

Short Communication

OsDOF11 Promotes Crown Root Formation via Cytokinin in Oryza Sativa

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Abstract

Background: Crown root is the main part of root system, which performs an important role in rice growth and development, especially in nutrition and water assimilation. Previously, we reported negative feedback regulation loop between Oryza sativa DNA BINDING WITH ONE FINGER I1 (OsDOF11) and cytokinin by Oryza sativa CYTOKININ OXIDASE/DEHYDROGENASE 4 (OsCKX4) in rice development. Methods: Reverse transcription quantitative RT-PCR analyses was used to analyze the related gene transcript level. Nitrogen and hormone were measured by CHN-Nitrogen analyser and Liquid chromatography mass spectrometer, respectively. Exogenous application of cytokinin and $[^{13}C]$ sucrose labeled stable isotope uptake experiments help us to explain the relationship between OsDOF11 and cytokinin. Results: We demonstrate the role of OsDOF11 in root development. We note that the loss function of OsDOF11 displays the reduced crown roots number, low activity of nitrogen assimilation allow content of cytokinin and auxin. The expression level of WUSCHEL-related homeobox (OsWOX11), A-type response regulator 2 (OsRR2), OsRR3, and OsCKX4 were decreased in osdof11-1, as well as in OsDOF11 RNA interference 9 mutants (RNAi-9 lines). Through Exogenous application of multiple concentrations of cytokinin as treatment to osdof11-1 mutant, RNAi-9 lines, and wild type (WT). We found that the crown roots number of osdof11-1 plants were rescued as the cytokinin concentration increased gradually from 1 μ M to 10 μ M, but the effect was weaker in RNAi-9 line. And cytokinin inhibited sucrose uptake activity from Murashige-Skoog medium with 3.0% sucrose (MS30) by OsDOF11 in rice root. Conclusions: OsDOF11 promotes crown root formation via cytokinin in oryza sativa. These results provide a physiological basis for further analysis of the OsDOF11 function of in rice root development.

Keywords: OsDOF11; cytokinin; nitrogen; crown root; rice

1. Introduction

Plant architecture is an important factor in biomass, such as of the root system, tiller number, panicle structure [1,2]. Several development processes or reactions directly or indirectly affect the plant architecture, such as: nutrition transport activity and distribution efficiency of assimilation, plant hormones signaling and mechanism, and so on. Nutrients are assimilated by root system, which provides the fundamental elements for plant development [3,4]. Crown root (also known as adventitious roots or shoot-borne roots) acts as one type of the root component of plant root system, which displays much more contributions to nutrition and water uptake in crops, including rice [5].

The endogenous/exogenous phytohormones are essential for crown roots development, such as auxin, and cytokinin [6,7]. Auxin may induce *Oryza sativa CROWN ROOTLESS 1* (*OsCRL1*) by two auxin responsive elements at promoter region, which is essential for crown root formation in rice [8]. Also, overexpression of *OsYUCCA1* or RNA interference of rice *PIN-formed 1* (*PIN1*) transgenic

plants displayed reduced crown roots by altering auxin signal transfer or transport, respectively [9,10]. Oryza sativa CYTOKININ OXIDASE/DEHYDROGENASE 4 (OsCKX4) functions in cytokinin degradation. OsCKX4 activation line ren-1 demonstrate more crown roots with lower level cytokinin. Both RNAi-32 and RNAi-42, OsCKX4 RNA interference lines, have reduced number of crown roots. Two different type response elements of auxin and cytokinin existed in OsCKX4 promoter. Auxin response factor of Os-ARF25, and B-type response regulator of ORR2 and ORR3 could bind OsCKX4 promoter by Yeast-one experiments [11]. In addition, OsCRL5 and WUSCHEL-related homeobox (OsWOX11) are also mediated in the cross talk of auxin and cytokinin signaling pathways in regulating crown root formation [12,13]. Over expression of *Receptor-like* Protein Kinase (OsRPK1), which encodes a leucine-rich repeat-receptor-like kinase, reduces crown roots number by auxin transport inhibition. This gene is also regulated by abscisic acid and salt stress [14].

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Multiple extrinsic nutrition factors could affect crown root emerging from the stem. PHOSPHORUS UP-TAKE 1 (PUP1)/PHORUS-STARVATION TOLERANCE 1 (PSTOL1), expresses in the zone of crown roots initiation of the stem base, might affect crown roots establishment and elongation by contributing to nutrient uptake [15]. Oryza sativa DNA BINDING WITH ONE FINGER 11 (Os-DOF11) is a transcription factor that mediates sucrose transport by binding to the promoter of sucrose transport genes, Sucrose Transporter (SUT) and Sugars Will Eventually be Exported Transporters (SWEET) genes. Recently, we reported that the osdof11 mutant and WT germinated on Murashige-Skoog medium without sucrose (MS0) for 7 days. We found that the primary root length and crown roots number were reduced in osdof11 mutants [16], which were similar with published data of OsCKX4 RNAi transgenic plant root phenotype [11]. Here, we demonstrated that OsDOF11 modulates crown roots initially by inducing cytokinin signaling.

2. Materials and Methods

2.1 Plant Materials and Growth Conditions

Japonica rice (*Oryza sativa* 'Dongjin') plants were grown in controlled environment rooms. Seeds were germinated either on an MS medium without sucrose, as previously reported. Progeny of homozygous *osdof11-1* plants and segregating WT plants were selected, as well as *RNAi-9* [17]. Seedlings were cultivated for 7 days at 28 °C under continuous light before being transferred to soil in the greenhouse.

2.2 Nitrogen Content

WT, osdof11-1 and RNAi-9 seeds were geminated in Yoshida medium with or without nitrogen for 7 days. The seedling plant was harvested, ground in liquid nitrogen, and then filtered through a $100-\mu m$ sieve. The total nitrogen content was measured using a CHN-Nitrogen analyser (Vario EL cube, Elementar Analysensysteme Gmbh, Langenselbold, Germany). The protein contents in the seedling plant and effective leaf blade were calculated on a dry basis.

2.3 RT-PCR Analyses

Total RNA was isolated from seedling roots with stem at 7 DAG using RNAiso Plus (TaKaRa, Shiga, Japan; http://www.takarabio.com). The cDNAs were synthesized and quantitative real-time RT-PCR was performed as previously described [17]. Expression levels were normalized with rice UBQ5 (LOC_Os01g22490). All experiments were conducted at least three times, with three or more samples taken at each point. To ensure primer specificity, we performed the experiments when the melting curve showed a single sharp peak. All primers are listed in **Supplementary Table 1**.

2.4 Extraction, Purification, and Quantification of Hormones

WT, *osdof11-1* and *RNAi-9* seeds germinated and grew in water for 10 days at growth chamber. The various hormones studied here were extracted, purified and measured as previously reported [18].

2.5 Cytokinin Treatment Arrays

WT, osdof11-1 and RNAi-9 were germinated in MS medium without sucrose, which contained multiple concentration of kinetin (1 μ M, 4 μ M, 10 μ M, and 50 μ M).

2.6 Statistical Analysis

Student's *t*-test by Excel 2010 (Microsoft, Washington, USA) was performed to determine any statistically significant differences among values measured from WT, osdof11-1, and RNAi-9 samples in each experiment. Each data point represents the mean from at least four different plants. Student's *t*-test was used to compare means at a significance level of p < 0.05 or p < 0.01.

3. Result and Discussion

OXI-Orvza sativa **CYTOKININ** DASE/DEHYDROGENASE 4 (OsCKX4) is a cytokinin inhibitor, which plays a positive role in crown roots formation [11]. Previously, we reported that Oryza sativa DNA BINDING WITH ONE FINGER 11 (OsDOF11) mediated sucrose transport by sucrose transporter genes and cytokinin degradation by OsCKX4 [16,19]. To further analyze the function of OsDOF11 at seedling stage, we chose T-DNA insertion line osdof11-1 and OsDOF11 RNA interference line 9 (RNAi-9) for analysis, as well as background line of cultivar Dongjin (WT). We found that the crown roots number was reduced in OsDOF11 mutant (Fig. 1A,B) which was similar with published data of OsCKX4 RNAi transgenic plant [11]. Reverse transcription quantitative PCR (RT-qPCR) analyses demonstrated that the expression level of WUSCHEL-related homeobox (OsWOX11), A-type response regulator 2 (OsRR2), OsRR3 and OsCKX4 was reduced in the osdof11 mutant root, as well as RNAi-9 (Fig. 1C-F).

Sucrose not only acts as a type of carbohydrate for providing energy, but is also utilized to synthesize other organic materials. We described that *OsDOF11* participated in sugar distribution and nitrogen assimilation [17,19]. Furthermore cytokinin metabolism and signal are closely associated with nitrogen availability [20], which plays key roles in root development [21,22]. We germinated *OsDOF11* mutant and *RNAi-9* in Yoshida medium for 10 days. Compared with WT, nitrogen assimilated contents were reduced to 45.62% and 38.34% in the *OsDOF11* mutant and *RNAi-9* lines, respectively (Fig. 1G).

We further measured cytokinin, IAA, and ABA contents of the total seedling plant at 10 DAG. These results showed that zeatin contents in *osdof11-1* and *RNAi-9* were



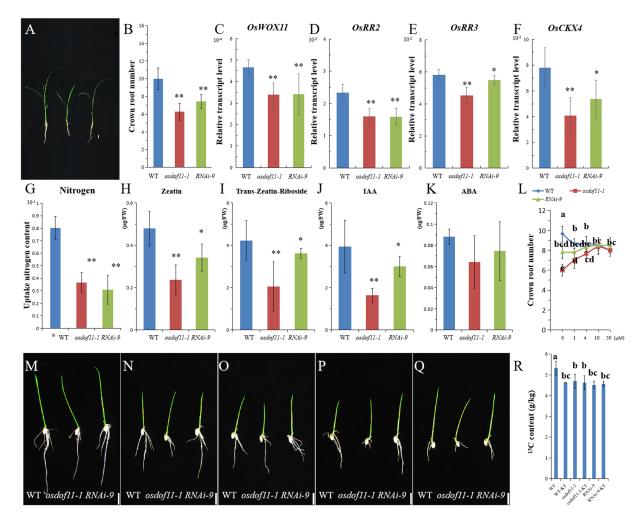


Fig. 1. OsDOF11 promotes crown roots formation by cytokinin. (A,B) Crown root number of WT, osdof11-1, and RNAi-9. (A) Plants at 14 DAG; (B) Crown root number of OsDOF11 mutant and WT plants at 7 DAG. Bar: A = 2 cm. (C–F) Expression levels of CK-related genes relative to OsUBQ5, evaluated in 7 DAG total seedling plant from WT and osdof11 mutants. (C) OsWOX11; (D) OsRR2; (E) OsRR3; (F) OsCKX4. (G) The increased nitrogen content of WT, osdof11-1, and RNAi-9 seedlings grown on MS0 media with or without Nitrogen for 7 days. (H–K) CK, IAA, and ABA content in WT and osdof11 mutant at 7 DAG. (H) Zeatin; (I) Transzeatin-riboside; (J) IAA; (K) ABA. (L–Q) Crown roots number by the treatment of multiple concentration of Kinetin for 7 days. (L) Crown roots number; (M) 0 μ M; (N) 1 μ M; (O) 4 μ M; (P) 10 μ M; (Q) 50 μ M. (R) 13 C-sucrose content. 13 C-sucrose was added into MS medium with 3.0% sucrose and content of the stable isotope labeled sucrose was detected after 3 d. Error bars represent STDEV of at least 3 samples. (B–K): Student's t-test was used for statistical analysis. *, p < 0.05; **, p < 0.01. (L, R): Values in the same column with different letters are significantly different (p < 0.05).

reduced to approximately 49.41% and 71.70%, respectively (Fig. 1H). In addition trans-zeatin-riboside levels were also reduced to about 48.48% and 85.78% (Fig. 1I). This implies that less cytokinin in OsDOF11 mutant plants might be due to lower activity in synthesis or transport. And the IAA contents in osdof11-1 and RNAi-9 were reduced to 41.3% and 75.92%, respectively (Fig. 1J). But the ABA contents was not changed (Fig. 1K). To further analyze the role of cytokinin in osdof11-1 plants, we applied multiple concentrations of cytokinin (0 μ M, 1 μ M, 4 μ M, 10 μ M and 50 μ M) for treatment. We found that crown roots number of WT was inhibited, but that of the osdof11-1 plants was rescued as the cytokinin concentration increased gradually from 1

 μ M to 10 μ M (Fig. 1L–Q). These results indicated that *OsDOF11* promoted crown roots number by cytokinin.

OsDOF11 mediates sucrose transport activity. We germinated WT and osdof11 mutant seeds on MS medium without sugar for 7 days, and then move to MS liquid medium with 3.0% sucrose (labeled stable isotope [13 C]) for 3 days. Compared with WT, the 13 C content in osdof11-1 and RNAi-9 seedlings was decreased to 88.28% and 84.88% (Fig. 1R). To analyze the role of cytokinin in sucrose transport, we added 10 μ M cytokinin in this sucrose uptake experiment. We found that the 13 C labeled sucrose content in WT seedlings was reduced by 13.18% under the cytokinin treatment, but osdof11-1 and RNAi-9 seedlings



were not affected (Fig. 1R). These results demonstrated that cytokinin inhibited sucrose uptake by *OsDOF11*.

Cytokinin acts as an important factor in rice root development. The concentrations of cytokinin ribosides were reduced in *OsCKX4* activation-tagging mutant [11]. OsDOF11 appeared to mediate expression of *OsCKX4* directly through binding to the target promoters, and further induced the content of cytokinin in leaf [16]. Defect in sugar transport may cause reduced content of cytokinin and IAA in *OsDOF11* at 10 DAG. The set genes of *OsIPT3*, *OsIPT7*, and *OsIPT8* expressed in leaf blade, which may synthesize the cytokinin [23]. We do not rule out a possibility that cytokinin transport and synthesis are also the reason why cytokinin was abnormal in *OsDOF11* mutant.

4. Conclusions

We considered that defect in crown roots number was caused by reduced sugar transport activity and hormone level, especially in cytokinin. Meanwhile, OsDOF11 controlled sucrose transport and nitrogen metabolism. Cytokinin induced OsDOF11 transcript levels. However, sucrose uptake activity was inhibited by the $10~\mu M$ cytokinin treatment. It also indicated that high level of cytokinin decreased root activity. There is the possibility of a relationship between OsDOF11 and auxin due to the binding of OsCKX4 to OsARF25. Further studies are required to clarify the relationship between hormone and sucrose transport or uptake at the molecular level.

Author Contributions

XD, WH, XH and YZ perfomed experiments and analyzed data. YW and FX designed the experiment. YW, GC and FX supervised the experiment. YW, and MZ wrote and edited the manuscript.

Ethics Approval and Consent to Participate

Not applicable.

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Conflict of Interest

The authors declare no conflict of interest.

Supplementary Material

Supplementary material associated with this article can be found, in the online version, at https://doi.org/10.31083/j.fbl2708248.

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