

7. Identification of enhancer trap lines with tissue-specific GUS activities in rice

Y. ITO and N. KURATA

Plant Genetics Laboratory, National Institute of Genetics, Mishima, 411-8540 Japan

Department of Genetics, School of Life Science, Graduate University for Advanced Studies,
Mishima, 411-8540 Japan

To establish an experimental system to identify mutants and tissue-specific genes and to clone corresponding genes we have been producing enhancer trap lines of rice using vectors based on a maize transposable element *Ac/Ds* and a GUS reporter gene. We previously reported that the genes trapped by the GUS were efficiently identified in the system (Ito et al. 2004).

To identify various tissue-specific enhancers and genes with a larger scale we screened about 3,000 *Ds* transposed lines by a GUS staining. The GUS staining was carried out using various organs at several developmental stages, an entire germinating seed at 1-day after imbibition, an entire 2-week seedling and a leaf, root, young panicle and flower at around a heading stage. By this screening, 151 lines (5%) with tissue-specific GUS activities in 160 organs were obtained. Some lines showed the GUS activities in two organs. Classification of the GUS-positive lines was shown in Table 1, and their examples were shown in Fig. 1. In vegetative organs 23 lines showed the GUS activities in germinating embryo, two in shoot apex, two in stem, three in tiller, 53 in leaf and 19 in root. In reproductive organs 15 showed the GUS activities in panicle and 37 in flower. Seven lines showed the GUS activities in developing embryo.

These lines would be useful materials to identify genes with tissue-specific expression, which may play a role in development or function of the tissues. These lines also are adequate materials to analyse functions of genes in which *Ds* inserted. Thus, this enhancer trap system provides a useful experimental system for gene and enhancer identification, generation of tissue-specific marker lines and functional analysis of the genes.

Reference

Ito, Y., M. Eiguchi and N. Kurata, 2004. Establishment of an enhancer trap system with *Ds* and GUS for functional genomics in rice. *Mol. Gen. Gen.* 271: 639-650.

Table 1. Number of GUS positive lines in organs

| Organ | | Number |
|------------------|---------------|----------|
| Germinating seed | | 23 |
| Shoot apex | | 2 |
| Stem | | 2 |
| Tiller | | 3 |
| Leaf | 1st leaf | 3 |
| | Lamina joint | 40 |
| | Bundle sheath | 2 |
| | Blade | 1 |
| | Wound | 7 |
| Root | Entire | 7 |
| | Tip | 12 |
| Panicle | Young | 11 |
| | Pedicel | 4 |
| Flower | Awn | 1 |
| | Lodicule | 2 |
| | Anther | 15 |
| | Pollen | 12 |
| | Ovary | 5 |
| | Style | 1 |
| Embryo | | 7 |
| Total | | 160(151) |

The number in parentheses indicates the number of lines.

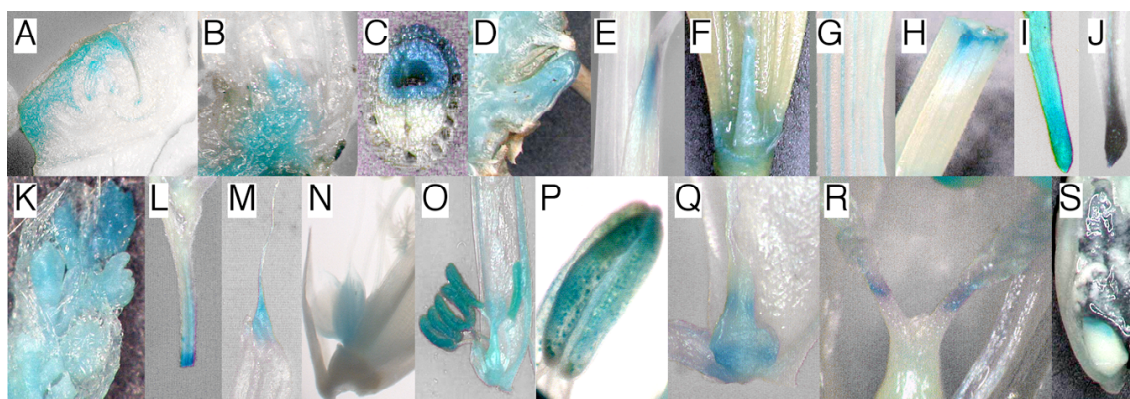


Fig. 1. GUS activities observed in enhancer trap lines. A: 1-day germinating seed. B: shoot. C: stem. D: tiller. E: first leaf. F: lamina joint. G: bundle sheath of leaf. H: wounded leaf. I: root. J: root tip. K: young panicle. L: pedicel. M: awn. N: lodicule. O: anther. P: pollen. Q: ovary. R: style. S: embryo.