these proteins likely act in concert to carry out their biological effects.
MATERIALS AND METHODS

DNA Constructs and Cell Cultures
LPPR1, LPPR3, LPPR4 and LPPR5 cDNA were amplified from a mouse brain cDNA library. Full length LPPR1 (amino acids 1~325), LPPR1 lacking the last 43 or 19 amino acid of the C-terminal region (LPPR1ΔC43, amino acids 1~282; LPPR1ΔC19, amino acids 1~306) and the C-terminus of LPPR1 (LPPR1CT; amino acids 283~325) were fused into the pEGFP-C1 vector using the In-Fusion cloning system (Clontech, Mountain View, CA). A construct expressing C-terminal HA-tagged LPPR1 (LPPR1-HA) was kindly provided by Dr. Andrew J. Morris, University of Kentucky (Sigal et al., 2007). EGFP-tagged full length LPPR5 (EGFP-LPPR5), C-terminal 39 amino acid truncated LPPR5 (EGFP-LPPR5ΔC39) and 3×Flag-tagged LPPR5 (Flag-LPPR5) constructs were obtained by cloning LPPR5 or LPPR5ΔC39 cDNA into pEGFP-C1 or pCMV-3×Flag. The Flag-LPPR3, Flag-LPPR4, tdTomato-LPPR3 and tdTomato-LPPR4 were constructed using the Gateway cloning system (Life Technologies, Frederick, MD). The pmCherry-Mem construct which fused mCherry to a membrane localization sequence (Mem-Cherry) was from Clontech. The tdTomato-F-tractin construct was a gift of Dr. Michael Schell (Johns Hopkins University); the GFP-Myosin X construct was a gift of Dr. Richard Cheney (University of North Carolina, Chapel Hill); the mCherry-Tubulin construct was a gift of Dr. Roger Tsien (University of California, San Diego).

Neuro2A cells, Cos-7 cells, HEK293 cells or human fibroblasts were grown in DMEM supplemented with 10% FBS. Cells were transfected with the indicated constructs using Lipofectamine LTX reagent (Life Technologies). Cells were fixed for imaging or cell lysates were collected for western blot analysis at 20-24 hours after transfection. In some cases, Neuro2A cells were grown on PLL and laminin (5 μg/mL) coated surfaces.

Affinity purification of LPPR1 and its binding proteins
Neuro2A cells growing on 10-cm dishes were transfected with pEGFP, pEGFP-LPPR1 or pEGFP-LPPR1ΔC43. After 24 hours, cells were washed with PBS, followed by extraction with 0.5 mL/dish of lysis buffer [10 mM Tris/Cl pH7.5, 150 mM NaCl, 0.5 mM EDTA, 1% NP-40, 1× protease inhibitor cocktail (Calbiochem, La Jolla, CA)]. Cells were lysed for 15 min on a rotating device at 4°C and kept on ice for another 15 min. Cell extracts were centrifuged at 12000 × g for 15 min at 4°C to remove insoluble material. Affinity purification of EGFP fusion proteins and their interacting proteins were performed using Chromotek-
GFP-Trap agarose beads (Allele Biotechnology, San Diego, CA) according to the manufacturer’s instructions. Briefly, two experiments were performed from two independent cultures. For the first experiment, the GFP-Trap beads were first washed three times with dilution buffer [10 mM Tris/Cl pH7.5, 150 mM NaCl, 0.5 mM EDTA, 1× protease inhibitor cocktail] and resuspended in 400 μL of dilution buffer. The same volume of cell lysate was added into the beads and incubated with end-over-end rotation at 4ºC for 2 hours. Samples were then washed three times with 1mL of washing buffer (0.5% NP-40 in dilution buffer). Protein complexes were eluted using 20 μL of 2× SDS sample buffer containing 5% β-mercaptoethanol and boiled for 10 min. For the second immunoprecipitation experiment, we increased both the detergent concentration (1% NP-40) and salt concentration (500 mM NaCl) in order to increase the stringency of the affinity purification.

**In-gel Digestion and LC-MS/MS Analysis**

The eluted proteins were separated using a 4-12% Bis-Tris gradient gel (Invitrogen) and stained with Coomassie Blue. Independent lanes corresponding to GFP-Trap immunoprecipitated protein complexes from extracts of pEGFP, pEGFP-LPPR1 or pEGFP-LPPR1ΔC43 transfected cells were cut into 20 gel slices per lane and subjected to in-gel digestion. Briefly, individual gel slices were diced into small cube pieces and placed into 1.5 ml tubes. After destaining Coomassie Blue with 25 mM NH₄HCO₃ in 50% acetonitrile (ACN), the gel samples were reduced at 56ºC for 30 min in 10 mM DTT in 25 mM NH₄HCO₃ following by alkylation in the dark for 30 min with 55 mM iodoacetamide in 25 mM NH₄HCO₃ at room temperature. The gel pieces were dried out using a Speed Vac prior to trypsin digestion. A solution of 12.5 ng/μL trypsin in 25 mM NH₄HCO₃ was added in a volume just enough to cover the gel pieces. Trypsin digestion was performed overnight at 37ºC. Sequential extraction of peptides from the gel was done twice with 5% formic acid (FA)/50% ACN. The extracts were pooled together and the organic solvent was dried off in a Speed Vac. The dried peptide extract was resuspended in 20 μL of 0.1% FA and desalted with μ-C18 ZipTips. The peptides bound to the ZipTip were eluted with 60% ACN in 0.1% FA solution. After drying in the Speed Vac, the peptide sample was resuspended in 0.1% FA and subjected for LC-MS/MS analysis.

LC-MS/MS was performed using an Eksigent nanoLC-Ultra 2D system (Dublin, CA) coupled to an Orbitrap Elite mass spectrometer (Thermo Scientific, San Jose, CA). The peptide sample was first loaded onto a Zorbax 300SB-C18 trap column (Agilent, Palo Alto,
CA), and then separated on a reversed-phase BetaBasic C18 PicoFrit analytical column (New Objective, Woburn, MA) using a linear gradient of 5-35% B (buffer A: 0.1% formic acid in water; buffer B: 0.1% formic acid in acetonitrile). Eluted peptides were sprayed into the Orbitrap Elite equipped with a nano-spray ionization source. Survey MS spectra were acquired in the Orbitrap, and data-dependent MS/MS scans were performed in the linear ion trap with dynamic exclusion.

**Database Search and Bioinformatics**

Raw data files generated from the Orbitrap Elite were searched by the MASCOT search engine using the Proteome Discoverer software (ver. 1.4, Thermo Scientific). Protein identifications were assigned by searching against the mouse UniprotKB/SwissProt database (Release date: 20130206; Number of entries: 16648). Peptide identifications were restricted to tryptic peptides with no more than 2 miscleavages. Carbamidomethylation of cysteine was set as fixed modification, and oxidation of methionine, N-acetylation as well as deamidation of asparagines and glutamine were searched as variable modifications. Database searches were performed with a peptide precursor ion tolerance of 25 ppm and a MS/MS fragment mass tolerance of 0.8 Da. Peptide-spectrum matches (PSMs) were filtered to achieve an estimated false discovery rate (FDR) of 1% based on a target-decoy database search strategy.

**Co-immunoprecipitation and Western Blot Analysis**

To validate the interaction between LPPR1 and other LPPR members, EGFP-LPPR1 or EGFP-LPPR1ΔC43 were co-transfected with Flag-tagged LPPR3, LPPR4 or LPPR5 in Neuro2A cells, the cell lysates were collected and immunoprecipitated either with EZview Red ANTI-FLAG M2 Affinity Gel (Sigma) or with Chromotek-GFP-Trap agarose beads (Allele Biotechnology). Empty EGFP and Flag vectors were used as controls. The precipitated products were blotted with chicken anti-GFP antibody (1:2000, Abcam) or anti-Flag M2 antibody (1:1000, Sigma). To determine the interaction of LPPR1 with LPP1 and LPP2, the EGFP- or EGFP-LPPR1-transfected HEK293 cell lysate was subjected to co-immunoprecipitation using GFP-Trap beads and the eluted proteins were blotted with rabbit anti-LPP1 antibody (1:250, Exalpha Biologicals, Shirley, MA) or with rabbit anti-LPP2 antibody (1:500, Exalpha Biologicals). To validate the interaction of LPPR1 with mTOR and PTEN, the EGFP, EGFP-LPPR1 or EGFP-LPPR1ΔC43 transfected cell lysate was subjected to co-immunoprecipitation using GFP-Trap beads and the eluted proteins were blotted with rabbit anti-mTOR antibody (1:1000, Cell Signaling Technology, Beverly, MA) or with rabbit
anti-PTEN antibody (1:1000, Cell Signaling Technology). To access the alteration in LPPR protein levels after co-expression of two LPPR members, the co-transfected cell lysates were blotted with chicken anti-GFP antibody (1:2000, Abcam), anti-Flag M2 antibody (1:1000, Sigma) or rabbit monoclonal anti-phospho-S6 ribosomal protein (Ser235/236) antibody (1:1000, Cell Signaling Technology).

**Confocal Microscopy**

Neuro2A cells transfected with the indicated constructs were fixed with 4% PFA and stained with one of the following antibodies: rabbit anti-HA antibody (1:200, Santa Cruz), mouse anti-Flag antibody (1:1000), or rabbit anti-calreticulin (1:100, Millipore). Stacks of images were collected using a Zeiss LSM510 or a Zeiss LSM780 confocal microscope (Carl Zeiss MicroImaging, Jena, Germany) with a 63×1.4 NA oil immersion objective. To address the relationship between LPPR1 and LPPR5, stacks of images collected throughout the depth of cell were analyzed in 3D with Imaris software v7.6.3 (Bitplane, Belfast, UK).

Quantification of co-localization was assessed in 3D, and pixel co-distribution was calculated for green and red staining patterns. Co-localized pixels were displayed as a 2-color histogram (scattergram-fluorogram). 2D fluorograms represent quantification of the co-localization as distribution of pairs of pixel intensities (aligned to a diagonal, perfect co-localization, randomly scattered, or towards one channel in case of lack of co-localization). In addition Pearson coefficients in the co-localized volume were computed and compared (1, perfect correlation; 0, no correlation; −1, perfect inverse correlation). To quantify the distribution shift of EGFP-LPPR1 after co-expressing with Flag-LPPR5, cells growing on laminin-coated surfaces were co-transfected with EGFP-LPPR1 and Flag, or with EGFP-LPPR5 and Flag-LPPR5. Stacks of images were obtained and the intracellular and total fluorescence intensity of EGFP-LPPR1 for individual cell was measured using Image J (Schneider et al., 2012). The percentages of intracellular and cell surface LPPR1 were calculated based on the intracellular EGFP-LPPR1 fluorescence intensity and the total EGFP-LPPR1 fluorescence intensity.

**Super-resolution Microscopy**

To further assess the co-localization of LPPR family members on the plasma membrane protrusions, super-resolution microscopy was performed using Stimulated Emission Depletion (STED) methodology. Neuro2A cells co-transfected with EGFP-LPPR1 and Flag-LPPR5 were stained with mouse anti-Flag primary antibody followed by Cy3-conjugated
F(ab')₂ fragment donkey anti-mouse IgG. Two-color STED images were obtained using a Leica SP8 STED 3X system (Leica Microsystems), equipped with a white light laser and a 592nm and 660nm STED depletion lasers. A 100×1.4 NA oil immersion objective lens (HCX PL APO STED white, Leica Microsystems, Mannheim, Germany) was used for imaging. To better visualize the actin filaments within the LPPR-induced membrane protrusions, super-resolution microscopy was performed using 3D structured illumination (3D-SIM). Neuro2A cells co-transfected with EGFP-LPPR1 and Flag-LPPR5 were stained with anti-Flag antibody followed by Alexa 647-conjugated goat anti-Mouse IgG secondary antibody, and with Alexa Fluor 568-Phalloidin to label the F-actin. 3D-SIM microscopy was performed using the Delta-Vision OMX V4 (GE Healthcare, Issaquah, WA) imaging system. Images were taken with an Olympus PlanApo N 60× 1.42 NA oil objective. Stacks of z-sections were taken over a cell thickness at a spacing of every 125 nm. The microscope is calibrated prior to experiments to calculate both the lateral and axial limits of image resolution under our experimental conditions. All raw images were processed and reconstructed in 3D using DeltaVison SoftWoRx software.

**Quantification of membrane protrusions**

Cos-7 cells growing on plain glass coverslips or Neuro2A cells growing on laminin-coated coverslips were transfected with the indicated Control or LPPR constructs. For Cos-7 cells, a membrane-targeting mCherry (mem-mCherry) construct was co-transfected for visualizing the overall cell morphology and to allow counting of protrusions. The density of protrusions along the edge of each cell was calculated. For Neuro2A cells, cells were stained with phalloidin to label F-actin, and the total number of F-actin-rich protrusions for each cell was counted. Data were collected from at least 3 independent experiments and were presented as Mean ± SEM. Statistical analysis was performed using one-way ANOVA and Tukey’s multiple comparison test. The level of significance was set at $p < 0.05$.

**Live cell imaging**

Neuro2A cells co-transfected with pEGFP-LPPR1 and pCMV-Flag-LPPR5 were stained with a plasma membrane staining dye (CellMask deep red, Invitrogen) in living cells 24 h after transfection and live cell images were acquired with a 63×1.4 NA oil immersion objective using a Leica SP5 confocal system (Leica Microsystems). In other cases, Neuro2A cells were co-transfected with pEGFP-LPPR1 and pCMV-Flag-LPPR5 together with
tdTomato-F-tractin to label the actin filaments. The effect of actin polymerization on the motility of LPPR-induced plasma membrane protrusions was tested by adding 1 μM Cytochalasin D. Time-lapse images of the same area were taken before and after adding Cytochalasin D using a Zeiss LSM510 confocal microscope.

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References


Fig. 1. C-terminal deletion of LPPR1 abolished its plasma membrane localization. (A and B) Representative images of Neuro2A cells expressing EGFP-LPPR1 (A) or LPPR1-HA (B), showing similar distribution pattern. (C and D) Representative images of Neuro2A cells expressing EGFP-LPPR1 (C) or EGFP-LPPR1ΔC43 (D) together with a plasma membrane targeted mCherry (mem-Cherry) for visualization of overall cell morphology. The inset in C is a higher magnification image of the boxed area, showing the discontinuous and punctate distribution pattern of EGFP-LPPR1 along membrane protrusions (arrows). The inset in D is a higher magnification image of the boxed area, showing EGFP-LPPR1ΔC43 was absent from membrane protrusions (arrowheads). (E) Quantification of the relative amount of intracellular and cell surface LPPR1. (F and G) Representative images of Neuro2A cells expressing EGFP (F) or EGFP-LPPR1CT (G). (H and I) Representative images and quantification of the protrusion numbers in cells overexpressing EGFP, EGFP-LPPR1, EGFP-LPPR1ΔC43 or EGFP-LPPR1CT. Scale bar: 20 µm.
Fig. 2. Proteome-wide Identification of the LPPR1-interacting proteins. (A) Coomassie blue staining pattern of the co-immunoprecipitated proteins. Neuro2A cells transfected with pEGFP, pEGFP-LPPR1 or pEGFP-LPPR1ΔC43 constructs were subjected to co-immunoprecipitation using GFP-Trap beads. Two independent co-immunoprecipitation experiments were performed with different detergent and the salt concentrations. (B) Functional annotation of the putative LPPR1 binding proteins by DAVID. Significantly enriched GO terms of the Biological Process and KEGG Pathways were plotted according to the number of proteins. (C) Validation of the interaction of mTOR and PTEN with LPPR1 using co-immunoprecipitation.
Fig. 3. Validation of the interaction between LPPR1 family members. (A) Co-precipitation of EGFP-LPPR1 by Flag-LPPR3 or Flag-LPPR4, but not by Flag. (B) Co-precipitation of EGFP-LPPR1, but not EGFP by the Flag-LPPR5. (C) Co-precipitation of Flag-LPPR5 by EGFP-LPPR1 or EGFP-LPPR1ΔC, but not by EGFP. The C-terminus of LPPR1 is not required for its interaction with LPPR5. (D) Co-precipitation of EGFP-LPPR5 by Flag-LPPR3 or Flag-LPPR4. (D) No interaction was detected between EGFP-LPPR1 and LPP1 as well as LPP2.
Fig. 4. Co-transfection two of the LPPR members, except for co-transfection of LPPR3 and LPPR4, increased their protein levels. (A) Western blot and quantification showing increase in the EGFP-LPPR1 protein amount when co-transfecting EGFP-LPPR1 with either Flag-LPPR3, Flag-LPPR4 or Flag-LPPR5, compared to co-transfection with Flag control. (B) Western blot showing increase in the protein amount of Flag-LPPR3, Flag-LPPR4 or Flag-LPPR5 when co-transfected with EGFP-LPPR1, compared to co-transfection with EGFP control. (C) Western blot showing increase in the Flag-LPPR3 or the Flag-LPPR4 protein amount when co-transfection EGFP-LPPR5 with Flag-LPPR3 or with Flag-LPPR4, coinciding with an increase in EGFP-LPPR5. (D) Western blot showing no change in their protein level with co-transfection of LPPR3 with LPPR4, compared to transfecion with LPPR3 alone or LPPR4 alone. (E) Western blot showing co-expression of EGFP-LPPR1 with either Flag-LPPR3, Flag-LPPR4 or Flag-LPPR5 increased the phosphorylation of S6 ribosomal protein.
**Fig. 5. Co-localization of LPPR5 and LPPR1 on plasma membrane protrusions (A-D)**

Neuro2A cells were transfected with EGFP-LPPR1, EGFP-LPPR1ΔC43, EGFP-LPPR5 or EGFP- LPPR 5ΔC39 separately. Representative z-stack confocal images collected throughout the depth of cells showing the protein distribution of EGFP- LPPR1 (A), EGFP- LPPR ΔC43 (B), EGFP- LPPR 5(C) or EGFP- LPPR5ΔC39 (D). LPPR1 was expressed in endomembrane
systems as well as plasma membrane protrusions, while deletion of C-terminus of LPPR1 (LPPR 1\(\Delta\)C43) abolished its localization towards plasma membrane protrusions. LPPR5 was expressed mainly in plasma membrane protrusions and in some vesicle-like structures inside the cells (arrow, in C'), C-terminal truncated LPPR5 (LPPR5\(\Delta\)C39) displayed similar distribution pattern as full length LPPR5. A’-D’ are high magnification single plane images of cell body areas boxed in A-D, respectively. (E-H) Neuro2A cells were co-transfected with EGFP-LPPR1 and Flag-LPPR5, or EGFP-LPPR1\(\Delta\)C43 and Flag-LPPR5. Cells were stained with anti-Flag antibody and DAPI. Co-expression of LPPR1 with LPPR5 showing LPPR1 was co-localized with LPPR5 at plasma membrane protrusions (E and G). Co-expression of LPPR1\(\Delta\)C43 with LPPR5 showing co-localization of LPPR1\(\Delta\)C43 with LPPR5 and some LPPR1\(\Delta\)C43 can be targeted to plasma membrane protrusions (F and H). (I-L) STED super-resolution images showing the co-localization of LPPR1 with LPPR5 on plasma membrane protrusions. The boxed area in K was highlighted in L, showing a strong colocalization observed along the two opposed membranes of the filopodia (arrows). Scale bar: 20 \(\mu\)m in A-D; 5 \(\mu\)m in A’-D’, E-L; 1 \(\mu\)m in O.
Fig. 6. Co-localization of LPPR1 family members exclusively at plasma membrane protrusions. Representative images of Neuro2A cells co-transfected with: (A-C) EGFP-LPPR1 and tdTomato-LPPR4; (D-E) EGFP-LPPR1 and tdTomato-LPPR3; (G-H) EGFP-LPPR5 and tdTomato-LPPR4; (J-L) EGFP-LPPR5 and tdTomato-LPPR3; Scale bar: 20 µm.
Fig. 7. LPPR5 facilitated the localization of LPPR1 to the plasma membrane, which further increased the number of plasma membrane protrusions. (A-E) Representative images and quantification of the distribution shift of LPPR1 by LPPR5. Neuro2A cells plated on laminin were transfected with EGFP-LPPR1 and Flag (A and C), or EGFP-LPPR1 and Flag-LPPR5 (B, D). C and D showing the fluorescence intensity of EGFP-LPPR1 in a heat map format. The percentages of intracellular LPPR1 and cell surface LPPR1 were measured and the quantification was shown in E. More EGFP-LPPR1 was localized to plasma membrane when co-expressing with LPPR5 (p < 0.001, by two-way ANOVA and Bonferroni posttests). Scale bar: 20 µm. (F) Coexpression of LPPR1 with LPPR5 produced an enhanced induction of plasma membrane protrusions. *, p < 0.05; ***, p < 0.001, compared to EGFP control group; #, p < 0.05, compared to LPPR5 group; ### p < 0.001, compared to LPPR1 group (by one-way ANOVA and Turkey’s multiple comparison test).
Fig. 8. Characterization of the plasma membrane protrusions induced by LPPRs. (A) Representative image of Neuro2A cells co-transfected with EGFP-LPPR1 and Flag-LPPR5 together with Cherry-tubulin, showing the absence of microtubules in the LPPR-induced protrusions. (B) Representative image of Neuro2A cells co-transfected with EGFP-LPPR1 and Flag-LPPR5 together with GFP-myosin X, showing the localization of myosin X at the tips of the LPPR-induced protrusions. (C) Live cell imaging showing retraction of LPPR-induced plasma membrane protrusions after treatment with 1 µM cytochalasin D. (D)
Quantification of protrusions after cytochalasin D treatment. (E and F) SIM super-resolution images demonstrating the presence of actin filaments labeled by phalloidin (red) inside LPPR1 (green) and LPPR5 (blue) labeled membrane protrusions. The dashed boxed area in E was highlighted in F showing actin filaments (red) surrounded by LPPR1 (green) and LPPR5 (blue) distributed along the two opposed membrane layer (arrows). Scale bar: 20 µm in A; 10 µm in B and C; 5 µm in E; 2 µm in F.