LABORATORY OF BIOLOGICAL DIVERSITY

HOSHINO Group

Assistant Professor:	*HOSHINO, Atsushi*
Technical Assistant:	*NAKAMURA, Ryoko* *TAKEUCHI, Tomoyo* *ITO, Kazuyo*

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 had a large impact on gene expression and evolution. To understand these genome dynamics in eukaryotes, especially in plants, we are characterizing the flower pigmentation of morning glories.

I. Flower pigmentation patterns of the morning glories

Ipomoea nil (Japanese morning glory), *I. purpurea* (the common morning glory), and *I. tricolor* have been domesticated well as floricultural plants, and their various spontaneous mutations have been isolated. The wild type morning glories produce flowers with uniformly pigmented corolla, whereas a number of mutants displaying particular pigmentation patterns have been collected. Because flower pigmentation patterns are easily observed, the molecular mechanisms underlying these phenomena provide fine model systems for investigating genome variability.

Margined, *Rayed* and *Blizzard* of *I. nil* are dominant mutations. While these mutants show distinct flower pigmentation patterns, the same pigmentation gene is repressed by non-coding small RNAs in the whitish parts of the corolla. It is suggested that distinct regulation of these small RNAs cause the difference in pigmentation patterns. The recessive mutations, *duskish* of *I. nil* and *pearly-v* of *I. tricolor*, confer variegated flowers, and epigenetic mechanisms are thought to regulate their flower pigmentation. We are currently characterizing detailed molecular mechanisms of these mutations.

II. *de novo* sequencing of the Japanese morning glory genome

Although morning glories are studied worldwide, especially in plant physiology and genetics, no whole nuclear genome sequences of any *Ipomoea* species are available. To facilitate the studies of our group as well as all morning glory researchers, we are conducting *de novo* genome sequencing of *I. nil*. We chose a standard line for genome sequencing, and employed shotgun sequencing using a single molecule real time sequencing system. We recently obtained a draft genome sequence consisting of 15 pseudo-chromosomes with reasonable size, and are going to characterize more details of the genome sequence.

III. BioResource of morning glories

NIBB is the sub-center for the National BioResource Project (NBRP) for morning glory. In this project, we are collecting, maintaining and distributing standard lines, mutant lines for flower pigmentation, and DNA clones from EST and BAC libraries of *I. nil* and its related species. *I. nil* has been one of the most popular floricultural plants since the late Edo era in Japan. It has an extensive history of genetic studies and also has many advantages as a model plant; simple genome, large number of mutant lines, and efficient self-pollination. Our collection includes 235 lines and 157,000 DNA clones.

IV. Pale- and dull-colored flower formation

Anthocyanin is responsible for the colors of many flowers and is usually glucosylated by 3GT (UDP-glucose:flavonoid 3-*O*-glucosyltransferase). We first demonstrated that absence of 3GT results in pale and dull flower coloration by using the recessive *3GT* mutants of *I. nil* and *I. purpurea* (Figure 1). Anthocyanin analysis revealed that 3GT is essential for maintaining proper production quantity, acylation, and glucosylation of anthocyanin. Incomplete acylation and glucosylation of anthocyanin results in dull flower coloration in *Ipomoea*. One of the *I. nil* mutants produces flower variegations that are thought to be epigenetically regulated (Figure 1c). We are currently studying a molecular mechanism of the flower variegation.

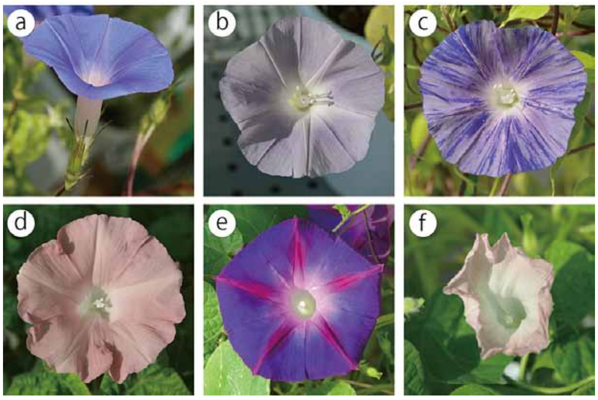

Figure 1. Wild type (a) and *3GT* deficient mutant of Japanese morning glory (b-d). Wild type (e) and *3GT* deficient mutant of common morning glory (f).

Publication List:

〔Original paper〕

- Morita, Y., Ishiguro, K., Tanaka, Y., Iida, S., and Hoshino, A. (2015). Spontaneous mutations of the UDP-glucose: flavonoid 3-*O*-glucosyltransferase gene confers pale and dull colored flowers in the Japanese and common morning glories. Planta *242*, 575-587.

〔Original paper (E-publication ahead of print)〕

- Azuma, M., Morimoto, R., Hirose, M., Morita, Y., Hoshino, A., Iida, S., Oshima, Y., Mitsuda, N., Ohme-Takagi, M., and Shiratake, K. A petal-specific InMYB1 promoter from Japanese morning glory: a useful tool for molecular breeding of floricultural crops. Plant Biotechnol. J. 29 Apr 2015.