

DIVISION OF DEVELOPMENTAL BIOLOGY

(ADJUNCT)

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Availability of sugars and the inter-organ transport and distribution of sugars are essential in the growth and development of the plant body. Expression of a variety of plant genes is regulated, either positively or negatively depending on the gene, by the level of sugars at the sugar-importing sink sites as well as at the sugar-exporting source sites of the plant body. Thus, sugars are not only important as sources for cellular energy and the synthesis of macromolecules but also as a signal controlling the pattern of gene expression in various parts of the plant body. Our research attention is focused to elucidate the mechanisms involved in the regulation of gene expression in response to sugars and the role of such regulation in the growth and development of plants.

During the growth of plants, new organs develop as carbohydrate sink, and many vegetative organs show sink-to-source transition after their maturation. Sugar affects many aspects of these organ developments in plants. To obtain insights into the role of sugar-regulated gene expression in the growth and development of plants, we took genetic approach using *Arabidopsis thaliana*. To aid this purpose, we established more than 7,000 independent lines of *Arabidopsis* plants transformed with T-DNA containing multiple copies of the enhancer sequence. Among these lines, we screened for mutants that not only showed defects in the development of leaves or anomalies in the flowering time but also showed the altered patterns of the sugar-inducible expression of a gene for β -amylase (*At β -Amy*). More than 20 such mutants, designated as *uns* (*unusual sugar response*), were isolated. Similar to *lba1* and *hba1* mutants of *Arabidopsis* isolated previously [Mita, S., Murano, M., Akaike, M. and Nakamura, K., *Plant J.*

11: 841-851 (1997); Mita, S., Hirano, H. and Nakamura, K. *Plant Physiol.* **114**: 575-582 (1997)], the sugar-inducible expression of *At β -Amy* in *uns* mutants was either significantly reduced or enhanced compared to that in the wild-type plants depending on the mutant line.

In several of *uns* mutants, we could identify mutated genes responsible for the mutant phenotypes. One of them, *UNS6*, codes for a protein that shows amino acid sequence similarity to a gene of *Saccharomyces cerevisiae*, which is essential in yeast and has been suggested to play a role in the assembly of the transcription preinitiation complex. The *uns6* mutant plants show enhanced sugar-inducible expression of *At β -Amy* and several other genes and defects in leaf development. However, despite *UNS6* is a single-copy gene in *Arabidopsis*, mutant plants do not show severe developmental defects other than leaf development. Furthermore, the sugar-responsive expression of several other genes is not affected in the mutant plants. Thus, *UNS6* may have some unique function other than a general role in transcription initiation in *Arabidopsis*.

Selected Publication:

- Iwata, Y., Kuriyama, M., Nakakita, M., Kojima, H., Ohto, M. and Nakamura, K., (1998) Characterization of a calcium dependent protein kinase of tobacco leaves that is associated with the plasma membrane and is inducible by sucrose. *Plant Cell Physiol.* **39**(11): 1176-1183.
- Koide, Y., Matsuoka, K., Ohto, M. and Nakamura, K., (1999) The N-terminal propeptide and the C terminus of the precursor to 20-kilo-dalton potato tuber protein can function as different types of vacuolar sorting signals. *Plant Cell Physiol.* **40**(11): 1152-1159.
- Nakamura, K., Morikami, A., Ohto, M., Tomiya, T., Hayashi, S., Saijo, T., Yamada, M. and Furukawa, Y. (2000) Mutants of *Arabidopsis thaliana* with altered response to sugars. In "Proceedings of the 2000 Japan-Korea Joint Symposium of Plant Science; Plant Responses to Environments", The Symposium on Plant Biotechnology **14**: 91-94.