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Two interacting PPR proteins are major Arabidopsis editing factors in plastid and mitochondria

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RNA editing is converting hundreds of cytosines into uridines during organelle gene expression of land plants. The pentatricopeptide repeat (PPR) proteins are at the core of this posttranscriptional RNA modification. Even if a PPR protein defines the editing site, a DYW domain of the same or another PPR protein is believed to catalyze the deamination. To give insight into the organelle RNA editosome, we performed tandem affinity purification of the plastidial CHLOROPLAST BIOGENESIS 19 (CLB19) PPR editing factor. Two PPR proteins, dually targeted to mitochondria and chloroplasts, were identified as potential partners of CLB19. These two proteins, a P-type PPR and a member of a small PPR-DYW subfamily, were shown to interact in yeast. Insertional mutations resulted in embryo lethality that could be rescued by embryo-specific complementation. A transcriptome analysis of these complemented plants showed major editing defects in both organelles with a very high PPR type specificity, indicating that the two proteins are core members of E+-type PPR editosomes.

RNA editing | organelles | pentatricopeptide repeat

In vascular plant organelle RNAs, hundreds of specific cytidines are converted into uridines by the so-called RNA editing mechanism (C to U editing). This phenomenon remained very enigmatic for a long time, raising numerous questions about its purpose, its evolution, and the molecular mechanism behind its very high specificity. Even if editing finality is still a matter of debate, many components of plant editosomes and the molecular elements required for editing specificity have been described (1, 2).

The editable cytidine is identified by a pentatricopeptide repeat (PPR) protein through the recognition of 20–25 bases upstream of the cytidine (1). However, the 5' cis-elements, defining RNA editing sites, are not conserved between sites. Each editing site is targeted by a specific PPR protein. For example, in *Arabidopsis thaliana*, a total of 56 PPR proteins were shown so far to be each required for the editing of one to eight specific sites (Table S1). The PPR domain is a degenerated polypeptide showing a conserved structural conformation able to bind RNA molecules when it is repeated in tandem (3–5). A code for RNA recognition by PPR proteins was proposed (6–10). In this code, the nucleotide recognition is achieved by the combination of three amino acids of each PPR motif.

The nature of the PPR domains within proteins is used to divide the PPR family into two subfamilies, the PPR-P and the PPR-PLS. This last subfamily is subdivided in subgroups according to their E1, E2, E+, and DYW C-terminal domains (11, 12). Most members of the P-type PPR subfamily have been implicated in RNA metabolism such as 5' or 3' transcript stabilization and processing, splicing, and translation (5), whereas most editing PPR proteins belong to the PLS subfamily (1). Although a function in selecting editing sites is well defined for their PPR domains, the functions of the E1, E2, E+, and DYW domains remain unclear and controversial. Molecular and phylogenetic evidences suggest that the DYW domain is required for the editing activity (13, 14). Despite the lack of definitive biochemical evidence, it has been hypothesized that it could contain the RNA editing enzymatic activity

required for the deamination of cytidines into uridines (13–16). However, some editing PPRs do not carry any DYW domain and end with either an E1, E2, or E+ domain (1). Moreover, the DYW domain could be deleted in some PPR-DYW proteins without affecting their function in editing (17). To reconcile the different pieces of evidence, it has been proposed that the cytidine deaminase activity could be provided either in cis by a PPR-DYW specificity factor or in trans when a PPR-E factor is required for the site recognition. This was shown, for example, for the editing of the chloroplastic *ndhD-1* site, where the target site is recognized by CRR4, a PPR-E specificity factor, whereas a DYW domain is provided by DYW1, a small protein containing only a DYW domain (18).

Besides PPR proteins, numerous additional proteins were shown to be required for the same editing events, suggesting the existence of high molecular mass editosome protein complexes (2). In particular, three classes of essential non-PPR components of the editosomes were shown to be involved in C to U RNA editing. These proteins are members of small families and are suspected to have partially redundant functions as general factors involved

Significance

Breaking the “central dogma” of molecular biology, RNA editing is a specific posttranscriptional modification of RNA sequences. In seed plant organelle editosomes, each editable cytidine is identified by a specific pentatricopeptide repeat (PPR) protein. Some of these sequence-specific proteins contain an additional C-terminal “DYW” domain, which is supposed to carry the catalytic activity for editing. However, many PPR editing factors lack this domain. In this article, we show that a subfamily of about 60 Arabidopsis proteins might all require two additional PPR proteins for the editing of their sites. One of them, DYW2, is a specific cofactor containing a DYW domain, supporting the hypothesis that this domain might bring the cytidine deaminase activity to these editosomes.

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Table 1. Proteins purified by TAP using CLB19 as bait in *Arabidopsis* cell suspension culture PSB-L

AGI*	Name [†]	Prot. mass, KDa	Loc. [‡]	No. identified in four TAPs [§]
AT1G05750	CLB19	56.4	C (26)	4
AT2G15690	DYW2	66.3	M/C (42)	4
AT3G49240	NUWA	71.7	M/C (34)	4

**Arabidopsis* genome initiative annotation identifier in TAIR database version 9.

[†]CLB19, ChLoroplast Biogenesis 19.

[‡]Loc., subcellular localization of proteins.

[§]See Dataset S1 for mass spectrometry analysis details.

in the editing of organelle transcripts (2). In *Arabidopsis*, nine Multiple Organellar RNA editing Factors (MORF/RIPs) were described as required for many editing sites of plant organelles (19–21). Members of the ORRM family and the CP31 protein, containing RNA Recognition Motifs (RRMs), were also found to influence RNA editing in plant organelles (22, 23). More recently, OZ proteins were found to copurify with components of the editosomes and also be required for organellar editing (24).

Although extensive studies of plant editosomes have already identified many factors, further studies are needed to discover new components as well as their relations in the protein network. Here, we implemented a tandem affinity purification (TAP) approach to gain insight into the composition of a chloroplast editing complex. We use the known chloroplast editing factor CHLOROPLAST BIOGENESIS 19 (CLB19) required for *rpoA* and *clpP* editing (25) as bait for purification. Two unknown PPR proteins, dually targeted to mitochondria and chloroplasts and required for *Arabidopsis* embryo development, were identified in the CLB19 editing complex. A transcriptome analysis of the mutants showed major editing defects in both organelles with a very high PPR-type specificity indicating that the two proteins are core members of E+-type PPR editosomes.

Results

Exploring the CLB19 Chloroplast Editing Complex. To improve our knowledge of the in vivo composition of an RNA editing complex of land plant chloroplasts, a TAP approach was performed using the previously characterized chloroplast editing factor CLB19 as bait. CLB19 was fused to a G protein and a streptavidin-binding peptide (GS) tag at its C terminus (26, 27) and was expressed under the control of the cauliflower mosaic virus (CaMV) 35S promoter (Fig. S1A). In *clb19-1* mutant plants, the CLB19-TAP tag protein was able to complement the macroscopic phenotype of the mutant (Fig. S1B and C), indicating that the fusion protein was functionally similar to the wild-type protein. After production in *Arabidopsis* cell suspension culture PSB-L, two proteins were copurified with CLB19-GS in four independent experiments (Table 1 and Dataset S1). The fourth sample was subjected to RNase treatment before purification without any modification of the proteins identified in the complex (Dataset S1). Both identified proteins, AT3G49240 and AT2G15690, are members of the PPR family. According to the PPR classification, AT3G49240 belongs to the P-type PPR subfamily. This protein was recently shown to be encoded by a maternal imprinted gene named *NUWA* (28). AT2G15690 belongs to the PPR-DYW subfamily and was named DYW2 (detailed in *DYW2 and NUWA Are Two Distant PPR Proteins*).

To identify proteins interacting with CLB19, NUWA, and DYW2, we screened these three PPR proteins against a library of more than 12,000 *Arabidopsis* proteins using an improved high-throughput binary interactome mapping pipeline based on yeast two-hybrid (Y2H). Among the interactions involving DYW2, we identified a direct link between NUWA and DYW2 (Fig. S2). In contrast, we did not identify any interactor of the CLB19 protein in this screen.

DYW2 and NUWA Are Two Distant PPR Proteins. DYW2 is an atypical PPR-DYW protein containing five predicted PPR domains and a C-terminal DYW domain separated by an amino acid sequence that do not clearly correspond to an E domain (11) (Fig. 1A). This unusual architecture of a PPR protein carrying a DYW domain without any regular E1 and E2 domains is shared by only five other proteins in the *A. thaliana* genome, among which is the DYW1 chloroplast editing factor (18). The other members of this small subfamily (Fig. S3), called here after the DYW1-like subfamily, are two mitochondrial editing factors, MEF8 and MEF8S (29), and two uncharacterized proteins, AT2G34370 (DYW3) and AT1G29710 (DYW4).

In silico prediction of PPR domains using the PPR Gene Database (11) and TPRpred (30) websites showed that NUWA harbors up to 12 PPR domains covering most of its amino acid sequence. As reported previously (28), a coiled-coil domain is predicted in the N-terminal region of the NUWA protein, whereas a 106-amino acid sequence without any conserved domain is present upstream of the PPR motifs (Fig. 1B). Its closest homolog in the *Arabidopsis* genome is GRP23, a nuclear and mitochondrial PPR (31, 32). GRP23 shares 34% amino acid identity with NUWA but does not carry any coiled coil domain (31).

NUWA and DYW2 Are Dually Targeted to Chloroplast and Mitochondria.

Several independent experiments previously showed that *A. thaliana* NUWA and DYW2 proteins, or some of their orthologs, are dually targeted to mitochondria and plastids. Whereas NUWA was recently published as localized in mitochondria (28), AT3G49240 (NUWA) was identified in several proteomic data either in *A. thaliana* mitochondria (33, 34) or chloroplastic samples (35, 36). In accordance with these results, we and Andrés-Colás et al. (32, 37) observed NUWA presequence and full-length fusions to fluorescent proteins in mitochondria and chloroplast (Fig. S4). The two maize orthologs of DYW2 (GRMZM2G073551 and GRMZM2G017821) were identified in plastid nucleoids (38), whereas its rice ortholog was described in mitochondria (39) samples. In *A. thaliana*, AT2G15690 (DYW2) was observed in both mitochondria and plastids when fused to a GFP protein (Fig. S4) (37, 40). These dual subcellular localizations were further confirmed by reverse

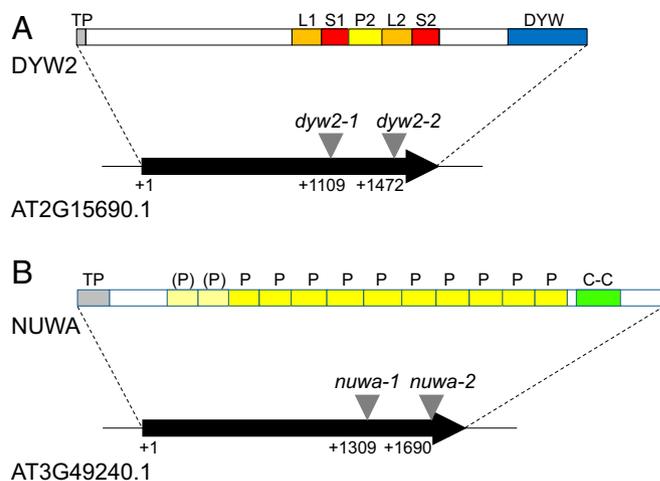


Fig. 1. DYW2 and NUWA are members of the PPR family. (A) DYW2. (B) NUWA. Schematic structures of the loci and the proteins. Predicted targeting peptide (TP, gray box), S (red), L (orange), P (yellow), DYW (blue), and coiled-coil region (C-C, green) domains are labeled on the protein sequence. The targeting peptide was predicted using the TargetP software at www.cbs.dtu.dk/services/TargetP/ for plant organisms using no cutoffs. S, L, P, and DYW domains were located according to the PPR Gene Database (11) and using the TPRpred software at <https://toolkit.tuebingen.mpg.de/#/tools/tpred> [(P), light yellow]. Sequence-verified locations of the T-DNA insertions used in this study are indicated (+1 is the transcription start).

genetic analyses and the identification of molecular phenotypes in both mitochondria and plastids of *dyw2* and *nuwa* mutants (see *DYW2 and NUWA Proteins Are Functionally Linked and Involved in Editing of Chloroplast and Mitochondria Transcripts*).

NUWA and DYW2 Proteins Are Required for Embryo Development. A reverse genetics approach was used to identify the molecular functions of DYW2 and NUWA proteins. Two T-DNA insertions in each gene were selected from the T-DNA Express database (41) and were named *dyw2-1* (GK_332A07), *dyw2-2* (FLAG_435F11), *nuwa-1* (SALK_069042), and *nuwa-2* (SAIL_784_A11). The position of each T-DNA was confirmed by sequencing and is indicated in Fig. 1. *nuwa-1* and *nuwa-2* were previously characterized as two embryo-defective alleles of the *EMBI796* locus during the seed-genes project (42). Similarly, another T-DNA insertion mutant, *nuwa*, was recently shown to be affected in early embryogenesis and endosperm development (28). Accordingly, no homozygous seedling for *nuwa-1* and *nuwa-2*, but also *dyw2-1* and *dyw2-2*, insertions was found from large screens of heterozygous plant progenies, whereas aborted embryos were observed when opening siliques of heterozygous plants (Fig. 2A). Pollen viability was assayed by Alexander staining of mature anthers from heterozygous plants. Results indicated that all pollen grains were viable in both heterozygous mutants and that mutations did not affect male gametophyte viability (Fig. 2A). Finally, genetic complementation assays between, on one hand, *dyw2-1* and *dyw2-2* lines and, on the other hand, *nuwa-1* and *nuwa-2* lines confirmed that *dyw2-1* and *dyw2-2* and *nuwa-1* and *nuwa-2* are allelic mutations responsible for the observed embryo lethal phenotype (Table S2).

Complementation of *dyw2* and *nuwa* in Embryos and Seeds. To bypass the embryo lethality of the mutants, we complemented them by expressing NUWA and DYW2 wild-type proteins under the control of the embryo-specific *ABI3* promoter (43). After seedling development, the *ABI3* promoter is expected to be no longer active, leading to its absence of expression in seedlings and at the adult stage. This strategy allowed the development of homozygous *dyw2* and *nuwa* mutant embryos in siliques of heterozygous plants and the germination of homozygous seedlings in their progeny (Fig. 2B). The absence of expression of *NUWA* and *DYW2* transcripts in adult plants was confirmed by qRT-PCR (Fig. 2C) and subsequently when analyzing RNA-sequencing (RNA-seq) data (see *dyw2-1* and *nuwa-2* Complete Transcriptome Analysis). Whereas the *nuwa* mutants were almost indistinguishable from WT, the *dyw2* mutants were small pale green plants producing sterile flowers (Fig. 2B and D).

DYW2 and NUWA Proteins Are Functionally Linked and Involved in Editing of Chloroplast and Mitochondria Transcripts. As DYW2 and NUWA are PPR proteins interacting with the editing PPR protein CLB19, we tested their involvement in editing of organelle RNA by total RNA-seq analysis of the rescued *dyw2-1* and *nuwa-2* mutants. The organellar editing quantification identified 392 and 223 differentially edited sites in *dyw2-1* and *nuwa-2*, respectively (Fig. 3A and B and Dataset S2 A and B). The differentially edited sites were either mitochondrial or chloroplastic and included previously unidentified editing sites (109 in *dyw2-1* and 44 in *nuwa-2*). Surprisingly, one site (position 20299 of the plastid genome) was edited only in *dyw2-1*. Targeted Sanger sequencing of

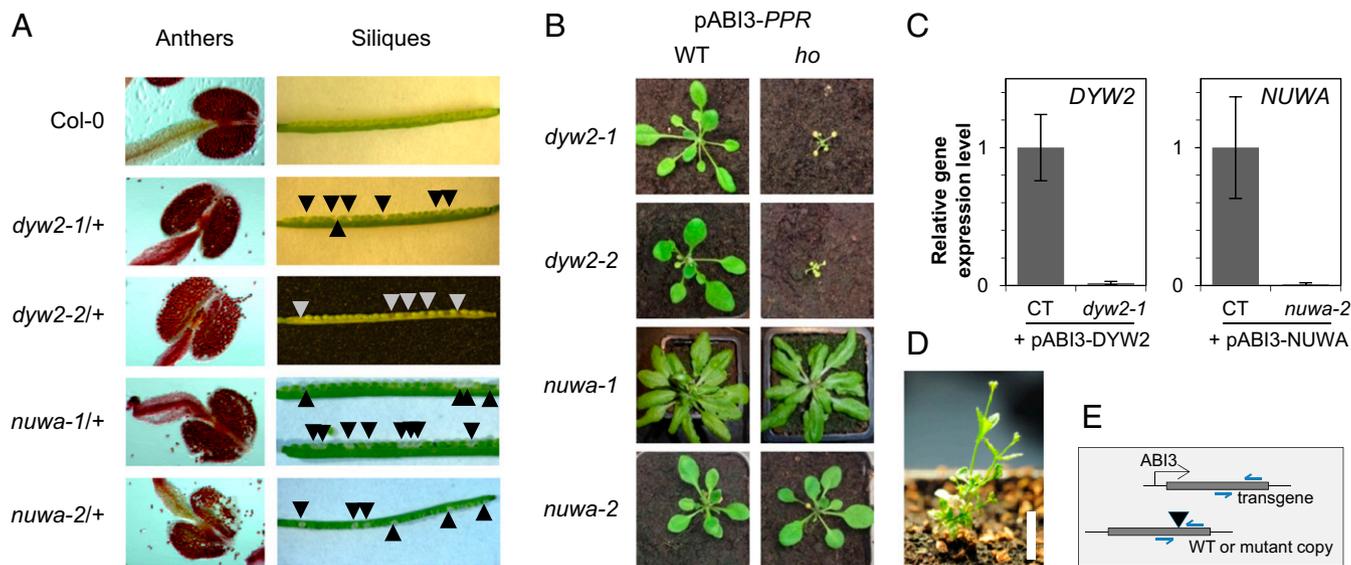


Fig. 2. Characterization of *dyw2* and *nuwa* mutants. (A) Phenotype of pollen and embryo observed on heterozygous *dyw2* and *nuwa* plants. (Left) The viability of pollen was assayed by Alexander staining of wild-type and heterozygous plant anthers. (Right) Siliques resulting from wild-type or heterozygote self-pollination were opened 10 d after pollination. Abnormal seeds (arrows) accounted for ~25% of the total observed. (B) Macroscopic phenotype of 1-mo-old homozygous mutant plants obtained after complementation with an embryo-specific construct. Heterozygous plants for *dyw2-1* and *dyw2-2* mutations were transformed with full-length DYW2 under the control of the embryo-specific *pABI3* promoter, whereas heterozygous plants for *nuwa-1* and *nuwa-2* mutations were transformed with full-length NUWA under the control of the *pABI3* promoter. Progeny seedlings of heterozygous T1 plants were genotyped to identify wild-type (Left), heterozygous (not shown), and homozygous (Right) sibling plants carrying the *pABI3* embryo-specific construct. After germination on MS + hygromycin media, 10-d-old seedlings were transferred onto soil in a growth chamber with long-day conditions. (C) *DYW2* and *NUWA* gene expression in homozygous mutant plants obtained after complementation with an embryo-specific construct. Gene expression of 1-mo-old plants grown in long-day conditions was measured by qRT-PCR using total RNA extracted from leaves of four biological replicates of *dyw2-1* and *nuwa-2* homozygous plants expressing the corresponding *pABI3* construct and of control sibling plants. For each biological replicate, the mean expression level of three technical qRT-PCR replicates was normalized with the mean of *actin2-8* expression, used as reference gene. Controls (CTs) refer to siblings of homozygous mutant plants coming from the same self-progeny, wild type or heterozygous for the mutation, and carrying the corresponding *pABI3* transgene. (D) Adult phenotype of *dyw2* mutant expressing *pABI3-DYW2*. A homozygous *dyw2-2* adult plant was observed after 7 wk of culture in soil in greenhouse with short day condition (white bar, 1 cm). Flower buds were produced but did not further develop in flowers and siliques. (E) Schematic representation of the primers used for qRT-PCR in Fig. 2C. Primers are surrounding positions of T-DNA insertion. Thus, in homozygous plants expressing *pABI3* construct, the expression level reflects the expression of the *pABI3* construct, whereas, in CT plants, the expression level corresponds to the expression of both endogenous and transgenic genes.

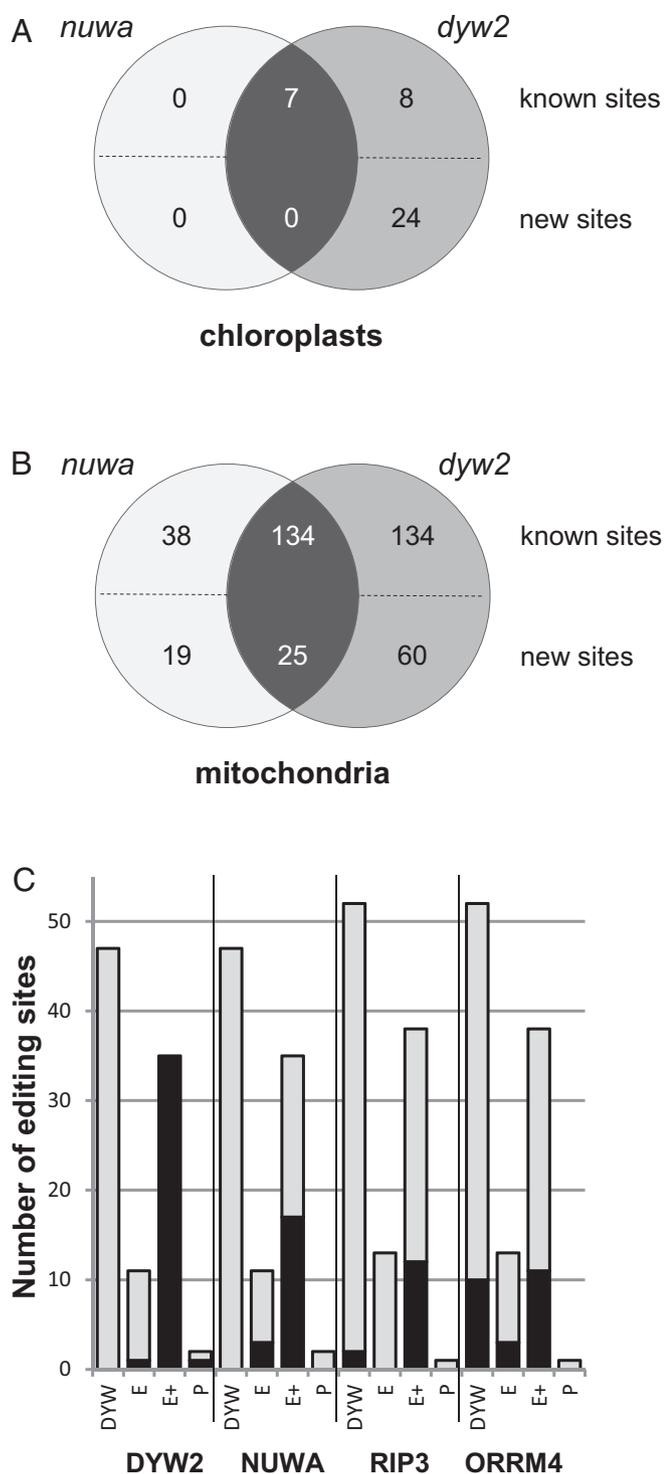


Fig. 3. Editing activity of DYW2 and NUWA. The detailed results are provided in [Dataset S2 A–D](#) and [Dataset S3](#). (A) Plastidial editing sites affected in *dyw2* and *nuwa*. (B) Mitochondrial editing sites affected in *dyw2* and *nuwa*. Venn diagrams summarizing the number of differentially edited sites in *dyw2-1* and *nuwa-2*. The known sites correspond to the sites identified in Bentolilla et al. (44), Sun et al. (24), Shi et al. (60), and Shi et al. (45). The new sites are the editing sites identified in this study. (C) DYW2 and NUWA-dependent sites are targeted by PPR-E+ proteins. The PPR specificity of DYW2, NUWA, RIP3, and ORRM4 was estimated by counting the dependent (black) and independent (gray) editing sites associated with PPR of the various subfamilies [DYW, E, E+, and pure (P)]. An editing site is considered as depending on a particular

several RT-PCR products from the corresponding second allele (rescued *dyw2-2* and *nuwa-1*) mutants showed similar results ([Dataset S3](#)), indicating that editing defects were genetically linked to mutations in either *DYW2* or *NUWA* locus. Interestingly, *dyw2-1* and *nuwa-2* shared 166 differentially edited sites, a number significantly higher to what would be randomly expected ($P = 0$), and these common sites included the *clpP* and *rpoA* editing sites associated with CLB19. This result strongly suggests that CLB19, DYW2, and NUWA are editing partners supporting the physical interactions previously observed.

DYW2 and NUWA Are Required for Editing by PPR-E+. As DYW2 and NUWA are working together with CLB19 (this work) and SLO2 (37), two PPR-E+s, we explored their association with PPR-E+ in general. Using the same criteria as Bentolilla et al. (44), we considered only the editing sites depending on DYW2 or NUWA. There was a strong positive bias for sites associated with PPR-E+ proteins. Out of 47 analyzed sites associated with PPR-DYW proteins, none are depending on DYW2 or NUWA. Conversely, the 35 known PPR-E+ sites analyzed in this study are depending on DYW2 and 17 of them are depending on NUWA (Fig. 3C). Applying the same statistical analysis for RIP3 (44) (Fig. 3C and [Dataset S2C](#)) and ORRM4 (45) (Fig. 3C and [Dataset S2D](#)), two editing factors controlling numerous chloroplastic and mitochondrial sites, showed no such specificity. These results and the work of Andrés-Colás et al. (37) support an extension of the function of DYW2 and NUWA to all PPR-E+ proteins.

***dyw2-1* and *nuwa-2* Complete Transcriptome Analysis.** The total RNA-seq approach allowed further complete and parallel quantitative analyses of nuclear, mitochondrial, and plastidial transcriptomes. As PPR proteins of the pure subfamily such as NUWA have rarely been involved in editing (46) and to confirm that DYW2 and NUWA function primarily in RNA editing, total RNA-seq data were used to quantify organelle transcript splicing, processing, and accumulation in *nuwa-2* and *dyw2-1*. The organelle transcriptome of *dyw2-1* was highly impacted with 182 differentially expressed genes out of 239 and 21 differentially spliced introns out of 37 ([Dataset S2 E–G](#)). Noteworthy, the plastid gene expression profile of *dyw2-1* was similar to the expression profile of *clb19* as described by Chateigner-Boutin et al. (25), suggesting that the perturbations in the *dyw2-1* transcriptome were the consequences of the numerous editing defects, especially in *rpoA*, which encodes a subunit of the plastid encoded RNA polymerase. On the other hand, the organelle transcriptome of *nuwa-2* showed limited perturbations with only 28 differentially expressed genes and 6 differentially spliced introns, including only one that was partially impaired ([Dataset S2 E, F, and H](#)). As most of these perturbations were also found in *dyw2-1* and no strong processing defect likely to explain the editing defects of *nuwa-2* was detected ([Dataset S2I](#)), these results strongly suggest that both DYW2 and NUWA are genuine editing factors.

The analysis of the nuclear transcripts confirmed that no functional RNA of *DYW2* or *NUWA* was detected in the corresponding mutants. Indeed, although reads were mapping to the genes, the mutants showed no read overlapping the T-DNA insertion sites as opposed to the controls, indicating that despite normal counts, no full-length RNA was produced in these mutants. The nuclear transcriptome analysis also showed that 12,485 genes were differentially expressed in *dyw2-1* versus only 1,097 in *nuwa-2*, in agreement with their macroscopic phenotype ([Dataset S2J](#)). Interestingly, the analysis of the nuclear transcriptome with MapMan

protein if it is differentially edited between CT and mutant (P value < 5% after Bonferroni correction) and its editing extent is decreased by 10% or more in the mutant. It is independent otherwise. Editing sites associated with known PPRs are listed in [Table S1](#) with their corresponding primary references. Values for RIP3 and ORRM4 were obtained by applying our statistical protocol to the raw data from Bentolilla et al. (44) and Shi et al. (45), respectively. The total number of sites differs from one study to the other because of missing data from some editing sites in each study.

showed that the PPR gene family was significantly affected in both mutants ($P = 0$; [Dataset S2K](#)), suggesting that the organelle gene expression was impacted. In particular, *NUWA* was induced four times in *dyw2-1*, and *DYW2* was induced twice in *nuwa-2*. Although major, these nuclear transcriptome modifications very probably reflected secondary effects of severe organelle dysfunctions as expected in mitochondria and plastid mutants because of organelle-nuclear signaling (47).

Discussion

Different RNA editing complexes have been described in several organisms, some of them having high molecular mass quaternary structures such as the 20S editosome of *Trypanosoma brucei* (48), for example. In contrast, it was first suggested that plant editing complexes could simply constitute one or two (PPR) proteins (18, 49, 50), similarly to the initial model of C-to-U mammal editosome where a specificity factor, ACF, binds the RNA sequence and recruits APOBEC-1, the enzyme catalyzing the reaction (51). The composition of plant RNA editosomes recently appeared to be more convoluted and heterogeneous with numerous additional proteins whose functions are still poorly understood (2). In these complexes, one or two PPR proteins of the PLS subfamily are considered to be key factors providing both the specificity and probably the enzymatic activity. Here, we show that two PPR proteins, *DYW2* and *NUWA*, are physically and functionally part of the E+ editosomes and required for the editing activity of probably all PPR-E+ proteins.

Our results predicted that at least three different PPR proteins are at the core of each E+ editosome: a PPR-E+ specific of the target site and two common PPR proteins, *DYW2* and *NUWA*. Whereas, in such a complex, the function of the PPR-E+ is well known as the specificity factor binding the target RNA, the molecular functions of the two other PPR proteins remain unclear. Unexpectedly for PPR proteins, reverse genetics analyses indicated that they could have numerous potential binding sites without any sequence similarity. This suggests that unlike most PPR proteins, *DYW2* and *NUWA* may not bind to RNA or bind RNA with low sequence specificity. As proposed in the companion paper from Andrés-Colás et al. (37) and supported by our results, an interesting hypothesis is that *NUWA* may bridge and stabilize the interaction between PPR-E+ and *DYW2* proteins. As proposed for the *DYW1* protein, which brings a *DYW* domain to the *CRR4* protein (18), it is probable that *DYW2* brings the cytidine deaminase activity to the E+ editosomes. Thus, the core of any plant organelle editosome would be organized with a PPR protein targeting the editing site and a *DYW* domain bringing the enzymatic activity. This domain is provided in cis by the PPR specificity factor when it belongs to the PPR-*DYW* subfamily or could be brought in trans by a member of the *DYW1*-like clade when the specificity factor is a PPR-PLS, PPR-E, or PPR-E+ protein.

In addition to the severe editing defects observed in E+ sites, we also showed that *dyw2* and *nuwa* mutants had numerous minor negative as well as positive defects in non-E+ editing sites. These results suggested that *DYW2* and *NUWA* editosomes compete with other editosomes for unknown editing factors, supporting Sun et al.'s (2) recent review, which proposed that editosomes result from complex assembly equilibria of numerous editing factors. However, we tested the functional overlap of *DYW2* and *NUWA* with RIP/MORFs, ORRM1s, and OZ1 by comparing the

lists of impacted editing sites, but none of these comparisons showed significant overlaps. Surprisingly, whereas the bait protein used in our approach, *CLB19*, is required for editing of two plastidial sites, which are also targets of general factors such as MORF2, MORF9, and ORRM1, we were not able to purify them together with *CLB19*, *NUWA*, and *DYW2*. One possible explanation of the absence of these proteins could be due to weak and/or transient interactions of these factors within the complex. Indeed, when screening the Y2H library with *CLB19*, *NUWA*, and *DYW2*, we were not able to identify any of these editing factors.

Besides these targeted questions regarding the molecular functions of *NUWA* and *DYW2* PPR proteins, an intriguing observation of our study is the requirement of both of them during embryo development, whereas they are dispensable for further plant growth. Mutant studies showed that a large number of nuclear mutations impairing embryo development are associated with proteins targeted to organelles (42). Interestingly, most of these proteins are involved in the regulation of organelle gene expression, from editing to translation via splicing and processing on different RNA targets. The general consensus is that the embryo lethal phenotype of mitochondrial *emb* mutations is associated with a lack of energy production (52, 53), whereas the understanding of the essential role of plastid function in plant embryogenesis is still very limited. *NUWA* and *DYW2* are required for numerous editing events in both mitochondria and plastids. The impact of these defects on embryo development is not surprising. However, further studies will be needed to understand why, in contrast, these editing defects are not lethal at the adult stage, especially in *NUWA* mutants that do not show any macroscopic phenotype.

Materials and Methods

Plant Material and Phenotype Characterization of T-DNA Insertion Lines. The T-DNA insertional mutants, GK_332A07 (*dyw2-1*), FLAG_435F11 (*dyw2-2*), SALK_069042 (*nuwa-1*), and SAIL_784_A11 (*nuwa-2*), were obtained from the ABRRC stock center. *NUWA* and *DYW2* wild-type ORFs were cloned under the control of the embryo-specific *pABI3* promoter using the pH7WG-ABI3 vector from Aryamanesh et al. (43). Detailed information on the plant methods used in this study is included in [SI Materials and Methods](#). All sequences of primers used in this study are available in [Table S3](#).

Protein Interaction Methods. The detailed methods of TAP and Y2H screening are given in [SI Materials and Methods](#). In brief, constructions and *Arabidopsis* transformation were carried out as previously described (54), protein complex purification was done as described in Van Leene et al. (55), and peptide isolation and analysis were performed according to Van Leene et al. (56). Protein identification details are listed in [Dataset S1](#).

RNA-Seq Analysis. The detailed methods are given in [SI Materials and Methods](#). In brief, the RNA-seq analysis was performed following the recommendations of Rigauil et al. (57). The organelle transcriptome was studied after mapping of the reads with STAR (v020201) (58) using in-house scripts adapted from the ChloroSeq package (59).

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