A Highly Efficient Agrobacterium-Mediated Method for Transient Gene Expression and Functional Studies in Multiple Plant Species

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https://doi.org/10.1016/j.xplc.2020.100028

ABSTRACT

Although the use of stable transformation technology has led to great insight into gene function, its application in high-throughput studies remains arduous. Agro-infiltration have been widely used in species such as Nicotiana benthamiana for the rapid detection of gene expression and protein interaction analysis, but this technique does not work efficiently in other plant species, including Arabidopsis thaliana. As an efficient high-throughput transient expression system is currently lacking in the model plant species A. thaliana, we developed a method that is characterized by high efficiency, reproducibility, and suitability for transient expression of a variety of functional proteins in A. thaliana and 7 other plant species, including Brassica oleracea, Capsella rubella, Thellungiella salsuginea, Thellungiella halophila, Solanum tuberosum, Capsicum annuum, and N. benthamiana. Efficiency of this method was independently verified in three independent research facilities, pointing to the robustness of this technique. Furthermore, in addition to demonstrating the utility of this technique in a range of species, we also present a case study employing this method to assess protein–protein interactions in the sucrose biosynthesis pathway in Arabidopsis.

Key words: transient expression, agro-infiltration, subcellular localization, protein-protein interaction

been widely used in agriculture and is indeed indispensable for many aspects of plant science, recent attention has also been devoted to transient plant transformation (Wu et al., 2014; Krenek et al., 2015). Indeed the transient agro-infiltration method developed by Li et al. (2009) allows for rapid and scalable recombinant protein production, studies of protein subcellular localization and protein–protein interactions, as well as development of functional genomics assays.

An efficient tool to study the function of gene products, transient gene expression provides a convenient alternative to stable transformation. Although agro-infiltration has been widely used in Nicotiana benthamiana for the rapid evaluation of gene function and protein interaction studies (Sparkes et al., 2006), its use is limited to processes that naturally occur in this species. Thus, for the study of non-N. benthamiana appropriate, species-specific aspects of metabolism, development, or stress tolerance, use of this technique may be limiting (Krenek et al., 2015). At present, transient expression does not work efficiently in many other plant species/tissues, including Arabidopsis leaf tissue. Arabidopsis remains the most widely transformed species (predominantly by floral dipping-based transformation methods) (Provart et al., 2016), due to the wealth of genetic tools and resources available (Clough and Bent, 1998). Although stable transformation systems, such as floral dipping, have provided the potential for mutant complementation, as well as the ability to couple gene expression to marker proteins for examination of global gene expression (Chang et al., 1994), transient expression systems have provided a convenient alternative by virtue of time and labor efficiency (Krenek et al., 2015). Agrobacterium-mediated seedling transformation has been successfully used to express a wide variety of constructs driven by different promoters in cotyledons of Arabidopsis plants of diverse genetic backgrounds (Marion et al., 2008; Li et al., 2009; Wu et al., 2014; Wang et al., 2018). Furthermore, the transient transformation of Arabidopsis seedlings and perception of Agrobacterium (Mangano et al., 2014; Zhu et al., 2016; Rosas-Diaz et al., 2017). Given this, another transient transformation method was developed but was limited to transgenic plants expressing AvrPto under the control of a dexamethasone-inducible promoter (Tsuda et al., 2012). This background, however, is unlikely to be universally appropriate given that it is itself a mutant. Similar to A. thaliana, methods for stable transformation of Brassica oleracea (De Block et al., 1989), Thellungiella halophila (Li et al., 2007), Solanum tuberosum (Sheerman and Bevan, 1988; Zhang et al., 2014), and Capsicum annuum (Mahto et al., 2019) are well established, yet transient transformation methods are still lacking. Furthermore, neither transient nor stable transformation methods are well established in Capsella rubella and Thellungiella salsuginea. Because a method for reliable transient gene transformation in different species could significantly enhance our ability to evaluate protein function, localization, and interaction in a species-dependent or -independent manner, there is an urgent need for such a method to be developed.

Given that Arabidopsis has the advantage of having that harbours near-saturation level collections of T-DNA insertion mutants, we present a rapid and highly efficient transient expression assay for this species using simple infiltration of intact leaves with Agrobacterium. We additionally demonstrate its efficiency in B. oleracea, C. rubella, T. salsuginea, T. halophila, S. tuberosum, C. annuum, and N. benthamiana. In addition to demonstrating the utility of this method in a range of plant species, we also provide a case study of its utility in addressing protein–protein interactions. A recent paper has highlighted the utility of the recombination strategy for this purpose (Hu et al., 2019). Despite the great advances offered by this technique in aiding in the cloning of large genes, in Arabidopsis at least, it currently largely remains reliant on stable transformation techniques. Here, we demonstrate the capability of our transient expression system to investigate interactions of one of the key enzymes of sucrose biosynthesis in Arabidopsis.
Figure 2. The High-Efficiency Agro-Infiltration of Arabidopsis Leaves.

(A) Agrobacterium was streaked on YEB-induced medium, diluted with infiltration medium, and injected into leaves of Arabidopsis.
(B) Mitochondria-targeted citrate synthase with C-terminal GFP (CYS4-GFP) was infiltrated into Arabidopsis leaves using the standard protocol described in this paper.

(legend continued on next page)
RESULTS

Transient Expression in Arabidopsis Leaves

Here, we describe a robust transient expression method that is characterized by high efficiency, reproducibility, and suitability for a variety of functional Arabidopsis proteins with diverse biological activities and subcellular localizations (Figure 1). Two- to 3-week old Arabidopsis plants cultivated under 8-, 12-, or 16-h photoperiods were transformed before bolting and were used for proof-of-concept studies. For this purpose, the mitochondrial citrate synthesis 4 (CSY4) GFP fusion protein (Supplemental Tables 1–3) was transformed into the Agrobacterium strains to artificial fluorescence being observable under the confocal microscope.

For our case study, localization of the mitochondrial fusion protein was visualized by confocal microscopy. Infiltration with 0.005% Silwet L-77 resulted in 80%–90% of cells being transformed (Figure 2B and 2E), while only very few cells were transformed when plants were not kept in the dark for 24 h after infiltration (Figure 2C). No cells were transformed in the absence of Silwet L-77 (Figure 2D). In addition, the agrobacteria AGL1 strain resulted in higher transformation ratios of 95%–100% compared with the GV3101 strain (Figure 2F).

Transient Expression in the Leaves of Different Plant Species

To further test this method, we grew plants of several plant species commonly used in our research. Four Brassicaceae family species (B. oleracea, C. rubella, T. halophila, and S. tuberosum) were grown in the greenhouse under 8-, 12-, and 16-h photoperiods for 2–3 weeks. Younger leaves had higher transformation ratios compared with older leaves. Six-week-old S. tuberosum Deseree, C. annuum, and N. benthamiana were also cultivated in the greenhouse under 12-h photoperiods.

After growing AGL1 agrobacteria transformed with a mitochondrial CSY4 GFP fusion protein in induction medium (Supplemental Table 4) for approximately 2 days, the transformed agrobacteria were moved into wash solution (Table 1), diluted in infiltration solution, and injected into plant leaves using a disposable plastic syringe (Table 1). After drying the leaves and maintaining the plants in the dark for 24 h, the transformed plants were moved into the greenhouse for 2 days and examined under the microscope. B. oleracea transformation resulted in a success rate of only approximately 20% (Figures 3A and 4A), which is in contrast to the high success rates obtained for the other Brassicaceae family species used, where young leaves displayed transformation ratios of around 60%–80% (Figures 3B–3D and 4A). In S. tuberosum and C. annuum, a lower concentration of Silwet L-77 0.001% was used for infiltration, resulting in a transformation ratio of between 60% and 80% (Figures 3E and 4A), as it was observed that concentrations of 0.005%–0.01% Silwet L-77 could damage the leaves of these two species. In addition, the method we describe here also resulted in high levels of transiently expressed protein in N. benthamiana (Figure 3G), suggesting that it works efficiently in a broad range of species.

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transient transformation (Figure 2B–2D). Without Silwet L-77 or dark treatment after infiltration, the transformation ratio was as low as in previously published protocols (Mangano et al., 2014). Similarly, concentrations of Silwet L-77 that were too high and the lack of a leaf-drying step resulted in tissue damage leading to artificial fluorescence being observable under the confocal microscope.

Table 1. The Infiltration Solution for the Agrobacteria Infiltration

<table>
<thead>
<tr>
<th>Washing Solution</th>
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<tbody>
<tr>
<td>MgCl₂</td>
<td>10mM</td>
</tr>
<tr>
<td>Acetosyringone</td>
<td>100µM</td>
</tr>
<tr>
<td>Infiltration Solution (PH6.0, fresh)</td>
<td></td>
</tr>
<tr>
<td>Murashige and Skoog medium (sigma M5519)</td>
<td>1.1g</td>
</tr>
<tr>
<td>Sucrose</td>
<td>1%</td>
</tr>
<tr>
<td>Acetosyringone</td>
<td>100µM</td>
</tr>
<tr>
<td>Silwet L-77</td>
<td>0.01%</td>
</tr>
</tbody>
</table>

For Acetosyringone 100mM stock, dissolve 9.8mg in 0.5ml DMSO.

For infiltration solution needs to freshly prepared, while MS with 1% sucrose (pH=6.0) could be prepared as stock.

(C) Agro-infiltration protocol with transformed plants kept in darkness for 2 days.
(D) Agro-infiltration protocol without the addition the 0.005% Silwet L-77.
(E) Transformation efficiency of wild-type Arabidopsis plants. Dark method, CYS4-GFP was infiltrated into Arabidopsis leaves and plants were kept in the dark for 2 days. Light method, CYS4-GFP was infiltrated into Arabidopsis leaves without 0.005% Silwet L-77 and plants were kept in the light. New method, CYS4-GFP was infiltrated into Arabidopsis leaves using the standard protocol described in this paper. Old method, CYS4-GFP was infiltrated into Arabidopsis leaves using a previously published method (Mangano et al., 2014). The transformation efficiency was calculated from eight different replicates.
(F) Both agrobacteria strains, GV3101 and AGL1, were transformed into Arabidopsis leaves. Agro-infiltration of AGL1 into Arabidopsis leaves was achieved with high efficiency agro-infiltration of leaves.
The standard *Arabidopsis* transient transformation protocol described above was used without modifications for the transformation of *Brassica oleracea* (A), *Capsella rubella* (B), *Thellungiella salsuginea* (C), *Thellungiella halophila* (D), *Solanum tuberosum* (E), *Capsicum annuum* (F), and *Nicotiana benthamiana* (G).

**Figure 3. The High-Efficiency Agro-Infiltration of the Leaves of Different Plant Species.**

The standard *Arabidopsis* transient transformation protocol described above was used without modifications for the transformation of *Brassica oleracea* (A), *Capsella rubella* (B), *Thellungiella salsuginea* (C), *Thellungiella halophila* (D), *Solanum tuberosum* (E), *Capsicum annuum* (F), and *Nicotiana benthamiana* (G).
Using the Agro-Infiltration Method to Test for Novel Protein–Protein Interactions

In addition, AtSPS-GFP and GFP (Supplemental Table 2) were transformed into Arabidopsis leaves to further test the use of this method for the discovery of novel protein–protein interactions. Both GFP and AtSPS-GFP could be expressed to a high level in Arabidopsis leaves (Figure 4B and 4C). For each construct, four plants were used for infiltration and kept in the greenhouse for 6 days to produce approximately 2–3 g of plant material for affinity purification (AP). Because AP-mass spectrometry (AP-MS) experiments have been widely used to generate meaningful interaction networks (Puig et al., 2001; Bürckstümmer et al., 2006; Morris et al., 2014; Zhang et al., 2017b, 2018, 2019), it follows that they could be used to produce information-rich data concerning both within-pathway and extra-pathway protein–protein interactions. Such interactions would aid in the characterization of interacting protein function, provide detailed catalogs of proteins involved in forming protein complexes, and reveal networks of biological processes at local and proteome-wide scales (Morris et al., 2014).

The success of AP-MS greatly depends on tagged protein expression for AP, and the efficiency of trypsin digestion and the recovery of tryptic peptides for MS analysis (Zhang et al., 2017b, 2019). Unlike in digestion-based AP-MS, in which a gel is cut into pieces for several independent trypsin digestions (Morris et al., 2014), we used a proteomics-based in-solution digestion method to directly digest proteins on the beads that they were bound following AP (Zhang et al., 2017b, 2018). Thus, in an AP-MS experiment a single sample is used for the liquid chromatography-mass spectrometry (LC-MS) measurement. In subsequent data analysis, normalized signal intensities were processed to determine fold change in abundance (FC-A) scores using the SAINT algorithm embedded within CRAPome software (Choi et al., 2012; Morris et al., 2014). A total of 22 protein–protein interactions were obtained, displaying in excess of four-fold changes in abundance (Supplemental Table 3). We considered only the protein pairs for which the intensity scores were in the top 2% compared with GFP, which corresponded to FC-A values of at least 4 in a minimum of three of the four replicates as positive interactions. Because of the possible mis-targeted subcellular localization of AtSPS following high-level overexpression, only the cytosol localized preys were selected for network generation. Screening of the SUBA4 database...
(Hooper et al., 2016) revealed a total of 11 interactions between cytosol-localized AtSPS1 and cytosol target proteins, which comprise the interaction network (Figure 4D). Of these 11 interactions, 2 have been previously reported: ATSPS2F (Bahaji et al., 2015) and 14-3-3OMEGA (Toroser et al., 1998). These two previously known and nine novel interactions are shown in Figure 4D.

Colocalization of Selected Interaction Pairs and Confirmation of Interactions by BiFC

As the FC score from the AP-MS analysis is indicative of the interaction intensity (Mellacheruvu et al., 2013), we randomly selected two protein interactors with a high FC score (AtSPS2F and AtRHM1) and two interactors with a low score (AtCYT1 and 14-3-3OMEGA) to analyze the protein interaction network (Figure 4C). Colocalization refers to the observation of spatial overlap between two different fluorescent labels (mCitrine and mCherry), each having a separate emission wavelength, to see if the different “targets” are located in the same area of the cell or very near to one another, which provides support for their interaction. Because these proteins have the same suggested subcellular localization in SUBA4, we used two fluorescence signals to analyze the colocalization of these interaction pairs (Figure 5). In our experiment, both AtSPS1 and the four identified interactors were localized to the plasma membrane, suggestive of possible interactions. Moreover, we used two vectors co-infiltrated into Arabidopsis leaves with a previous

Figure 5. Subcellular Co-localization of Four AtSPS1 Interactors.
(A) AtSPS2F-mCitrine/AtSPS1-mCherry.
(B) AtCYT1-mCitrine/AtSPS1-mCherry.
(C) AtRHM1-mCitrine/AtSPS1-mCherry.
(D) 14-3-3OMEGA-mCitrine/AtSPS1-mCherry. The panels from left to right show the mCitrine fluorescence, mCherry fluorescence, autofluorescence, blank, and the merged image, respectively. AtSPS2F (AT5G11110) is an isoform of sucrose phosphate synthase. AtCYT1 (AT2G39770) is GDP-mannose pyrophosphorylase/mannose-1-pyrophosphatase. AtRHM1 (AT1G78570) is a UDP-L-rhamnose synthase. 14-3-3OMEGA (AT1G78300) is a 14-3-3 protein.
high efficiency of transformation. In addition, we also used bimolecular fluorescent complementation (BiFC) assays for analysis of these binary protein interactions (Figure 6). All four selected interactions were independently validated by BiFC assays, which enabled qualitative but highly sensitive detection of protein–protein interactions with subcellular localization information. Importantly, no BiFC signal was detected for any of the enzyme pairs that were not defined in our AP-MS interaction network.

**DISCUSSION**

We have developed a novel transient transformation method that enables unprecedentedly high transformation efficiency in a range of plant species, including *Arabidopsis* Col-0 seedlings. We believe a good transient expression system needs to fulfill several criteria: namely it should be highly reproducible in different labs, offer considerable time savings in comparison with stable transformation methods, and have a high transformation efficiency. Finally, it should achieve this without producing significant detrimental effects or artifacts and should be broadly applicable to different types of functional assays. Generally, the overall transformation efficiency achieved by agro-infiltration depends on the presence of mild concentrations of Silwet L-77 (Kim et al., 2009), streaking agrobacteria on agar plates, and keeping *Agrobacterium*-treated plants in the dark for 24 h. This method is optimized for transient expression of genes in *Arabidopsis* leaves, and routinely results in transformation of up to 70%–90% of cells. Furthermore, our method is applicable to very diverse types of proteins and experimental designs. We expect that this method can be readily adopted for other types of functional assays both in wild-type and mutant *Arabidopsis* plants. Importantly, this method nicely complements commonly used *Arabidopsis* mesophyll–protoplast transformation methods, *Agrobacterium* plant cell culture transformation, and *Agrobacterium*-mediated infiltration of *N. benthamiana* leaves (Sparkes et al., 2006) and would seem likely to be a great boon for researchers wanting to functionally complement studies in a medium- to high-throughput manner.

However, use of this method is not restricted to *Arabidopsis*, with data presented here revealing high-efficiency transformation of close *Arabidopsis* relatives, including *C. rubella*, *T. salsuginea*, and *T. halophilia*. Although a high transformation efficiency could not be obtained for *B. oleracea*, increased use of the other three Brassicaceae species tested here (Tohge et al., 2016, 2017, 2018) suggests that availability of a transient expression system for them will likely be highly useful to many researchers. Beyond Brassicaceae, we also demonstrate that the protocol could be used for transient expression in *S. tuberosum*, *C. annuum*, and *N. benthamiana*. Although the latter is commonly used for transient expression (Martin et al., 2009; Li et al., 2013), the fact that our protocol also works in this species may prove useful in instances where it is preferable to assess the effect of transient expression in several species. Although potato was one of the earliest stably transformed plants (Fernie and Willmitzer, 2001; Hofius et al., 2001) using virus-induced gene silencing (VIGS) (Brigneti et al., 2004; Faivre-Rampant et al., 2004), only a single report of transient overexpression has been, to date, reported in this species (Ma’u et al., 2018). This situation is even more severe in *C. annuum*, with only a handful of laboratories even reporting successful stable transformation to date (Manoharan et al., 1998; Kumar et al., 2012). Therefore, having a functional transient expression system will likely be a great boon for this species and for many others. Indeed both potato and *C. annuum* have advanced genetic resources available, including high-quality genomes (Potato Genome Sequencing Consortium, 2011; Qin et al., 2014) and ample transcriptomics datasets (Li et al., 2016), and are relatively well characterized at the proteomic and metabolomics levels (Palma et al., 2018; Shekhar et al., 2016).
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Furthermore, both mapping populations and a global panel of accessions for both species have been generated or collected allowing quantitative trait loci and genome-wide association studies, respectively, to be performed. Thus the transient expression method we describe here will likely also find great utility as a tool for the rapid validation of candidate genes. Although VIGS is one strategy for transient expression, as we mention above this system is not currently developed for C. annuum. We should note here that the method proved successful for every species tested, with the exception of B. oleracea, suggesting that its range and hence its utility likely exceeds that we report here.

In addition to the development of the technique, we describe one experiment designed to provide rapid insight into Arabidopsis biology. For this purpose, we investigated the protein binding partners of sucrose phosphate synthase. We chose this protein because of a hypothesis raised following the elucidation of the crystal structure of an enzyme from the sucrose synthesis pathway, sucrose phosphate phosphatase (from cyanobacteria), which suggested that sucrose phosphate synthase and sucrose phosphate phosphatase may operate in tandem to channel sucrose phosphate (Fieulaine et al., 2005). We recently demonstrated that plants harbor the canonical glycolysis metabolon (Zhang and Fernie, 2018) as well as a novel plant-specific channel within the TCA cycle (Zhang et al., 2017a; Fernie et al., 2018). Furthering this investigation, here we adopted the same approach but used transient rather than stable transformation of Arabidopsis cultures to assess the protein–protein interactions of sucrose phosphate synthase. We were unable to find an association between sucrose phosphate synthase and sucrose phosphate phosphatase, suggesting that it is highly unlikely that they channel sucrose 6-phosphate. However, 11 other interacting proteins were found with a similar subcellular location. These sucrose phosphate synthase interactors include a different isoform of sucrose phosphate synthase (Bahaji et al., 2015) and the known regulatory protein 14-3-3Ω (Toroser et al., 1998), in phosphate synthase (Bahaji et al., 2015) and the known synthase interactors include a different isoform of sucrose with a similar subcellular location. These sucrose phosphate synthase and sucrose phosphate phosphatase may operate in tandem to channel sucrose phosphate (Fieulaine et al., 2005). We recently demonstrated that plants harbor the canonical glycolysis metabolon (Zhang and Fernie, 2018) as well as a novel plant-specific channel within the TCA cycle (Zhang et al., 2017a; Fernie et al., 2018). Furthering this investigation, here we adopted the same approach but used transient rather than stable transformation of Arabidopsis cultures to assess the protein–protein interactions of sucrose phosphate synthase. We were unable to find an association between sucrose phosphate synthase and sucrose phosphate phosphatase, suggesting that it is highly unlikely that they channel sucrose 6-phosphate. However, 11 other interacting proteins were found with a similar subcellular location. These sucrose phosphate synthase interactors include a different isoform of sucrose phosphate synthase (Bahaji et al., 2015) and the known regulatory protein 14-3-3Ω (Toroser et al., 1998), in addition to nine other proteins with various functions, including metabolic enzymes, transport proteins, and chaperones, as well as proteins with little known functions. This study was able to rapidly evaluate the hypothesis that sucrose 6-phosphate is channeled in plants and also to provide a list of candidate regulatory proteins that may aid in the assembly or stability of sucrose phosphate synthase. We identified a similar set of proteins when assembling the extra-pathway TCA cycle interactome (Zhang et al., 2018), and feel that this may prove to be a common feature in metabolism-associated protein–protein interaction networks.

In summary, this technical report presents a protocol for transient expression in Arabidopsis that can also be applied to a range of other species. In addition, we demonstrate its utility in protein localization and protein–protein interaction studies as well as proving its usefulness as a means to rapidly test previous biological postulates. We strongly believe that this protocol will prove highly useful for a wide number of laboratories since it improves greatly on existing protocols for Arabidopsis as well as opening up new avenues of research in several other species of ecological, environmental, and agronomic importance. Although the tremendous interest and development of CRISPR-based strate-

Plant Communications 1, 100028, September 14 2020 © 2020 The Authors.
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localization of the tagged proteins were evaluated by visualizing GFP fluorescence using confocal microscopy. The transformed plant materials were collected 6 days after their transfer to the greenhouse. After grinding tissue into a fine powder using a ball mill (MM301, Retch, Haan, Germany), proteins were extracted by mixing 2 g of material with 2 ml extraction buffer (25 mM Tris–HCl [pH7.5], 15 mM MgCl2, 5 mM EGTA, 1 mM dithiothreitol, and 1 mM phenylmethylsulfonyl fluoride). Following removal of cell debris by repeated centrifugation at 22 000 g, 4 °C for 5 min, the supernatant was mixed with 25 μl of GFP-Trap A slurry (ChromoTek, Martinsried, Germany) equilibrated with extraction buffer and incubated for 1 h at 4 °C with rotation. The beads were collected by centrifugation at 3000 g, 4 °C for 3 min and washed three times each with extraction buffer containing different concentrations of NaCl (0, 250, and 500 mM) (Zhang et al., 2019).

The proteins remaining on the beads were subsequently subjected to proteolysis via in-solution digestion with LysC and trypsin and the resulting peptides were purified (Wisniewski et al., 2009). LC-tandem MS (LC-MS/MS) analysis was performed on a Q Exactive Plus (Thermo Fisher Scientific) machine. Quantitative analysis of MS/MS measurements was performed with Progenesis IQ software (Nonlinear Dynamics, Newcastle, UK). Proteins were identified from spectra using Mascot (Matrix Science, London, UK). Mascot search parameters were set as follows: TFA:R10 protein annotation, requirement for tryptic ends, one missed cleavage allowed, fixed modification (carbamidomethylation [cysteine]), variable modification (oxidation [methionine]), peptide mass tolerance ± 10 ppm, MS/MS tolerance ± 0.6 Da, allowed peptide charges of +2 and +3. A decoy database search was used to limit the false discovery rate to 1% at the protein level. Peptide identifications below rank 1 or with a Mascot ion score below 25 were excluded. Mascot results were imported into SAINT (Nesvizhskii, 2012) using tandem affinity purification-mass spectrometry data with SAINT. Curr. Opin. Chem. Biol. 11:263–271 to restrict defined interactors to those proteins that are co-localized to the cytosol (Zhang et al., 2019).

BIFC Confocal images were taken using a DM6000B/SP5 confocal laser scanning microscope (Leica Microsystems, Wetzlar, Germany). BIFC and MitoTracker fluorescence were imaged with 488 and 555 nm laser excitation, and emission fluorescence was captured by 500–520 and 560–580 nm band-pass emission filters, respectively.

Co-subcellular Localization Analysis Constructs (Supplemental Table 2) were transiently expressed in Arabidopsis leaves by agro-infiltration as mentioned above for the protein co-subcellularization analysis. Confocal images were taken using a DM6000B/SP8 confocal laser scanning microscope.

SUPPLEMENTAL INFORMATION
Supplemental Information is available at Plant Communications Online.

FUNDING
This work was supported by funding from the Max Planck Society (A.R.F. and Y.Z.) and the European Union’s Horizon 2020 project PlantsSYST (SGA-CSA no. 739582 under FPA no. 664620 (A.R.F. and Y.Z.).

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