

## HOSHINO Group

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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 had a large impact on gene expression and evolution. To understand such genome dynamisms 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 RNA in the whitish parts of the corolla. It is suggested that distinct regulation of small RNA causes 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 flower pigmentation. We are currently characterizing detailed molecular mechanisms of these mutations.

### II. *de novo* sequencing of 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 the Tokyo-kokei standard line for genome sequencing, and employed shotgun sequencing using a single molecule real time sequencing system. We could recently obtain thousands of assembled sequences having reasonable size, and are going to characterize details of the genome sequence.

### III. BioResource of morning glories

NIBB is the sub-center for 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 230 lines and 157,000 DNA clones.

### IV. A novel flower color enhancing protein

Anthocyanin is a type of flavonoid pigment and is responsible for the colors of many flowers. The depth of flower color is determined by the amount of anthocyanin. We characterized *I. nil* mutants displaying pale colored flowers (Figure 1), and successfully isolated a novel enhancer of flavonoid production (EFP). The EFP deficient mutants fail in efficient flavonoid production resulting reduction of anthocyanin accumulation. The presence and action of EFP are conserved among diverse plants. The amino acid sequence of EFP resembles an enzyme catalyzing flavonoid biosynthesis, however, it has no enzymatic activities. We are currently studying a molecular mechanism of flavonoid production enhancement by EFP.



Figure 1. Wild type (right) and EFP deficient mutant of Japanese morning glory (left).

### Publication List

#### [Original papers]

- Faraco, M., Spelt, C., Blied, M., Verweij, W., Hoshino, A., Espen, L., Prinsi, B., Jaarsma, R., Tarhan, E., de Boer, A.H., Di Sansebastiano, G.-P., Koes, R., and Quattrocchio, F.M. (2014). Hyperacidification of vacuoles by the combined action of two different P-ATPases in the tonoplast determines flower color. *Cell Rep.* 6, 32-43.
- Morita, Y., Takagi, K., Fukuchi-Mizutani, M., Ishiguro, K., Tanaka, Y., Nitasaka, E., Nakayama, M., Saito, N., Kagami, T., Hoshino, A., and Iida, S. (2014). A chalcone isomerase-like protein enhances flavonoid production and flower pigmentation. *Plant J.* 78, 294-304.
- Park, K.I., Hoshino, A., Saito, N., and Tatsuzawa, F. (2014). Anthocyanins in the flowers of *Ipomoea tricolor* Cav. (Convolvulaceae). *Biochem. Syst. Ecol.* 54, 15-18.