LABORATORY OF BIOLOGICAL DIVERSITY

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While genomic structures (as well as their genetic information) appear to stably transmit into daughter cells during cell division, and also into the next generation, they can actually vary genetically and/or epigenetically. Such variability has a large impact on gene expression and evolution. To understand these genome dynamics in eukaryotes, especially in plants, we are analyzing the flower pigmentation of morning glories including *Ipomoea nil* (Japanese morning glory), *I. purpurea* (the common morning glory), and *I. tricolor*.

I. Flower pigmentation patterns

The wild type morning glories produce flowers with uniformly pigmented corolla. However, a number of mutants displaying particular pigmentation patterns have been collected for this study. Because flower pigmentation patterns are easily observable, the molecular mechanisms underlying these phenomena provide useful model systems for investigating genome variability.

The recessive mutations, *duskish* of *I. nil* and *pearly-v* of *I. tricolor*, confer variegated flowers. They are caused by a stable insertion of a transposable element into a gene for flower pigmentation. Furthermore, epigenetic mechanisms are thought to regulate this pigmentation (Figure 1). We are currently analyzing the detailed molecular mechanisms of these mutations.

Figure 1. The *duskish* mutant of *I. nil* shows variable flower phenotypes and produces variegated, fully pigmented, and pale grayish-purple flowers. It segregates offsprings that only show fully pigmented or pale grayish-purple flowers, and their phenotypes can be stably inherited by further generations.

II. Recreating the lost morning glory

I. nil cultivars are displayed in a wide variety of flower colors: red, peach, purple, brown and white. However, just as roses do not have blue flowers, morning glories do not have yellow flowers. Yellow-flowered morning glories have been recorded in illustrations from the Edo period, but this color variety has since been lost. For this reason, it has been called the 'phantom morning glory', and many efforts have been made to reproduce it over a long period. In the yellow-flowered snapdragon, yellow pigment aurones are synthesized by the chalcone glycosyltransferase and aurone synthase genes from chalcone. Although *I. nil* produces chalcone, it lacks an ability to produce large quantities of aurones. The two snapdragon genes were introduced in the *I. nil* mutant accumulating chalcones in its cream yellow flowers. The transgenic plants expressing both genes exhibited yellow flowers; a characteristic sought for many years. The flower petals of the transgenic plants contained the snapdragon aurones and a novel acylated aurone.

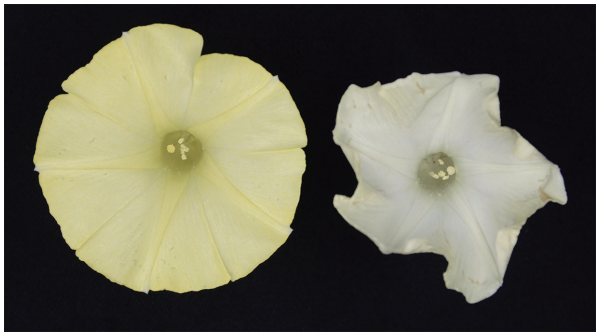

Figure 2. Flowers of the recreated 'phantom morning glory' (left), and the host plant (right). The host plant often exhibits shriveled flowers with necrotic cells, the transgenic plants produced fully opened flowers with few necrotic cells.

III. BioResource of morning glories

NIBB is the sub-center for the National BioResource Project (NBRP) for morning glories. In this project, we are collecting, maintaining and distributing standard and mutant lines for flower pigmentation, and DNA clones from EST and BAC libraries of *I. nil* and its related species. *I. nil* is one of the most popular floricultural plants in Japan, and has a 100-year history of extensive genetic studies related to it. Our collection includes 220 lines and 177,000 DNA clones. The whole genome sequence, the transcriptome sequences, as well as the end sequences of the DNA clones can be viewed via the *I. nil* genome database (http://viewer.shigen.info/asagao/index.php).

Publication List:

〔Original papers〕

- Hoshino, A., Mizuno, T., Shimizu, K., Mori, S., Fukada-Tanaka, S., Furukawa, K., Ishiguro, K., Tanaka, Y., and Iida, S. (2019). Generation of yellow flowers of the japanese morning glory by engineering its flavonoid biosynthetic pathway toward aurones. Plant Cell Physiol. *60*, 1871-1879. doi: 10.1093/pcp/pcz101
- Waki, T., Mameda, R., Nakano, T., Yamada, S., Terashita, M., Ito, K., Tenma, N., Li, Y., Fujino, N., Uno, K., Yamashita, S., Aoki, Y., Denessiouk, K., Kawai, Y., Sugawara, S., Saito, K., Yonekura-Sakakibara, K., Morita, Y., Hoshino, A., Takahashi, S., and Nakayama, T. (2020). A conserved strategy of chalcone isomerase-like protein to rectify promiscuous chalcone synthase specificity. Nat. Commun. *11*, 870. doi: 10.1038/s41467-020-14558-9