Molecular Mechanism of Mugineic Acid Family Phytosiderophores Secretion

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Iron (Fe) is essential for all living organisms, including humans and plants. To acquire Fe in the soil, graminaceous plants produce and secrete mugineic acid family phytosiderophores (MAs) from their roots. MAs chelate and solubilize insoluble Fe hydroxide in the soil. Subsequently, plants take up Fe-MAs complexes through specific transporters on the root cell membrane. MAs and nicotianamine (NA), an intermediate of the MAs biosynthesis, are both important for the translocation of Fe in the plant body. In this study, we analyzed molecular mechanism of MAs secretion. We show that the efflux of deoxymugineic acid, the primary MAs from rice and barley, involves the *TOM1* and *HvTOM1* genes, respectively [1]. We have also identified two genes encoding efflux transporters of nicotianamine, *ENA1* and *ENA2*. In addition, we analyzed *Yellow stripe 3* (*ys3*), the recessive mutants of maize (*Zea mays* L.) that show typical symptoms of Fe deficiency, and found that the expression level of a homolog of *TOM1* in maize decreased significantly in the *ys3* mutant, suggesting that *ZmTOM1* may be involved in the *ys3* phenotype [2]. Our identification of MAs efflux transporters has revealed the final piece in the molecular machinery of iron acquisition in graminaceous plants. We also analyzed the particular vesicles that are speculated to be involved in MAs biosynthesis. We developed transgenic rice plants that express rice nicotianamine synthase (NAS) 2 (*OsNAS2*) fused to synthetic green fluorescent protein (*sGFP*) under the control of its own promoter [3,4]. In root cells, OsNAS2:sGFP fluorescence was observed in a dot-like pattern, moving dynamically within the cell. This suggests that these vesicles are involved in MAs biosynthesis. Finally, we succeeded to produce the soybean plants overexpressing the barley NAS1 (*HvNAS1*) gene driven by the constitutive CaMV 35S promoter were produced using Agrobacterium-mediated transformation [5]. The NA content of transgenic soybean seeds was up to four-fold greater than that of non-transgenic (NT) soybean seeds and showed tolerance to low Fe availability in calcareous soil.

References

[1] Nozoye T., Nagasaka S., Kobayashi T., Takahashi M., Sato Y., Uozumi N., Nishizawa N.K.: J. Biol. Chem., 18: 5546-5554 (2011).

[2] Nozoye T., Nakanishi H., Nishizawa N.K.: PLoS One, 8: e62567 (2013).

[3] Nozoye T., Nagasaka S., Bashir K., Takahashi M., Kobayashi T., Nakanishi H., Nishizawa N.K.: Plant Journal, 77: 246-260(2014).

[4] Nozoye T., Tsunoda K., Nagasaka S., Bashir K., Takahashi M., Kobayashi T., Nakanishi H., Nishizawa, N.K.: Plant Signaling & Behavior, 4: 9 (2014).

[5] Nozoye T., Kim S., Kakei Y., Takahashi M., Nakanishi H., Nishizawa, N.K.: Bioscience Biotechnology Biochemistry 22: 1-8 (2014).