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Inhibition of phosphatidylinositol 3,5-bisphosphate production has pleiotropic effects on various membrane trafficking routes in Arabidopsis

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Phosphoinositides play an important role in various membrane trafficking events in eukaryotes. One of them, however, phosphatidylinositol 3,5-bisphosphate [PI(3,5)P2], has not been studied widely in plants. Using a combination of fluorescent reporter proteins and the PI(3,5)P2-specific inhibitor YM202636, here we demonstrated that in Arabidopsis thaliana, PI(3,5)P2 affects various membrane trafficking events, mostly in the post-Golgi routes. We found that YM201636 treatment effectively reduced PI(3,5)P2 concentration not only in the wild type but also in FAB1A-overexpressing Arabidopsis plants. In particular, reduced PI(3,5)P2 levels caused morphological dynamics of plasma membrane proteins, AUX1 and BOR1, with different trafficking patterns. Secretion and morphological characteristics of late endosomes and vacuoles were also affected by the decreased PI(3,5)P2 production. These pleiotropic defects in the post-Golgi trafficking events were caused by the inhibition of PI(3,5)P2 production. This effect is probably mediated by the inhibition of maturation of FAB1-positive late endosomes, thereby impairing late endosome function. In conclusion, our results imply that in Arabidopsis, late endosomes are involved in multiple post-Golgi membrane trafficking routes including not only vacuolar trafficking and endocytosis but also secretion.

Keywords: Arabidopsis thaliana • FAB1/PIKfyve • Phosphatidylinositol 3,5-bisphosphate • Post-Golgi membrane trafficking routes • YM201636.

Abbreviations: AUX1, auxin 1; BOR1, high boron 1; DMSO, dimethylsulfoxide; ER, endoplasmic reticulum; FAB1, formation of haploid and binucleate cells 1; FYVE, FAB1 YPTB VAC1 EEAE; GFP, green fluorescent protein; mRFP, monomeric red fluorescent protein; MS, Murashige and Skoog; PIKfyve, a FYVE finger-containing phosphoinositide kinase; PI3P, phosphatidylinositol 3-phosphate; PI(3,5)P2, phosphatidylinositol 3,5-bisphosphate; TGN, trans-Golgi network; TLC, thin-layer chromatography; VAMP727, vesicle-associated membrane protein 727; WT, wild type; YFP, yellow fluorescent protein. Sequence data from this article can be found in the Arabidopsis Information Resource (http://www.arabidopsis.org/) under the following accession numbers: AUX1 (At2g38120), AtVAM3/SYP22 (At5g66860), BOR1 (At2g47160), FYVE1 (At1g20110), FAB1B (At3g14270), FAB1A (At4g33240) and UBQ10 (At4g05320).

Introduction

Membrane trafficking in eukaryotes represents the process of transport of proteins and lipids from the endoplasmic reticulum (ER) to various membrane organelles including the Golgi apparatus, trans-Golgi network (TGN), endosomes, vacuoles or the plasma membrane, or the transport of secretory vesicles to the extracellular space via vesicular traffic underlying various biological processes. In this process, newly synthesized proteins in the ER are passing through the Golgi apparatus, then cargo proteins are sorted into the vacuolar sorting or secretory pathways in the TGN (Jahn et al. 2003, Bonifacino and Glick 2004). In mammalian cells, the TGN is usually localized to the trans-most side of the Golgi apparatus; however, in plants, the TGN not only overlaps the Golgi apparatus but also exists in the form of independent organelles dispersed throughout the cytoplasm (Uemura et al. 2004, Kang et al. 2011). In the plant secretory pathway, TGN-derived secretory vesicles form clustered structures, termed secretory vesicle clusters (Toyooka et al. 2009) or secretory vesicles released from the TGN (Staehelin and Chapman, 1987 Winter et al. 2007). Secretory vesicle clusters or secretory vesicles move directly to and fuse with the plasma membrane in various dividing and growing plant cells. In the vacuolar sorting pathway, cargo proteins use at least three distinct routes: (i) the RAB5/RAB7-dependent route via late endosomes; (ii) the multivesicular body/AP-3-dependent route; and (iii) the RAB5-dependent AP-3-independent route (Ebine et al. 2014). Morphologically and immunocytochemically, secretory vesicle clusters and secretory vesicles are clearly distinct from multivesicular bodies, suggesting that the plant secretory pathway never passes through multivesicular bodies to the plasma membrane (Kang et al. 2011). Nonetheless, unique to plants, late-endosomal RAB5, Arabidopsis RAB5...
spatially mimic FAB1A/B conditional mutant phenotypes in Arabidopsis (Hirano et al. 2015).

Here, we studied how PI(3,5)P_2 affects various transport pathways using a combination of the FAB1-specific inhibitor YM201636 and various fluorescent protein markers for the post-Golgi membrane trafficking in Arabidopsis thaliana. We found that the PI(3,5)P_2 concentration that is reduced by YM201636 treatment impairs borate-dependent endocytosis and degradation of a plasma membrane protein, BOR1 (high boron 1), as well as the uptake of an exogenous auxin, secretion of a fluorescent secretory marker protein and morphological characteristics of late endosomes and the central vacuole. These results suggest that in plants, most post-Golgi membrane trafficking routes converge on FAB1-positive late endosomes.

Results

Balanced PI(3,5)P_2 levels are crucial for Arabidopsis growth

We previously reported that a FAB1/PIKfyve inhibitor, YM201636, specifically inhibits PI(3,5)P_2 production in wild-type (WT) Arabidopsis seedlings (Hirano et al. 2015). Here, we first evaluated the inhibitory effect of YM201636 in two FAB1A-overexpressing A. thaliana lines. As reported previously, the FAB1A-overexpressing lines #10 and #34 overexpress FAB1A at different magnitudes and show accompanying growth inhibition (Hirano et al. 2011). Measurement of PI(3,5)P_2 levels in these two lines by 32P-labeling and thin-layer chromatography (TLC) revealed that the concentration of PI(3,5)P_2 was significantly increased in the two FAB1A-overexpressing lines compared with WT Arabidopsis (37.8% overexpression in line #10 and 107% overexpression in line #34 compared with the WT dimethylsulfoxide (DMSO) control), without affecting the level of other phospholipids (Supplementary Fig. S1). YM201636 (1 μM) decreased PI(3,5)P_2 levels by 50–80% (by 66.9% in the WT, by 76.1% in line #10 and by 81.1% in line #34; Fig. 1A). The growth inhibition of root length of the FAB1A-overexpressing line #34 was suppressed by treatment with YM201636 in a dose-dependent manner (Fig. 1B). Because we previously...
showed that the loss and gain of FAB1 function cause the same growth defect in Arabidopsis (Hirano et al. 2011), the present data indicate that balanced PI(3,5)P₂ levels are crucial for proper Arabidopsis growth.

Exogenous auxin uptake is reduced by YM201636 treatment

Previously, we reported that exogenous non-penetrating auxin-induced lateral root formation is inhibited by the reduction in FAB1 expression, suggesting that the influx carrier-dependent auxin uptake is impaired by inhibition of PI(3,5)P₂ synthesis (Hirano et al. 2011). Therefore, we next tested whether exogenous non-penetrating auxin uptake is also affected by YM201636. To visualize auxin uptake, Arabidopsis seedlings with the DR5rev:GFP auxin reporter line were treated with 1 μM non-penetrating auxin, i.e. IAA, in the presence of 1 μM YM201636. In the absence of exogenous IAA, the intensity of green fluorescent protein (GFP) fluorescence in the root tip region was unchanged in the presence or absence of YM201636 (Fig. 2A, B). In contrast, strong GFP fluorescence was detected in whole-root tissues grown on a medium containing IAA (Fig. 2C) although GFP fluorescence was significantly decreased when the seedlings were grown on a medium containing 1 μM YM201636, even though 1 μM IAA was exogenously administered (Fig. 2D). Conditional knockdown of FAB1/B genes gave similar results (Supplementary Fig. S2). These findings suggest that uptake of exogenous auxins is severely impaired by inhibition of PI(3,5)P₂ synthesis.

We hypothesized that the PI(3,5)P₂-dependent changes in auxin uptake might be caused by a change in the plasma membrane localization of the auxin influx carrier protein, auxin 1 (AUX1). To test this hypothesis, we analyzed the localization of the AUX1–yellow fluorescent protein (YFP) fusion protein in the root tip region in the presence and absence of YM201636. As shown in Fig. 2E and F, 5 h treatment with YM201636 dramatically decreased the intensity of AUX1–YFP fluorescence on the plasma membrane. To determine whether this decrease in AUX1–YFP fluorescence was due to proteasomal degradation or to endocytic retrieval from the plasma membrane, we treated the cells with a proteasome inhibitor, MG132 (6 h, 50 μM) or a V-ATPase inhibitor, concanamycin A (1 h, 2 μM). The YM201636-dependent decrease in AUX1–YFP fluorescence was not affected by MG132 treatment (Fig. 2G, R) but was abrogated by concanamycin A (Fig. 2H, R). We observed the same results in FAB1/A/B-artificial microRNA (amiRNA) plants (Supplementary Fig. S3). In the presence of YM201636, AUX1–YFP was internalized and formed punctate structures beneath the plasma membrane after 2.5 h incubation (Fig. 2L–N), then the structures disappeared after 5 h incubation (Fig. 2O–Q). Next, we measured the AUX1 mRNA expression level in 5-day-old WT seedlings after YM201636 treatment and found that AUX1 mRNA expression did not change after YM201636 treatment (Fig. 2S), suggesting that the YM201636-dependent inhibition of AUX1–YFP fluorescence does not take place at the transcriptional level. Because concanamycin A is known to block the endocytic transport pathway to the tonoplast from the TGN (Dettmer et al. 2006), the YM201636-dependent sequestration of AUX1–YFP is likely to be blocked in the TGN. Taken together, these results indicated that YM201636-induced down-regulation of AUX1 might be mediated by endocytosis and is followed by degradation in the vacuole.

PI(3,5)P₂ regulates degradation and expression of BOR1

Boron (B) is an essential micronutrient for plants. Excess B is toxic, but B homeostasis is important for plants (Sharrocks 1997). B is effectively taken up by plants through two distinct B transporters: BOR1 and nodulin-26-like major intrinsic protein (NIP5;1). BOR1 and NIP5;1 are an efflux-type and an influx-
type B transporter, respectively, and are polarly localized to the inner and outer plasma membrane domain of root epidermal cells. The DRSrevGFP transgenic line was grown on the medium in the presence (B, D) or absence (A, C) of YM201636 for 5 d, and then was incubated with (C, D) or without (A, B) 1 μM IAA for 6 h. The fluorescence of GFP was examined using confocal laser scanning microscopy. The letters v and c in the images denote vascular bundle and columella cells, respectively. Five-day-old seedlings of AUX1–YFP-expressing plants were treated with 0.01% DMSO (E, F), 50 μM MG132 for 5 h (G) or 2 μM concanamycin A for 1 h (H), and then the samples were incubated with 1 μM YM201636 for 5 h (F–H). For the FM4-64 labeling experiment, 5-day-old seedlings expressing AUX1–YFP were labeled with 2 μM FM4-64 for 5 min in the presence (L–Q) or absence (I–K) of 1 μM YM201636, and then were examined after 2.5 h (I–N) or 5 h (O–Q) by confocal laser scanning microscopy. The scale bar = 10 μm. (R) The fluorescence intensity of the root tip region of the AUX1–YFP line (n > 12) was measured by means of the ImageStudio software. (S) Expression of AUX1 mRNA without or with YM201636 was measured by real-time RT–PCR. The bars represent the mean ± SD (n = 8).

Fig. 2 Inhibition of FAB1 activity reduces the uptake of a non-penetrating auxin and alters the localization pattern of AUX1 in root epidermal cells. The DR5rev:GFP transgenic line was grown on the medium in the presence (B, D) or absence (A, C) of YM201636 for 5 d, and then was incubated with (C, D) or without (A, B) 1 μM IAA for 6 h. The fluorescence of GFP was examined using confocal laser scanning microscopy. The letters v and c in the images denote vascular bundle and columella cells, respectively. Five-day-old seedlings of AUX1–YFP-expressing plants were treated with 0.01% DMSO (E, F), 50 μM MG132 for 5 h (G) or 2 μM concanamycin A for 1 h (H), and then the samples were incubated with 1 μM YM201636 for 5 h (F–H). For the FM4-64 labeling experiment, 5-day-old seedlings expressing AUX1–YFP were labeled with 2 μM FM4-64 for 5 min in the presence (L–Q) or absence (I–K) of 1 μM YM201636, and then were examined after 2.5 h (I–N) or 5 h (O–Q) by confocal laser scanning microscopy. The scale bar = 10 μm. (R) The fluorescence intensity of the root tip region of the AUX1–YFP line (n > 12) was measured by means of the ImageStudio software. (S) Expression of AUX1 mRNA without or with YM201636 was measured by real-time RT–PCR. The bars represent the mean ± SD (n = 8).
grown on a 0.3–3.0 μM borate medium (Takano et al. 2005). At 3 μM borate, the fluorescence of BOR1 on the plasma membrane was unaltered in the presence or absence of YM201636 (Fig. 3C). Nevertheless, the amount of BOR1 on the plasma membrane was not changed at 30 μM borate when the seedlings were treated with 1 μM YM201636, although it decreased without YM201636 because BOR1 was degraded at the same borate concentration (Fig. 3D). In the presence of YM201636, endocytosis of a fluorescent endocytosis tracer, FM4-64, was strongly delayed, and this tracer never reached the central vacuolar membrane (Fig. 3E). In this condition, the mRNA expression of BOR1 in the presence of YM201636 was unchanged regardless of the presence of YM201636 (Fig. 3F). Thus, we concluded that PI(3,5)P2 regulates B-dependent BOR1 endocytosis and subsequent degradation in the vacuole through a FAB1-mediated endocytic pathway but not at the transcriptional level.

YM201636 inhibits protein secretion

Protein secretion plays pivotal roles in the assembly and modification of the plant cell wall and in various stress responses (Surpin and Raikhel 2004). In plants, the conventional secretion route to the plasma membrane is believed to go through the Golgi–TGN. In Arabidopsis, an alternative secretion pathway via multivesicular bodies/late endosomes was recently reported (Ebine et al. 2011). To test whether PI(3,5)P2 is involved in the protein secretion routes, localization of a fluorescent secretion marker, secGFP—which contains an N-terminal signal peptide and is secreted to the apoplast through the default secretory pathway (Batako et al. 2000, Zheng et al. 2004)—was used to determine whether the secretion process is affected by YM201636. In the absence of YM201636, weak secGFP fluorescence was observed only in the apoplastic space, indicating that secGFP is secreted from the cells normally (Fig. 4A, C). In the presence of YM201636, however, strong fluorescence of

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**Fig. 3** Sensitivity to a high concentration of borate is decreased by the inhibition of PI(3,5)P2 synthesis. Five-day-old seedlings of WT Arabidopsis grown on MGRL medium containing 0.3, 30 or 300 μM borate were transferred to the same MGRL medium in the presence or absence (Control) of 1 μM YM201636, and the root length (A) and the length of root hairs (B) were measured after 6 d. The data are presented as the mean ± SD of 20 seedlings (root length) or the 10 longest root hairs from 20 primary roots. Significant differences between seedlings incubated with or without YM201636 are indicated by an asterisk (Student’s t-test, \( P < 0.001 \)). Five-day-old seedlings of a BOR1–GFP-expressing plant grown on MGRL medium containing 3 or 30 μM borate were examined by confocal laser scanning microscopy with or without YM201636 treatment. Scale bars = 10 μm. (C and D). Endocytosis of FM4-64 was inhibited by incubation with YM201636. For the FM4-64 labeling experiment, 5-day-old seedlings of WT Arabidopsis were labeled with 2 μM FM4-64 for 5 min in the presence or absence of 1 μM YM201636; later, the plants were examined after 10 or 30 min by confocal laser scanning microscopy. Scale bars = 10 μm (E). Transcripts of BOR1 in WT seedlings grown on MGRL medium at different borate concentrations (0.3 and 30 μM) in the presence or absence of 1 μM YM201636 in the medium were analyzed by qRT-PCR. Bars represent the mean ± SD (n = 8) (F).
secGFP was observed in the cytosol in the form of complex membranous structures but was not observed in the apoplast (Fig. 4B, D). The internal membranous structures included tubular ER-like and punctate-endosome-like structures (Fig. 4B, D). The punctate structures were overlapping with the staining pattern of a Golgi marker, sialyltransferase (ST)—monomeric red fluorescent protein (mRFP) (Fig. 4E–G) and an late-endosome marker, mRFP–VAMP727 (Fig. 4H–J), suggesting that secGFP is accumulated in various single-membrane organelles in the secretory pathway. Similarly, conditional knockdown of FAB1A/B caused secretion defect of secGFP (Supplementary Fig. S4).

Therefore, we concluded that the default secretory pathway is severely impaired by inhibition of PI(3,5)P2 production.

YM201636 alters the morphological characteristics of late endosomes and vacuoles

In yeast, fab1 mutants show an enlarged vacuole phenotype (Gary et al. 1998, Morishita et al. 2002). Similarly, in mammalian cells that overexpress a dominant kinase-inactive mutant of PIKfyve, enlarged lysosomes are also observed (Ikonomov et al. 2001). Thus, a defect in PI(3,5)P2 production causes defects in the morphology of vacuolar/lysosomal compartments. To study the relationship between PI(3,5)P2 content and the vacuole morphology in Arabidopsis, the fluorescence patterns of a GFP-tagged vacuolar membrane marker, Arabidopsis vacuolar morphology 3 (AtVAM3)/syntaxin of plants 22 (SYP22)–GFP were examined in the presence and absence of YM201636. The vacuolar membrane structures clearly shrank and formed compact entities in the presence of YM201636 in epidermal cells (Fig. 5A–C) and cortical cells (Fig. 5D–F) of the root division zone. On the other hand, FAB1A–GFP-labeled late endosomes/multivesicular bodies mostly formed rounded structures in the presence of YM201636 (Fig. 6A–C), while the punctate fluorescence pattern of late-endosome/multivesicular body-localized GFP–FYVE1 was completely dispersed throughout the cytosol (Fig. 6D–F). Taken together, these data indicate that PI(3,5)P2 is important for the maintenance of not only late-endosomal structures but also central vacuole structures in Arabidopsis.

Discussion

Membrane dynamics of AUX1 and BOR1 are regulated differently by PI(3,5)P2

Our previous report revealed that non-penetrating auxin-dependent lateral root formation is severely inhibited by a knockdown or overexpression of FAB1A/B, suggesting that the expression and/or localization of an auxin influx transporter, AUX1, can be affected by abnormal FAB1A/B expression (Hirano et al. 2011, Hirano et al. 2011). In the present study, we demonstrated that the uptake of a non-penetrating auxin is...
strongly inhibited by YM201636 treatment. In the presence of YM201636, the AUX1–YFP fusion protein is internalized and probably degraded in the vacuole.

On the other hand, BOR1 internalization and subsequent degradation in the vacuole at higher B concentrations (Takano et al. 2010, Kasai et al. 2011, Scheuring et al. 2011) were strongly inhibited by YM201636 treatment at 30 μM borate. In contrast, at 0.3 μM borate, BOR1–GFP fluorescence was not significantly different from that in the control (Fig. 3C, D). We previously reported that FAB1 dysfunction delays endocytosis (Hirano et al. 2011). This delayed endocytosis was attributed to the maturation defect in late endosomes/multivesicular bodies caused by the decrease in PI(3,5)P2 content (Hirano et al. 2015). In this study, we also observed that the endocytosis process is severely impaired by YM201636 treatment (Fig. 3E). Given that the effect of YM201636 is the inhibition of the maturation of FAB1-positive endosomes thereby causing delayed endocytosis, the inhibition of BOR1 endocytosis by YM201636 may be mediated by the dysfunction of maturation of FAB1-positive endosomes, so that BOR1 can no longer be internalized and transported to the vacuole via the FAB1-positive late endosomes/multivesicular bodies.

AUX1, also a plasma membrane protein, behaved differently at low PI(3,5)P2 concentrations. Namely, YM201636 blocked the internalization of BOR1, while AUX1 was endocytosed and degraded. How can the differences in subcellular dynamics of these two proteins at low PI(3,5)P2 concentrations be explained? It is reported that AUX1 follows a trafficking pathway different from that of other polarized membrane proteins. For example, AUX1 dynamics show different sensitivity to inhibitors of trafficking and are independent of the endosomal trafficking regulator ARF-GEF, known as GNOM in Arabidopsis (Kleine-Vehn et al. 2006, Geldner et al. 2003). PIN2, but not AUX1 or PIN1, is transported through AtSNX1-containing endosomes, and AUX1 trafficking is not affected in either a snx1 or a vps29 mutant (Jaillais et al. 2006, Jaillais et al. 2007). Thus, there are multiple endocytosis and recycling pathways for plasma membrane proteins in Arabidopsis. Most probably, FAB1/PI(3,5)P2 is involved in the regulation of multiple endocytic pathways via distinct mechanisms.

The secretory pathway is affected by YM201636 treatment

Although newly synthesized secretory proteins are known to be transported from the ER through the Golgi apparatus to the TGN en route to the plasma membrane or to the extracellular medium (Richter et al. 2009), it is unknown whether the secretory pathway passes through late endosomes/multivesicular bodies. We found that the process of secretion of secGFP is inhibited by YM201636 (Fig. 4), suggesting that PI(3,5)P2-mediated membrane trafficking is involved in the default secretory process in Arabidopsis.

In plants, secretory traffic from the TGN to the plasma membrane is regulated by RABA4b and phosphatidylinositol-4 kinase β-1 (PI4Kβ-1). RABA4b and PI4Kβ-1 are co-localized to budding secretory vesicles in the TGN, and the pi4kb1pi4kb2 double mutant has aberrant sizes of secretory vesicles (Kang
et al. 2011). Furthermore, PI4P 5-kinases, PIP5K1 and PIP5K2, and their product, PI(4,5)P_{2}, are specifically enriched in the apical and basal polar plasma membrane domains, and PI(4,5)P_{2} influences polarization of PINs (auxin transporters) (Ischebeck et al. 2013, Tejos et al. 2014). We found that the secretion marker secGFP is down-regulated by YM201636 (Fig. 5), suggesting that PI(3,5)P_{2} also controls the secretory traffic. We previously reported that the loss of FAB1 function and inhibition of PI(3,5)P_{2} production cause a release of late-endosomal effector proteins, thereby impairing the early stage of late-endosome maturation (Hirano et al. 2015). Accordingly, the secretion defect caused by the inhibition of PI(3,5)P_{2} synthesis may result from the defect in the late-endosome maturation; therefore, the secretory route possibly passes through late endosomes in Arabidopsis.

### The defects in the vacuolar transport pathway and vacuolar structure

In yeast, FAB1 and PI(3,5)P_{2} regulate endosomal trafficking to the vacuole/lysosomes. PI(3,5)P_{2} is present on the external membrane of multivesicular bodies (Odorizzi et al. 1998). The yeast fab1 mutant shows enlarged vacuoles, with a defect in vacuolar acidification and osmoregulation. It also has a growth defect at elevated temperatures because of impairment of both the retrograde vesicle transport from vacuoles to the TGN and the anterograde pathway to the vacuole (Gary et al. 1998, Odorizzi et al. 1998). In Arabidopsis, the fab1a fab1b double mutant shows male gametophyte mortality. Mutant pollen grains have severe defects in vacuolar reorganization (Whitely et al. 2009), while a loss of FAB1 function impairs endomembrane homeostasis, including endocytosis, vacuole formation and vacuolar acidification (Hirano et al. 2011). Here, we found that YM202636 treatment diminished luminal vacuoles (Fig. 5) but caused circulation of FAB1-positive late endosomes/multivesicular bodies (Fig. 6A–C) and induced the release of GFP–FYVE1 from the endosome membrane (Fig. 6D–F).

The FAB1, YOTB, VAC1 and EEA1 (FYVE) domain-containing protein—FYVE1/FREE1—has been implicated in intracellular trafficking. FYVE1/FREE1 is localized to late endosomes and interacts with Src homology-3 domain-containing proteins. A T-DNA insertion mutant, fyve1/free1, shows abnormal vacuolar morphology where small fragmented vacuoles are interconnected, and is defective in ubiquitin-mediated protein degradation, vacuolar transport and autophagy (Gao et al. 2015, Kolb et al. 2015). Because we observed similar small vacuolar structures caused by the YM201636 treatment (Fig. 5), we assumed that the smaller vacuolar structure may be formed by a release of the FYVE1/FREE1 protein from the late-endosomal membrane because of lower PI(3,5)P_{2} concentrations.

Similar morphological defects in the vacuole and in late endosomes/multivesicular bodies were also reported in sand-1 (Singh et al. 2014) and after wortmannin treatment (Jaillais et al. 2006, Vermeer et al. 2006). Previously, we showed that FAB1, and/or its product PI(3,5)P_{2}, is involved in the early stages of late endosome/multivesicular body maturation, recruiting late-endosome effector proteins (Hirano et al. 2015). If the maturation of late endosomes/multivesicular bodies is inhibited by a reduction in PI(3,5)P_{2} concentration, then SAND-CCZ1-mediated Rab5 (ARA7 in Arabidopsis) to Rab7 (RABG3f in Arabidopsis) conversion may be stopped. Consequently, multiple membrane trafficking routes, including the recycling pathway of BOR1 and the secretion and vacuolar transport pathways, can be impaired. In the case of AUX1, alternative trafficking pathways rather than the late-endosome/multivesicular body-dependent pathway to the vacuole (Ebene et al. 2014) may be affected by a so far unknown PI(3,5)P_{2}-dependent mechanism (Fig. 7). Additional studies are needed to dissect the PI(3,5)P_{2}-mediated membrane trafficking pathways in plants.

### Materials and Methods

#### Plant growth conditions

The A. thaliana ecotype Col-0 served as the WT in all experiments in this study. The plants were grown under white light in a cycle of 16 h light and 8 h dark at 22°C on half-strength Murashige and Skoog (1/2 MS) medium or half-strength Murashige and Skoog medium with 4.5 mg L^{-1} of 2,4-D and 100 mg L^{-1} of 3,5-iodobenzoic acid (IBA).
**Confocal laser scanning microscopy**

GFP, mRFP and FM4-64 fluorescent signals and differential interference contrast (DIC) images were obtained using a laser scanning microscope (Eclipse E600; Nikon Corp.) equipped with a C1si-ready confocal system (Nikon Corp.) at the following wavelengths for excitation and detection: 488 and 515–530 nm for GFP and 543 and 605–675 nm for mRFP and FM4-64. The acquired images were processed in the vendor’s software (EZ-C1; Nikon Corp.).

**Quantitative RT-PCR (qRT-PCR)**

Total RNA was extracted from the transgenic lines. Then, reverse transcription was performed using ReverTra Ace qPCR RT Master Mix (TOYOBO) for cDNA synthesis from 1 μg of total RNA in the reaction mixture; a 1 μl sample was taken for a subsequent PCR. For qRT-PCR, gene expression was monitored using 1 μl of diluted cDNA in the Thunderbird SYBR qPCR Mix (TOYOBO). qRT-PCR was performed using primer pairs AUX1-F (5’-CCGCTCAACGTGCTAC-TTACC-3’) and AUX1-R (5’-GGATCTAAAGACGCTGGTGCCTC-3’) for AUX1 and BOR1-F (5’-AGAACACAGAAGGGCACTA-3’) and BOR1-R (5’-TTGTGACCATGCTCATATTAGC-3’) for BOR1 and UBQ10-F (5’-GGCTTGTTAATCCCGTGATGAA-3’) and UBQ10-R (5’-AAAGAGATACACGAGCGCAAA CATAGT-3’) for ubiquitin 10 (UBQ10, At4g05320), which served as an internal standard. Quantification of five independent samples was performed for each data point.

**Measurement of root length**

Roots were examined in 5-day-old seedlings grown on 1/2 MS agar plates supplemented with 1 μM YM201636, 1 μM 17β-estradiol or 0.01% DMSO (control). Their lengths were measured using ImageJ software (National Institutes of Health, USA).

**YM201636 treatment and phosphoinositide analysis**

Polyphosphoinositide levels were measured according to the method of Munnik and Zarza (2013). Briefly, radioactive PIP2 levels were measured by labeling 5-day-old seedlings (three per tube in triplicate) of WT and FAB1A-overexpressing lines with 0.37 MBq of carrier-free [32P]orthophosphate overnight (~16 h). The next day, seedlings were incubated with or without 1 μM YM201636 for 2 h, after which lipids were extracted, separated by TLC (Meijer et al. 1999) and quantified by means of Image Studio software (LI-COR).

**Disclosures**

The authors have no conflicts of interest to declare.

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