Plastid translation is essential for lateral root stem-cell patterning in Arabidopsis thaliana

Miyuki T. Nakata¹*, Mayuko Sato², Mayumi Wakazaki², Nozomi Sato³, Koji Kojima⁴,³, Akihiko Sekine⁴, Shiori Nakamura⁴, Toshiharu Shikanai³, Kiminori Toyooka³, Hirokazu Tsukaya⁵,⁶, Gorou Horiguchi¹,⁴,§

¹ Research Center for Life Science, College of Science, Rikkyo University, Toshima, Tokyo 171-8501, Japan
² Center for Sustainable Resource Science, RIKEN, Tsurumi, Yokohama, Kanagawa 230-0045, Japan
³ Graduate School of Science, Kyoto University, Sakyo, Kyoto 606-8502, Japan
⁴ Department of Life Science, College of Science, Rikkyo University, Toshima, Tokyo 171-8501, Japan
⁵ Graduate school of Science, The University of Tokyo, Bunkyo, Tokyo 113-0033, Japan
⁶ Okazaki Institute for Integrative Bioscience, National Institutes of Natural Sciences, Okazaki, Aichi 444-8787, Japan

*Present address: Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology, Tsukuba, Ibaraki 305-8566, Japan
‡Present address: Department of Biomolecular Engineering, Graduate School of Engineering, Tohoku University, Sendai, Miyagi 980-8579, Japan
§Author for correspondence: ghori@rikkyo.ac.jp

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Summary statement
Successful plastid gene expression is required for stem-cell patterning in lateral root primordia as revealed by genetic and pharmacological impairment of plastid translation.
Abstract

The plastid evolved from a symbiotic cyanobacterial ancestor and is an essential organelle for plant life, but its developmental roles in roots have been largely overlooked. Here, we show that plastid translation is connected to the stem-cell patterning in lateral root primordia. The RFC3 gene encodes a plastid-localized protein that is a conserved bacterial ribosomal protein S6 of β/γ proteobacterial origin. The rfc3 mutant developed lateral roots with disrupted stem-cell patterning and associated with decreased leaf photosynthetic activity, reduced accumulation of plastid rRNAs in roots, altered root plastid gene expression, and changes in expression of several root stem-cell regulators. These results suggest that deficiencies in plastid function affect lateral root stem cells. Treatment with the plastid translation inhibitor spectinomycin phenocopied the defective stem-cell patterning in lateral roots and altered plastid gene expression observed in the rfc3 mutant. Additionally, when prps17 defective in a plastid ribosomal protein was treated with low concentrations of spectinomycin, it also phenocopied the lateral root phenotypes of rfc3. The spectinomycin treatment and rfc3 mutation also negatively affected symplasmic connectivity between primary root and lateral root-primordia. This study highlights previously unrecognized functions of plastid translation in the stem-cell patterning in lateral roots.
INTRODUCTION

The plastid evolved from a symbiotic cyanobacterial ancestor and is an essential organelle of plants as the site of a number of metabolic reactions represented by photosynthesis in chloroplasts. The plastid has its own genome and gene expression machinery. Plastids and the nucleus communicate with each other to regulate cellular physiology and plastid functions, especially those related to photosynthesis. Mutations or treatment with drugs that interfere with metabolic pathways and gene expression machinery of chloroplasts evoke retrograde signaling and suppress the expression of photosynthesis-associated nuclear genes (Bobik and Burch-Smith, 2015; Kleine and Leister, 2016). Impaired translation in chloroplasts is a trigger for retrograde signaling (Tiller and Bock, 2014). Recent studies in *Arabidopsis thaliana* (hereafter, Arabidopsis) have suggested that plastids also have a role in particular developmental events, e.g., flowering time, leaf adaxial-abaxial patterning, and callus formation, in shoots of higher plants (Moschopoulos et al., 2012; Tameshige et al., 2013; Mateo-Bonmatí et al., 2015; Wang and Dehesh, 2015; Wilson et al., 2016). In addition to the green chloroplasts found in photosynthetic tissues, non-green plastids are found in cells of heterotrophic organs, including roots (Robertson and Laetsch, 1974; Kobayashi et al., 2012); however, the role of translation in non-green plastids in root development is largely unknown.

We previously reported that a *regulator of fatty acid composition3* (*rfc3*) mutant of Arabidopsis strikingly forms abnormal lateral roots (LRs), in which function and stem-cell patterning of the root apical meristem are completely disrupted or severely compromised (Horiguchi et al., 2003). The RFC3 gene (*At3g17170*) encodes a protein harboring a plastid-localization signal and a bacterial ribosomal protein S6 (bRPS6)-like sequence (Horiguchi et al., 2003). There is an authentic *PLASTID RIBOSOMAL PROTEIN S6* (*PRPS6*) gene (*At1g64510*) whose ortholog in spinach was identified by a proteome analysis of the chloroplast 30S ribosomal subunit (Yamaguchi et al., 2000). Recent cryo-electron microscopy analysis of spinach chloroplast 70S ribosome also demonstrated the existence of PRPS6 as a component of the 30S ribosomal subunit (Bieri et al., 2017). The amino acid sequence of PRPS6 in spinach is 82% and 22% similar to that of *At1g64510* and RFC3. Although the RFC3 plastid-localization signal is functional (Horiguchi et al., 2003) and the possibility that RFC3 also functions as a plastid ribosomal...
protein can not be formally discarded, low amino acid sequence conservation between PRPS6 and RFC3 has rendered the function of RFC3 in plastids obscure.

A notable feature of the LR phenotype in *rfc3* is its sucrose sensitivity; *rfc3* forms abnormal LRs when grown in media containing 3% sucrose but not in media containing 0.5% sucrose (Horiguchi et al., 2003). Sucrose concentration shift experiments showed that primary roots grown under the 3% sucrose condition are no longer able to form normal LRs even when LRs are initiated after transfer to the 0.5% sucrose condition (Horiguchi et al., 2003). This suggests that the cause of defective LR development in *rfc3* is associated with primary root growth but not the process of LR formation itself. Here we suggest a role of plastid translation in the stem-cell patterning in lateral root primordia by showing that *rfc3* is defective in the accumulation of plastid rRNAs and examining the effects of mutants defective in plastid ribosome biosynthesis and plastid translation inhibitors.

RESULTS

The phylogenetic origin of RFC3 is different from PRPS6

To better understand the relationship between RFC3 and the bRPS6 family proteins, we performed an extensive phylogenetic analysis. We identified the bRPS6 family proteins from land plant, green algal, red algal, animal, and bacterial species (Table S1). The phylogenetic analysis revealed that the land plant sequences grouped into three different clades, such as the RFC3 clade, a clade that includes At1g64510, and a clade including At3g18760, a newly identified bRPS6 domain-containing protein from Arabidopsis (Fig. S1A). The plastid RPS6 (PRPS6) clade, which included At1g64510, *Chlamydomonas reinhardtii* PRPS6, and homologous genes of spinach PRPS6 (Yamaguchi et al., 2000; Yamaguchi et al., 2002; Tiller and Bock, 2014), was associated weakly with the Eurhodophytina and cyanobacterial RPS6s [bootstrap (BS) values, 20%]. The mitochondrial RPS6 (MRPS6) clade including At3g18760 was closely related to animal MRPS6s (BS values, 84%). In contrast, the RFC3 clade was most closely related to a clade containing both the β and γ proteobacterial RPS6s among the proteobacterial groups (BS values, 83%). The alignment shown in Fig. S1B indicates that the two α-helices (a1 and a2) and four β-sheets (b1–b4) in the bRPS6 domain are strongly conserved. The length of the amino acid sequence between b2 and b3 in land-plant RFC3s was the same
as bacterial RPS6s compared with PRPS6s and MRPS6s, indicating that the bRPS6 domain of RFC3 is more similar to bRPS6s than to PRPS6s and MRPS6s.

**RFC3 localization in leaf and root cells**

Transient expression analysis of \(35Sp::RFC3\):GREEN FLUORESCENT PROTEIN (**GFP**), \(35Sp::PRPS6::GFP\), and \(35Sp::MRPS6::GFP\) using mesophyll protoplasts detected GFP fluorescence from RFC3:GFP and PRPS6:GFP as a pattern of spots dispersed throughout the chloroplasts and GFP fluorescence from MRPS6:GFP predominantly as spots in the mitochondria (Fig. 1A). The same result was also observed in leaves of stable lines expressing the RFC3 genomic fragment fused to **GFP** that complemented the root and shoot phenotypes of \(rfc3\) (\(RFC3g::GFP\)/\(rfc3-2\); Fig. 1B, S2A-C). The GFP signal in roots of \(RFC3g::GFP\)/\(rfc3-2\) plants was found in root tips and differentiated portions of primary roots as well as LR primordia (Fig. S2D, E) and detected as numerous small spots that completely overlapped with a plastid marker [cyan fluorescent protein (CFP) fused to the RECA transit peptide (\(35Sp::RecA-TP::CFP\)); Fig. 1C], demonstrating that RFC3 also localizes to plastids in roots. These results indicate that **RFC3** encodes a conserved bRPS6 protein whose origin is separate from those of PRPS6 and MRPS6, which, similar to PRPS6, functions in plastids.

**Photosynthesis-related phenotypes of rfc3**

In our previous work, we focused on LR development in \(rfc3\) (Horiguchi et al., 2003). To better understand the general characteristics of \(rfc3\), we examined shoot and photosynthesis-related phenotypes. Both \(rfc3-1\) and \(rfc3-2\) are in the Landsberg erecta (**L. er**) background. These mutants have pale-green leaves and are smaller than wild type in young seedlings (Fig. 2A). However, leaves of \(rfc3-2\) reached to a size similar to **L. er** when they were grown until flowering (Fig. S3A, B). The number of leaves produced by the time of flowering was slightly fewer in \(rfc3-2\) than in wild type (Fig. S2C). Compared to **L. er**, \(rfc3\) alleles showed a significantly decreased maximum quantum yield of photosystem II (PSII) (\(Fv/Fm\)), and significantly decreased quantum yields of PSII (\(\Phi_{PSII}\)) according to analysis using a pulse amplitude modulation fluorescence system (Fig. 2B). In three of the four \(rfc3-1\) plants and two of the four \(rfc3-2\) plants tested, the steady state level of fluorescence (\(F_s\)) decreased below the \(F_0\) level upon exposure to actinic light.
(120 µmol photons m\(^{-2}\) s\(^{-1}\)), which was in contrast to wild-type plants (Fig. S4). Consequently, we concluded that photosynthetic electron transport was partially affected by the mutations. Additionally, two plastid-encoded proteins, D1 (encoded by \textit{psbA}) and the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (RBCL), were slightly less abundant in \textit{rfc3-2} shoots, whereas two nuclear-encoded cytosolic ribosomal proteins, RPS6 and RPL5, were slightly more abundant (Fig. 2C). A decrease in RBCL was also detected in \textit{rfc3-2} by Amido Black staining (asterisk in Fig. 2C). These results indicate that RFC3 contributes to chloroplast function.

\textbf{Plastid gene expression in \textit{rfc3}}

To test whether RFC3 has an active role in root plastid function, we investigated the effect of the \textit{rfc3} mutation on the expression of plastid-encoded genes in roots grown in media containing 3\% sucrose (Fig. 3A). Compared with cytosolic 18S rRNA (ct18S), the expression of plastid 16S (pt16S) and pt23S rRNAs was dramatically reduced, suggesting a corresponding decrease in plastid ribosomes. In addition, \textit{psbA}, and \textit{psbB} decreased significantly in \textit{rfc3-2} roots. In contrast, expression of \textit{rpoB}, \textit{prps18}, and \textit{clpP} increased significantly in \textit{rfc3-2}. However, the expression of plastid-encoded \textit{accD}, \textit{ndhA}, and \textit{rbcL}, and the expression of ct25S, mitochondrial 18S (mt18S), and mt26S rRNAs did not differ significantly between wild type and \textit{rfc3-2}.

Because abnormal LRs do not form in \textit{rfc3} grown in media containing 0.5\% sucrose (Horiguchi et al., 2003), we examined whether plastid rRNA levels are also affected by sucrose conditions. Hereafter, we designate sucrose conditions as follows: 0\% sucrose = Suc0, 0.5\% = Suc0.5, and 3\% = Suc3. Compared to wild type, expression levels of both pt16S and pt23S rRNAs in the \textit{rfc3-2} roots decreased by about 60\% and 30\%, respectively, even when they were grown in Suc0.5 media. These rRNA levels further decreased in Suc3 media (Fig. 3B). In \textit{rfc3-2} roots, the level of pt16S rRNA showed a greater decrease than pt23S rRNA in both Suc0.5 and Suc3 media (Fig. 3B). These results suggest that a high concentration of sucrose enhances a negative effect of the \textit{rfc3} mutation on LR development through decreases in plastid rRNA levels.
*rfc3* mutations result in abnormal stem-cell patterning in LRs

*rfc3*-1 and *rfc3*-2 grown on the Suc3 media form nodule-like LRs (Fig. 4A, yellow arrowheads) (Horiguchi et al., 2003) which are round or pointed and covered with epidermal and root hair cells. They were likely to lose distal tissues and the quiescent center (QC) cells (Fig. 4B) (Horiguchi et al., 2003). In this study, we noticed that *rfc3*-2 also formed stubby LRs, which occurred at a lower frequency than the nodule-like LRs (Fig. 4A, red arrowhead). The stubby LRs were shorter and thicker than the wild-type LRs, but had tissue resembling a root cap at the apex. A group of cells located between proximal and distal tissues in stubby LRs of *rfc3* was disorganized or multi-layered, indicating that the stem-cell alignment collapsed (Fig. 4B). We previously showed that *rfc3* forms nodule-like LRs when grown on the Suc3 media but it is able to develop normal LRs on the Suc0.5 media (Horiguchi et al., 2003). To examine if the observed stubby LRs are a milder LR phenotype, we cultured *rfc3* in media containing different concentrations of sucrose (Fig. S5A). Wild-type plants grown in all sucrose conditions examined and *rfc3*-2 grown in Suc0 media formed neither stubby nor nodule-like LRs. In *rfc3*-2, stubby and nodule-like LRs began to form in Suc0.5 media, although their frequencies were less than 5%. As expected, the frequency of stubby LRs was higher in intermediate sucrose concentrations than in lower or higher sucrose conditions. The frequency of nodule-like LRs was steadily increased as the sucrose concentration increased. These results suggest that stubby LR is a less severe form of the *rfc3* LR phenotype. On the other hand, the length of primary roots in *rfc3*-2 was always shorter than wild type in any sucrose condition tested (Fig. S5B). The growth defect of the *rfc3*-2 primary root was slightly enhanced in the presence of sucrose as indicated by the relative primary root length of *rfc3*-2 compared to wild type (Fig. S5B).

We also examined whether sucrose affected LR development as an osmoticum or metabolizable sugar (Fig. S5C). Three percent sucrose corresponds to 88 mM, and we examined the effect of glucose as another metabolizable sugar and mannitol as a non-metabolizable osmoticum at the same molar concentration. Growth under no metabolizable sugars often causes vitrification. To avoid this, 0.5% sucrose was added to media containing glucose or mannitol. In the presence of glucose but not mannitol, *rfc3* formed shorter primary roots and abnormal LRs (Fig. S5C), suggesting that the presence of metabolizable sugars is a trigger of abnormal LR development.
Irregular organization of LR cells motivated us to examine the expression of a number of well-characterized root stem-cell regulatory genes including WUSCHEL-RELATED HOMEOBOX5 (WOX5) (Sarkar et al., 2007), PLETHORA3 (PLT3), PLT7 (Galinha et al., 2007), and CLAVATA1 (CLV1) (Stahl et al., 2013), and ARABIDOPSIS CRINKLY4 (ACR4) (De Smet et al., 2008) (Fig. 4C). The expression levels of WOX5, PLT3, PLT7, CLV1, and ACR4 were higher in roots of rfc3-2 grown in Suc3 media. Expression of WOX5p::GFP was limited to the QC in LR primordia of the wild type but was more widespread in almost all LR primordia of rfc3-2 grown in Suc3 media (Fig. 4D, E). Conversely, GFP fluorescence was not found in approximately 5% of rfc3-2 LR primordia (Fig. 4E). These LRs formed root hairs on their apical parts, suggesting that cells in these LRs were fully differentiated. These results indicate that RFC3 is required for normal LR development and for the proper expression of a subset of root stem-cell regulatory genes.

Experiments with Suc3 media may not reflect natural growth. To minimize the effect of exogenous sucrose, we used Suc0.5 media and checked expression patterns of WOX5p::GFP (Figs 4E, S6). Although rfc3-2 grown on Suc0.5 media had only a few nodule-like LRs, we found a slight expansion of GFP signal in the LR apex of approximately 35% of rfc3-2 plants (Figs 4E, S6). These results, together with a finding that rfc3 grown in Suc0.5 media had less plastid rRNAs (Fig. 3), suggest that RFC3 is required to accumulate plastid rRNAs to a sufficiently high level to ensure normal LR development under a near-physiological condition. Suc3 further decreased plastid rRNA levels in rfc3-2 and this is very likely a cause of sugar-sensitive LR defects.

Spec-treated L. er plants phenocopy the rfc3 root defects
Our findings suggest that the rfc3 mutation impaired plastid gene expression, resulting in abnormal LR stem-cell patterning. Because RFC3 is a bRPS6 family protein and its mutation is associated with a reduction in pt16S and pt23S rRNAs, impaired translation may have effects similar to those observed in rfc3. Therefore, we investigated the effect on LR development of three bacterial ribosome inhibitors, Spec, kanamycin, and streptomycin, which inhibit plastid translation (Fromm et al., 1987; Svab and Maliga, 1991; Kavanagh et al., 1994; Rosellini et al., 2004; Conte et al., 2009; Parker et al., 2014)
in Suc3 media. We observed that plants treated with 4 and 10 mg L\(^{-1}\) Spec (designated Spec4 and Spec10, respectively, and so forth) in Suc3 media formed nodule-like and/or stubby LRs with misaligned stem cells that resembled those of \(rfc3\) (Figs 5A, S7). Treatment with Spec2 but not Spec1 produced slight irregularities in LR stem-cell patterning without generating macroscopic morphological changes (Fig. 5A). Increasing the Spec concentration from Spec0 to Spec2 resulted in gradual increases in the expression of \(WOX5\), \(PLT3\), and \(PLT7\) and more widespread expression of \(WOX5p::GFP\) (Fig. 5B, C). In addition, the kanamycin and streptomycin treatments induced nodule-like and/or stubby LR formation in \(L. \text{er}\) plants (Fig. S7).

We also examined the effect of Spec2 and Spec4 on \(L. \text{er}\) plants and found that plastid rRNA levels and \(psbA\) and \(psbB\) transcripts were downregulated (Fig. 5D, E), whereas the transcript levels of plastid-encoded genes \(rpoB\), \(prps18\), \(clpP\), and \(ndhA\) were upregulated. A good correlation was observed between the RNA levels of plastid-encoded genes in \(rfc3\) and Spec4-treated wild-type plants (Fig. 5F).

In general, drug treatment at a high concentration may cause nonspecific deleterious effects on development. To further confirm the relationship between plastid translation and abnormal LR development, we analyzed the effects of Spec treatment on the \(WOX5p::GFP\) expression pattern in \(rfc3\) LRs formed in Suc0.5 media (Fig. 4E). We first examined wild type and found that Suc0.5 combined with Spec0.33 or Spec0.67 did not affect the \(WOX5p::GFP\) expression pattern (Figs 4E, S6). On the other hand, \(WOX5p::GFP\) expression in \(rfc3-2\) LR primordia was expanded or disappeared even in Spec0.33 media (Figs 4E, S6). Most of the LRs with altered \(WOX5p::GFP\) expression were stubby or nodule-like ones (Fig. S6). Abnormal LRs induced at a low concentration of Spec suggest that this phenotype results from the inhibitory effects on plastid translation rather than nonspecific effects.

**Plastid translation-deficient mutants trigger an \(rfc3\)-like LR phenotype with a low concentration of Spec**

The similar effect of \(rfc3\) mutation with Spec and other drugs supports the idea that abnormality in LR stem cell patterns is due to impaired plastid translation. For further confirmation, we examined plastid translation-deficient mutants. First, we studied the phenotype of \(prps17-1\), which is an \(L. \text{er}\) background mutant deficient in a nuclear-
encoded plastid ribosomal protein (Romani et al., 2012). The shoot size of \textit{prps17-1} was smaller than wild type and \textit{rfc3-2} (Fig. 2A). On the other hand, primary root growth of \textit{prps17-1} was suppressed but the severity was milder than \textit{rfc3-2} (Fig. 6A). Growth of LRs in \textit{prps17-1} was not slowed (Fig. 6B) but showed a slightly irregular stem-cell alignment (Fig. 6C) with a slightly expanded GFP fluorescence pattern of \textit{WOX5p::GFP} (Fig. 6E), and the expression of \textit{WOX5}, \textit{PLT3}, and \textit{PLT7} increased slightly (Fig. 6D). Then, we applied a low concentration of Spec to \textit{prps17-1}. Unlike Spec1-treated \textit{L. er} plants, Spec1-treated \textit{prps17-1} plants formed nodule-like LRs (Fig. 6C) with a widely distributed GFP signal of \textit{WOX5p::GFP} (Fig. 6E) that resembled those of untreated \textit{rfc3} mutants (Fig. 4D).

As described above, \textit{prps17-1} showed the same effect as \textit{rfc3-2} in low concentration Spec treatments. To examine the genetic interaction between these two mutations, we attempted to create a \textit{prps17-1 rfc3-2} double knockout mutant. However, we were unable to find any \textit{prps17-1 rfc3-2} double homozygous mutants in the F2 population. \textit{prps17-1 rfc3-2/+} plants were selected and the genotype of their descendants was examined. Among the 56 plants, 23 and 33 plants had the \textit{prps17-1} and \textit{prps17-1 rfc3-2/+} genotypes, respectively, but no \textit{prps17-1 rfc3-2} double mutant was found. Seed development and maturation in fruits of the \textit{prps17-1} single mutant and \textit{prps17-1 rfc3-2/+} double mutant were observed (Fig. S8A). All seeds of \textit{prps17-1} fruits grew green during seed maturation (n = 91), while 21.6% of \textit{prps17-1 rfc3-2/+} fruit seeds remained albino (Fig. S8A, central panel, n = 218). We did not detect albino seeds from the fruits of \textit{L. er} and \textit{rfc3-2} (n = 134 and 120, respectively). In the \textit{prps17-1 rfc3-2/+} fruits, the green seeds were in the mature green stage and the embryos were spherical (Figs S8A and B) but those in albino seeds were still in a globular stage (Figs S8C, D). In the late stage of \textit{prps17-1 rfc3-2/+} fruit, there was no albino seed, but brown shrinking seeds were found (Fig. S8A, lower panel). Shrinking seeds were not observed in \textit{prps17-1} fruit. It is assumed that albino/shrinking seeds are \textit{prps17-1 rfc3-2} double mutants, and both mutations work synergistically, resulting in the arrest of embryonic development during the globular phase. Similar to this observation, mutations in several nuclear-encoded plastid ribosomal protein genes result in an embryonic lethal phenotype (Romani et al., 2012). The synergistic effects of the \textit{rfc3} and \textit{prps17} mutations suggest that the function of RFC3 is closely related to the function of PRPS17, most likely translation or plastid
ribosome biogenesis, during development.

Next, we examined Col-0-background plastid translation-deficient mutants, rap-1 and rbf1-2. RAP and RBF1 are involved in the maturation of pt16S rRNA (Fristedt et al., 2014; Kleinknecht et al., 2014). LR phenotypes of rap-1 and rbf1-2 were indistinguishable from wild-type Col-0 (Fig. 6F). Then, we analyzed the Spec sensitivity of wild-type Col-0 and their mutants. Spec4-treated Col-0 plants formed rfc3-like stubby LRs with abnormal stem cell alignment (Fig. 7A). Spec1-treated Col-0 LR did not differ from untreated Col-0 (Fig 7A), but Col-0 plants treated with Spec2 showed variable LR phenotypes: 85.2% of the plants showed a wild-type-like phenotype but the others (14.8%) showed weak stratification of stem cells (n = 27; Figs 6F, 7A). On the other hand, all of the Spec2-treated rap-1 mutants formed nodule-like LRs and/or stubby LRs with a severe defect in stem cells (n = 18) and most Spec2-treated rbf1-2 mutants had abnormal LRs with a weak or severe stem cell defect (88.9%, n = 27; Fig. 6F).

The synergistic effects of plastid translation-deficient mutants, prps17-1, rap-1 and rbf1-2, and Spec treatment on the LR phenotype support the hypothesis that impaired plastid translation and/or plastid ribosome biogenesis triggers abnormal LR development.

**Spec treatment alters characteristics of LR meristematic cells**

As described above, Spec4 treatment results in LR deformation. We then investigated the effect of Spec4 treatment on root meristem markers. The GFP signal from a SCARECROW (SCR) reporter line (SCRp::GFP:SCR/scr-3) was detectable in both the endodermis and the QC in untreated plants, but was faint in the meristematic region of stubby LRs in Spec4-treated plants (Fig. 7B). Additionally, no signals were detected from the QC-specific markers QC25 and QC46 in Spec4-treated plants (Fig. 7B). We also found that QC25 expression in stubby and nodule-like LRs of rfc3-2 was absent while its expression was maintained in the primary root tip (n = 10, Fig. S9). These results, together with the altered expression of WOX5p::GFP (Fig. 5C), indicate that the stubby LRs formed in Spec-treated wild-type plants also have abnormal meristematic characteristics.

The SUCROSERO-PROTON SYMPORTER2p (SUC2p)::sGFP line can be used to visualize symplasmic connectivity between the phloem and the meristematic regions in roots by monitoring cytosolic GFP (Imlau et al., 1999). GFP fluorescence was detected in the meristematic region of LRs in untreated SUC2p::sGFP plants, whereas it was
detected only in the phloem of LRs in Spec4-treated SUC2p::sGFP plants (Fig. 7C). SUC2p::sGFP in rfc3-2 also showed restricted diffusion of GFP into LR primordia (Fig. 7D). These results show that the symplastic connectivity between phloem tissues and LR primordia is controlled by the common pathway affected by the Spec treatment and the rfc3 mutation.

The intracellular distribution of plastids was altered in rfc3

RAP encodes an octotricopeptide repeat protein localized in chloroplasts and its loss of function results in a pt16S rRNA maturation defect (Kleinknecht et al., 2014). Interestingly, an earlier report of rap described its enhanced resistance to pathogen infection (Katiyar-Agarwal et al., 2007). A recent study also highlighted the involvement of chloroplasts in an immune response during which chloroplasts elongate tubular structures known as stromules. These stromules make contact with the nucleus and this dynamic behavior of chloroplasts is proposed to have a signaling role (Caplan et al., 2015). Curiously, we also found that rfc3-2 and Spec-treated wild type shared abnormalities in behavior of root plastids. In experiments using 35Sp::RecA-TP:CFP, the CFP fluorescence in wild-type plants was observed as small spots scattered throughout the root cells (Fig. 8A). Conversely, the CFP fluorescence in rfc3-2 mutants and Spec4-treated plants was visible as abnormal aggregations in the center of cells and small spots in the mature parts of the primary root (Fig. 8A, S10). Similar aggregation was observed in Spec4-treated RFC3g:GFP/rfc3-2 (Fig. S10). Transmission electron microscopy observations revealed that plastids in the pericycle cells of mature untreated L. er primary root were dispersed, whereas those of rfc3 primary roots often formed large plastid clusters that contained mitochondria and other structures (Figs 8B, S11). The cluster of plastids was also observed in cells of Spec-treated wild-type primary roots (Figs 8B, S11). These findings demonstrate that impaired translation in plastids affects intracellular distribution of root plastids.

DISCUSSION

We reported the RFC3 gene, which was cloned nearly 15 years ago as a member of PRPS6 but with a very low similarity compared to authentic PRPS6 in Arabidopsis and spinach (Horiguchi et al., 2003). In this study, detailed phylogenetic analyses supported that RFC3
and its orthologs present only in land plants and are likely of β/γ-proteobacterial origin (Fig. S1). We found that rfc3 reduces plastid rRNAs in roots (Fig. 3), suggesting that RFC3 as a non-ribosomal protein, plays a role either during ribosome biogenesis or in stabilizing mature ribosomes.

In this study, we also demonstrated that rfc3 grown in Suc3 media, Spec-treated wild-type plants, and plastid ribosome-related mutants commonly produced abnormal LRs that lacked typical stem-cell patterning (Figs 4-6). These findings suggest a link between impaired translation and/or ribosome biogenesis in plastids and abnormal LR development. However, there are two critical issues concerning the rfc3 phenotype and Spec treatment. For rfc3, its sucrose-sensitive abnormal LR formation raises a question about whether the observed phenotype is physiologically relevant. We found that stubby and nodule-like LRs begin to form at a low frequency in a media containing sucrose as low as 0.5% and the frequency of their appearance increased as sucrose concentration increased (Fig. S5). Thus, rfc3-2 grown in a low sucrose condition is already vulnerable to impaired plastid translation. Further reduction in plastid rRNA levels by sucrose (Fig. 3) is a likely cause of sucrose-sensitive abnormal LR development. For Spec-treatment, nodule-like LRs were induced at a concentration higher than 4 mg L^{-1}, which might have resulted from nonspecific deleterious effects (Fig. 5). However, similar phenotypes were found when wild-type plants were treated with plastid translation inhibitors kanamycin and streptomycin that are structurally unrelated to Spec (Fig. S7). In addition, rfc3 grown in Suc0.5 media formed abnormal LRs at an increased frequency when they were treated with Spec0.33 while wild-type plants developed normal LRs (Figs 4, S6). Taking these results together, we propose that rfc3 and Spec-treatment induce abnormal LRs specifically through their negative effects on ribosome biogenesis or translation in plastids.

Our finding that exogenous sucrose has an effect to further reduce plastid rRNA levels in rfc3 (Fig. 3B) raises a next question concerning the action of sucrose. We ruled out the possibility that osmotic stress induced by exogenous sugars is the cause of the rfc3 phenotypes since sucrose and glucose but not mannitol induced abnormal LR formation in rfc3 (Fig. S5C). Sucrose is metabolized into glucose and both sugars act as energy source. At the same time, glucose has a signaling role by which diverse processes
from gene expression, metabolism, and development are regulated (Sheen, 2014). Whether the sucrose-dependent \textit{rfc3} phenotypes were induced via glucose signaling network would be examined by experiments on the relationship between ribosomal rRNA accumulation and glucose signaling regulators such as HEXOKINASE1, SNF-related protein kinases KIN10/11, TARGET OF RAPAMYCIN. Alternatively, plastid rRNA levels may be influenced by an indirect manner. Sucrose activates growth and cytosolic ribosome biogenesis through transcriptional induction of ribosome biogenesis factors (Kojima et al., 2007; Maekawa et al., 2017). Since plastids are one of major sites of the primary metabolism, demand of plastid gene expression machineries would be increased in response to exogenous sucrose to support growth stimulation. If cytosolic and plastid ribosomes are coordinately increased, the relative levels among cytosolic and plastid rRNAs will be unaltered significantly. The rRNA levels shown in Fig. 3 were expressed relative to 18S rRNA level. Thus, reduced plastid rRNA levels in \textit{rfc3} grown in the Suc3 media might result from increased cytosolic rRNA levels. Interestingly, the leaf variegation phenotype of \textit{variegated2 (var2)}, which is defective in plastid-localized metalloprotease, is enhanced by mutations in cytosolic ribosomal protein genes but this enhancement was cancelled by a mutation for the plastid ribosomal protein L24 (PRPL24) gene (Wang et al., 2017). This finding suggests that an appropriate balance between plastid ribosomes and cytosolic ribosomes are maintained during growth and development by an unknown mechanism and its disruption affects plastid development. Whether disruption of such a balance is linked to abnormal LR development in \textit{rfc3} would be an interesting issue to be examined.

Common defects included not only failure of LR stem-cell patterning and altered expression of root stem-cell regulatory genes (Figs 4-6), but also reduced symplasmic connectivity (Fig. 7), and cluster formation of plastids in the roots (Fig. 8). Each of these phenotypes was highly reproducible and specific but are they mutually related in the context of LR development? The first two defects are obviously related to each other, yet further experiments are needed to understand relationship between them. It is possible that deregulated cell proliferation in LR primordia leads to altered expression of stem-cell regulatory genes or vice versa. This dilemma may be solved by generating double or higher order multiple mutants between \textit{rfc3} and \textit{wox5}, \textit{plt3} and/or \textit{plt7}.
The altered expression of root stem-cell regulatory genes, however, might be rather downstream events. We previously showed that sucrose-sensitive developmental process of rfc3 can be traced back to primary root growth rather than to LR developmental processes (Horiguchi et al., 2003). Although how plastid function ensures LR development should be investigated in a future study, it is interesting to note that plastid function (or dysfunction) influences symplasmic communication and spatial organization of the root apical meristem (Benitez-Alfonso et al., 2009; Burch-Smith et al., 2011; Stonebloom et al., 2012; Dmitrieva et al., 2017). The intercellular movement of key transcription factors, such as SHORT ROOT (SHR) and WOX5 (Nakajima et al., 2001; Pi et al., 2015), and symplasmic communication in the stem cell niche (Liu et al., 2017) are crucial for establishing and maintaining the root apical meristem. However, these regulations occur in the root apical meristem and probably in developing LR primordia, as well. In Spec-treated wild-type roots and in rfc3-2 roots grown in Suc3 media, GFP diffusion from the primary root into LR primordia was strongly inhibited (Fig. 7), suggesting that upon impaired plastid translation in primary roots, a symplasmic boundary is generated between primary roots and LR primordia. This interpretation is consistent with the suggestion that the sucrose-sensitive event in rfc3 is expected to reside in the primary root (Horiguchi et al., 2003). This idea also fits with the finding that symplasmic connectivity between xylem pole pericycle cells from which LRs are initiated, and neighboring cells including LR founder cells are regulated spatially and temporally (Benitez-Alfonso et al., 2013). Manipulating callose deposition in these cells in future experiments could help examine whether reduced symplasmic connectivity and plastid translation is linked to regulating LR development.

If reduced symplasmic communication is relevant to abnormal LR development, the last question concerning plastid translation and LR development in this study is how impaired plastid translation affects the processes between plastids and other cellular compartments. In this regard, plastid clusters formed adjacent to the nucleus are interesting if we consider chloroplast stromule-nucleus contacts are proposed to have a signaling function during the immune response (Caplan et al., 2015). However, plastid clusters found in this study and immunity-induced stromules are not very similar to each other except that both of them have a close association with the nucleus (Fig. 8). In addition, stromule-nucleus contact might have a more passive role (Erickson et al., 2017).
Therefore, developmental meanings of plastid cluster and its association with the nucleus, if any, should be carefully investigated in the future.

Several reports suggest that retrograde signaling is triggered by impaired plastid translation and it links to developmental processes (Moschopoulos et al., 2012; Tameshige et al., 2013; Mateo-Bonmatí et al., 2015), although these mutations affect leaf adaxial-abaxial polarity and signaling mechanisms behind this phenotype are unclear. Interestingly, root initiation defective2 (rid2) shows both leaf polarity and LR defects; rid2 roots form abnormal LRs similar to stubby LRs found in rfc3 when they are cultured in root-inducing medium (Konishi and Sugiyama, 2003). The rid2 mutation also affects leaf adaxial-abaxial polarity and produces pointed leaves (Ohbayashi et al., 2011; Matsumura et al., 2016). RID2 encodes a cytosolic ribosome biogenesis factor (Ohbayashi et al., 2011). Surprisingly, rid2 phenotypes are suppressed by a second mutation in NO APICAL MERISTEM, ARABIDOPSIS TRANSCRIPTION ACTIVATION FACTOR1/2, and CUP-SHAPED COTYLEDON2 (NAC) transcription factor gene SUPPRESSOR OF RID TWO 1 (SRIW1)/ANAC082 (Ohbayashi et al., 2017). Although speculative, phenotypic commonality between mutants defective in plastid and cytosolic ribosome related genes might have overlapping signaling components. In this perspective, the LR phenotypes of the temperature-sensitive mutants rid1-1 and shoot redifferentiation defective2-1 (srd2-1), which form nodule-like LRs at 28°C (Ohtani et al., 2010; Ohtani et al., 2013), are strikingly similar to those of rfc3. The pattern of SCR and WOX5 expression in the root meristem of rid1-1 (Ohtani et al., 2013) also resembles that of rfc3-2. However, RID1 and SRD2 function in pre-mRNA splicing in the nucleus (Ohtani et al., 2010; Ohtani et al., 2013) and are unlikely to be directly associated with plastid gene expression. Elucidating commonality and differences in the subcellular and molecular phenotypes among rfc3, rid1, rid2, and srd2 will further advance our understanding of the role of plastid function in LR stem-cell patterning as well as regulatory mechanisms that respond to defects of a broad category of gene expression systems. Finally, although the developmental functions of housekeeping genes have often been overlooked, there are increasing examples of housekeeping gene mutations that produce specific developmental defects (Tsukaya et al., 2013). As our study illustrates, there may be additional unidentified molecular processes that involve housekeeping genes.
MATERIALS AND METHODS

Plant materials and growth conditions
L. er and Col-0 were used as wild-type Arabidopsis plants. rfc3-1 and rfc3-2 (Horiguchi et al., 2003), rap-1/SAIL_1223_C10 (Kleinknecht et al., 2014), rby1-2/SALK_058490 (Fristed et al., 2014), prps17-1 (Romani et al., 2012), WOX5p::GFP (Blilou et al., 2005), SCRp::GFP:SCR/scr-3 (Nakajima et al., 2001), and QC markers (Sabatini et al., 1999) were described previously. The WOX5p::GFP and QC25 and were backcrossed with L. er and/or rfc3-2 at least three times. Plants were cultured on a solid medium leaning backward a few degrees from the vertical position under a long-day condition (16 h light, 8 h dark) at 22°C to observe the root phenotypes. The solid medium included 0.5× Murashige and Skoog (MS) salts, 0.05% (w/v) MES-KOH pH 5.7, sucrose at an indicated concentration, and 0.5% (w/v) gellan gum. Plants were cultured on rock wool under the long-day condition to observe leaf phenotypes. Stock solutions of plastid ribosome inhibitors dissolved in distilled water or ethanol were added to autoclaved 0.5× MS Suc3 medium before solidification. Spectinomycin dihydrochloride pentahydrate (Wako Pure Chemical, Osaka, Japan), kanamycin sulfate (Wako), and streptomycin sulfate (Wako) were used as plastid ribosome inhibitors and were added to 0.5× MS Suc3 or Suc0.5 at various concentrations.

Plasmid construction and plant transformation
The cDNA sequences were subcloned into pENTR/D-TOPO with the TOPO cloning kit (Thermo Fisher Scientific, Rockford, IL, USA) to construct of 35Sp::RFC3:GFP, 35Sp:PRPS6:GFP, and 35Sp::MRPS6:GFP and transferred into the pH35WG vector (G. Horiguchi and H. Tsukaya, unpublished data) using Gateway LR clonase II (Thermo Fisher Scientific). The transit-peptide sequence of the RecA gene was subcloned into pENTR/D-TOPO (called pENT-RecA-TP) after referring to a previous study (Kohler et al., 1997) to construct 35Sp::RecA-TP:CFP. The 35S promoter cloned into pDONRP4P1R and pENT-RecA-TP was reacted with R4pGWB543 (Nakagawa et al., 2008) using LR clonase II plus (Thermo Fisher Scientific). A genomic RFC3 fragment from the 4,044-bp 5′-region upstream of the region just before the RFC3 stop codon (in
total, 5,709 bp) was cloned into pENTR/D-TOPO (Thermo Fisher Scientific) to construct RFC3g:GFP and then transferred into a Gateway binary vector containing a promoterless GFP cassette, pHWG (Horiguchi and Tsukaya, unpublished). The SUC2 promoter and sGFP fragment were amplified by polymerase chain reaction (PCR) and reacted with the linearized binary vector pSMAH621 (Kubo et al., 2005) using the In-Fusion HD cloning kit (TaKaRa Bio, Shiga, Japan) to construct SUC2p::sGFP, 35Sp::RecA-TP:CFP and RFC3g:GFP were introduced into wild-type L. er and/or rfc3-2 and SUC2p::sGFP was introduced into Col by floral dipping using Agrobacterium tumefaciens strain ASE or C58C1. A SUC2p::sGFP line was crossed with rfc3-2 three times. We used medium containing 0.5× MS salts pH 5.7, Suc3 or Suc0.5, 0.3% (w/v) gellan gum, 20 mg·L⁻¹ hygromycin, and 500 mg·L⁻¹ cefotaxime to select T1 plants. Primer sequences used for construction are shown in Table S2.

Quantitative RNA analyses

RNA samples were extracted from roots of 8-days post sown seedlings frozen in liquid nitrogen using the TRI reagent (Molecular Research Center, Cincinnati, OH, USA) according to the manufacturer’s instructions. SuperScript III Reverse Transcriptase (Thermo Fisher Scientific) and its accessory primers were used for reverse transcription. Oligo(dT) primers and random hexamers were used for the expression analysis of nuclear-encoded genes (except for cytosolic rRNAs) and of plastid-encoded genes and cytosolic rRNAs, respectively. Quantitative PCR analysis was performed using GoTaq qPCR Master Mix (Promega, Madison, WI, USA) with an Applied Biosystems 7500 Fast Real-Time PCR system (Thermo Fisher Scientific). Relative expression levels of nuclear-encoded genes and plastid-encoded genes were calculated with the ΔΔCT method, and normalization was based on ACT2 and ct18S expression, respectively. The primer sequences are shown in Table S2.

Phylogenetic analysis

The sequences analyzed were identified with BLAST searches at several websites: TAIR (https://www.arabidopsis.org/index.jsp), Phytozome (ver. 9.1; http://www.phytozome.net/), GreenPhyl (ver. 3; http://www.greenphyl.org/v3/), and NCBI (http://www.ncbi.nlm.nih.gov/). Sequences of Marchantia polymorpha RFC3,
PRPS6, and MRPS6 homologs were identified from RNA-seq data generated in the Kohchi laboratory (http://marchantia.info/genome/index.php/). The sequences identified were aligned with the MAFFT program (Katoh et al., 2002, 2013) and sites containing > 50% gaps were excluded with the trimAl tool (Capella-Gutierrez et al., 2009). Phylogenetic tree were prepared according to the maximum likelihood (ML) method with the JTT model was analyzed with the RAxML program (Stamatakis, 2006). Alignment files were converted to PDF files with the ClustalX program (http://www.clustal.org/clustal2/), and phylogenetic trees were displayed with MEGA6 software (Tamura et al., 2013).

**Transient expression analysis using leaf mesophyll protoplasts**

Leaf mesophyll protoplasts of 1-month-old plants grown on rock wool were prepared according to the Tape-Arabidopsis sandwich method (Wu et al., 2009). Vectors were isolated from transformed Escherichia coli DH5α with the JetStar Plasmid Midi Kit (Veritas Genetics, Danvers, MA, USA) and transfected by the PEG method, based on a previous report (Yoo et al., 2007). After a 16-h culture at 22°C, transfected protoplasts were mounted with WI solution (0.5 M D-mannitol, 20 mM KCl, 4 mM MES-KOH pH 5.7). MRPS6:GFP-transfected protoplasts were treated with 50 µM MitoTracker Red (Thermo Fisher Scientific) to stain mitochondria on a slide for 30–60 min at 22°C and washed with WI solution before mounting the protoplasts. Stained and unstained protoplasts were observed with an LSM 710 laser scanning microscope (Carl Zeiss, Zena, Germany) (GFP, λ_{ex} = 488 nm, λ_{em} = 493–556 nm, chlorophyll autofluorescence, λ_{ex} = 633 nm, λ_{em} = 647–721 nm, and MitoTracker Red, λ_{ex} = 561 nm, λ_{em} = 568–614 nm).

**Chlorophyll fluorescence measurements**

Chlorophyll fluorescence parameters were measured with a MINI-PAM (pulse-amplitude modulation) portable chlorophyll fluorometer (Walz, Effeltrich, Germany) in ambient air at room temperature (25°C). Minimum chlorophyll fluorescence at the open PSII center (Fo) was determined by measuring light at 0.05–0.1 µmol photons m^{-2} s^{-1}. A saturating pulse of white light (800 ms, 3,000 µmol photons m^{-2} s^{-1}) was applied to determine the maximum fluorescence level at the closed PSII center in the dark (Fm). Maximum fluorescence level at the closed PSII center (Fm’) and the steady-state fluorescence level
(Fs) in actinic light (120 µmol photons m\(^{-2}\) s\(^{-1}\)) were determined. The maximum PSII activity and PSII (Φ\(_{PSII}\)) quantum yield were calculated as \((Fm – Fo)/Fm\) and \((Fm’ – Fs)/Fm’\), respectively.

**Immunoblot analysis**

Aerial parts of 10-days post sown seedlings of L. er and rfc3-2 grown on rock wool were homogenized in protein extraction buffer [20 mM Tris-HCl, pH 6.8, 2% (w/v) sodium dodecyl sulfate, 24% (v/v) glycerol] on ice using a hand-operated homogenizer, and sediment was removed by two centrifugation steps. The concentrations of extracted protein samples were determined with a DC Protein Assay Kit (Bio-Rad, Hercules, CA, USA) before adding 1/10 volume of 1 M dithiothreitol. Approximately 100 ng and 3.5 µg total protein from extracts were electrophoresed on 10% (w/v) isocratic polyacrylamide gels containing SDS, transferred to Amersham Hybond LFP 0.2 PVDF membranes (GE Healthcare, Piscataway, NJ, USA), reacted with each antibody, and detected with Amersham ECL Prime (GE Healthcare) and the ImageQuant LAS 4000mini (GE Healthcare) for immunoblotting of D1 and the other proteins. Antibodies to anti-RPS6 and anti-RPL5 detected both of the paralogous ribosomal proteins (RPS6A/B and RPL5A/B, respectively). After detection, the membranes were stained by Amido Black solution [1 mg/mL Amido Black, 45% (v/v) methanol, and 10% (v/v) acetic acid].

**Detection of ribosomal proteins in polysomal fractions**

Total cell extracts were prepared from 5 mL of frozen ground seedlings and suspended in polysome extraction buffer (PEB) containing 200 mM Tris-HCl (pH 9.0), 200 mM KCl, 50 mM ethylene glycol tetraacetic acid, 100 mM MgCl\(_2\), 6 mM β-mercaptoethanol, 2 mM phenylmethylsulfonyl fluoride (PMSF), 1% (v/v) Triton X-100, 1% (v/v) Brij 35, 1% (v/v) Tween-40, 1% (v/v) NP-40, 2% (v/v) polyoxyethylene 10 tridecyl ether, 1% deoxycholic acid, 50 µM cycloheximide, 50 µM chloramphenicol, and 1 mg mL\(^{-1}\) heparin. Procedures for sucrose density gradient sedimentation analyses were carried out according to the methods described by Natori et al. (2007) and Nanamiya et al. (2010). After removing cell debris by centrifugation (12,000 g, 15 min, 4°C), aliquots of the supernatant were layered onto 15–60% (w/v) sucrose density gradients in Buffer I (20 mM Tris-HCl pH 7.6, 10 mM magnesium acetate, 100 mM ammonium acetate, 6 mM...
β-mercaptoethanol, and 2 mM PMSF) and centrifuged (65,000 g, 17.5 h, 4°C, Hitachi P40ST rotor). Samples were taken with a Piston Gradient Fractionator (BioComP, Fredericton, NB, Canada), and absorbance profiles were monitored at 254 nm using a Bio-mini UV Monitor (ATTO, Tokyo, Japan). Polysomal fractions were subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis and immunoblot analysis (Fig. S12). Rabbit antiRPS6 and RPL5 antibodies were raised against the synthetic peptides, DTEKPRMRGPKRASKIRC and VEA TedFSVEPTDSRRC, respectively.

Transmission electron microscopy

*A. thaliana* roots were cut into 2–3-mm pieces and fixed with 4% (w/v) paraformaldehyde and 2% (v/v) glutaraldehyde in 50 mM sodium cacodylate buffer (pH 7.4) overnight at 4°C. They were post-fixed with 1% (w/v) osmium tetroxide in 50 mM cacodylate buffer for 2 h at 21°C. After dehydration in a graded methanol series [25, 50, 75, 90, and 100% (v/v)], the samples were infiltrated with increasing concentrations of Epon812 resin [propylene oxide: Epon812 = 3:1, 1:1, 1:3, and 100% (v/v)] and embedded. Ultrathin sections (80 nm) were cut with a diamond knife on an ultramicrotome (Leica EM UC7, Leica Microsystems, Buffalo Grove, IL, USA) and mounted on formvar-coated copper grids. The ultrathin sections were stained with 4% (w/v) uranyl acetate followed by lead citrate solution and examined with a transmission electron microscope (JEM-1400; JEOL Ltd., Tokyo, Japan) at 80 kV.

Other procedures

We mounted the samples treated with or without 10 µg mL\(^{-1}\) propidium iodide (PI) for 5 min on a slide to observe GFP and CFP patterns in root cells and leaf mesophyll cells. The samples were observed with the LSM 710 (GFP only, \(\lambda_{\text{ex}} = 488\) nm, \(\lambda_{\text{em}} = 493–598\) nm, GFP/Chl, \(\lambda_{\text{ex}} = 488\) nm/633 nm, \(\lambda_{\text{em}} = 493–598\) nm/647–721 nm, GFP/PI, \(\lambda_{\text{ex}} = 488\) nm, \(\lambda_{\text{em}} = 493–556\) nm/593–719 nm, CFP/PI, \(\lambda_{\text{ex}} = 405\) nm/514 nm, \(\lambda_{\text{em}} = 454–581\) nm/593–719 nm, and CFP/GFP, \(\lambda_{\text{ex}} = 405\) nm/488 nm, \(\lambda_{\text{em}} = 454–581\) nm/493–598 nm). The modified pseudo-Schiff-PI (mPS-PI) method was performed as described previously (Truernit et al., 2008) with some changes. Roots were fixed with 50% (v/v) ethanol and 10% (v/v) acetic acid overnight or for several days at 4°C and treated with 80% (v/v) ethanol for 3 min before washing and treatment with 1% (w/v) periodic acid solution. The
treated samples were stained with 100 µg mL⁻¹ PI for 2 h, cleared in a clearing solution (chloral hydrate:glycerol:water = 8:1:2) overnight at 4°C, mounted, and scanned with the LSM 710 (λ_ex = 514 nm, λ_em = 566–719 nm). The roots were soaked in a β-glucuronidase (GUS) solution [500 mg/L 5-bromo-4-chloro-3-indolyl-β-D-glucuronic acid, 100 mM NaPO₄, pH 7, 3 mM potassium ferricyanide, 10 mM EDTA, 0.1% (v/v) TritonX-100] overnight at 37°C for GUS staining, washed in 70% (v/v) ethanol twice, and mounted in clearing solution. We used a Leica M165FC equipped with a DFC300FX camera (Leica) as a stereomicroscope, and a Leica DM2500 equipped with a DFC420C camera (Leica) as a differential contrast interference microscope. Adjustments and format conversions of confocal images were performed using Fiji software (Schindelin et al., 2012). Statistical analyses and drawing graphs were performed using the ‘R’ software (R_Development_Core_Team, 2010) or Excel 2008 for Mac (Microsoft, Redmond, WA, USA). Captions, diagrams, and coloring for explanation were superimposed on the figures using Adobe Illustrator CS4 software (Adobe Systems, San Jose, CA, USA).

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Competing interests

The authors declare no competing or financial interests.
Author contributions
M.T.N. and G.H. designed the research; N.S. and T.S. measured chlorophyll fluorescence; M.S., M.W., and K.T. performed the TEM analysis; K.K. generated the anti-RPS6 and anti-RPL5 antibodies; M.T.N., A.S., S.N., and G.H. constructed and isolated the transgenic lines; M.T.N. contributed to data collection and analyses of the experiments; and M.T.N., M.S., M.W., K.T., T.S., H.T., and G.H. contributed to the manuscript drafting and revisions.

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**Fig. 1. Subcellular localization of RFC3:GFP.** (A) Transient expression assays in Arabidopsis mesophyll protoplasts. GFP signals (GFP), chlorophyll autofluorescence (Chl), the bright field (BF) image, and MitoTracker Red (Mito) are shown. (B) RFC3:GFP localization in mesophyll cells of leaves of a stable RFC3g:GFP line. (C) Colocalization analysis of RFC3:GFP and RecA-TP:CFP in the meristematic region of lateral roots (LRs). Scale bars, 20 µm (A), 5 µm (middle and right panels in the bottom row of A), 50 µm (B and upper panels of C), 5 µm (lower panels of C).
Fig. 2. RFC3 function in chloroplasts. (A) Shoots from different alleles of *rfc3* and *prps17-1* mutant plants. Scale bar indicates 1 cm. (B) The photosynthetic parameters of *L. er* and two *rfc3* alleles \([Fv/Fm \text{ and } (Fm' - Fs)/Fm' = \Phi_{PSII}]\). The maximum fluorescence level at the closed PSII center \((Fm')\) and the steady-state fluorescence level \((Fs)\) were determined in actinic light \((120 \mu\text{mol photons m}^{-2} \text{s}^{-1})\). (C) Immunoblot analysis and Amido Black staining of proteins extracted from *L. er* (shown as “L”) and *rfc3-2* (shown as “r3”) shoots. Statistical analyses in (B) were carried out using the paired Student’s *t*-test and statistical significance is indicated by double asterisks \((p < 0.01)\).
Fig. 3. Expression of plastid encoded genes in L. er and rfc3-2 roots. (A) Relative RNA levels in roots estimated by RT-qPCR analysis. Plants were grown in media containing 3% sucrose. (B) Effects of sucrose on the levels of plastid 16S (pt16S) and pt23S rRNAs in wild-type and rfc3-2 roots grown in media containing 0.5% or 3% sucrose. Data are represented as the mean ± s.d. (n = 3). Statistical analyses in (A) was carried out using the paired Student’s t-test and statistical significance is indicated by single (p < 0.05), double (p < 0.01), and triple asterisks (p < 0.001) while those in (B) using ANOVA with Tukey HSD test (P <0.05). In (A) and (B) ct25S, mt18S, and mt28S indicate cytosolic 25S rRNA and mitochondrial 18S and 28S rRNAs.
Fig. 4. Characterization of the *rfc3* LR phenotype. (A) The LR phenotype of *rfc3* alleles. (B) Nodule-like LRs (left panel) and stubby LRs (middle and right panels) observed by modified pseudo-Schiff-propidium iodide (mPS-PI) staining. (C) Relative expression of root stem-cell regulatory genes in roots measured by RT-qPCR (n = 3). Statistical analyses were carried out as described in Fig. 3. (D) WOX5p::GFP patterns (green) merged with bright field images in LR primordia. (E) Phenotype frequencies of WOX5p::GFP in *L. er* and *rfc3-2* LRs grown in different concentrations of sucrose and Spec. Sucrose and Spec concentrations are indicated by percentage and mg L⁻¹, respectively. Individual LR primordia were classified into normal, slightly expanded, widely expanded and disappeared WOX5p::GFP expression patterns. LR primordia beyond stage VI and LRs up to 200 µm were scored. The total number of LR primordia plus LRs in each condition was more than 76. Scale bars, 1 mm (A) and 100 µm (B, D).
Fig. 5. Effect of the plastid translation inhibitor Spec on LR development. (A) mPS-PI-stained LRs of L. er plants grown on medium containing various Spec concentrations. (B) Relative expression levels of WOX5, PLT3, and PLT7 in Spec-treated plants (n = 3). (C) Distribution of GFP fluorescence (green) in WOX5p::GFP merged with bright field images. (D, E) Relative transcript levels of plastid ribosomal RNAs (D) and plastid-encoded genes (E) in roots (n = 3). (F) Correlation analysis of changes in expression (Log2) in plastid-encoded genes resulting from the rfc3 mutation and 4 mg L⁻¹ Spec treatment. R, Pearson’s correlation value. Statistical analyses were carried out as described in Fig. 3.
Fig. 6. LR phenotype of plastid translation-defective mutants with/without Spec.

(A) Primary root length of L. er, prps17-1 and rfc3-2 at 8 days post sowing. Data are represented as mean ± s.d. (n ≥ 46). ***P < 0.001 by Tukey’s HSD test. (B) LR phenotype of L. er and prps17-1 with or without Spec. Yellow arrowheads, nodule-like LRs. (C) mPS-PI-stained LR phenotype of L. er and prps17-1 with or without Spec. Orange arrows, the position of the QC cells. (D) Relative expression levels of WOX5, PLT3 and PLT7 in L. er and prps17-1 roots without Spec. Data are represented as mean ± s.d. Experiments were performed in biological triplicate. ***P < 0.001 and *P < 0.05 by paired Student’s t-test. (E) The GFP signal (green) of WOX5p::GFP in prps17-1 background with or without Spec. The differential interference contrast images were merged. (F) mPS-PI-stained LR phenotype in rap-1 and rbf1-2 with or without Spec. In (F), arrowheads indicate the position of the QC cells and brackets indicate the area occupied by disorganized or staritified cells. Scale bars, 1 mm (B), 50 µm (C, E, F).
Fig. 7. Spec treatment of Col-0-background meristem marker lines and the SUC2p::sGFP line. (A) mPS-PI-stained LRs of Col-0 plants treated with Spec. (B) SCRp::GFP:SCR/scr, QC25, and QC46 expression patterns. (C, D) GFP patterns in LRs of Spec4-treated SUC2p::sGFP in the wild-type Col-0 (C) and rfc3-2 (D) backgrounds. The green signals in (B), (C), and (D) are GFP fluorescence; the blue signal in (B) is β-glucuronidase (GUS)-stained cells. Scale bars, 50 µm (A, B) and 100 µm (C, D).
Fig. 8. Plastid distribution in root cells. (A) Intracellular distribution of CFP in the 35Sp::RecA-TP:CFP lines in L. er and rfc3-2 backgrounds. CFP fluorescence is shown in green and roots were stained with PI (magenta). (B) Ultrastructure of plastids in pericycle cells of primary roots in L. er, rfc3-2, and Spec4-treated L. er. Scale bars, 50 µm (A) and 1 µm (B).
**Figure S1. Phylogenetic tree and alignment of bRPS6 family proteins.** (A) An unrooted phylogenetic tree of bRPS6 family proteins by ML method with JTT model. Numbers indicate bootstrap values (% of 1000 times). Arrowheads show Cyanidiophyceae species. Detailed name of each species and accession numbers of used sequences are shown in Table S1. (B) Alignment of the bRPS6 domain. Ath, *Arabidopsis thaliana*; Bdi, *Brachypodium distachyon*; Mpo, *Marchantia polymorpha*; Cre, *Chlamydomonas reinhardtii*; Ppu, *Porphyridium purpureum*; animal mitochondria Homo, *Homo sapience* mitochondrial RPS6; Drosophila, *Drosophila melanogaster* mitochondrial RPS6; the others, RPS6s from bacterial species (refer to Table S1). “a1” and “a2” indicate the first and second alpha helices and “b1” to “b4” indicate the first to fourth beta sheets, respectively.
Figure S2. Subcellular localization of RFC3:GFP in stable lines of RFC3g:GFP/rfc3-2. (A-C) Phenotype of primary roots (A), LRs (B) and shoots at 20-days-post-sowing (C) in rescued lines of RFC3g:GFP/rfc3-2. (D-E) RFC3:GFP pattern (green) in primary roots (D), an LR primordium (E, left panel) and an LR (E, right panel). Propidium iodide (PI)-stained cell wall is shown as white in (E). An arrow in D indicates QC cells. An arrowhead in (E) indicates an LR primordium. Scale bars equal 1cm (A, C), 1 mm (B) and 100 µm (D, E).
Figure S3. Shoot phenotypes of rfc3-2. (A) Shoots of L. er and rfc3-2 grown for 23 days. Bar indicates 1cm. (B) Leaf blade area. (C) Number of leaves per plant. Data are mean ± s.d. (n = 12). Statistical analyses in (B) and (C) were carried out using the paired Student’s t-test and statistical significance is indicated by triple asterisks (p < 0.001).
Figure S4. Chlorophyll fluorescence induction pattern of *rfc3* alleles. Results from four independent experiments (Ex1-Ex4). Vertical blue bars represent the Fo levels. Chlorophyll fluorescence was analyzed under the measuring light (ML). Photosynthesis was induced by actinic light (AL, 120 µmol photons m⁻² s⁻¹). Saturating flushes (SF) were applied every 1 min to monitor Fm and Fm'.

- *L. er* rfc3-1 rfc3-2
- Ex1
- Ex2
- Ex3
- Ex4
- Fo
- Fm
- MLon
- ALon
- Fm'
- ALoff
- Fs
- SF
- SF
- SF
- SF SF SF
- 1 min

**Figure S5.** Effects of sugars on LR development. (A) Frequencies of normal, stubby, and nodule-like LRs in *L. er* and *rfc3-2*. (B) Primary root length. (C) *L. er* and *rfc3-2* grown in media containing various sugar conditions. *L. er* (*n* = 20) and *rfc3-2* (*n* = 30) primary roots grown for 8 days were examined. In (A), LRs beyond stage VI and all LRs were scored. In (B), data are presented as mean ± s.d. and relative primary root lengths of *rfc3-2* to *L. er* are also indicated on the top of graph. Scale bars in (C) indicate 1 cm.
Figure S6. *WOX5p::GFP* pattern in LR primordia of *rfc3-2*. *L. er* and *rfc3-2* were grown in media containing 0.5% sucrose and Spec at indicated concentration (mg L⁻¹). GFP fluorescence images were merged with differential interference contrast images. Bars indicate 100 μm.
Figure S7. The effect of plastid translation inhibitors on LR development. (A) LR phenotype of wild-type L. er plants treated with plastid translation inhibitors. Yellow arrowheads, nodule-like LRs; red arrowheads, stubby LRs. The numbers described in Figures are the concentration of each inhibitor (mg L^{-1}). (B) LR phenotype of kanamycin (Kan)-treated and streptomycin (Strep)-treated plants stained by mPS-PI methods. Scale bars equal 1 mm (A) and 100 μm (B).
Figure S8. Genetic interaction between *rfc3* and *prps17*. (A) Developing ovules from immature to mature fruits. (B-D) Ovules containing a green embryo (B) and an albino embryo (C), respectively. An enlarged image of a square in (C) is shown in (D). Scale bars equal 1 mm (A) and 100 µm (B, C).
Figure S9. Expression of QC25 marker. QC25 reporter lines in L. er and rfc3-2 backgrounds were subjected to GUS staining. Bars indicate 100 μm.
Figure S10. Plastid marker aggregations in mature root cells of Spec-treated L. er plants. The patterns of stroma markers of root plastids in the mature region of PRs. The fluorescence pattern of 35Sp::RecA-TP::CFP or RFC3g::GFP are shown in green and propidium iodide is shown in magenta. Scale bars, 50µm.
Figure S11. Enormous plastid clusters in mature root cells of rfc3-2 and Spec-treated L. er plants. Ultrastructure of root plastids in untreated L. er, rfc3-2 and 4 mg L⁻¹ Spec-treated L. er plants. Figure 8B corresponds to magnified views of orange squares of this figure. Scale bars equal 2 μm.
Figure S12. Detection of RPL5 and RPS6. Polysomal fractions from wild type (WT) seedlings were isolated and subjected immunoblot analysis. Both anti-RPL5 and -RPS6 antibodies detected proteins at the estimated molecular weights of RPL5 and RPS6, respectively. M, Molecular weight marker.

Table S1. Information of RPS6 sequences for phylogenetic analysis

Click here to Download Table S1

Table S2. Information of primers used in this study

Click here to Download Table S2