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1 **Functions of anionic lipids in plants**

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12 **Abstract:** (150 words max)

13 Anionic phospholipids, which include phosphatidic acid, phosphatidylserine, and
14 phosphoinositides, represent a low percentage of membrane lipids. They are able to modulate
15 the physical properties of membranes, such as their surface charges, curvature or clustering of
16 proteins. Moreover, by mediating interactions with numerous membrane-associated proteins,
17 they are key components in the establishment of organelle identity and dynamics. Finally,
18 anionic lipids also act as signalling molecules, as they are rapidly produced or interconverted
19 by a set of dedicated enzymes. As such, anionic lipids are major regulators of many
20 fundamental cellular processes, including cell signalling, cell division, membrane trafficking,
21 cell growth or gene expression. In this review, we describe the functions of anionic lipids with
22 a cellular perspective. Using the localization of each anionic lipids and their related metabolic
23 enzymes as starting points, we summarize their roles within the different compartments of the
24 endomembrane system and address their associated developmental and physiological
25 consequences.

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27 **Keywords:** (6 max)

28 membrane contact sites, endocytosis, exocytosis, autophagy, nanodomains, plant-microbe
29 interphase

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32 **Main text**

33 **1. INTRODUCTION**

34 Biological membranes delimit cellular compartments, as well as the inner and outer of the cell.
35 Each compartment has its proper chemical environment allowing numerous and specialized
36 chemical reactions in the same cell. To enable the proper localization of proteins, each
37 membrane has its own biochemical and biophysical identity. Membranes are composed of lipids
38 forming a bilayer and transmembrane or membrane-associated proteins (63).
39 Glycerophospholipids associated with sphingolipids and sterols are the main lipid components
40 within the eukaryotic **endomembrane system**. Among the glycerophospholipids some present
41 negative charges and, as such, are anionic phospholipids. Anionic phospholipids include
42 phosphatidic acid (PA), phosphatidylserine (PS), phosphatidylinositol and phosphatidylinositol
43 phosphates (PIPs also referred to as phosphoinositides), the phosphorylated forms of
44 phosphatidylinositol (Figure 1.a). Phosphatidylinositol display an inositol ring that can be
45 phosphorylated in three different positions - 3, 4 and 5 - creating a total of seven possible
46 phosphoinositide species: 3 phosphoinositide monophosphates (PI3P, PI4P, PI5P), 3
47 phosphoinositide biphosphates (PI(3,4)P₂, PI(3,5)P₂, PI(4,5)P₂) and one phosphoinositide
48 triphosphate (PI(3,4,5)P₃).

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50 These lipids are present in low to very low abundance in eukaryotic membranes. In Arabidopsis
51 leaf, phosphatidylinositol represents about 7% of total phospholipids, PA ~2% and PS ~1%. In
52 addition, all phosphoinositides combined account for less than 1% of the total phospholipid
53 content (72, 135). However, anionic lipids are key components of cell membranes. They are
54 involved in the regulation of nearly all membrane-associated events including cell signalling,
55 trafficking, cell division, and cell growth. Consequently, over-expression lines or loss-of-function
56 mutants for lipid enzymes that perturb anionic lipid homeostasis lead to severe and pleiotropic
57 phenotypes at the plant level, including defects in development, immunity, reproduction and
58 stress adaptation (24, 94).

59 Anionic phospholipids are detected in most endomembrane compartments: endoplasmic
60 reticulum (ER), Golgi, **trans-Golgi network/early endosomes** (TGN/EE), plasma membrane
61 (PM), Late endosomes/**multi-vesicular bodies** (LE/MVB), vacuoles and autophagosomes. In
62 this review, we first describe the key physicochemical properties of anionic lipids that mediate
63 lipid-protein interactions and regulate protein dynamics in cell membranes. Then, we discuss
64 the functions of anionic lipids with a cellular perspective, using as a starting point the
65 localization of each anionic lipids and their related metabolic enzymes. We summarize the roles
66 of anionic lipids within the different compartments of the endomembrane system and address
67 their associated developmental and physiological consequences.

68 It should be noted that anionic lipids also accumulate in mitochondria and plastids where they
69 play a role in division, lipid synthesis and photosynthesis. Anionic lipids, such as PA, PI4P and
70 PI(4,5)P₂ are also found in the nucleoplasm of the nucleus where they may regulate
71 transcription factors, chromatin status and epigenetic landmarks (125) but this will not be
72 further discussed, as we decided to focus this review on the endomembrane system.

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75 **2. ANIONIC LIPIDS ARE DYNAMIC LANDMARKS OF BIOLOGICAL MEMBRANES**

76 **2.1. Anionic phospholipids as landmarks for organelle identity**

77 Cell compartments are enriched in different anionic lipids, which give specific properties to their
78 membrane and thereby contribute to their identity. **Lipids binding domains** (LBDs) can
79 mediate the interaction with the membrane (63, 126) (Figure 2.d). They allow the targeting of
80 proteins to membranes by stereospecific interactions with a given phospholipid species. Those
81 domains are, for example, Pleckstrin Homology (PH) domains, Fab1/YOTB/Vac1/EEA1 (FYVE)
82 domains, Phox (PX) domains and C2 domains. The characterization of these domains and their
83 specificity allowed the engineering of a set of anionic phospholipid biosensors by fusion of these
84 domains with a fluorescent protein (92). These so called genetically encoded biosensors enable
85 the study of the subcellular accumulation pattern and to some extent the dynamics of anionic

86 phospholipids *in vivo* (112, 127–129). However, in some cases, lipid-binding domains are not
87 sufficient to target the protein to its proper compartment. Indeed, some proteins require the
88 present of both, an anionic lipid and another protein (or lipid) to localize to the right
89 compartment, in a mechanism called “**coincidence binding**” (Figure 2.d). For instance, the
90 ubiquitin ligase PLANT-U-BOX13 (PUB13), which regulates the trafficking of the PM receptor
91 FLAGELIN-INSENSITIVE 2 (FLS2), is recruited to the TGN via the concomitant interaction with
92 RabA4b and PI4P (2). Furthermore, LBDs may also recognize additional membrane feature such
93 as curvature or electrostatics. As such, results obtained with lipid biosensors should always
94 been taken with care as their localization may not only reflect the accumulation of a single lipid
95 species. This is exemplified by the fact that biosensors designed to bind to the same lipid species
96 do not always have the exact same localization (112, 113). If possible, the potential
97 accumulation of a lipid at a given membrane should be also supported by biochemical evidences
98 and/or by the localization of their metabolic enzymes.

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100 The combined study of the localization of anionic lipid generating enzymes and genetically
101 encoded lipid sensors suggest that in Arabidopsis epidermal root cells, the PM accumulates PI4P,
102 PI(4,5)P₂, PA and PS (Figure 3) (93, 112, 113, 127, 128). TGN/EE are enriched in PI4P, PS and to
103 a lesser extent PI3P (93, 113, 114, 128). LE/MVBs accumulate both PI3P and PI(3,5)P₂, although
104 both lipids localize in distinct compartments (37, 38, 112, 129). Finally, the tonoplast and
105 autophagosomes carry PI3P (112, 129). However, this subcellular accumulation pattern may
106 vary according to the cell type or the stress status of the cell (Figure 3) (34, 41, 44, 48, 57 in
107 revision, 61, 110, 115). For example, PI(3,5)P₂ is found in LE/MVBs in most cell type but
108 accumulates at the PM in elongating root hairs (34) (Figure 3). PI(4,5)P₂ and PA are
109 constitutively produced at the PM at low or moderate levels, respectively, in resting condignition
110 but upon stimulation, such as salt stress, they can be massively produced, which triggers specific
111 stress responses (82, 121, 127). Alternatively, PI(4,5)P₂ production can be inhibited by external
112 stimuli such as pathogen-associated molecular patterns (80).

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2.2. Dynamics of anionic lipids: rapid production and turnover thanks to a set of lipid-modifying enzymes

2.2.1. PA production and stress responses

PA is structurally the simplest phospholipid. As such, it is a key intermediate for other phospholipid biosynthesis (94, 121). Multiple pathways involving different enzymes at various locations can lead to PA synthesis and are summarized in Figure 1.b. The rapid accumulation of PA is induced by numerous abiotic stresses including salt, cold, heat, or osmotic stress, but also by biotic stresses in case of pathogen infection (121). Moreover, PA synthesis is regulated in physiological and developmental context including hormonal responses such as SA, ABA, and auxin (121). In each case, PA accumulation leads to different adapted cellular responses raising the question: how can PA integrate different inputs to lead to specific outputs relevant to the physiological situation? One of the main hypothesis is that PA accumulation never occurs alone but rather that PA is one second messenger among others that together lead to concerted cellular responses (94). To know more about this topic, the different hypotheses to answer this question are discussed by Pokotylo *et al.* in a recent review.

2.2.2. PIPs and rapid inter-conversion

The phosphorylation of the inositol ring of phosphatidylinositol is mediated by PI-kinases that are specific of the phosphate position (Figure 1.d). In plants, the genome does not encode for type-I and type-II PI3-kinases (PI3Ks), able to phosphorylate PI4P or PI(4,5)P₂ (84). As a consequence, PI(3,4)P₂ and PI(3,4,5)P₃ likely do not exist and have not been detected in plants. The dephosphorylation of PIPs is mediated by PI-phosphatases that belong in plants to three main families, the SUPPRESSOR OF ACTIN (SAC) domain-containing proteins (SAC1 to SAC9), the 5PTase family (5PTase1 to 15) and the PHOPHATASE AND TENSIN Homolog (PTEN) family (PTEN1 to 3) (24) (Figure 1.d). PI-kinases and phosphatases are highly processive enzymes *in*

140 *vivo* and thereby PIPs can be quickly interconverted, cycling between two states or creating
141 cascade regulations (86). Because anionic lipid pools can be enzymatically modified within
142 second, they are able to respond to various stimuli and to act in fast cellular events such as
143 membrane trafficking.

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145 *In vitro* experiments testing PI-kinases activity often require the use of detergents, which
146 destroy liposomal structures and free lipid substrates in order to increase kinase activity (52).
147 These results suggest that PI-kinases have difficulties to recognize their substrate embedded
148 into the membrane and might get “help” *in planta*. The main candidates to fulfil this function are
149 the SEC14 lipid transfer proteins. The yeast Sec14 protein is able to transfer
150 phosphatidylcholine and phosphatidylinositol from distinct membranes *in vitro*, possibly by-
151 passing the classical vesicular transport of lipids (52, 103). However, the current model, based
152 on crystallographic data, advocates the idea that Sec14 dislodges the phosphatidylinositol head
153 from the TGN membrane making it accessible for PI4-kinases (Figure 4.a). Based on sequence
154 homology, Arabidopsis contains 32 Sec Fourteen Homologs (AtSFHs), each containing a highly
155 conserved sec14 domain. The sec14 domain of several AtSFHs displays the same *in vitro* activity
156 than the yeast sec14 and can rescue the sec14 yeast mutant (40, 130). So far, the best-
157 characterized AtSFH protein is AtSFH1. AtSFH1 belongs to a subclass of 13 members that
158 contains a Nlj16 domain in C-terminal. This domain has two functions. It contains a polybasic
159 patch that localizes at the PM in a PI(4,5)P₂-dependent manner and a coiled-coiled domain that
160 mediates homo-oligomerization (25). The model built with the combination of yeast and
161 Arabidopsis data is that AtSFH1 is targeted at the root hair tip PM by PI(4,5)P₂ where it
162 stimulates the activity of PI-kinases (PI4K or PIP5K), thereby enhancing the production of PIPs
163 (directly PI(4,5)P₂ or PI4P that will then be converted into PI(4,5)P₂). PI(4,5)P₂ recruit new
164 AtSFH1 which oligomerizes and further creates PI(4,5)P₂ clusters at the root hair tip PM (Figure
165 3).

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168 **2.3. PS synthesis and trafficking**

169 Contrary to PA and PIPs that can be synthesized by several enzymes, a single enzyme produces
170 PS in Arabidopsis: the Phosphatidylserine Synthase 1 (PSS1) (91, 93, 140) (Figure 1.b). PSS1 is
171 an ER transmembrane protein which synthesizes PS in the luminal leaflet of this compartment
172 (140). Therefore, by contrast to PIPs, PS is not locally produced directly at the membranes
173 where it acts. This implies that PS must be transported from the luminal leaflet of the ER to the
174 cytosolic leaflet of the endomembrane system. Two non-exclusive mechanisms may explain the
175 localization of PS.

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177 **2.3.1. Flippases and vesicular trafficking**

178 As PS faces the lumen in the ER but the cytosol once at the PM or endosomes, it must switch
179 membrane leaflet at some point. **Flippases** are proteins able to flip phospholipids from the
180 luminal membrane leaflet to the cytosolic membrane leaflet (85) (Figure 4.b). The Arabidopsis
181 genome encodes for 12 aminophospholipid flippases (ALAs) and at least ALA1, ALA2, ALA3 and
182 ALA10 are able to flip PS in yeast (27, 70, 71, 85, 97). ALA proteins localize in the ER (ALA1, 2
183 and 3) but also all along the endocytic pathway (ALA1 at the PM, ALA2 in LE/MVBs, ALA3 in the
184 Golgi and TGN/EE) (9, 70, 71, 74, 96). Their localization, and function, depends on ALA
185 interacting β -subunits, ALIS. These localization suggest that PS could be directly flipped in the
186 ER and then be transported through vesicular trafficking to the PM and endosomes. Another
187 hypothesis would be that PS is first transported by vesicular trafficking on the luminal side of
188 organelle and then flipped in specific compartments, such as TGN/EE or PM. In yeast, the activity
189 of the PS flippase Drs2p is promoted by PI4P (4, 123). As PI4P is present in the same
190 compartments than PS along the endocytic pathway in plants, this could be an argument in
191 favour of the later hypothesis. In any case, if the flippase activity occurs at the ER membrane, PS
192 is then actively exported out of this compartment, since the ER cytosolic leaflet does not
193 accumulate PS (93, 113).

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2.3.2. PS transfer at membrane contact sites

Another hypothesis suggests that PS bypasses classical vesicular trafficking and rather directly translocates from the ER to the PM, at **membrane contact sites** (MCSs). MCSs are static microdomains where membranes from two different organelles are bring together (at a distance lower than 30nm) and stabilize by **tethering proteins** (107). In animal and yeast, MCSs are major sites of lipid flow and are particularly important to control the localization of nearly all anionic lipids (138). **Lipid transfer proteins** present at MCS are able to transport lipids between two membranes extracting the lipid from the donor membrane, transferring it through the cytosol and inserting it in the acceptor membrane. Notably, proteins from the oxysterol-binding related protein (ORP) family localize at MCS via interactions with suppressor of choline sensitivity Scs2p (VAPS in animal cells) in the ER and PIPs at the PM (3, 138). Several ORPs transfer PS (among other lipids) from the ER to the PM and then counter transport PI4P from the PM back to the ER (Figure 4.c). The PI4P phosphatase SAC1, an ER resident protein, hydrolyses the incoming PI4P, thereby maintaining the PI4P gradient between the PM and ER membrane and fuelling PS export from the ER (3). Note that PS transfer at MCS has not been described so far in plants but that ORP proteins are conserved in plant genomes.

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3. ANIONIC LIPIDS AS DETERMINANT OF MEMBRANE PHYSICOCHEMICAL PROPERTIES

3.1. Surface charges

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As they carry negative charges, anionic phospholipids generate an **electrostatic field** on the cytosolic leaflet of membranes (76) (Figure 1.a and 2.b). The strength of this electrostatic

219 field depends upon the relative concentration in anionic phospholipids and their respective
220 negative charges, which vary from -1 for PS to -5 for PI(4,5)P₂. In plants, TGN/EEs are less
221 electronegative than the PM but more electrostatics than MVB/LEs, whereas ER-derived
222 compartments (ER, nuclear membrane, peroxisomes) are neutral (93, 113). Consequently, an
223 electrostatic gradient is formed from the PM to the tonoplast, which follows the endocytic
224 route and specifies an “**electrostatic membrane territory**” within the endomembrane system
225 (93). The extensive use of biosensors locating anionic lipids and assessing membrane surface
226 charge *in vivo* shows that the high electronegativity of the plant PM relies concomitantly on
227 PI4P, PS and PA, with a major role of PI4P, whereas the surface charge of TGN/EE depends
228 of both PI4P and PS (93, 113).

229 The surface charges of membrane compartments are a key determinant to control the
230 localization of many membrane-associated proteins. For example, proteins which contain
231 polybasic patches interact with the negative charges of the anionic phospholipids of the
232 membrane by non-specific electrostatic interactions (Figure 2.d). Very often, such motifs also
233 contain hydrophobic residues or are found adjacent to hydrophobic lipid anchors. For
234 example, the plant AGC kinases PINOID and D6PK, which are well-characterized regulators
235 of auxin efflux transporters from the PIN family, localize at the PM through this mechanism
236 (5, 61, 113). Another prominent example of plant proteins, which rely, at least in part, on
237 electrostatic interactions with anionic lipids for localization is the small GTPases from the
238 Rho-Of-Plant (ROP) family, which have a polybasic stretch adjacent to a prenylation site (i.e.
239 a geranylgeranylation lipid modification) (91).

240 There is no precise study on the number of proteins encoded in plant genomes that might
241 contain such polybasic/hydrophobic stretches and localize to electrostatic membranes
242 through this mechanism but it is likely a general mechanism that contributes to the
243 localization of many proteins within the electrostatic membrane territory.

244

245 **3.2. Curvature**

246 Anionic phospholipids present different geometries (Figure 2.a). Indeed, PI and PIPs have a large
247 head group that carries the phosphorylation, whereas PA has a very small one (10). The bulk of
248 the lipid directly influences the curvature of the membrane. Thus, the conical shape of PIPs will
249 enhance positive curvature while the inverted conical shape of PA and PS will favour negative
250 curvature (Figure 2.a). Membrane curvature is of prime importance to form endocytic vesicles at
251 the PM, **secretory vesicles** at the TGN/EE or to internalize proteins in MVB for instance (10,
252 78). Similar than surface charges, the curvature of the membrane can also induce lipid-protein
253 interactions, via curvature sensing domain such as Bib-Amphiphysin-Rsv (BAR) domains (7, 63)
254 or the Amphipathic Lipid Packing Sensor (ALPS) motif, which recognizes packing defects found
255 in curved membrane. This motif can be found in association with a small stretch of positive
256 amino acids to form a so-called +ALPS motif, which allows the coincidence detection of
257 membrane charge and curvature (139). In plants, the PI4-kinase PI4K β 1 relies on such motif to
258 localize to the curved and electrostatic membrane of TGN/EEs (93).

259

260 → Include the sidebar "**Lipid molecular species and lipid packing defects**" here

261

262 **3.3. Clustering**

263 Proteins and lipids can also laterally segregate in membrane domains, thereby creating sub-
264 compartmentalization inside the membranes (Figure 2.c). Such clustering is often required for
265 the protein to fulfil its biological function. While sterol has long been associated with membrane
266 domain formation, it recently emerged that anionic lipids are also key determinant of protein
267 clustering.

268 For example, Remorins (REM) are proteins that laterally segregate at the PM in domains of
269 about 100nm in size (hence termed **nanodomains**) (46) (Figure 5.a). REMs are involved in
270 biotic and abiotic responses, although their exact molecular function is still unknown (47). For

271 example, *Solanum tuberosum* REMORIN group 1 isoform three (StREM1.3) limits the spreading
272 of Potato Virus X (PVX), and regulates **plasmodesmata** permeability (100). A combination of
273 super-resolution microscopy and biophysical experiments showed that StREM1.3 targeting into
274 nanodomains is dependent upon the presence of both sterol and PI4P and is required for
275 function (29) (Figure 5.a). PI4P is not the only anionic lipid involved protein nanoclustering into
276 membrane nanodomains. Indeed, PS stabilizes the small GTPase ROP6 into nanoclusters of
277 about 50 to 70nm in diameter (91) (Figure 5.b). By contrast to REM proteins, which are
278 constitutively localized in PM nanodomains, ROP6 clustering is triggered by its activation (i.e.
279 GTP-loading) upon auxin treatment. ROP6 directly binds to PS (and other anionic lipids) via a
280 polybasic region located next to its geranylgeranylation site (91). ROP6 localization into
281 nanoclusters is essential for function since ROP6 signalling is impaired in mutant lines lacking
282 PS biosynthesis or when the PS-binding site in ROP6 is mutated. Single molecule imaging and
283 super resolution microscopy of PS biosensors at the plasma membrane suggest that PS itself, not
284 only ROP6, is present in PM nanodomains (Figure 5.b). However, unlike ROP6, PS are present in
285 PM nanodomains both in the absence or presence of auxin (91). Therefore, there are
286 prepatterned nanoplatforms of PS at the PM, which recruit GTP-loaded ROP6 upon auxin
287 treatment. Future studies are needed to uncover whether such PS nanoplatforms also contain
288 additional lipids, such as sterol or PI4P and how they are formed. The cell wall and the
289 cytoskeleton influence protein diffusion into membrane (73, 75). It will therefore be interesting
290 to understand the interplay between anionic lipid-induced clustering, cell wall constraints and
291 cytoskeleton dynamics, the latter being itself regulated by anionic lipids (24).

292

293 All the mechanisms described above converge on the idea that anionic lipids are key
294 determinant of membrane identity, which ultimately allows the precise recruitment of proteins
295 in space and time. There are countless examples of proteins that are targeted to specific
296 membranes by anionic phospholipids either constitutively or upon certain stimuli. These
297 examples will not be individually reviewed here. Instead, we will dedicate the rest of this

298 review to one of the key questions of cell biology: how compartments maintain a specific
299 identity despite the constant flow and exchange of proteins and lipids between compartments.
300 We will in particular highlight how anionic lipids may contribute to membrane contact sites
301 establishment and analyse the interplay between membrane trafficking and anionic lipids.

302

303 **4. ANIONIC LIPIDS AND ER/PM MEMBRANE CONTACT SITES IN PLANTS**

304 Several reports began to put EPCS (ER/PM MCS) at the centre of essential cellular processes
305 including immune secretory pathway, viral movement at plasmodesmata, stabilization of the
306 cortical ER network, endocytosis, membrane integrity, pollen, seed and root hair development
307 (53, 64, 65, 90, 104, 134, 141). Lipid exchange at EPCSs is still an open question in plants but
308 a clear role for anionic lipids in EPCS establishment is documented.

309

310 In Arabidopsis, three types of EPCSs have been described (Figure 6): the S-EPCSs, which are
311 stabilized by synaptotagmins (SYTs, orthologs of the mammalian extended synaptotagmins
312 (E-SYT)) (6, 90), the V-EPCSs that contain the vesicle-associated membrane-associated
313 protein 27s (VAP27s) and VAP27-related proteins (orthologs of the mammalian VAPS and
314 yeast Scs2) (102, 132, 134) and the PD-EPCSs, which are specifically enriched at
315 plasmodesmata (PD) and contain MULTIPLE C2 AND TRANSMEMBRANE PROTEIN
316 (MCTP) proteins (11). Importantly, all three classes of tethering molecules, VAP27s, SYTs,
317 and MCTPs are directly interacting with anionic phospholipids and likely require these lipids
318 to interact with the PM. Nonetheless, S-EPCS and V-EPCS are spatially separated within the
319 same cell suggesting a tethering signature model where the abundance of one type of EPCS at
320 the expense of the other could vary in response to environmental or developmental cues
321 (111). Another model, the tethering arrangement model, proposes that the organization of
322 EPCS could change in response to stimuli such as lipids or calcium fluxes (26). These two

323 models are not mutually exclusive.

324

325 **4.1. V-EPCS**

326 VAP27 are ER transmembrane proteins that are conserved among eukaryotes (138). Ten
327 homologs of VAP27 exist in Arabidopsis (134). Three of them localize at the ER-PM contact
328 sites: VAP27-1, VAP27-3, and VAP27-4, together with the actin binding protein
329 NETWORKED 3C, NET3C (133) (Figure 6). VAP27-1 and VAP27-3 interact with PIPs *in*
330 *vitro* (116). Moreover, VAP27-3 is able to interact with a lipid transfer protein from the ORP
331 family, ORP3a, that is able to bind sterol *in vitro*, suggesting possible lipid transfer similar to
332 what has been described in yeast and animal cells (3, 102).

333

334 **4.2. S-EPCS**

335 The mammalian E-SYT1 is able *in vitro* to trigger glycerolipids exchanges between
336 liposomes (105). E-SYTs contain C2 domains that bind anionic phospholipids from the PM in
337 a Ca²⁺ depend manner (144). In favour of the tethering arrangement model, E-SYTs Ca²⁺
338 binding leads to clustering of E-SYTs proteins and an increase of the interactions between E-
339 SYTs and PM anionic lipids (26). This results in stabilization and tightening of S-EPCS (26,
340 138, 144). In Arabidopsis, ionic stress triggers the expansion of S-EPCS in association with
341 accumulation of PI(4,5)P₂ at the PM supporting the tethering arrangement model (62).
342 Furthermore, the C2 domains of Arabidopsis SYT1 bind PS in a Ca²⁺ dependent-manner *in*
343 *vitro* (90) (Figure 6). The relevance of this Ca²⁺-dependent PS binding *in vivo* is currently
344 unknown but also argues in favour of the tethering arrangement model.

345

346 **4.3. PD-EPCS**

347 PD pores interconnect virtually all cells within the plant body, establishing direct PM and
348 cytoplasmic continuity. A striking feature of PD is a strand of endoplasmic reticulum (ER)

349 running through the pores and tethered tightly to PM, making PD a unique case of EPCS in
350 eukaryotes. While SYT1 localize to PD to some extent (64, 90), several MCTP proteins are
351 specifically enriched at PD and likely contribute to ER-PM tethering at the PD pore (11)
352 (Figure 6). Molecular dynamics suggest that MCTP4 C2 domains interact with anionic lipids
353 at the PM, in particular PS and PI4P. Accordingly, pharmacological experiments support that
354 PI4P is required for MCTP4 PD-specific localization. PDs have a specific composition in
355 term of sterol and sphingolipid (28). By extension, an attractive hypothesis that remains to be
356 tested, would be that the PM at PD has a unique anionic lipid signature that could contribute
357 to MCTP PD-specific localization.

358

359 Communication between organelles and lipid exchanges occur not only at MCSs but also
360 during vesicular trafficking. Vesicular trafficking implies exchange of membranes between
361 compartments and anionic lipids are key actors of those exchanges. Therefore, compartments
362 must maintain a specific lipid identity despite the constant flow and exchange of proteins and
363 lipids that happen during vesicular trafficking. The interplay between membrane trafficking
364 and anionic lipids will be detailed in the following section of this review.

365

366 **5. TRAFFICKING BETWEEN THE PM AND THE TGN**

367 **5.1. Clathrin mediated endocytosis**

368 In animal cells, it is well documented that anionic lipids play a fundamental role in
369 endocytosis. Clathrin-mediated endocytosis mainly involves PI(4,5)P₂ produced from PI4P by
370 PIP5P kinases (PI4P-5Ks) (81). PI(4,5)P₂ allows the initiation and stabilisation of the
371 **clathrin-coated pits** by the recruitment of several components of the endocytic machinery
372 including the adaptor protein AP2 (51, 95). Moreover, PIP5Ks are directly recruited at the site
373 of endocytosis by AP2, creating a local pool of PI(4,5)P₂, which induces a high rate of

374 clathrin-coated pit nucleation (81). Then, both PI(4,5)P₂ and PI(3,4)P₂ are involved in pit
375 maturation (81).

376

377 **5.1.1. PI(4,5)P₂ a main actor in clathrin-mediated endocytosis**

378 In plant cells, the recruitment of the endocytic machinery to the PM is far less understood.
379 However, the role of PI(4,5)P₂ in endocytosis has been demonstrated indirectly using PIP5Ks
380 over-expression and loss-of-function approaches (43, 146). Notably, a *pip5k1pip5k2*
381 (hereafter designed as *pip5k1k2*) mutant has abnormal **clathrin-coated pits**, which are less
382 dense than in the wild type but bigger (43). This mutant, as well as PIP5K1 and PIP5K2
383 overexpression line, have defects in PIN endocytic trafficking, which ultimately impact both
384 their accumulation at the PM, their polar targeting and hence auxin distribution, leading to
385 various degrees of auxin-related developmental defects (43, 79, 120). Over-expression of
386 PIP5K also induces a phloem differentiation phenotype (30). PIP5K overexpression redirects
387 the trafficking toward the vacuole leading to protein degradation and vacuole biogenesis,
388 which in protophloem file induces vascular discontinuities (30). However, it is unclear if this
389 increase in vacuolar trafficking is caused by an overall heightened endocytic rate at the PM or
390 by regulation of downstream trafficking steps. In any case, PI(4,5)P₂ levels are constantly
391 kept in check in the root phloem by two PM-localized PI(4,5)P₂ 5-phosphatases,
392 COTYLEDON VASCULAR PATTERN 2 (CVP2) and CVP2-LIKE 1, whose double mutant
393 shows similar phloem discontinuity as PIP5K overexpression lines (101).

394 In growing pollen tube, the exocytosis at the tip is balanced by endocytosis in the subapical
395 regions (Figure 3). These regions are marked by PI(4,5)P₂ locally produced by PIP5Ks and
396 restricted by degradation into diacylglycerol (DAG) by Phosphoinositide Phospholipase C
397 (PI-PLC) (17, 32) (Figure 3). Loss-of function mutants of PIP5Ks show reduced endocytosis,
398 which lead to low pollen germination rate and slow tube elongation (41, 115). Conversely,

399 pollens overexpressing PIP5K6 show PM invagination and the formation of several tip
400 branches due to a higher rate of endocytosis at the tip of pollen tube (146). The expression of
401 a clathrin dominant negative can rescue the PIP5K6-OE phenotype indicating that PI(4,5)P₂
402 synthesis enhances clathrin-mediated endocytosis (146). A similar mechanism was proposed
403 in responses to salt treatment which increases the level of PI(4,5)P₂ and induces the formation
404 of **clathrin-coated vesicles** in a PIP5K1 and PI5PK2-dependent manner (43, 56).

405

406 **5.1.2. PA as another regulator of clathrin-mediated endocytosis?**

407 Salt tolerance studies suggest a role for PA in endocytosis. Indeed, the level of PA is
408 drastically increased under salt treatments (83). In addition of inducing membrane curvature,
409 PA is able to bind clathrin heavy chain (CHC) and domain clathrin assembly proteins (77).
410 Upon salt treatment, PA production by the phospholipase PLDζ₂ induces the internalisation
411 of PIN2 in TGN/EE (21), whereas in normal condition PA and PLDζ₂ are necessary for the
412 proper cycling of PIN2 in root cells (66). This mechanism decreases the amount of PIN2 at
413 the PM on the salt-side and induces auxin redistribution that allows the plant to redirect its
414 root growth away from highly salt concentrated soil (21). This data suggest that PA could act
415 as a mediator of the auxin response by activating the endocytosis of PIN proteins upon high
416 salinity conditions.

417

418 To conclude, a role for PI(4,5)P₂ in clathrin-mediated endocytosis is established in different
419 cell types and developmental contexts. Nevertheless, the proteins regulated by PI(4,5)P₂
420 during endocytosis are still largely unknown. In addition, the role of other anionic lipids such
421 as PI4P and PA in the regulation of the endocytic machinery needs to be clarified.

422

423 **5.2. Polar secretion and exocytosis: the targeting of the exocyst**

424 Exocytosis is led by a **tethering complex** called exocyst, which is conserved among
425 eukaryotes and that targets exocytic vesicles to the PM (88). In many cases, exocytosis does
426 not occur homogenously along the PM but it is polarized. Polar exocytosis has been reported
427 in growing tip cells such as root hair and pollen tube (8, 14, 67, 108, 118, 136), for the polar
428 localization of auxin efflux carriers from the PIN family (18, 89, 119), in the establishment of
429 the casparian strip (48) or the Ortmannian ring in trichomes (57 in revision, 58–59).

430

431 **5.2.1. PI(4,5)P₂ targets the Exocyst to the PM**

432 The exocyst complex is targeted to the PM via two subunits, SEC3 and EXO70 known to
433 bind anionic phospholipids, in particular PI(4,5)P₂. In Arabidopsis, SEC3 contains a PH
434 domain that binds to PI(4,5)P₂ *in vitro* (8). The extensive use of biosensors and the
435 localization of lipid metabolic enzymes in plants allowed the cartography of anionic lipids in
436 cells exhibiting polar secretion highlighting specific lipid accumulation patterns, notably for
437 PI(4,5)P₂ (Figure 3) (41, 42, 57, 60, 61, 115, 117, 146). Interestingly, the localizations of
438 SEC3 and/or EXO70 isoforms often correlate with the PI(4,5)P₂ subcellular accumulation
439 pattern, suggesting that PI(4,5)P₂ contribute to their localization (8, 48, 108). In pollen tube,
440 SEC3 and EXO70A1 partially colocalize with PI(4,5)P₂ biosensors (8, 108). Since PIP5K
441 mutants display slower tube elongation and reduced secretion of cell wall materials (41, 115),
442 it is likely that PI(4,5)P₂ participates in targeting exocyst complexes to specific PM domains.

443

444 **5.2.2. PI(4,5)P₂ and PA: working together to confine exocytosis**

445 EXO70A1 and EXO70B1 are expressed in growing pollen tube and partially colocalize with
446 both PI(4,5)P₂ and PA biosensors (108). Therefore, it is possible that the coincidence
447 detection of PI(4,5)P₂ and PA in pollen tube restricts the site of exocytosis to the narrow PM
448 strip that contains both lipids (Figure 3). These EXO70 subunits may directly recognize each

449 lipid. Alternatively, they may be sensitive to the overall membrane surface charges. One may
450 speculate that in pollen tube, the PM membrane domain that contains a combination of both
451 PI(4,5)P₂ and PA is highly electronegative and thereby could recruit specific EXO70
452 isoforms. Additional experiments are required to distinguish between these two possibilities.
453

454 **5.3. Proper secretion requires PI4P production in the TGN**

455 Exocytosis not only requires specific anionic lipids at the PM but also a regulation of the lipid
456 composition in the TGN for proper vesicle formation. Indeed, root hair studies revealed the
457 importance of the pool of PI4P in the TGN for polar secretion (49, 99, 122, 143). PI4Kinases,
458 PI4Kβ1 and PI4Kβ2, as well as the PI4P phosphatase ROOT HAIR DEFECTIVE 4,
459 RHD4/SAC7, localize to the TGN. *pi4kβ1β2* and *rhd4* mutants display short or bulged root
460 hairs (49, 99, 122). Ultrastructural studies by electron tomography showed the presence of
461 enlarged, likely deficient, **secretory vesicles** in the TGN of *pi4kβ1β2* double mutant,
462 suggesting that PI4Kβs are indeed involved in secretion (49). PI4Kβs and RHD4/SAC7 have
463 opposite catalytic activities, yet apparently, locate to the same compartment. It is possible that
464 PI4Kβs and RHD4/SAC7 localize in different TGN subdomains. Consistent with this
465 scenario, PI4Kβ1 localizes specifically in the secretory vesicle subdomain of the TGN (49).
466 According to this hypothesis, PI4Kinases could be necessary for the production of the pool of
467 PI4P at the TGN which confers the proper physical properties (mild electrostatics, high
468 curvature) necessary for secretory vesicle formation. By contrast, RHD4/SAC7 could localize
469 in a different TGN subdomain, perhaps directly connected to endocytosis. In such model,
470 RHD4/SAC7 would degrade incoming PI4P from the PM to maintain the PI4P gradient along
471 the endocytic pathway (113).

472

473 **5.4. Cell plate establishment and the creation of a new PM**

474 The cell plate is an organelle formed from the secretion and fusion of vesicles from the TGN
475 and will form the new PM of the two daughter cells (13). A combination of clathrin-mediated
476 endocytosis and exocytosis occurs at the cell plate. During this process, the lipid composition
477 of the cell plate varies from the bulk PM. Lipid binding biosensors suggest that PI4P, PA and
478 PS accumulate and confer a highly electronegative field at the cell plate to a similar extent, or
479 even higher, than at the PM (16, 93, 113) (Figure 3). However, PI(4,5)P₂ is excluded from the
480 cell plate during its creation and extension and appears at the edges of the cell plate just
481 before its full attachment to the PM (16, 113, 127). Knowing that PI(4,5)P₂ is a major
482 regulator of both exocytosis and endocytosis, it is therefore likely that specific trafficking
483 mechanisms occur at the cell plate compared to the bulk PM, which have yet to be uncovered.
484 This difference of membrane composition between the bulk PM and the cell plate is crucial
485 for proper cell division. Indeed, several mutants for enzymes involved in anionic lipid
486 homeostasis show cell plate and/or cytokinesis phenotypes. Those include mutants for PI4P
487 production (*pi4kβ1β2*), PI4P/PI(4,5)P₂ interconversion (*sac9*, *pi5k1k2*), and PI3P/PI(3,5)P₂
488 interconversion (*fab1afab1b*, *fra7/sac1*) (49, 120, 131, 137, 148). Some of these enzymes
489 directly act at the cell plate. For instance, PI4Kβ1 localizes at the cell plate and the absence of
490 PI4Kβ1 and PI4Kβ2 directly affect the vesicular trafficking along phragmoplast microtubules
491 (68). However, others might act indirectly on cell division, such as FORMATION OF
492 APLOID AND BINUCLEATE CELLS 1, FAB1A and FAB1B proteins, that do not localize
493 at the cell plate (36, 137). It is therefore likely that the *fab1afab1b* cell plate phenotype results
494 from a broad alteration of membrane trafficking. We refer the reader to a recent review on
495 this subject, which details the potential involvement of each anionic lipid during cytokinesis
496 (13).

497

498 **5.6. Anionic phospholipid remodelling at the Plants-Fungi interface**

499 Fungi infection and mycorrhizal symbiosis induce PM reorganization, which include lipid
500 patterning at the PM with likely consequences on both endocytosis and exocytosis.

501

502 **5.6.1. Periarbuscular membrane**

503 During the endosymbiotic association of roots with arbuscular mycorrhizal (AM) fungi in *M.*
504 *truncatulla*, the fungus develops intracellular branched hyphae called arbuscules (44). In
505 response, the root cortical cells form a new membrane in continuity with the PM called
506 periarbuscular membrane (PAM) (31). The PAM envelops the hyphal branches and is thought
507 to be generated by polar exocytosis. Indeed, subunit of the exocyst complex and SNARE
508 proteins known to be involved in exocytosis and membrane fusion are required for the PAM
509 formation (31, 145). By analogy to tip growing cells, anionic lipids might regulate this
510 particular case of polarized secretion. So far, only the pattern of localization of PI4P,
511 PI(4,5)P₂ and PA were documented during AM interaction (44) (Figure 3). Both PI4P and PA
512 are found in the PAM to similar extent than the PM. However, in the trunk part of hyphal
513 branches, discrete regions where PI(4,5)P₂, PI4P and PA reporters co-accumulate can be
514 observed (44). This accumulation could correspond to an accumulation of membranes before
515 formation of small bulges. Furthermore, anionic lipids accumulation could influence
516 membrane curvature and thereby physically contribute to the establishment of the PAM.

517

518 **5.6.2. Extra invasive hyphal membrane**

519 Using another model of fungi-plant interactions, it was recently shown in *Arabidopsis*
520 infected by *Colletotrichum* that extra invasive hyphal membrane (EIHM), which is formed in
521 continuity with the PM, strongly accumulates PI(4,5)P₂ and PIP5K3 all along the membrane
522 (Figure 3), as well as a subunit of the exocyst complex and SNARE proteins (39, 109, 110).
523 This accumulation of PI(4,5)P₂ seems to be specific to *Colletotrichum* (110). PI(4,5)P₂

524 production by PIP5K at the EIHM could increase polar exocytosis thereby allowing the
525 formation of the EIHM and thus the successful infection by the fungi.

526

527 All together, these recent data suggest that anionic lipid patterns are modified in response to
528 fungi and allow the symbiosis or infection to take place, possibly by induction of polar
529 exocytosis to the membrane that surround the hypha.

530

531 **6. ANIONIC LIPIDS IN VACUOLAR TRAFFICKING**

532 Most membrane-associated proteins are degraded in the vacuole. To reach the vacuole, PM
533 proteins are first polyubiquitinated, which induces endocytosis and targeting to TGN/EEs
534 (19). Then TGN/EEs mature into LE/MVBs. During this maturation, endosomal-sorting-
535 complex-required-for-transport (ESCRT) internalizes membrane proteins into intraluminal
536 vesicles. Once the external membrane of MVB fuses with the tonoplast, the intraluminal
537 vesicles containing the proteins are released into the vacuole and degraded. Non-ubiquitinated
538 cargo can be retrieved in MVBs by the action of the retromer complex that antagonize the
539 ESCRT complex (86).

540

541 **6.1. From PI4P to PI3P and PI(3,5)P₂: PIP cascade leading to protein sorting**

542 One of the main characteristics of PIPs is to be quickly interconverted by kinases and
543 phosphatases (Figure 1.c). This is well illustrated along the road leading to protein
544 degradation into the vacuole in which the different maturation steps correlate with a PIP
545 interconversion (Figure 7). PI(4,5)P₂ from the PM is converted into PI4P by 5-phosphatases
546 either in TGN/EEs or during the endocytic process. At the surface of TGN/EEs, PI4P is
547 gradually replaced by PI3P through the combined action of 4-phosphatases (e.g. RHD4/SAC7
548 in root hair) and the PI3K, VPS34. Some MVBs exhibit PI(3,5)P₂ due to the action of the

549 PI3P5K from the FAB1 family (36, 38, 112) (Figure 7). The acquisition of PI3P is essential
550 for **protein sorting**. Indeed, FYVE1/FREE1, a component of the ESCRT complex that binds
551 ubiquitinated cargo, localizes in the MVB by interacting with PI3P (22, 55). Similarly,
552 SORTING NEXIN 1 (SNX1), a component of the retromer complex also localizes at the
553 MVB through interactions with PI3P and/or PI(3,5)P₂ (98). In addition, PI3P and/or PI(3,5)P₂
554 also mediate the association of endosomes with the cytoskeleton, since the loss of FAB1
555 releases MVBs from cortical microtubules (35, 36) and SNX1 interact with the microtubule
556 regulator CYTOPLASMIC LINKER ASSOCIATED PROTEIN, CLASP (1).

557

558 **6.2. Autophagosome and protein degradation**

559 Cytosolic cargoes can also be degraded by autophagy (20). In this process, cargoes are
560 encapsulated by a double membrane to form autophagosomes. The outer membrane of the
561 autophagosomes fuses with the tonoplast and the internal membrane, together with its luminal
562 content, is subsequently degraded in the vacuole (20). The autophagosome is initiated by the
563 formation of a **phagophore** that will expand, surround the cargoes and close. AuTophagy-
564 related (ATG) proteins were first discovered by genetic screens in yeast but most of the
565 actors of autophagy are conserved among eukaryotes (20). In all eukaryotes, PI3P is critical
566 for autophagy. In animal and yeast, PI3P is produced at the initiation step of phagophore
567 formation by a PI3K complex that contains the PI3K VPS34 (20). A member of the complex,
568 ATG14, targets the PI3K complex to the phagophore (15). Furthermore, the production of
569 PI3P is essential to recruit and stabilize autophagy-related proteins at the membrane of the
570 phagophore. In addition, the geometry of the head group of PI3P could also directly help the
571 curvature of the phagophore. In plants, the precise dynamics of PI3P during autophagy is not
572 well understood. Furthermore, ATG14 does not exist, which raises the question of the
573 recruitment of the PI3K complex at the phagophore (20). Yet, inhibitor of PI3Ks blocks

574 autophagy in plants (142), suggesting that, like in other eukaryotes, PI3P is important for this
575 process.

576

577 In addition to stabilizing ATG-related protein at the membrane of the phagophore, several
578 plant-specific proteins, involved in autophagy, directly interact with phosphoinositides. SRC-
579 HOMOLOGY3-CONTAINING-PROTEINs SH3P2 and SH3P3 are two BAR-domain
580 containing proteins that localize at the phagophore (149). As BAR domains can induce
581 membrane curvature, they may participate in the membrane shaping of the phagophore.
582 SH3P2 interacts with PI3P (and other phosphoinositides) and co-localize with ATG8 in the
583 phagophore in a VPS34-dependent manner (149). SH3P2 interacts with ATG8 and the PI3K
584 complex. *fyve1/free1* mutant presents autophagy-related phenotype with accumulation of
585 autophagic structures (22, 149). FYVE1/FREE1 interacts with ATG8, the PI3K complex and
586 SH3P2 (23). As such, FYVE1/FREE1 may play a role in phagophore maturation or closing.
587 Another hypothesis argues for an indirect role of the ESCRT and retromer complexes in
588 autophagy. Indeed, SNARE proteins, necessary for autophagosome fusion with the vacuole,
589 need to be properly sorted to the tonoplast. It is therefore possible that the *fyve1/free1*
590 phenotype results, at least in part, of a miss sorting of SNARE proteins (50).

591

592 **6.3. PIPs and vacuole morphology**

593 Mutant for the retromer and the ESCRT complexes present small unfused vacuoles (22, 23,
594 45, 54, 55). This phenotype is also found with the loss-of- function of VTI11, a SNARE
595 protein involved in the docking and fusion of MVB with the tonoplast (124). It is suggested
596 that the PI3P-dependent protein sorting is important for the proper localization of SNARE
597 proteins and thus vacuole fusion. Moreover, the vacuole phenotype of *vti11* mutant can be
598 rescued by inhibition of PI3K activity suggesting a role of PI3P in fusion of homeotic

599 vacuoles (147). The homotypic fusion and vacuolar protein sorting (HOPS) tethering complex
600 is required for vacuole morphology (12). VACUOLAR PROTEIN SORTING33 (VPS33) and
601 VPS45, two HOPS complex members, binds phosphoinositide in vitro and localize to the
602 vacuole in a PI3P-dependent manner (12). SAC2, SAC3, SAC4 and SAC5 are likely
603 PI(3,5)P₂ 5-phosphatases that localize at the tonoplast and could hydrolyse the incoming
604 PI(3,5)P₂ from MVB into PI3P (87) (Figure 7). Loss-of-function and overexpression of these
605 SAC proteins lead to abnormal vacuolar morphology consistent with deficit in vacuole fusion
606 due to lack of PI3P (87). PI4P is also involved in the morphological changes of the vacuole
607 that are regulated by auxin in the root (69, 106). However, the molecular mechanism
608 connecting PI4P to vacuole morphology are so far unknown.

609

610

611 **7. CONCLUSIONS, PERSPECTIVES AND FUTURE CHALLENGES**

612 Many aspects of the role and operation of anionic lipids along the endomembrane system are
613 conserved among eukaryotes, including many of the enzymes. However, the anionic lipid
614 distribution of plant cells present several specificities compare to yeast or animal cells,
615 starting with the high and low abundance of PI4P and PI(4,5)P₂ at the PM, respectively. Thus,
616 the establishment of the anionic lipid distribution in plant is still not fully understood.
617 Moreover, the mechanisms by which this distribution is maintained despite the constant
618 exchanges of membrane between compartments due to vesicular trafficking must be explored.
619 This includes the coupling between the enzymes that produce anionic lipids and the ones that
620 convert or degrade them. Additionally, links or compensatory effects could exist between the
621 different lipid pathways at the level of enzymatic activity, membrane recruitment or
622 expression. Recently, MCS appeared as a new path of lipids exchanges independent from

623 vesicular trafficking. The mechanisms, the nature of the exchanged lipids as well as relevance
624 for the cell and plant life remains to be fully appreciated.

625 The role of anionic lipids in the regulation of membrane trafficking has been clearly
626 established in all eukaryotes. The sorting of many of the proteins involved in membrane
627 trafficking depends on anionic lipids. At the same time, many of the proteins involved in
628 anionic lipids pathways are membrane-associated proteins. Thus, their sorting depends of
629 vesicular trafficking. The constant flow of membrane trafficking and the interconnections
630 between lipids and protein sorting make it difficult to sort the direct and indirect
631 consequences of lipid perturbation using loss-of-function strategy only. The situation is
632 further amplified by the fact that anionic phospholipids are highly interconnected, and
633 perturbation of one lipid is likely to impact others. Similarly, although anionic lipids are of
634 major importance for many developmental and physiological responses, including stress,
635 cytokinesis or cell differentiation, the chain of events explaining the observed phenotype is
636 often not solved. New live imaging and inducible perturbation technics to study lipid
637 dynamics in its physiological context are therefore urgently needed in order to untangle direct
638 from indirect effects of anionic phospholipids. Similarly, it will also be key to uncover and
639 functionally characterized anionic lipid effectors (i.e. proteins that interact with anionic
640 phospholipids for function and localization) as most of them are plant specific proteins.

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644 • **Summary Points list:** *highlight the central points of your review (as many as 8), in*
645 *complete sentences; insert above the Acknowledgments and/or Literature Cited section*
646

- 647 1. Anionic lipids influence the physicochemical properties of cell membranes, such as
648 their surface charges, curvature, packing and nanoscale organization.
- 649 2. Anionic lipids define an “electrostatic membrane territory” in plants, which
650 corresponds to post-Golgi membranes.
- 651 3. Enrichment of specific anionic lipid combination in different compartments
652 participates to the establishment of organelle identity and the specific recruitment of
653 proteins.
- 654 4. The distribution of anionic lipids inside a membrane is not homogeneous in term of
655 lateral segregation and membrane leaflet accumulation. Anionic lipids, together
656 with other lipids and proteins, organize in nanoclusters and are mostly oriented
657 toward the cytosolic leaflet.
- 658 5. Most of the enzymes related to anionic lipids are conserved among eukaryotes,
659 while anionic lipid effectors tend to be plant specific.
- 660 6. Anionic lipids can be transported either via vesicular trafficking or via lipid
661 transport proteins at MCS. Conversely, anionic lipids are themselves master
662 regulators of both vesicular trafficking and MCS.
- 663 7. Phosphoinositide kinases and phosphatases allow the fast production and
664 interconversion of PIP, which ensure relatively stable patterns of phosphoinositide
665 subcellular accumulation despite the constant flow of anionic lipids between
666 organelles.
- 667 8. Anionic lipid repartition is a dynamic feature of the cell and can change according
668 to its physiological (infection, symbiosis, stress...) or developmental (**polar**
669 **growth**, cytokinesis, aperture establishment, casparian strip formation, trichome...)
670 status.

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- **Future Issues list:** *note where research may be headed (as many as 8), in complete sentences; insert above the Acknowledgments and/or Literature Cited section*
 1. How the cell maintains the lipid homeostasis at both cellular and developmental levels? Addressing this question will require a deep understanding on how lipid production and degradation/consumption are coupled and regulated, and how each anionic lipid may work in functionally and physically independent pools within the same cells.
 2. Most enzymes involved in anionic lipid homeostasis have been described, but how their activity is regulated is still unknown. The role of post-translational modifications (e.g. phosphorylation) has been spear headed by Ingo Heilmann's group and this is an area of research that is likely to expand in the future (33, 80).
 3. It is difficult to determine the direct or indirect consequences of the perturbation of an anionic lipid in a given compartment. A key future research direction will be to address what is the chain of events linking defects in anionic lipids to the observed cellular or whole plant phenotypes? One of the key to unlock such question will be the development of fast inducible systems to perturb anionic phospholipids.
 4. What are the feedbacks and crosstalk between anionic lipids and the other membrane lipids, including phospholipids, sterol and sphingolipids? In particular, what is the importance of the membrane bilayer asymmetry in the way lipid pools contact and regulate each other, and what is the contribution of the cell wall/PM/cytoskeleton continuum in lipid interactions across the membrane bilayer?
 5. Compartment morphodynamics is a highly complex system. Understanding how anionic phospholipids contribute to membrane morphodynamics will require the development of minimal membrane systems in vitro and computer simulation together with continued efforts in molecular genetics and cellular biology.
 6. Anionic lipids are key molecules for membrane contact sites, yet the importance and mechanisms of MCS formation, regulation and function are still largely enigmatic in plants. It will be particularly interesting to investigate membrane contacts which include plant specific organelles, such as the chloroplast, tonoplast, plasmodesmata or TGN.
 7. The development of anionic lipid sensors compatible with live imaging and super-resolution microscopy techniques has allowed analysing the function of anionic lipids with unprecedented spatial and temporal resolution. However, given the current technical revolution in the field of super-resolution microscopy, we expect this line of research to rapidly grow in the future.
 8. A bottleneck in the field is our ability to biochemically detect the different anionic phospholipid molecular species with subcellular resolution. Efforts should be given to improve the current methods of anionic lipid identification by mass spectrometry and cellular fractionation.

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714

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- **Reference Annotations:** *brief (15 words maximum) explanation of citations' importance (as many as 10); insert below the Literature Cited section*
 1. **Brault et al., 2019:** Proposes MCTP proteins, a class of putative PS/PI4P binding proteins, as tethering factors at PD-EPCS.
 2. **Gronnier et al., 2017:** Describes how anionic lipids and sterol influence REMORIN conformation, localization and activity by forming nanoclusters.
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 4. **Lin et al., 2019:** Establishes that PI4P production at the cell plate contributes to cytokinesis and phragmoplast dynamics.
 5. **Kang et al., 2011:** Uses electron tomography to reveal distinct TGN subdomains with PI4KB1 highlighting the secretory vesicles subdomain.
 6. **Lee et al., 2019:** Proposes that S-EPCS dynamics is regulated by PI(4,5)P₂-SYT interactions and is remodelled during osmotic stresses.
 7. **Platre et al., 2018:** Proposes the concept of an “electrostatic membrane territory” in plants, which corresponds to post-Golgi membranes.
 8. **Steffano et al., 2018:** Identifies that plant VAP27 proteins directly interact with anionic phospholipids and regulate endocytic trafficking.
 9. **Simon et al., 2016:** Establishes the importance of membrane electrostatics and PI4P in defining the plant PM identity.
 10. **Ghosh et al., 2015:** Proposes a model for Sec14-nodulin function as PI-kinase helper protein mediating PI(4,5)P₂ polar localization.

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- 1176 • **Sidebar** (50 words minimum, 200 words maximum) briefly discussing a fascinating
1177 adjacent topic. Please give the sidebar a title and insert it below the Literature Cited
1178 section, but be sure to call out the sidebar in text; it will be typeset near the section
1179 containing the callout. The sidebar cannot contain figures or tables.

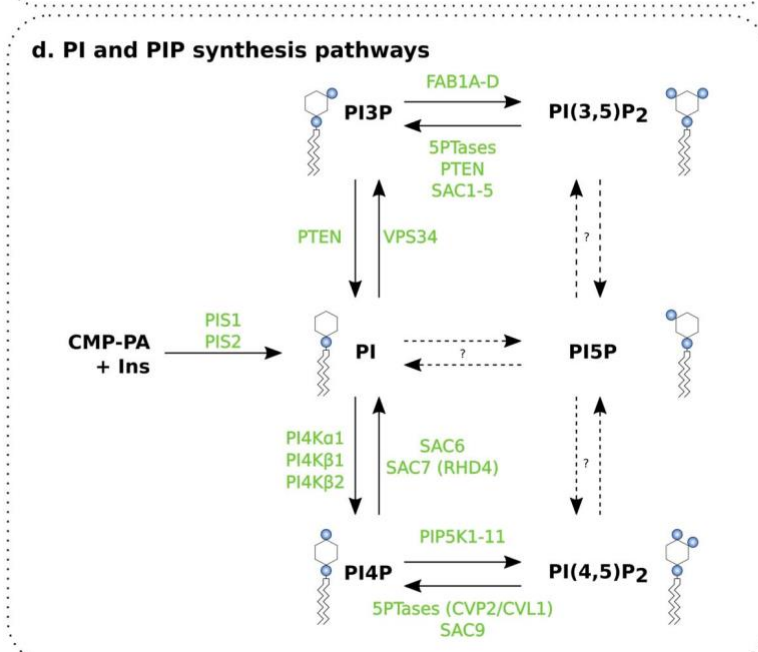
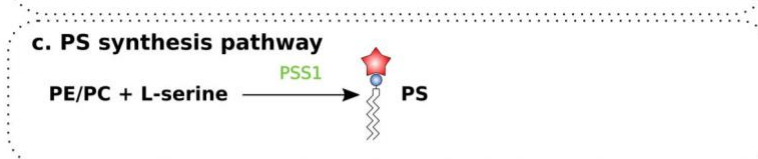
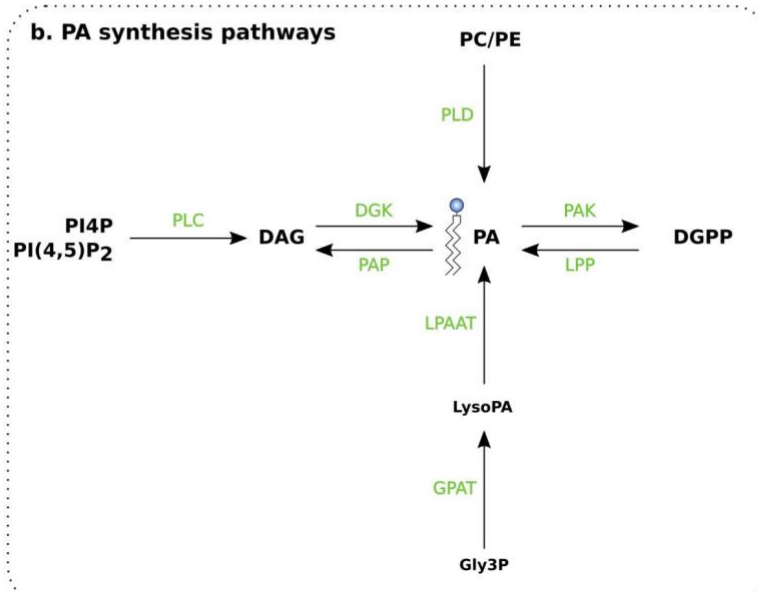
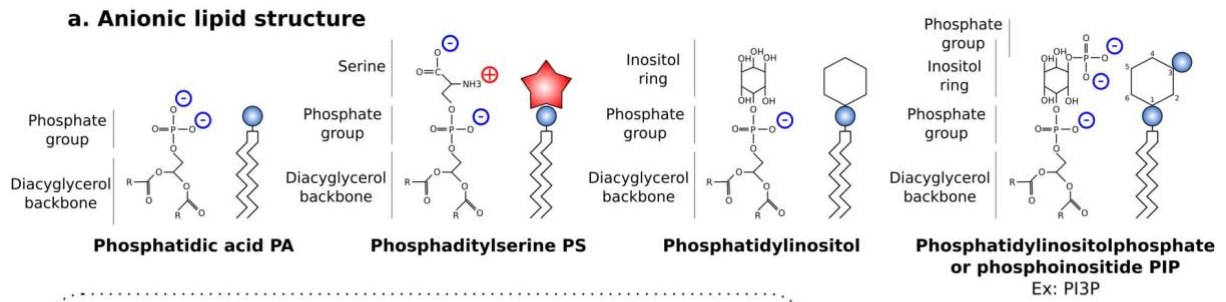
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1181 **Lipid molecular species and lipid packing defects (7):** Anionic lipids are defined by their
1182 head group. However, they are also constituted of two fatty acid chains that can vary in length
1183 and unsaturation degree. These parameters influence membranes physical properties, notably
1184 their fluidity and curvature, and thus, the recruitment and dynamics of membrane associated
1185 proteins. In addition to membrane charge and curvature, another physical feature of the
1186 membrane is of particular interest for protein targeting and is directly influenced by fatty acid
1187 composition. Indeed, the density of lipids in the membrane is not homogeneous. The regions
1188 with low density are called lipid-packing defects. Membrane curvature and conical shape
1189 lipids (which can be linked to the degree of unsaturation) can induce packing defects. In this
1190 region, the hydrophobic tails of the lipids are transiently exposed. Membrane associated
1191 proteins can recognize and target specifically membrane with packing defects by inserting
1192 hydrophobic residues into the membrane. In animal cells, high packing defects are found in
1193 ER and cis-Golgi membrane while TGN and PM present low level of packing defects except
1194 in highly curved-membranes. The relevance of lipid packing defects for protein recruitment in
1195 plants is largely unexplored.

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- 1197 • **Terms and Definitions list:** *provide definitions for as many as 20 of the most important*
 1198 *abbreviations or key terms, limited to 20 words maximum; insert below Literature Cited*
 1199 *section*
- 1200 **Endomembrane system:** membranes system connected directly or through vesicular
 1201 transport including nuclear envelop, ER, Golgi, PM, endosomes/vesicles,
 1202 lysosomes/tonoplast, but not chloroplasts/mitochondria.
- 1203 **Lipid Binding Domain (LBD):** Protein domain that selectively recognize and target
 1204 membranes via direct interactions with lipid(s) either via specific, non-specific and/or
 1205 multivalent interactions.
- 1206 **Electrostatic field:** Field created by electric charges that exert forces able to attract or repel
 1207 other charges entering the field.
- 1208 **Electrostatic membrane territory:** Within the endomembrane system, corresponds to
 1209 negatively-charged membranes, whose cytosolic leaflet harbours anionic phospholipids (Post-
 1210 Golgi compartments), as opposed to neutral membranes (ER-derived).
- 1211 **Nanodomain or nanocluster:** Small membrane zone below 100 nm, enriched in one or
 1212 several lipid species or proteins.
- 1213 **Membrane Contact site (MCS):** Close (below 30nm) and stable apposition via tethering
 1214 elements of two membranes allowing inter-organelle communication, without membrane
 1215 fusion.
- 1216 **Protein sorting:** Delivery process of proteins to their appropriate cellular destination, based
 1217 on information contained in the protein sequence and/or structure.
- 1218 **Polar secretion:** Delivery of proteins or material steered in one or several specific directions
 1219 within the cell.
- 1220 **Cell plate:** Organelle formed by delivery of cell wall and membranes by Golgi-derived
 1221 vesicles at the plane of cell division in plants.
- 1222 **trans-Golgi Network/Early endosome (TGN/EE):** Golgi-derived but Golgi-independent
 1223 compartment involved in secretion, which also serves as early endosome in plants and
 1224 involved in endocytic trafficking.
- 1225 **Secretory vesicles (SV):** specific subdomain of the TGN/EE made of uncoated vesicles
 1226 involved in secretion.
- 1227 **Multivesicular bodies (MVB):** late endosome characterized by their spherical morphology,
 1228 and containing intraluminal vesicles destined for vacuolar degradation.
- 1229 **Plasmodesmata (PD):** pores that connects plant cells by passing through their cell wall
 1230 thereby allowing cytoplasmic, PM and ER continuity from cell-to-cell.
- 1231 **Phagophore:** a double membrane that encloses and isolates cytoplasmic components during
 1232 autophagy.
- 1233 **Coincidence binding:** Recruitment of a protein at a specific membrane by interaction with

- 1234 several membrane landmarks, which together provides high targeting specificity.
- 1235 **Lipid transfer protein (LTP):** Proteins responsible for shuttling lipids between different
1236 membranes via non-vesicular trafficking.
- 1237 **Flippase:** membrane transporters which translocates phospholipids from the luminal to the
1238 cytosolic membrane leaflet, thereby maintaining lipid asymmetry across the bilayer.
- 1239 **Clathrin-coated vesicle (CCV):** vesicles decorated by a membrane-deforming Clathrin coat,
1240 involved in many vesicular-mediated trafficking pathway within the cell.
- 1241 **Clathrin-coated pit (CCP):** clathrin-coated vesicles at the PM, corresponding to the initial
1242 step of membrane deformation during endocytosis.
- 1243 **Tethering complex:** protein complex which brings together two membranes, either
1244 transiently before fusion or in a more sustained manner at contact sites.
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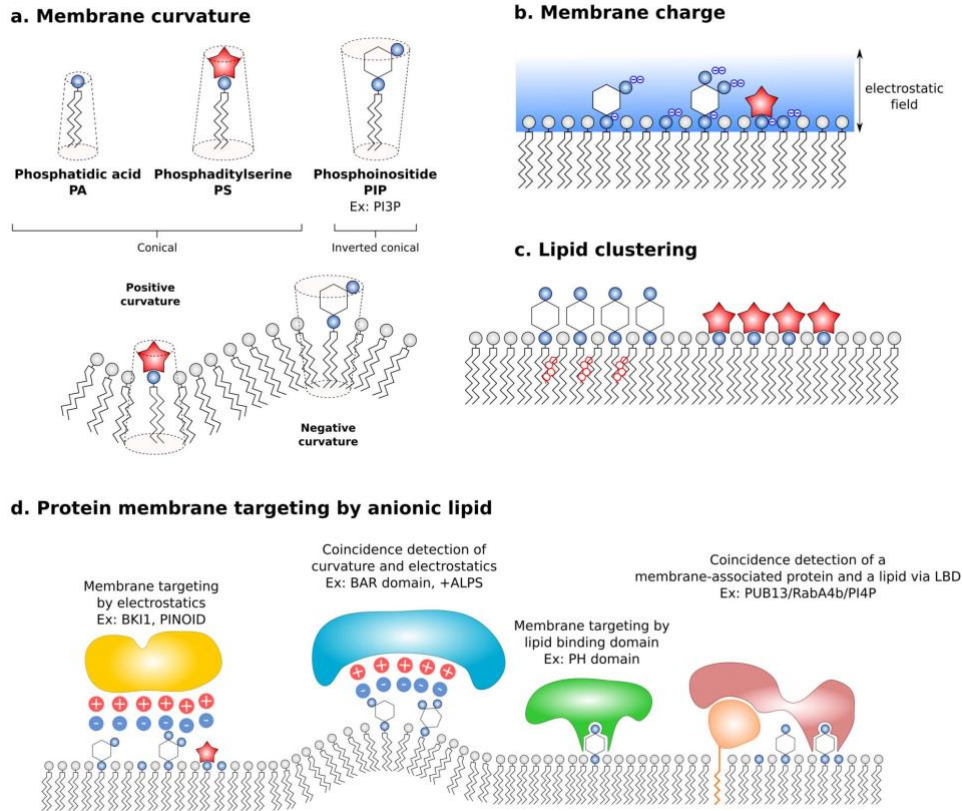


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Figure 1: Anionic lipids.

(a) Skeletal formula and schematic representation of anionic lipids: phosphatidic acid (PA), phosphatidylserine (PS), phosphatidylinositol (PI) and phosphoinositide (PIP). Anionic lipids

1253 are composed of a diacylglycerol backbone attached to a phosphate group. PS and PI display a
1254 serine (star) and an inositol ring (hexagon), respectively, linked to the glycerol by a
1255 phosphodiester linkage. PI can be phosphorylated in position 3, 4 and 5 to form 7 different
1256 PIPs: Phosphatidylinositol 3-phosphate (PtdIns3P or PI(3)P), Phosphatidylinositol 4-
1257 phosphate (PtdIns4P or PI(4)P), Phosphatidylinositol 5-phosphate (PtdIns5P or PI(5)P),
1258 Phosphatidylinositol 3,4-bisphosphate (PtdIns(3,4)P₂ or PI(3,4)P₂), Phosphatidylinositol 3,5-
1259 bisphosphate (PtdIns(3,5)P₂ or PI(3,5)P₂), Phosphatidylinositol 4,5-bisphosphate
1260 (PtdIns(4,5)P₂, PI(4,5)P₂ or PIP₂), Phosphatidylinositol 3,4,5-trisphosphate (PtdIns(3,4,5)P₃
1261 or PI(3,4,5)P₃). Pathways for PA (**b**), PS (**c**), PI and PIP (**d**) production and degradation. PC,
1262 phosphatidylcholine; PE, phosphatidylethanolamine; DAG, diacylglycerol; DGPP,
1263 Diacylglycerol pyrophosphate; Gly3P, Glycerol 3-phosphate; PLC, Phospholipase C; PLD,
1264 Phospholipase D; DGK, Diacylglycerol kinase; PAP, Phosphatidate phosphatase; PAK,
1265 PA Kinase; LPP, lipid-phosphate phosphatase; LPAAT, lyso-phosphatidic acid
1266 acyltransferase; GPAT, Glycerol-3-phosphate acyltransferase; PSS1, PS Synthase1; CMP-
1267 PA, Cytidine Monophosphoryl-Phosphatidic Acid; Ins, Inositol; SAC, SUPPRESSOR OF
1268 ACTIN; PTEN, PHOPHATASE AND TENSIN Homolog; FAB1, FORMATION OF
1269 APLOID AND BINUCLEATE CELLS 1; RHD4, ROOT HAIR DEFECTIVE 4; CVP2,
1270 COTYLEDON VASCULAR PATTERN 2; CVL1, CVP2-LIKE1; PI4K, PI 4-Kinases.
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Figure 2: Physicochemical properties of membranes and membrane targeting by anionic lipids.

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Anionic lipids can confer several properties to the membranes. **(a)** Curvature: The geometry of the head group of anionic lipids gives a conic shape to the lipid which influences positively (in the case of PIP) or negatively (in the case of PA and PS) the curvature of the membrane.

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(b) Electrostatics or membrane surface charge: Accumulation of anionic lipids confers a negative charge to the membrane leading to an electrostatic field. **(c)** Clustering: Anionic lipids can cluster together to form nanodomains in which one or several lipid species accumulate.

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(d) These properties can directly participate in the recruitment of proteins to the membrane through electrostatic interactions between the negative charges of the lipids and the positive charged amino acids, curvature recognition or lipid-binding domain that targets a specific lipid.

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In some cases, proteins can be recruited to the membrane by coincidence detection of several membrane features (electrostatics and curvature, or an anionic lipid and a membrane-associated protein for instance).

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Note that for clarity purpose only the cytoplasmic membrane leaflet was drawn. BK11, BRI1 KINASE INHIBITOR 1; BAR, Bib-Amphiphysin-Rsv; +ALPS, Amphipathic Lipid Packing Sensor; PH, Pleckstrin Homology; PUB13, PLANT-U-BOX13; PA, Phosphatidic Acid; PS, Phosphatidylserine; PIP, Phosphoinositide; PI3P, Phosphatidylinositol 3-phosphate; PI4P, Phosphatidylinositol 4-phosphate.

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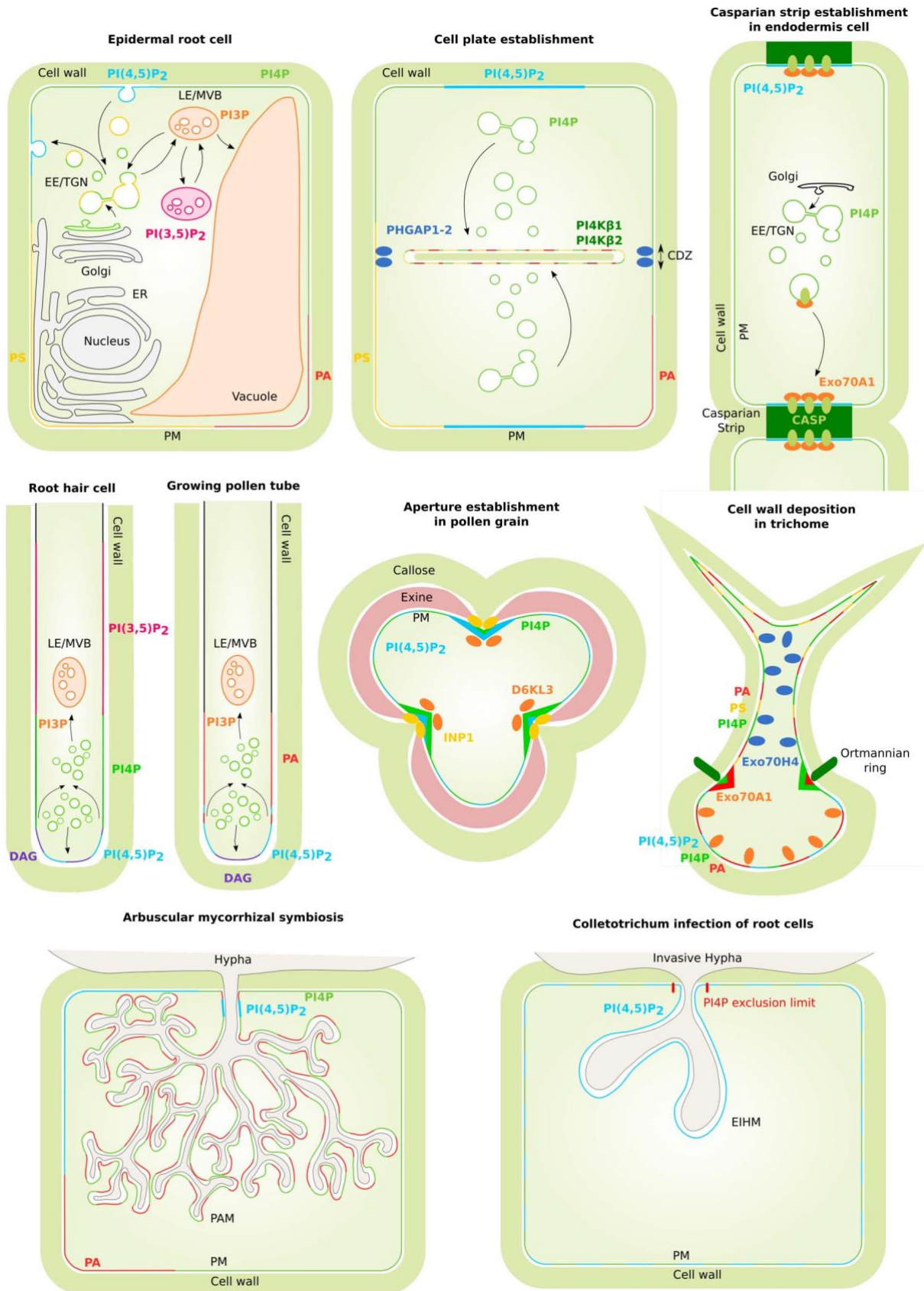
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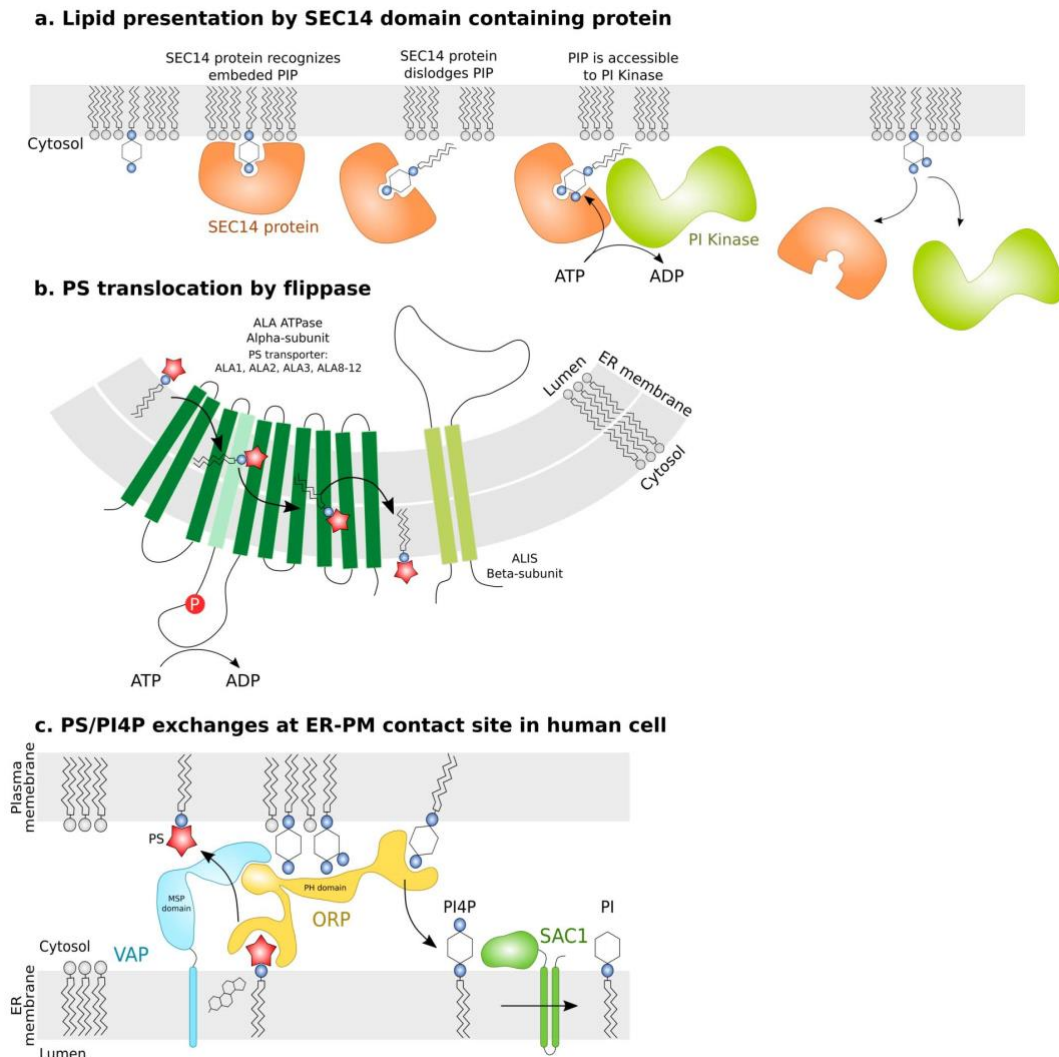
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Figure 3: Anionic lipid distribution in plant cells.

The localization of anionic lipids in between the different cellular compartment can change depending of the developmental and physiological context. Here, the distribution of anionic lipids in epidermal root cells is first represented. Anionic lipids can accumulate in specific

1298 zone of the PM during polarized cell growth (pollen tube, root hair cell for instance), when
1299 interacting with another organism (symbiosis, infection), to determine the position of
1300 developmental structure (aperture of the pollen grains, casparian strip, trichomes). PM,
1301 plasma Membrane; EE/TGN, Early Endosome/Trans-Golgi Network; LE/MVB, Late
1302 Endosome/Multi Vesicular Bodies; ER, Endoplasmic Reticulum; PAM, PeriArbuscular
1303 Membrane; EIHM, Extra Invasive Hyphal Membrane; PA, Phosphatidic Acid; PS,
1304 Phosphatidylserine; PI3P, Phosphatidylinositol 3-phosphate; PI4P, Phosphatidylinositol 4-
1305 phosphate; PI(4,5)P₂, Phosphatidylinositol 4,5-bisphosphate; DAG, Diacylglycerol; PI4K,;
1306 PI4P Kinases; PHGAP, Pleckstrin Homology GTPase Proteins; D6KL3, D6 PROTEIN
1307 KINASE-LIKE3; INE1, INAPERTURATE POLLEN1; CASP, CASPARIAN STRIP
1308 MEMBRANE DOMAIN PROTEIN; Exo70, Exocyst Complex Component 70.
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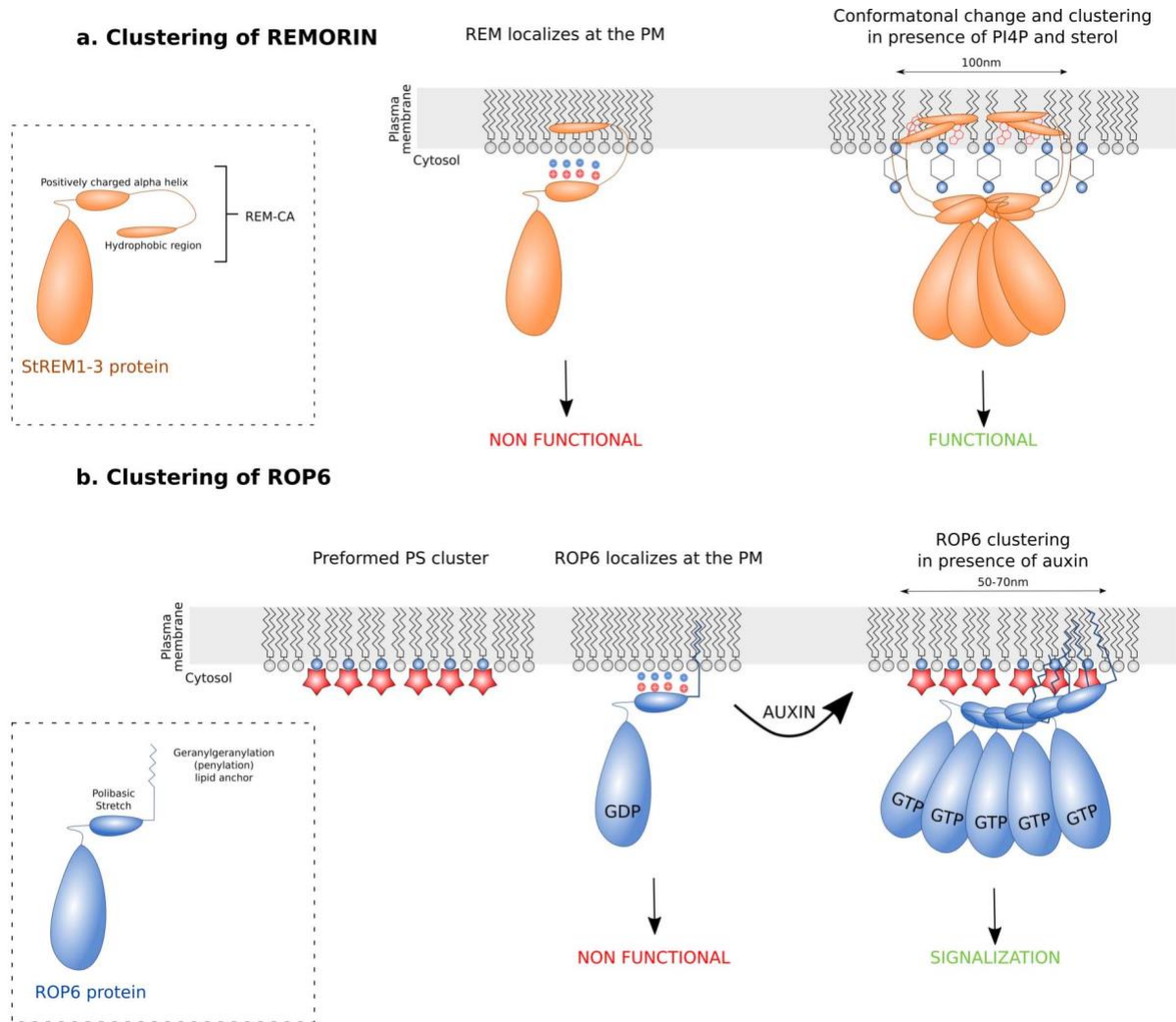


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Figure 4: Mechanisms of lipid presentation and transport.

(a) A mechanism of PIP presentation has been proposed to explain the high processive of PI-kinases. In this model, SEC14 protein digs up PI or PIP from the membrane and presents it to the PI-kinase for phosphorylation. (b) The translocation of PS from the luminal leaflet to the cytosolic leaflet of the ER membrane depends on flippase proteins composed of a alpha subunit called ALA which hydrolyses ATP and translocate PS and a beta-subunit called ALIS which specify the localization of the flippase at different membrane compartments and is essential for activity. (c) Lipid exchanges take place at membrane contact sites. In human, ORP5 and 8 tether the ER and the PM by direct interaction with the ER-resident protein VAP and the PM-localized lipid PI4P. ORP5/8 then transfer PS from the ER membrane to the PM via its lipid transfer domain and then counter transport PI4P to the ER. PI4P is then dephosphorylated by SAC1 in the ER membrane maintaining the PI4P gradient between the two membranes. Note that for clarity purpose in panel a and c only the cytoplasmic membrane leaflet was drawn. ER, Endoplasmic Reticulum; EPCS; ER Plasma membrane Contact Site; PS, Phosphatidylserine; PI, Phosphatidylinositol; PIP, Phosphoinositide; SEC14; ALA, aminophospholipid flippase; ALIS, ALA interacting beta-subunit; VAP, VAMP Associated Protein; SAC1, SUPPRESSOR OF ACTIN 1; ATP, Adenosine triphosphate; ADP, Adenosine diphosphate; ORP, OSBP-Related Protein; VAP, vesicle-associated membrane protein-associated proteins.

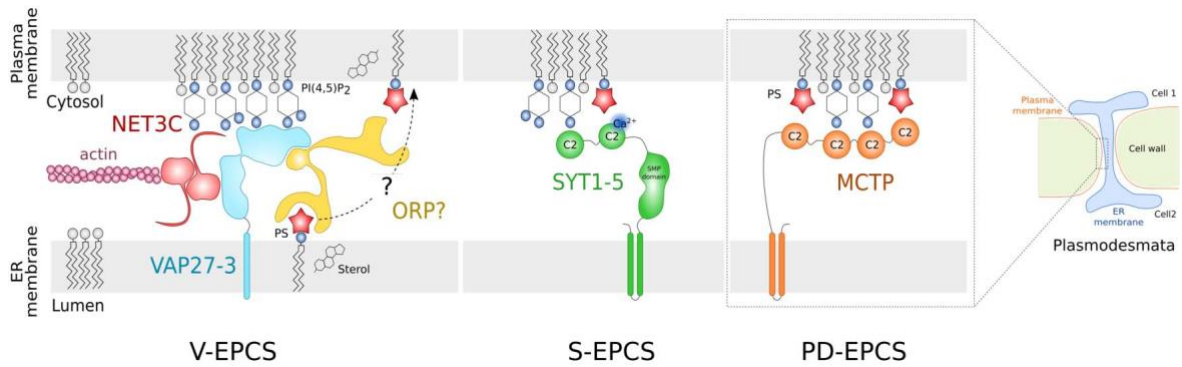
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Figure 5: Protein/lipid clustering into nanodomains

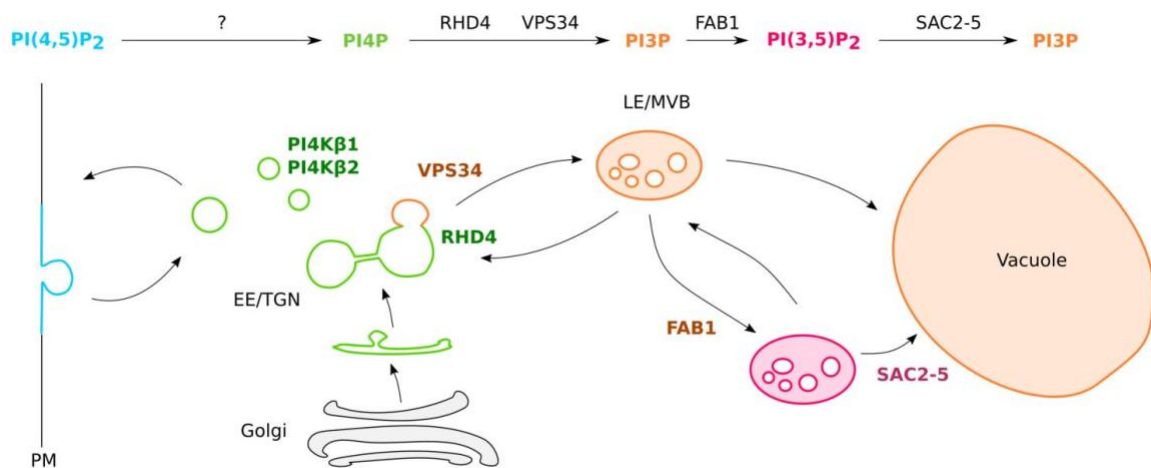
Lipids can accumulate in small regions of the membrane to form nanoclusters in which proteins are constrained. (a) StREM1.3 localizes at the PM through electrostatic interactions thanks to a positively charged alpha helix and hydrophobic interactions via a hydrophobic region that is embedded in the membrane. In presence of PI4P and cholesterol, StREM1.3 undergoes a conformational change that leads to its clustering. The distribution of StREM1.3 in cluster appears necessary to fulfill its function. (b) ROP6 localizes at the PM thanks to a polybasic patch and a lipid anchor. Upon auxin signaling, GTP-bound ROP6 relocates in pre-existing PS clusters. The clustering of ROP6 into PS nanodomains is necessary for ROP6 signaling. PM, Plasma Membrane; REM, REMORIN; ROP6, Rho-of-Plant 6; GDP, Guanosine diphosphate; GTP, Guanosine triphosphate; PS, Phosphatidylserine; PI4P, Phosphatidylinositol 4-phosphate.



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Figure 6: ER-PM Membrane Contact Sites in plant

Schematic representation of the three different classes of EPCS in plant and their relation with anionic lipids. Note that for clarity purpose only the cytoplasmic membrane leaflet was drawn. ER, Endoplasmic Reticulum; EPCS; ER Plasma membrane Contact Site; PD, Plasmodesmata; PS, Phosphatidylserine; PI(4,5)P₂, Phosphatidylinositol 4,5-bisphosphate; VAP27, VAMP Associated Protein 27; ORP, OSBP-Related Protein; NET3C, NETWORKED 3C; VAP27, vesicle-associated membrane protein-associated proteins; SYT, SYNAPTOTAGMINE; MCTP, MULTIPLE C2 AND TRANSMEMBRANE PROTEIN, SMP, Synaptotagmin-like mitochondrial-lipid-binding domain.



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Figure 7: Phosphoinositide cascade during endocytic trafficking to the vacuole

Kinases and phosphatases create a phosphoinositide cascade along the endocytic route. PM, plasma Membrane; EE/TGN, Early Endosome/Trans-Golgi Network; LE/MVB, Late Endosome/Multi Vesicular Bodies; PI3P, Phosphatidylinositol 3-phosphate; PI4P, Phosphatidylinositol 4-phosphate; PI(4,5)P₂, Phosphatidylinositol 4,5-bisphosphate; PI(3,5)P₂, Phosphatidylinositol 3,5-bisphosphate; PI4K., PI4P Kinases; RHD4, ROOT HAIR DEFECTIVE 4; FAB1, FORMATION OF APLOID AND BINUCLEATE CELLS 1; SAC, SUPPRESSOR OF ACTIN.