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 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 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, 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.

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 (Figure 1). We are currently characterizing detailed molecular mechanisms of these mutations.

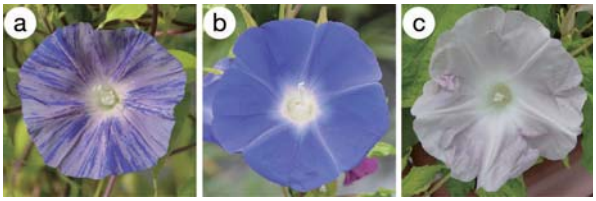

Figure 1. Flower phenotypes of the *duskish* mutant of *I. nil*. The phenotype is variable and displays variegated flowers (a), fully pigmented flowers (b), and pale grayish-purple flowers (c). As the flowers have the same genotype, epigenetic mechanisms are involved in the variable phenotypes.

II. Membrane transport of flower pigments

Anthocyanins are the most common flower pigments in Angiosperms including *I. nil*. They are synthesized in the cytosols and accumulate in the central vacuole in plant cells. Anthocyanin transport across the vacuolar membrane has long been debated. The transcriptional regulatory network of anthocyanin pigmentation supports involvement of an ATP binding caste (ABC) protein in the anthocyanin transport in *I. nil*. We started an international collaboration with researches in the Netherlands and Switzerland to reveal the function of the ABC protein.

III. Genome sequence information of the Japanese morning glory

In 2016, we reported an *I. nil* draft genome sequence with a scaffold N50 of 2.88 Mb, covering 98% of the 750 Mb genome. Scaffolds covering 91% of the genome sequence are anchored to 15 pseudo-chromosomes. A genome database for the genome sequence was built and opened to the public in 2017 (Figure 2). It includes a genome browser that enables users to analyze the 3,416 scaffolds (assembly name, Asagao_1.1), the 15 pseudo-chromosomes with the 3,095 scaffolds not anchored to the pseudo-chromosomes (Asagao_1.2), and the circular genomes of chloroplasts and mitochondria. The database provides BLAST, BLAT and keyword search services.

The genome sequence was also archived and used by several online databases and tools. The National Center for Biotechnology Information (NCBI) provides their own gene predictions (NCBI Ipomoea nil Annotation Release 100). The predicted genes are catalogued by the Kyoto Encyclopedia of Genes and Genomes (KEGG), and their functional information is visualized in the PATHWAY database that contains graphical representation of cellular processes (e.g. metabolism and signal transduction). Database Center for Life Science (DBCLS) equipped GGGenome and CRISPRdirect with the genome sequence. These tools facilitate ultrafast sequence search and rational design of CRISPR/Cas based genome editing target, respectively.

IV. 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* is one of the most popular floricultural plants in Japan, and has a 100 year history of extensive genetic studies. Our collections include 240 lines and 160,000 DNA clones. The end sequences of the DNA clones can be viewed from the *I. nil* genome database (Figure 2).

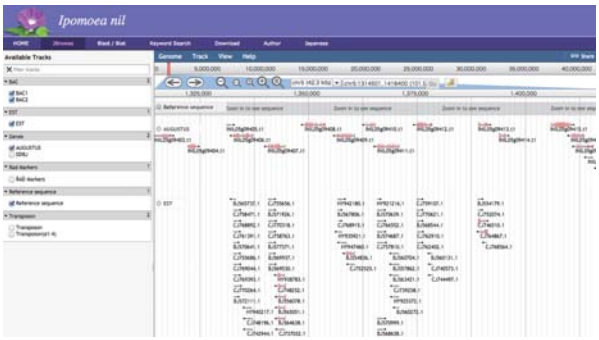

Figure 2. The *I. nil* genome database.
http://viewer.shigen.info/asagao/index.php