Concerted Action of Evolutionarily Ancient and Novel SNARE Complexes in Flowering-Plant Cytokinesis

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SUMMARY

Membrane vesicles delivered to the cell-division plane fuse with one another to form the partitioning membrane during plant cytokinesis, starting in the cell center. In *Arabidopsis*, this requires SNARE complexes involving the cytokinesis-specific Qa-SNARE KNOLLE. However, cytokinesis still occurs in *knolle* mutant embryos, suggesting contributions from KNOLLE-independent SNARE complexes. Here we show that Qa-SNARE SYP132, having counterparts in lower plants, functionally overlaps with the flowering plant-specific KNOLLE. *SYP132* mutation causes cytokinesis defects, *knolle syp132* double mutants consist of only one or a few multi-nucleate cells, and SYP132 has the same SNARE partners as KNOLLE. SYP132 and KNOLLE also have non-overlapping functions in secretion and in cellularization of the embryo-nourishing endosperm resulting from double fertilization unique to flowering plants. Evolutionarily ancient non-specialized SNARE complexes originating in algae were thus amended by the appearance of cytokinesis-specific SNARE complexes, meeting the high demand for membrane-fusion capacity during endosperm cellularization in angiosperms.

INTRODUCTION

Plants and non-plant eukaryotes diverged in evolution from single cells more than one billion years ago (Hedges et al., 2004; Yoon et al., 2004). Both fungal and animal cells initiate cytokinesis at the plasma membrane, with the formation of a contractile actomyosin ring that constricts the cell from the periphery, resulting in a central cytoplasmic bridge ("midbody") between the forming daughter cells, which is eventually severed by ESCRTIII-mediated constriction ("abscission") (Mierzwa and Gerlich, 2014). There are SNARE proteins localizing to the midbody (Low et al., 2003; Gromley et al., 2005). However, their role in abscission is controversial (Nakayama, 2016). Although contributing to furrow extension, membrane traffic appears to play a rather indirect role in animal cytokinesis (Schiel and Prekeris, 2013). In contrast, plant cells initiate cytokinesis in the center of the division plane through the targeted delivery of *trans*-Golgi network-derived secretory membrane vesicles, which fuse with one another to form the partitioning membrane known as the cell plate (Richter et al., 2014). This plant-specific mode of cytokinesis requires the assistance of a dynamic cytoskeletal array called the phragmoplast whose center-out remodeling drives centrifugal expansion of the cell plate until the margin of the latter fuses with the parental plasma membrane (Staehelin and Hepler, 1996).

Membrane fusion requires the formation of SNARE complexes that bridge the gap between adjacent membranes. Mutant analysis in the flowering plant *Arabidopsis* identified two genes specifically required for membrane vesicle fusion in cytokinesis: *KNOLLE*, encoding a cytokinesis-specific Qa-SNARE, and *KEULE*, encoding a KNOLLE-interacting Sec1/Munc18 protein (Lukowitz et al., 1996; Lauber et al., 1997; Assaad et al., 2001; Park et al., 2012). KNOLLE forms two kinds of SNARE complexes that act redundantly in cytokinesis: a trimeric complex comprising KNOLLE and its partners Qbc-SNARE SNAP33 and R-SNARE VAMP721 or VAMP722, whereas the other, tetrameric complex comprises KNOLLE and its partners Qb-SNARE

NPSN11, Qc-SNARE SYP71, and also R-SNARE VAMP721 or VAMP722 (El Kasmi et al., 2013). Interestingly, loss of *KNOLLE* function does not arrest embryo development at the zygote stage, indicating that cytokinesis is not completely blocked. In contrast, the *knolle keule* double-mutant embryo dies as a huge single cell with many nuclei, with no trace of cytokinesis detectable (Waizenegger et al., 2000). Thus, the membrane-fusion machinery appears to be more complex, with other Qa-SNAREs also forming SNARE complexes that contribute to cytokinesis. KNOLLE (also known as SYP111) is a member of the SYP1 family of "plasma membrane" Qa-SNAREs (Enami et al., 2009). Its closest relative, SYP112, essentially behaves like KNOLLE if expressed like KNOLLE. However, *SYP112* is not essential, and the *knolle syp112* double mutant looks identical to the *knolle* single mutant (Müller et al., 2003).

The plant-specific mode of phragmoplast-assisted cytokinesis originated within the clade of green algae that gave rise to land plants (Sawitzky and Grolig, 1995; Cook, 2004; Buschmann and Zachgo, 2016). In contrast, cytokinesis-specific Qa-SNARE KNOLLE appears to have arisen only with the advent of angiosperms several hundred million years later (Sanderfoot, 2007; see below). A possible candidate Qa-SNARE contributing to cytokinesis is the plasma membrane-localized SYP132, which is evolutionarily conserved in the plant lineage and able to complement *Arabidopsis knolle* mutant plants when expressed from the *KNOLLE* promoter (Sanderfoot, 2007; Reichardt et al., 2011). SYP132 appears to play diverse biological roles in different plant species. It is involved in biotic interactions, such as pathogen defense in tobacco and wheat, and nitrogen-fixing symbiosome formation and arbuscular mycorrhiza interactions in *Medicago* (Catalano et al., 2007; Kalde et al., 2007; Limpens et al., 2009; Pan et al., 2016; Wang et al., 2014; Huisman et al., 2016). In *Arabidopsis*, SYP132 mediates tip growth of root hairs, as indicated by conditional root hair defects caused by inducible knock down (Ichikawa et al., 2014). Importantly, *Arabidopsis* SYP132 protein does not cycle between the plasma membrane and endosomes in interphase, and is thus not retargeted in cytokinesis. Rather it accumulates as a newly synthesized protein in the cell-division plane (Enami et al., 2009; Reichardt et al., 2011). SYP132 forms an SDS-resistant SNARE complex with Qbc-SNARE SNAP33 and R-SNARE VAMP721 or VAMP722 *in vitro* when the proteins are mixed in equimolar amounts (Yun et al., 2013). SYP132 also interacts with VAMP721, VAMP722, and VAMP724, but not VAMP723, in split-luciferase complementation assays in transfected protoplasts (Ichikawa et al., 2014). In addition, Qb-SNAREs NPSN11 and NPSN13, and Qc-SNARE SYP71 and R-SNARE VAMP721, have been identified as SYP132 interactors by mass spectrometric analysis of immunoprecipitate from transgenic *Arabidopsis* plants (Fujiwara et al., 2014).

Here we address two puzzling questions regarding the membrane-fusion machinery in *Arabidopsis* cytokinesis and its evolutionary origin: (1) Why does the knock out of the cytokinesis-specific Qa-SNARE KNOLLE not prevent cytokinesis at the zygote stage of embryogenesis? (2) Might this residual capacity for cytokinesis provide clues to the evolution of present-day angiosperm cytokinesis, compared with the phragmoplast-assisted cytokinesis that occurs in the absence of the cytokinesis-specific Qa-SNARE KNOLLE in lower plants? Our results suggest that the Qa-SNARE SYP132, a member of an ancient clade present already in charophyte algae, interacts with the SNARE partners of KNOLLE to form evolutionarily ancient but still active SNARE complexes, which serve both secretory and cytokinetic membrane fusion in *Arabidopsis*. This contrasts with KNOLLE, which only arose with the advent of flowering plants, and specifically mediates formation of the partitioning membrane in cytokinesis and endosperm cellularization.

RESULTS

Zygotic Disruption of *SYP132* Gene Function Results in *Knolle*-like Cytokinesis-Defective Embryo and Seedling Phenotypes

The Qa-SNARE KNOLLE is the only one of nine *Arabidopsis* members of the SYP1 family of plasma membrane Qa-SNAREs that is strongly expressed during late-G2 to M phase, and turned over rapidly at the end of cytokinesis (Lukowitz et al., 1996; Lauber et al., 1997; Müller et al., 2003; Reichardt et al., 2007, 2011; Sanderfoot, 2007). Unlike KNOLLE, SYP132 is uniformly expressed in all organs and at all stages, stably accumulating at the plasma membrane (Enami et al., 2009; Schmid et al., 2005). However, SYP132 also accumulates at the plane of cell division, which appears to depend on *de novo* synthesis during late-G2 to M phase (Enami et al., 2009; Reichardt et al., 2011). Furthermore, SYP132 is functionally similar to KNOLLE in that it can rescue *knolle* mutant plants when expressed from the *KNOLLE* promoter, whereas another SYP1 family Qa-SNARE PEN1 (also known as SYP121) involved in pathogen defense and K+ channel regulation is unable to do so (Collins et al., 2003; Grefen et al., 2010; Reichardt et al., 2011). Unfortunately, there is no *syp132* knockout mutant available. Attempts to identify ethyl methanesulfonate-induced knockouts by TILLING were also unsuccessful, yielding only functionally intact variants (Figure S1A; mutations R210H and D230N when introduced into KNOLLE as R218H and D238N did not compromise KNOLLE function, as indicated by the ability of these KNOLLE variants to rescue *knolle* mutant plants) (Till et al., 2003). A transfer DNA (T-DNA) insertion in the promoter region of *SYP132* (*syp132*^{T}) showed a comparatively weak phenotype: bushy plants with almost no seeds, and the seedlings also seemed to be abnormal because they often formed adventitious roots instead of a single primary root (Figures 1B and S1B–E). The *syp132*^{T} mutant embryos displayed a mild phenotype and were often indistinguishable from wild-type embryos (Figures 1G and S2A–S2D). This *syp132*^{T} mutant was restored by the expression of transgene *SYP132::GFP-SYP132* (Figure S1K), indicating the specificity of *syp132*^{T}. To obtain an independent mutant allele of *SYP132*, we generated an artificial microRNA construct, using the Artificial microRNA Designer program (Schwab et al., 2006). Two-component expression of *amiR(SYP132)* from a strong ribosomal protein promoter, which is active in embryogenesis from fertilization onward (Weijers et al., 2003), (*RPS5A::GAL4* X *UAS::amiR*(*SYP132*), abbreviated as *syp132*^{amiR}), caused abnormal seedlings. These seedlings displayed a disorganized shoot meristem and the hallmarks of defective cytokinesis, such as multi-nucleate cells, cell-wall stubs, cell-wall fragments, and a band of unfused vesicles in the plane of cell division

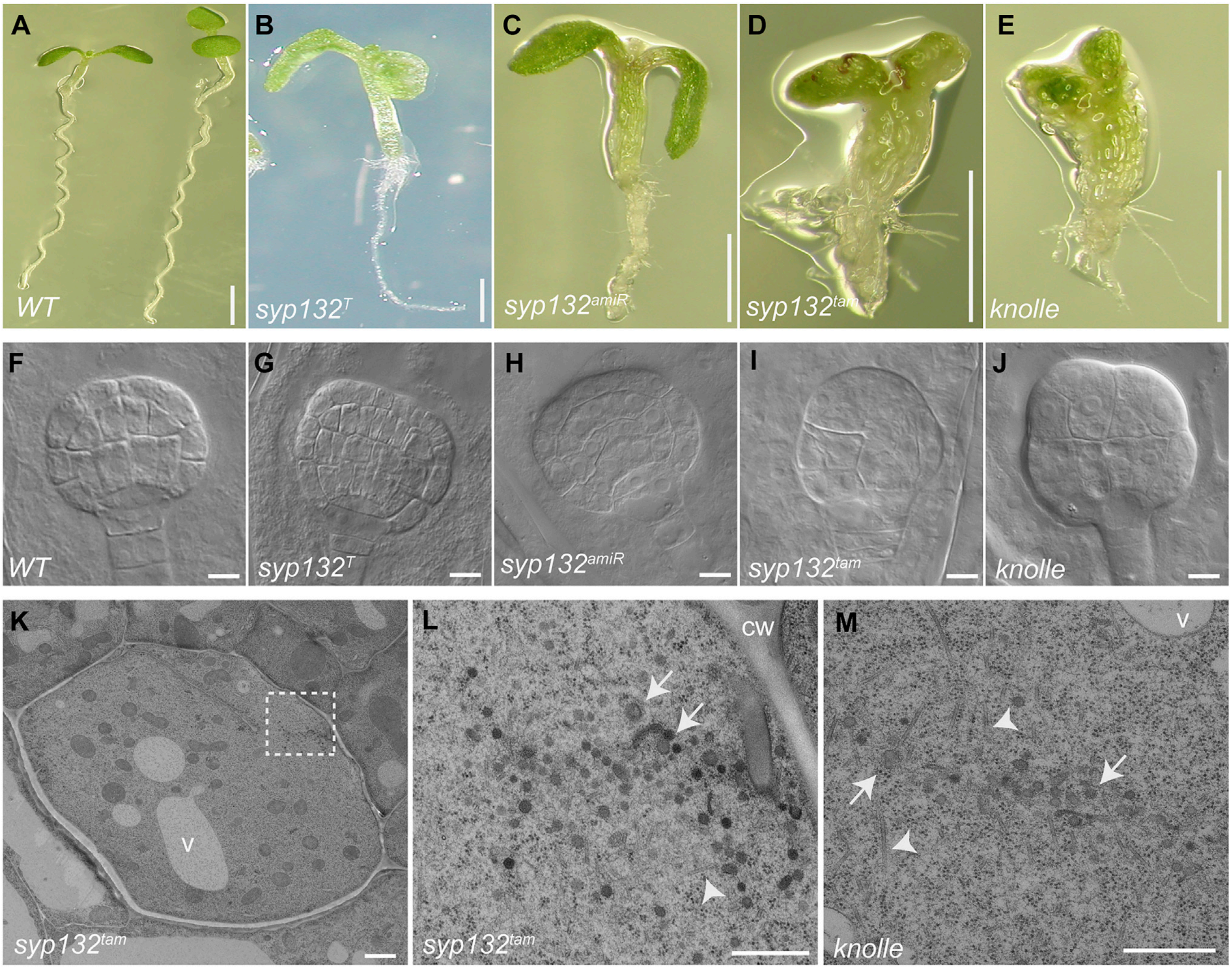


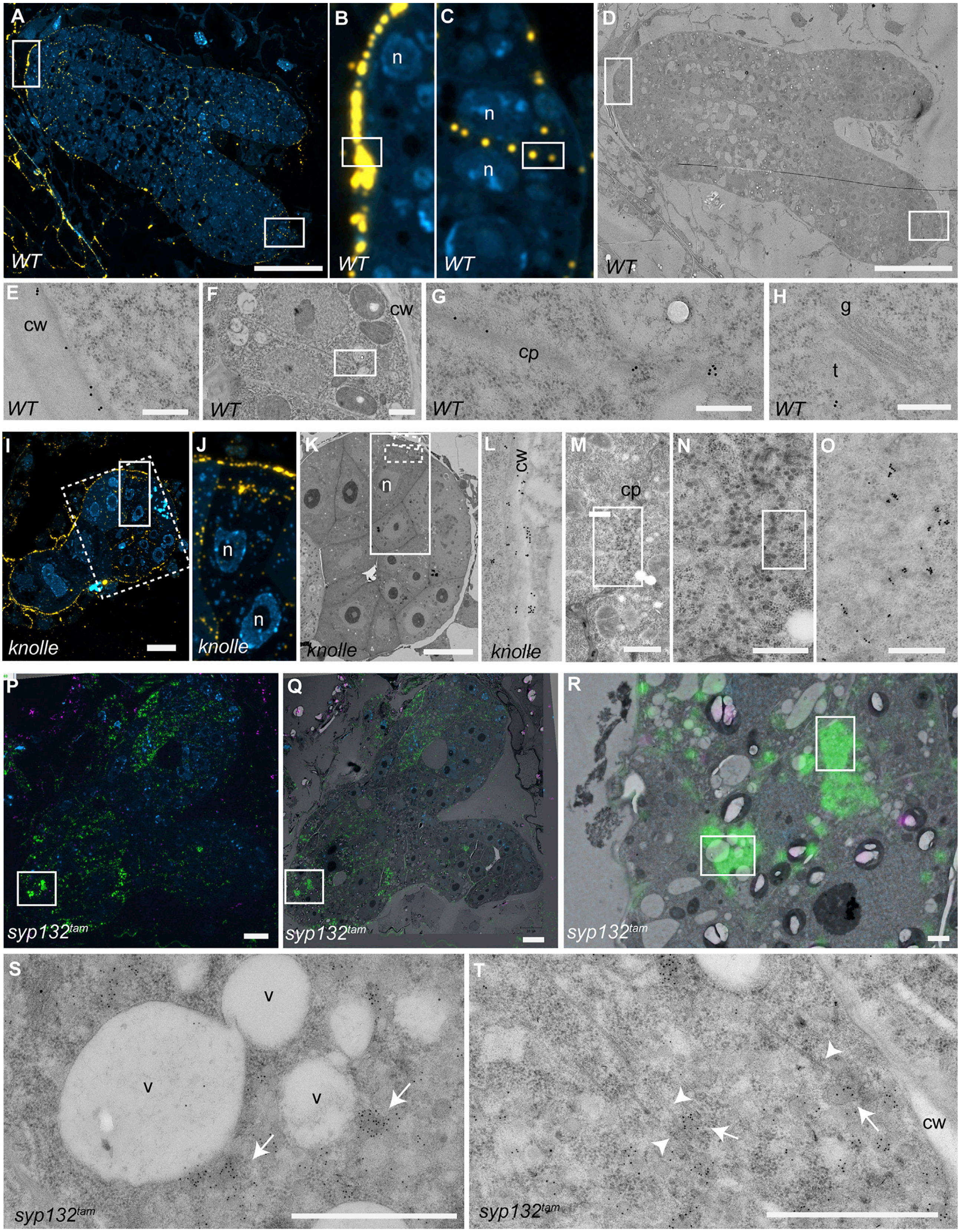
Figure 1. ***syp132*** **Mutants Displaying Defects in Cytokinesis**

(A–J) Seedlings (A–E), embryos (F–J): wild-type (A and F), *syp132^{T}* (B and G), *syp132^{amiR}* (C and H), *syp132^{tam}* (D and I), and *knolle* (E and J).

(K–M) Transmission electron microscopy (TEM) image after cryo-fixation and freeze-substitution of *syp132^{tam}* (K and L), (L) boxed area in (K) at higher magnification, and *knolle* (M); note unfused vesicles (arrows) near microtubule arrays (arrowheads) in the plane of cell division (L and M).

For genetic analysis, see Tables S1 and S2. WT, wild-type. Scale bars, 5 mm (A and B); 1 mm (C–E); 10 μm (F–J); 1 μm (K); and 0.5 μm (L and M). See also Figures S1 and S2 and Tables S1, S2, and S4.

(Figures 1C and S1F–S1J). Thus, Qa-SNARE SYP132 is required for cytokinesis. Like the *syp132^{T}* allele, the *syp132^{amiR}* mutant presented a relatively mild phenotype in developing embryos (Figures 1H and S2E–S2H). To verify that the mutant phenotype was caused by the artificial microRNA against *SYP132*, we generated a *SYP132_SYP123* chimeric gene that was resistant to *amiR(SYP132)* because the relevant sequence was no longer complementary to the artificial microRNA. *SYP123* is a close homolog of *SYP132*, and encodes the same peptide sequence from the different *amiR(SYP132)* target sequence. As expected, *KNOLLE::vYFP:SYP132_SYP123* rescued the *syp132^{amiR}* mutant (Figures S1L–S1N), revealing that *SYP132* is the specific target of *amiR*(*SYP132*). Then we combined *syp132^{amiR}* with the *syp132^{T}* allele for generating a *SYP132* mutant with an enhanced mutant phenotype, which we named two-alleles mutant of *syp132* (*syp132^{tam}*). The *syp132^{tam}* mutant embryos and seedlings displayed mutant phenotypes that were nearly indistinguishable from *knolle* mutant embryos and seedlings, respectively (Figures 1D and 1I, compare with 1E and 1J; Figures S2I–S2L). Notably, the *syp132^{tam}* embryos had cytokinesis defects including variably enlarged multi-nucleate cells, sometimes with enlarged nuclei. Like *knolle* mutant embryos, these *syp132^{tam}* embryos displayed bands of unfused vesicles (Figures 1K and 1L, compare with 1M). These results suggested that SYP132 plays an important role in cytokinesis. Since SYP132 protein accumulates at the plasma membrane in interphase (Enami et al., 2009; Reichardt et al., 2011), we also examined effects on secretory trafficking in *syp132^{tam}* mutant embryos/seedlings, using the cell-wall hemicellulosic polysaccharide xyloglucan (detectable with monoclonal antibody CCRC-M1) as a marker for secretion from the cell (Stierhof and El Kasmi, 2010; Zhang and Staehelin, 1992). Unlike wild-type



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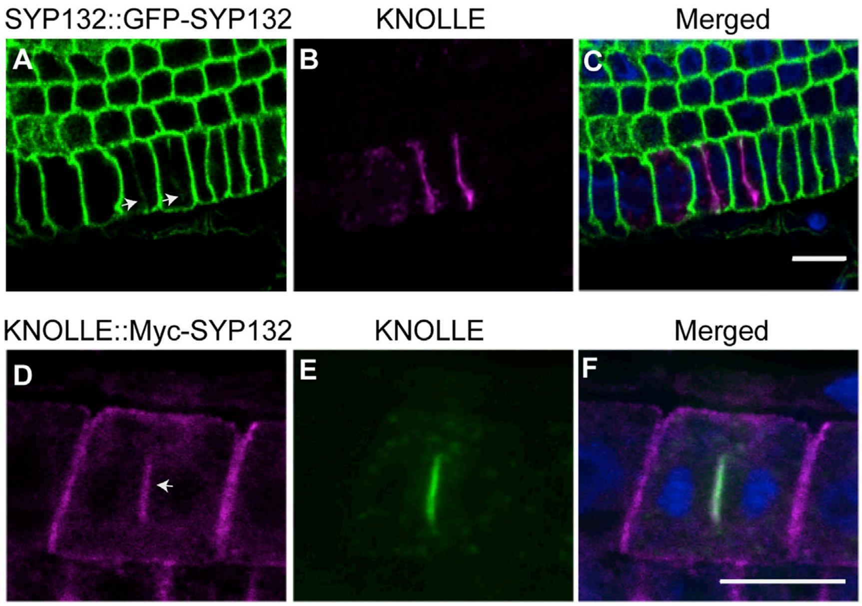

Figure 3. Subcellular Localization of Qa-SNAREs SYP132 and KNOLLE in Seedling Root Cells

(A–C) Co-localization of (A) SYP132::GFP-SYP132 (green), and (B) KNOLLE (magenta) labeled with anti-KNOLLE antiserum; (C) merged image plus DAPI staining of chromatin (blue).

(D–F) Co-localization of (D) KNOLLE::Myc-SYP132 (magenta) and (E) KNOLLE (green) labeled with anti-Myc and anti-KNOLLE antisera, respectively; (F) merged image plus DAPI staining of chromatin (blue).

Arrows indicate planes of cell division (A and D). Scale bars, 10 μm (C and F). See also Figures S3 and S4.

and *knolle* mutant embryos, which displayed an undisturbed extracellular accumulation of xyloglucan, *syp132*^{tam} mutant embryos accumulated massive amounts of the secretory marker in intracellular membrane vesicles (Figures 2A–2T). In conclusion, Qa-SNARE SYP132 appears to be required, like KNOLLE, for making the partitioning membrane in cytokinesis. Unlike KNOLLE, however, SYP132 appears to be also required for secretory trafficking to the plasma membrane in interphase.

Subcellular Localization of SYP132 Relative to KNOLLE in Cytokinesis

Unlike *KNOLLE*, *SYP132* mRNA is expressed at high level essentially in all cells of all developmental stages (Figure S3A) (Schmid et al., 2005). SYP132 protein fused to GFP and, expressed from the *SYP132* regulatory sequences, accumulated strongly at the plasma membrane but only weakly in the cell-division plane (Figures 3A–3C and S3B–S3D) (Enami et al., 2009). However, expression of SYP132 from the *KNOLLE* promoter yielded comparable accumulation of SYP132 to endogenous KNOLLE in the plane of cell division (Figures 3D–3F) and rescued the *knolle* deletion mutant (Reichardt et al., 2011). These different levels of expression correlate with the presence of two mitosis-specific activator (MSA) sequences that are close to each other in the *KNOLLE* promoter (Haga et al., 2007), but more than 100 base pairs apart in the *SYP132* promoter (Figure S4). The two closely spaced MSA elements in the *KNOLLE* promoter are essential for expression and KNOLLE function in cytokinesis (Haga et al., 2007). In contrast, *SYP132::GFP-SYP132* rescued the *knolle* mutant only partially, whereas it rescued the *syp132*^{T} mutant fully (Figure S1K; Table S3), suggesting that the MSA elements in the *SYP132* promoter are not sufficient for expressing the required amount of SYP132 protein in cytokinesis.

Nearly Complete Inhibition of Cytokinesis in *Knolle syp132*^{tam} Double Mutants

If both KNOLLE and SYP132 contributed to cytokinesis, then the *knolle syp132*^{tam} double mutant should exhibit a much stronger phenotype than either single mutant alone. Indeed, the double mutant was embryo lethal, whereas each single mutant completed embryogenesis, dying as abnormal seedlings (Figure 4; compare with Figures 1F–1J). *knolle syp132*^{amiR} or *knolle syp132*^{T} embryos consisted of a few multi-nucleate cells (Figures 4C and 4D; Table S1). Analysis of *knolle syp132*^{tam} yielded a high proportion of single-celled to few-celled embryos with multiple

Figure 2. *syp132* Mutants Displaying Defects in Secretory Pathway

Immunolocalization of xyloglucan in cryo-fixed and freeze-substituted embryos.

(A–H) Wild-type embryo (torpedo stage). (A–C) Fluorescently labeled xyloglucan (yellow): (B and C), enlarged boxes in (A) showing signals at cell wall (B) and in the plane of cell division (C). (D–H) Gold-labeled xyloglucan: (D) neighboring section (overview) imaged by TEM; (E) gold labeling of the cell wall in the region marked in (B) (white box); (F–G) gold labeling of cell plate shown in (C) (white box); (G) enlarged box in (F); (H) Golgi apparatus (G) with gold labeling in the *trans*-Golgi network (t). Note fluorescence and gold labeling on neighboring sections of the identical specimen block.

(I–O) *knolle* embryo (globular stage). (I and J) Fluorescently labeled xyloglucan; (J), enlarged detail of white box in (I). (K–O) Gold-labeled xyloglucan: (K) gold labeling of dashed box in (I); (L) enlarged view of smaller dashed box (K) showing cell wall labeling; (M) enlarged detail of bigger dashed box (K) showing cell plate labeling; (N) enlarged detail of (M) (white box) showing cell wall stubs and unfused vesicles between them; (O) same region of (M) showing vesicles. Note fluorescence and gold labeling on neighboring sections of the identical specimen block.

(P–T) *syp132*^{tam} embryo (torpedo stage). (P–R) Fluorescently labeled xyloglucan (green): (Q) overlay of fluorescence image and TEM image showing the identical section; (R) enlarged detail of (Q). Note that large numbers of fluorescent secretory vesicles are accumulated in intracellular region, unlike in wild-type and *knolle*. (S and T) Gold-labeled xyloglucan: (S) gold labeling of a region marked in (R); (T) gold labeling of the second region marked in (R) (rotated by 90°). Several microtubules, arrows in (T) are indicative of a cell plate with a large number of xyloglucan-positive unfused vesicles, arrowheads in (S) and (T). The light magenta color represents starch non-specifically labeled by anti-ARF1 antiserum (P–R). Note fluorescence and gold labeling on the identical section (P–T).

cw, cell wall; cp, cell plate; n, nucleus; v, vacuole. Scale bars, 20 μm (A and D); 10 μm (I, K, P, and Q); 1 μm (F, M, R, S, and T); 0.5 μm (N and O); and 0.25 μm (E, G, H, and L).

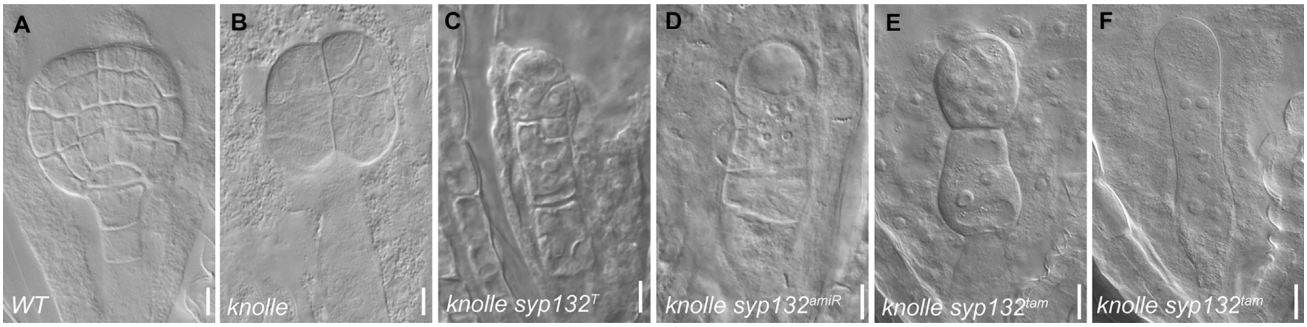

Figure 4. *syp132 Knolle* Double-Mutant Embryos Showing Strong Cytokinesis Defects

(A–F) Images of chloral hydrate-cleared whole-mount preparations of embryos. (A) Wild-type (WT); (B) *knolle* mutant; (C and D) *knolle syp132* double mutants: (C) *knolle syp132*^{T}; (D) *knolle syp132*^{amiR}; (E and F) *knolle syp132*^{tam}. Scale bars, 10 μm (A–F). See also Tables S1, S2, and S4.

nuclei (Figures 4E, 4F, and S2M–S2P; Table S1). These observations indicate that cytokinesis is almost completely abolished in the *knolle syp132*^{tam} double mutant from the zygote stage onward. The variability of the cytokinesis-defective phenotype can be attributed to the incomplete elimination of *SYP132* mRNA.

SNARE Interaction Partners of SYP132

To identify potential interaction partners of SYP132 among SNARE proteins, we investigated whether or not the knock out of individual KNOLLE partners enhanced the *knolle* knockout phenotype. If a KNOLLE partner also interacted with SYP132, double-mutant embryos lacking both KNOLLE and that specific SNARE protein would be expected to display a stronger mutant phenotype than *knolle* mutant embryos do on their own. In contrast, if that SNARE protein interacted with KNOLLE specifically, then no enhanced phenotype would be expected in the double mutant. We analyzed double-mutant embryos lacking KNOLLE and any one of its Qb-, Qc-, and Qbc-SNARE interaction partners: *knolle npsn11*, *knolle syp71*^{amiR}, and *knolle snap33*. For each combination, the double mutants died as embryos with an enhanced cytokinesis-defective phenotype: the embryos consisted of a few enlarged cells, sometimes with multiple nuclei, displaying cell-wall stubs (Figures 5A–5E, Tables S1, S2). This contrasted with the embryo viability of the single mutants (Heese et al., 2001; Zheng et al., 2002; El Kasmi et al., 2013). These results thus suggested that SNARE partners of KNOLLE might also be partners of SYP132.

To test for physical interaction between SYP132 and KNOLLE-interacting SNARE proteins, we performed co-immunoprecipitation experiments on protein extracts from transgenic plants expressing genomic *SYP132::GFP-SYP132* or *KNOLLE::Myc-SYP132* constructs. SYP132 did indeed interact with the SNARE partners of KNOLLE (Figures 5F and 5G). In the reciprocal experiment, the putative SNARE partners were immunoprecipitated, and each precipitate also contained both KNOLLE and SYP132 proteins (Figures 5H and 5I). In contrast, SNAP33 was not detected in the precipitates of YFP-NPSN11 and YFP-SYP71 (Figure 5H). Thus, like KNOLLE, SYP132 participated in two different complexes, since NPSN11 and SNAP33 had been shown before not to reside in the same KNOLLE complex (El Kasmi et al., 2013). One SYP132 complex contained the SNARE partners SNAP33 and VAMP721 or VAMP722, which cannot be distinguished with the antiserum available, whereas the other contained NPSN11 and SYP71 in addition to VAMP721 or VAMP722. These results indicate that the Qa-SNAREs SYP132 and KNOLLE each form complexes with the same SNARE partners to mediate membrane fusion in *Arabidopsis* cytokinesis.

Unlike KNOLLE, SYP132 Is Not Required for Endosperm Cellularization

The embryo-nourishing tissue called the endosperm originates together with the embryo through double fertilization; this is an evolutionary novelty of angiosperm reproduction (Floyd and Friedman, 2001; Friedman and Ryerson, 2009). Double fertilization involves two genetically identical haploid sperm cells, which each fertilize one of two genetically identical female gametes, the haploid egg cell and a diploid central cell, derived from the same meiotic product. In contrast to a series of cell divisions that transform the fertilized egg cell into a young embryo, the initial development of endosperm occurs within a large single cell, resembling *Drosophila* early embryogenesis: a series of nuclear division cycles is followed by the simultaneous formation of partitioning membranes that separate the many nuclei from each other, so-called cellularization (for review, see Mazumdar and Mazumdar, 2002). The Qa-SNARE KNOLLE is strongly expressed during endosperm cellularization and also during subsequent rounds of cytokinesis of the cellular endosperm (Figures 6A and 6C) (Day et al., 2008; Lauber et al., 1997). Furthermore, *knolle* mutant endosperm (almost) fails to cellularize, indicating that KNOLLE plays an essential role in endosperm development (Figure 6J, compare with 6I) (Sørensen et al., 2002). In contrast to KNOLLE, GFP-SYP132 was weakly and unevenly expressed in cellularizing endosperm, but subsequently accumulated strongly in the plasma membrane of endosperm cells (Figures 6B and 6D). To determine the functional requirement of SYP132 in the endosperm, the phenotype of *syp132*^{tam} developing embryo and endosperm within the same seed was analyzed. Although the *syp132*^{tam} mutant embryos displayed characteristic cytokinesis defects, resembling *knolle* mutant embryos, the associated endosperm essentially looked like wild-type, in contrast to the nearly complete elimination of endosperm cellularization in *knolle* mutants (Figure 6K, compare with 6I–6J). In conclusion, whereas KNOLLE is strictly required for endosperm cellularization SYP132 appears dispensable, although it plays an essential role in zygotic cytokinesis.

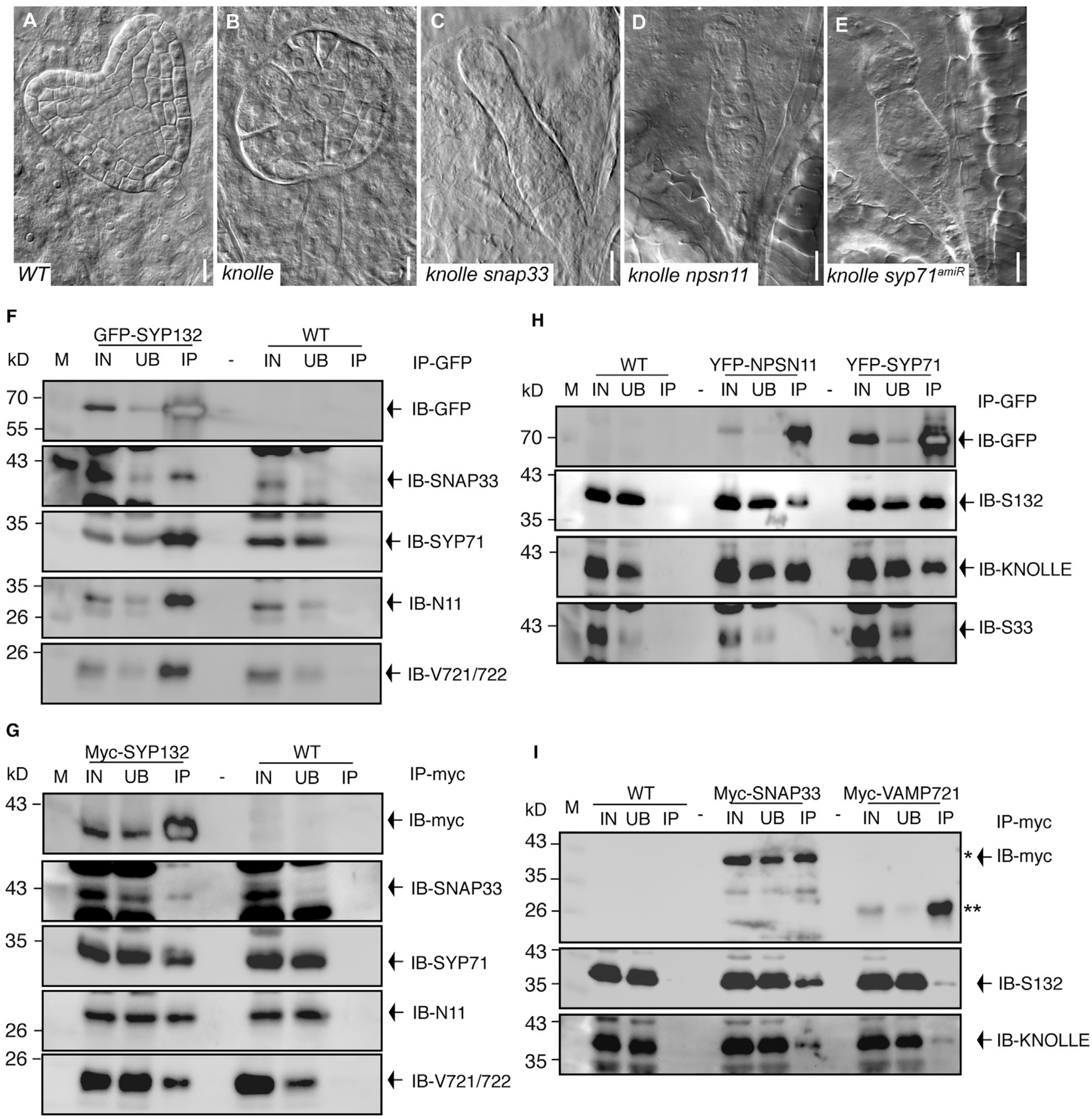

Figure 5. Genetic and Biochemical Interactions of SNAREs

(A–E) SNARE double-mutant embryos showing enhanced *knolle* mutant phenotypes. (A) Wild-type (WT); (B) *knolle* mutant; (C–E) double mutants of *knolle* and known KNOLLE-interacting Q-SNARE partners: (C) *knolle snap33*, (D) *knolle npsn11*, and (E) *knolle syp71^{amiR}*. Note that each double mutant shows more abnormal phenotype than each single mutant of *npsn11*, *snap33*, and *syp71^{amiR}*, which display no or only a slight cytokinesis phenotype (El Kasmi et al., 2013). Scale bars, 10 μm (A–E). See also Tables S1, S2, and S4.

(F–I) Co-immunoprecipitation analysis. Protein extracts from SYP132::GFP-SYP132 (F) and KNOLLE::Myc-SYP132 (G) seedlings were subjected to immunoprecipitation (IP) with anti-GFP and anti-Myc beads, respectively. (Col) was used as control. Immunoprecipitates were probed by immunoblotting (IB) for SNARE proteins NPSN11 (N11), SNAP33, SYP71, and VAMP721/722 (V721/722). (H and I) Reciprocal co-immunoprecipitation analysis. Protein extracts of YFP-NPSN11, middle in (H), or YFP-SYP71, right in (H), and Myc-SNAP33, left in (I), and Myc-VAMP721, right in (I) seedlings were subjected to IP with anti-GFP and anti-Myc beads, respectively. WT, left in (H) and (I) was used as control. Immunoprecipitates were probed by IB for Qa-SNAREs KNOLLE and SYP132 (S132), and for Qbc-SNAP33 (S33) in (H). Single asterisk (I) (upper panel), Myc-SNAP33; double asterisks (I) (upper panel), Myc-VAMP721. IN, input; UB, unbound; IP, immunoprecipitate. Molecular sizes (in kDa) are indicated on the left.

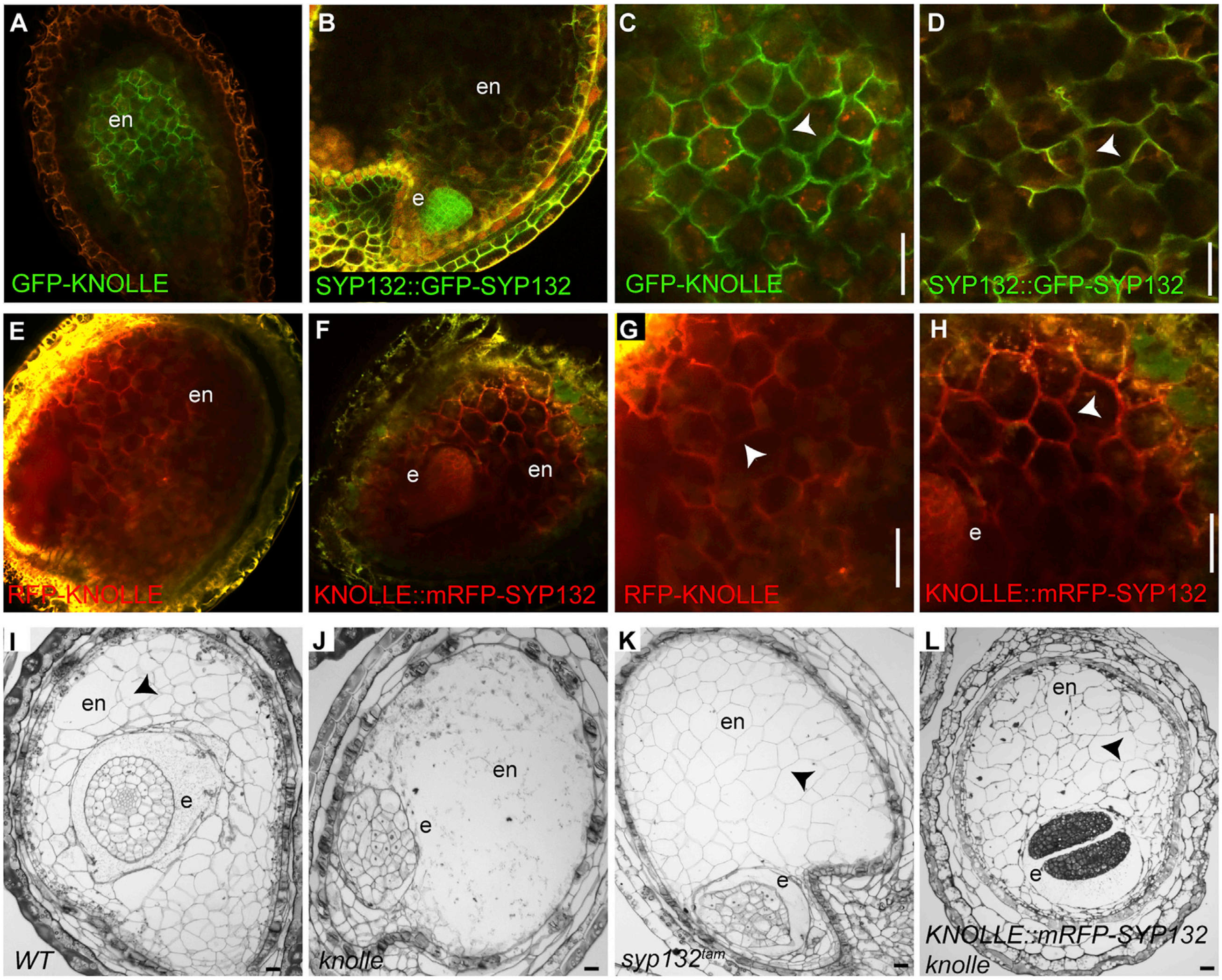

Figure 6. Qa-SNAREs SYP132 and KNOLLE in Endosperm Cellularization

(A–H) Localization of Qa-SNARE proteins in cellularizing endosperm: (A and C) KNOLLE::GFP-KNOLLE; (B and D) SYP132::GFP-SYP132; (E and G) KNOLLE::RFP-KNOLLE; (F and H) KNOLLE:mRFP-SYP132 *knolle*. (A, B, E, and F) Overviews. (C, D, G, and H) Highly magnified images taken from the peripheral endosperm at different or same focal planes. Note brightly stained embryo in (B and F). At the same detector setting, the GFP-KNOLLE signal was approximately 3-fold stronger than the GFP-SYP132 signal. In contrast, KNOLLE::mRFP-SYP132 expression was indistinguishable from KNOLLE::RFP-KNOLLE expression (E–H) (see also Figure S6 for immunofluorescent images and quantification analysis). Note that the counter colors, red in (A)–(D) and green in (E)–(H) represent an autofluorescent signal from the clearing.

(I–L) Endosperm in developing seeds of (I) WT (Col), (J) *knolle*, (K) *syp132*^{tam}, and (L) *KNOLLE::mRFP-SYP132 knolle*. Note the absence of cellular endosperm in *knolle* (J), but not in *syp132*^{tam} (K). In contrast, cellularization of the endosperm in *knolle* was rescued by *KNOLLE::mRFP-SYP132* (L), which resembled WT (I) and *syp132*^{tam} (K) ovules. Arrowheads indicate formation of partitioning membranes during cellularization (C, D, G, and H) and cell walls in cellular endosperm (I, K, and L). e, embryo derived from zygote; en, endosperm.

Scale bars, 20 μm (C, D, G, and H) and 10 μm (I–L). See also Tables S3 and S4.

To examine whether the differences in expression level might be responsible for the requirement of KNOLLE, as opposed to SYP132 in endosperm cellularization, we expressed SYP132 fused to mRFP from the *KNOLLE cis*-regulatory sequences in the *knolle* mutant background (Müller et al., 2003), which rescues the *knolle* mutant fully (Reichardt et al., 2011; Figure S5; Table S3). In the cellularizing endosperm, mRFP-SYP132 accumulated in midplane between adjacent nuclei, essentially like RFP-KNOLLE (Figures 6F and 6H, compare with 6E, 6G, and S6). Light microscopic analysis of sections of *KNOLLE::mRFP-SYP132 knolle* ovules revealed normal cellularization of the endosperm (Figure 6L). These results strongly suggest that the regulation of gene expression is the crucial feature of KNOLLE function in endosperm cellularization.

DISCUSSION

Our results suggest a plausible scenario for the evolution of membrane fusion during plant cytokinesis. The cytokinesis-specific Qa-SNARE KNOLLE is only conserved among flowering

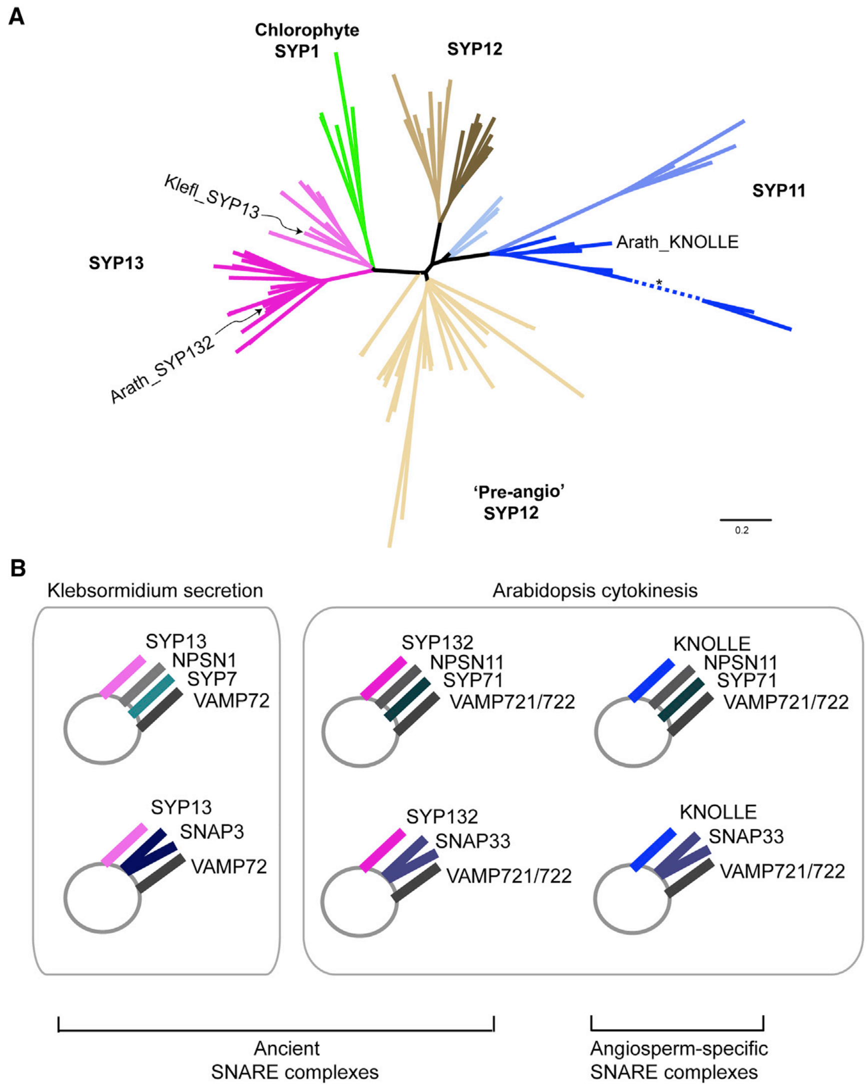

Figure 7. Evolution of Membrane Fusion in Plant Cytokinesis

(A) SYP1 phylogenetic tree (abridged). Proteins were aligned using MUSCLE in MEGA7. Phylogeny was generated using the Neighbor-Joining method in MEGA7. KNOLLE, SYP132 of *Arabidopsis thaliana* and SYP13 of *Klebsormidium flaccidum* are indicated. Note that the branch marked with an asterisk was shortened to 33%. See also Figure S7 for detailed phylogenetic tree.

(B) Model of SNARE complexes in cytokinesis. SYP132 complexes in *Arabidopsis* are evolutionarily ancient, resembling the putative secretory SYP13-containing SNARE complexes in the charophycean alga *Klebsormidium flaccidum* while KNOLLE complexes in *Arabidopsis* are angiosperm-specific SNARE complexes confined to cytokinesis.

plants (Figures 7A and S7), although the plant mode of phragmoplast-assisted cell-plate formation was already established in the charophycean algae that gave rise to the land plants (Doty et al., 2014; for review, see Buschmann and Zachgo, 2016). Unlike KNOLLE, SYP132 has counterparts in lower plants, starting in algae (Figures 7A and S7). In the sequenced genome of the charophycean alga *Klebsormidium flaccidum*, there are single-copy genes encoding putative SYP1 SNARE complex members (Hori et al., 2014): one SYP132-like Qa-SNARE (KfSYP13; kfl00435_0060; e-value, 4e-103), one SNAP33-like Qbc-SNARE (KfSNAP3; kfl00640_0070; e-value, 1e-42), one NPSN11-like Qb-SNARE (KfNPSN1; kfl00187_0180; e-value, 7e-93), one SYP71-like Qc-SNARE (KfSYP7; kfl00527_0090; e-value, 3e-95) and one VAMP721-like R-SNARE (KfVAMP72; kfl00515_0100; e-value, 7e-107). Taking into account the phylogenetic relationships between these proteins and their *Arabidopsis* counterparts as well as the interactions of the latter shown here, we propose that two different types of SYP1 SNARE complexes might already have existed in ancient algae giving rise to land plants: (1) SYP13-NPSN1-SYP7-VAMP72 and (2) SYP13-SNAP3-VAMP72 (Figure 7B). Those putative SNARE complexes would thus have involved the same single SYP1 Qa-SNARE related to SYP132 of *Arabidopsis* and the same single R-SNARE related to VAMP721 of *Arabidopsis*. Furthermore, those two complexes would have mediated membrane fusion both of secretory vesicles with the plasma membrane and of membrane vesicles with each other and the forming partitioning membrane during cytokinesis. Interestingly, *Klebsormidium* still displays centripetal furrowing as its prevalent mode of cytokinesis, thus superficially resembling the non-plant mode of cytokinesis, which is mediated by a contractile ring (Katsaros et al., 2011). Nonetheless, the only *SYP1* gene of *Klebsormidium* most closely relates to the *SYP13* clade of land plants, unlike the only *SYP1* gene of chlorophyte algae such as *Chlamydomonas*, which appears to be equally distantly related to SYP13 and SYP12 clades of plant SYP1 Qa-SNAREs (Kanazawa et al., 2016) (Figure S7).

Starting from the single SYP13 in *Klebsormidium*, the SYP1 family of Qa-SNAREs presumably evolved by gene duplication and diversification. A new branch of SYP12 members appears to have originated in the early land plants, as represented in the moss *Marchantia polymorpha* (Kanazawa et al., 2016) (Figure S7). Only much later was the SYP11 branch established. Although SYP11 proteins are encoded in the three gymnosperm genomes analyzed so far, they still appear different from the cytokinesis-specific KNOLLE protein of flowering plants, raising the possibility that KNOLLE-like proteins might only have acquired a novel essential role in angiosperms.

Although the charophycean algae established phragmoplast-assisted cell-plate formation as the plant-specific mode of cytokinesis several hundred million years ago, it appears that a cytokinesis-specific Qa-SNARE related to KNOLLE arose only with the advent of angiosperms. We propose that this led to the formation of SNARE complexes specifically involved in cytokinesis and playing no role in secretory traffic to the plasma membrane during interphase. The primary mechanism of KNOLLE sub-functionalization most likely was the acquisition of paired *cis*-regulatory elements such as MSA sequences required for strong expression during the G2/M phase of the cell cycle (Haga et al., 2007), which presumably was accompanied by changes causing KNOLLE protein degradation at the end of cytokinesis. Although cytokinesis-specific SNARE complexes exist in *Arabidopsis*, and most likely in other flowering plants as well (see Müller et al., 2003), there is still a contribution of the ancient SYP132-containing SNARE complexes to cytokinesis, in addition to their role in secretion. These observations beg the question of why KNOLLE was selected for in the flowering plants and, conversely, why the ancient Qa-SNARE SYP132 was nonetheless retained. Our results indicate that SYP132 is absolutely required for secretion and also plays a role in cytokinesis during embryogenesis. Conversely, KNOLLE, but not SYP132, is necessary not only for somatic cytokinesis but also for the cellularization of the endosperm (compare Figures 6J with 6K). In endosperm cellularization, membrane vesicles are delivered to the midplane between adjacent nuclei, where they fuse with one another to form partitioning membranes, as in somatic cytokinesis (Otegui et al., 2001). Thus, the role of KNOLLE in endosperm cellularization is mechanistically akin to its role in somatic cytokinesis: promoting the fusion of membrane vesicles delivered to the midplane between adjacent nuclei by forming SNARE complexes to generate the partitioning membranes, which separate hundreds of nuclei from each other simultaneously. However, compared with somatic embryogenesis, endosperm cellularization has a much higher demand for membrane-fusion capacity, which appears to be met by the very strong G2/M-phase expression of KNOLLE. This conclusion is strongly supported by the observation that SYP132 expressed from a transgene with *KNOLLE cis*-regulatory sequences accumulated like KNOLLE in midplane between adjacent nuclei during endosperm cellularization and was sufficient to rescue the cellularization defect of *knolle* mutant endosperm. It is interesting to note that the endosperm, which is an extra-embryonic nourishing tissue for the embryo, is a peculiarity of angiosperms, resulting from the double-fertilization event unique to flowering plants. It is thus tempting to speculate that the origin of this evolutionary novelty was facilitated by the emergence of a cytokinesis-specific Qa-SNARE.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

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SUPPLEMENTAL INFORMATION

Supplemental Information includes seven figures and four tables and can be found with this article online at https://doi.org/10.1016/j.devcel.2017.12.027.

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AUTHOR CONTRIBUTIONS

Investigation, Validation, Writing – Review & Editing, and Visualization, M.P.; Investigation, C.K., M. Karnahl, I.R., F.E.K., U.M., Y.-D.S., U.H., M.B., and M. Kientz; Resources, M.H.S., M.T.N., and J.L.D.; Resources and Investigation, A.A.S.; Conceptualization, Supervision, Project Administration, Writing – Original Draft Preparation, Writing – Review & Editing, and Funding Acquisition, G.J.

DECLARATION OF INTERESTS

The authors declare no competing interests.

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STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCES	SOURCE	IDENTIFIER
Antibodies		
Rabbit anti-KNOLLE	Lauber et al., 1997	N/A
Rabbit anti-SYP132	This paper	N/A
Rabbit anti-SNAP33	Heese et al., 2001	N/A
Rabbit anti-NPSN11	Zheng et al., 2002	N/A
Rabbit anti-SYP71	Sanderfoot et al., 2001	N/A
Rabbit anti-VAMP721/722	Kwon et al., 2008	N/A
Mouse anti-GFP	Roche	RRID: AB_390913
Rat anti-RFP	Chromotek	RRID: AB_2336064
Mouse anti-Myc 9E10	Millipore	RRID: AB_309725
Goat anti-rabbit IgG-POD	Millipore	Cat#AP307P
Goat anti-mouse IgG-POD	Sigma-Aldrich	Cat#A2554
Goat anti-rat IgG-POD	Sigma-Aldrich	Cat#A9037
Goat anti-rabbit Alexa488	Invitrogen	Cat#A11008
Goat anti-rabbit Cy3^{TM}	Dianova	Cat#111-165-144
Goat anti-rat Cy3	Dianova	Cat#112-165-062
Goat anti-mouse IgG-Cy3	Dianova	Cat#115-165-062
Goat anti-mouse IgG-Gold	Dianova	Cat#115-195-166
Mouse anti-Xyloglucan	Zhang and Staehelin, 1992	N/A
Anti-GFP agarose	Chromotek	RRID: AB_2631360
Anti-Myc agarose	Sigma-Aldrich	Cat#A7470
EDTA-free protease inhibitor cocktail	Roche	Cat#04693132001
Bacterial and Virus Strains		
Agrobacterium tumefaciens	ATCC	NCBITaxon:357
Chemicals, Peptides, and Recombinant Proteins		
DAPI	Sigma-Aldrich	Cat#D9542
FM4-64	Invitrogen	Cat#F34653; CHEBI-52078
BASTA	AgrEvo	N/A
LR-White Resin	Fluka	Cat#62662
EPON	Roth	Cat#8619
*Sma*I	Thermo Fischer scientific	Cat#ER0661
*Eco*RI	Thermo Fischer scientific	Cat#ER0271
Phusion Taq polymerase	Thermo Fischer scientific	Cat#F530L
Experimental Model: Organism		
Arabidopsis thaliana	NASC	NCBITaxon::3702
Plant Materials		
knolle$^{X37\text{-}2}$ mutant	Lukowitz et al., 1996	N/A
syp132^{T} mutant	This paper	N/A
syp132^{amiR} mutant	This paper	N/A
snap33 mutant	Heese et al., 2001	N/A
syp71^{amiR} mutant	El Kasmi et al., 2013	N/A
npsn11 mutant	Zheng et al., 2002	N/A
KNOLLE::Myc-SYP132	Reichardt et al., 2011	N/A
SYP132::GFP-SYP132	Enami et al., 2009	N/A
SNAP33::Myc-SNAP33	Heese et al., 2001	N/A

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Continued		
REAGENT or RESOURCES	SOURCE	IDENTIFIER
KNOLLE::YFP-NPSN11	El Kasmi et al., 2013	N/A
SYP71::YFP-SYP71	Suwastika et al., 2008	N/A
RPS5A::GAL4	Weijers et al., 2003	N/A
KNOLLE::vYFP-SYP132_SYP123	This paper	N/A
KNOLLE::mRFP-SYP132	This paper	N/A
Recombinant DNAs		
KNOLLE expression cassette	Müller et al., 2003	N/A
KNOLLE::vYFP-SYP132_SYP123	This paper	N/A
KNOLLE::mRFP-SYP132	This paper	N/A
Oligonucleotides		
amiR(SYP132) targeting sequence: AGCACAGGTAATGGACACCT	This paper	N/A
Primers for genotyping mutants	See Table S4	N/A
Primers for recombinant DNAs construction	See Table S4	N/A
Primers for genotyping transgenes	See Table S4	N/A
Other		
Chemiluminescence detection system	PEQlab	Fusion Fx7 Imager
Immunohistochemistry system	Intavis	InsituPro VSi
Confocal laser scanning microscope	Leica	SP8
Two-photon laser scanning microscope	Zeiss	LSM780NLO
Cryomicrotome	Supercut	Leica RM2065
Electron microscope	Jeol	TEM

CONTACT FOR REAGENT AND RESOURCE SHARING

Further information and requests for reagents and resources should be directed to and will be fulfilled by the Lead Contact, Gerd Jürgens (gerd.juergens@zmbp.uni-tuebingen.de).

METHOD DETAILS

Plant Material and Growth Conditions

Arabidopsis thaliana genotypes used were wild-type (*Col-0*), *knolle^{X37-2}* (*Ler/Nd*) (Lukowitz et al., 1996) and *snap33* (*Ws*) (Heese et al., 2001). In addition, T-DNA insertion lines were analyzed by PCR genotyping to identify homozygous *npsn11* (At2g35190; SALK_068094) and *syp132^{T}* (At5g08080, SAIL 403_B09) mutants. The following transgenic plant lines were used: *SYP132::GFP-SYP132* (Enami et al., 2009), *KNOLLE::Myc-SYP132* (Reichardt et al., 2011), *SNAP33::Myc-SNAP33* (Heese et al., 2001), *KNOLLE::YFP-NPSN11* (El Kasmi et al., 2013), *SYP71::YFP-SYP71* (Suwastika et al., 2008).

Plants were either grown on soil or on vertically oriented agar plates with 2.15 g/l Murashige and Skoog (1/2 MS) medium containing 1% sucrose in growth chambers at 23°C in continuous light. Transgenic plants were generated by transformation with *Agrobacterium tumefaciens* using the floral-dip method (Clough and Bent, 1998).

The homozygous *RPS5A::GAL4* activator line was transformed with *Agrobacterium* carrying *KNOLLE::vYFP-SYP132_SYP123.* T1 plants selected by spraying with 1:1000 diluted BASTA (183 g/l glufosinate; AgrEvo, Düsseldorf, Germany) were crossed with the homozygous *UAS::amiR(SYP132)* line. The resulting F1 was analysed for complementation test.

TILLING

Targeting induced local lesions in genomes (TILLING) of *SYP132* was performed as reported (McCallum et al. 2000). This approach is based on mismatch-specific endonuclease cleavage of heteroduplex DNA fragments formed upon PCR amplification of target gene sequences of individuals from a mutant population. To identify point mutations in *SYP132*, approximately 1500 M2 individuals from the ethyl methanesulfonat (EMS)-mutagenized population of *A. thaliana* (Col) were screened using two gene-specific primer pairs listed in Table S4. Seven mutations were identified in the *SYP132* gene: C2335T, C2363T and C2382T mutations in the introns; G2020A, G2221A and G2429A mutations in the exons. Of these, three mutations in the exons giving rise to point mutations (See Figure S1A for sequence comparison) were further analyzed. Seeds of lines carrying mutations in *SYP132* were obtained from the GABI-TILL Arabidopsis collection and screened twice independently.

Molecular Cloning and Genetic Analysis

Cloning of artificial microRNA (amiRNA) for SYP132 was done as described in Artificial microRNA Designer (http://wmd3.weigelworld.org/cgi-bin/webapp.cgi), using the primers listed in Table S4 (Schwab et al., 2006). For the two-component expression system, the amiRNA was cloned under the GAL4-responsive *UAS* element and these reporter lines were crossed with the *RPS5A::GAL4* activator lines (Weijers et al., 2003). The amino acid exchanges R218H and D238N were introduced into *KNOLLE* by site directed mutagenesis of *KNOLLE::Myc-KNOLLE*. The constructs were transformed in $knolle^{X37-2}$ heterozygous plants.

For *KNOLLE::vYFP-SYP132_SYP123*, a chimeric construct of *SYP132_SYP123* was generated with a primer-extension method. PCR product was digested with *Sma*I and *EcoR*I and subcloned in-frame downstream of *pKNOLLE::vYFP* cassette. For *KNOLLE::mRFP-SYP132*, *SYP132* was amplified by PCR using primers 132-start Sma1 and 132-stop EcoRI and subcloned in-frame downstream of *pKNOLLE::mRFP* cassette (*Sma*I/*EcoR*I). Genotyping PCR: X37-2 CIII and X37-2 DIII for $knolle^{X37-2}$ and *KNOLLE* (0. 5 kb and 1.5 kb, respectively); UASs and eGFP200rev for $syp132^{amiR}$ (0.4 kb); GALs and GALas for *GAL4* (0.7 kb); vYFP700sen and 132-stop EcoR1 for *vYFP-SYP132_SYP123* (1.2 kb); mRFP700sen and 132-stop EcoR1 for *mRFP-SYP132* (1.2 kb). See Table S4 for primer sequences.

Immunoprecipitation

The immunoprecipitation procedure was modified from the previous report (Park et al., 2012). Total protein extracts were prepared from approximately 2 g of five-day-old seedlings in buffer (50 mM Tris pH7.5, 150 mM NaCl, 1 mM EDTA, 0.5% Triton X-100) supplemented with EDTA-free protease inhibitor cocktail (Roche). 30 μl of agarose-conjugated lama anti-GFP (GFP-trap®; Chromotek) or anti-Myc (Anti-c-Myc agarose affinity gel, Sigma-Aldrich) were added to cleared protein extract and incubated at 4°C for 2 h on a rolling incubator. All immunoprecipitation experiments were repeated more than twice. Membranes were developed using a chemiluminescence detection system (Fusion Fx7 Imager, PEQlab, Erlangen, Germany). Antibody dilutions were as follows: rabbit anti-KNOLLE serum (1:5,000) (Lauber et al., 1997), rabbit anti-SYP132 serum (1:5,000) (a kind gift from A. Sanderfoot), rabbit anti-SNAP33 serum (1:5,000) (Heese et al., 2001), rabbit anti-NPSN11 serum (1:1,500) (Zheng et al., 2002), rabbit anti-SYP71 serum (1:2,000) (Sanderfoot et al., 2001), rabbit anti-VAMP721/722 serum (1:5000) (Kwon et al., 2008), mouse anti-GFP monoclonal antibody (1:1,000; Roche), mouse anti-Myc monoclonal antibody 9E10 (1:1,000; Millipore), rat anti-RFP monoclonal antibody (1:1000; Chromotek), goat anti-rabbit IgG-POD polyclonal antibody (1:10,000; Millipore), goat anti-mouse IgG-POD polyclonal antibody (1:10,000; Sigma), goat anti-rat IgG-POD polyclonal antibody (1:5,000; Sigma).

Immunofluorescence Imaging

Live imaging in roots of five-day-old seedlings was performed with 2 μM FM4-64 (Molecular Probes, Life Technologies) in liquid growth medium (1/2 MS medium, 1% sucrose, pH 5.6). Five-day-old seedlings were fixed in 4% (w/v) paraformaldehyde in MTSB (50 mM Pipes, 5 mM EGTA, 5 mM $MgSO_4$, pH 7.0) for 1 hr and stored at -20°C until used for immunostaining. For embryo and endosperm staining, ovules fixed in 4% paraformaldehyde in MTSB were squashed on the gelatin-coated slide (Lauber et al., 1997). For immunofluorescence, primary antisera anti-KNOLLE (1:4000, rabbit) (Lauber et al., 1997), mouse anti-Myc monoclonal antibody 9E10 (1:600; Millipore), rat anti-RFP monoclonal antibody (1:500; Chromotek), goat anti-rabbit Alexa488 (1:600, Invitrogen), goat anti-rat Cy3 (1:600; Dianova), and goat anti-rabbit Cy3™ (1:600, Dianova, Germany) were applied. PBS (pH 7.5) was used in all steps after fixation of the plant material. The primary antibody was incubated for 6 hours at 37°C after blocking for 3 hour with 3% BSA in PBS, the secondary antibody was incubated for 4 hours at 37°C. 1 μg/ml DAPI (1 mg/ml stock solution in H_2O) was used for staining nuclei. Samples were prepared manually or with an immunohistochemistry system (InsituPro VSi, Intavis, Cologne, Germany). Fluorescent images were taken using a 63x water-immersion objective in Leica SP8 confocal laser scanning microscope. Intensity profile was measured using Leica software. Images were processed with Adobe Photoshop CS3 only for adjustment of contrast and brightness.

Two-Photon Imaging of Cellularizing Endosperm

Experimental procedure was done as previously reported (Musielak et al., 2016). For whole-mount imaging of developing endosperm, immature seed of appropriate stage were dissected out of siliques and fixated in 4% paraformaldehyde in PBS buffer pH7.4 overnight at 4°C. After washing twice with water, the fixated ovules where cleared overnight and mounted in 50% thiodiethanol. Multi-photon imaging was performed with a Zeiss LSM780NLO equipped with a two-channel non-descanned GaAsP detector and a MaiTai DeepSee eHP IR laser. Excitation wavelength: GFP, 930 nm; mRFP, 745 nm; RFP, 755 nm. Images were taken with a Zeiss LD C-Apochromat 40x/1,1 W Korr objective.

Electron Microscopy and CLEM

For ultrastructural analysis, ovules were high-pressure frozen (HPM010) in 150 or 200 μm planchettes filled with hexadecane and freeze-substituted in acetone supplemented with 2.5% osmium tetroxide (35 h at -90°C, 6 h at -60°C, 6 h at -30°C, 2 h at 0°C). Thereafter samples were washed 5x with acetone (0°C), before they were infiltrated with 10%, 25%, 50%, 75%, 2x 100% epoxy resin (Roth, Germany). Infiltrated samples were polymerized at 60°C for two days. For ultrastructural analysis, 70 nm thin sections were cut and mounted on slot grids covered with pioloform. Sections were stained with 3% uranyl acetate in ethanol, followed by lead citrate and viewed in a Jeol JEM-1400plus TEM at 120 kV accelerating voltage. Images were taken with a 4K CMOS TemCam-F416 camera (TVIPS).

For resin section labeling with Xyloglucan-specific antibodies, ovules were high-pressure frozen as described above and freeze-substituted in acetone supplemented with 0.4% uranyl acetate and 1.6% methanol. After 50 h at -90°C, samples were warmed up to -50°C and washed 5x with acetone before they were infiltrated with 25%, 50%, 75% and 2x 100% Lowicryl HM20 at -50°C. Infiltrated samples were UV-polymerized for two days at -50°C. For immunolabeling, 70 nm thin sections were cut (Leica UC7) and mounted on coverslips for immunofluorescence microscopy or slot grids covered with Pioloform for immunoelectron microscopy and correlative light and electron microscopy (CLEM). For immunogold labeling of mounted sections on grids, unspecific binding sites were blocked with PBS containing 0.2% BSA and 0.2% milk powder. Sections were labeled as with mouse anti-xyloglucan antibodies (mAb CCRC-M1, 1:10; Carbosource Services, University of Gorgia) diluted in blocking buffer and goat anti-mouse IgG coupled to 6 nm gold (1:30; Dianova, Hamburg). In some cases, gold particles were silver-enhanced using R-Gent (Aurion, Wageningen) for 35-40 min. Resin sections were stained with 1% aqueous uranyl acetate for 4-5 min and lead citrate for 15-20 sec. For fluorescence labeling of coverslips, sections were labeled as described above with mouse anti-Xyloglucan antibodies (1:10) and goat anti-mouse IgG coupled to Cy3 (1:400; Dianova, Hamburg). Resin sections were stained for DNA with 1 μg/ml DAPI (4',6-diamidino-2-phenylindole) for 5 min and embedded in Moviol containing DABCO (1,4-diazabicyclo[2.2.2]octane) as anti-fading agent. Sections were viewed using a Zeiss Axioimager M2 with a 63x/1.40 oil immersion objective. Images were taken with a sCMOS Orca-flash4.0 camera (Hamamatsu). Contrast and brightness were adapted using Photoshop software.

For simultaneous double labeling with fluorescence and gold markers, sections mounted on slot grids were incubated with mouse anti-xyloglucan antibodies (1:10) as described above. Thereafter, sections were labeled with goat anti-mouse IgG coupled to 6 nm gold (6 min), directly followed by incubation with goat anti-mouse IgG coupled to Cy3. There were enough unbound first antibodies left for fluorochrome coupled marker molecules. Slot grids were then stained with DAPI and mounted on a slide under a coverslip with two additional coverslips laterally placed as spacer (in 50% glycerol) and fluorescent images were taken (see above). Thereafter, sections were washed with double distilled water and stained with 1% aqueous uranyl acetate (5 min) and in some cases with lead citrate (15-30 sec). Stained sections were examined in a Jeol TEM (see below). Alignment and overlay of light microscopic and electron microscopic images were performed with Picture Overlay Program (Jeol). Background was negligible in control experiments without first antibody. Contrast and brightness were adapted using Photoshop software.

Phylogenetic Tree Generation

Sequences of the plasma membrane-type Qa-SNAREs were acquired from NCBI (https://ncbi.nlm.nih.gov/BLAST) or from Phytozome v12 (https://phytozome.jgi.doe.gov/pz/portal.html) using taxa with complete genome sequences representative of the major plant branches. Proteins were aligned using MUSCLE in MEGA7 (Kumar et al., 2016). Phylogeny was tested using Neighbor-Joining (NJ) method (Seitou and Nei, 1987) in MEGA7. The optimal tree for just plant sequences had a branch length sum of 32.49052963, while the tree with additional non-plant taxa was 35.15907422. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replicates) is shown next to the branches (Felsenstein, 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method (Zuckerkandl and Pauling, 1965) and are in the units of the number of amino acid substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). The analysis involved 106 amino acid sequences. All ambiguous positions were removed for each sequence pair. There were a total of 541 positions in the final dataset.

Phenotypic Analysis

Seedlings and whole-mount chloral hydrate preparations of embryos were analyzed using a Leica MZFLIII binocular or a ZEISS Axiophot microscope (Heese et al., 2001). For structural analysis of endosperms, ovules were fixed in 4% paraformaldehyde, dehydrated with a series of ethanol and embedded in LR-White Resin (Figures 6I–6K) or Epon (Figure 6L). 1 to 5 μm-cut slices using cryomicrotome (Supercut 2065) were stained with toluidine blue. Images were taken with a Leica DC200 camera, using Adobe Photoshop CS3, or an AxioCam, using AxioVision 4.8.1 software. Images were processed with Adobe Photoshop CS3 and CS5.