**OB-05**

# The sequence variation on chloroplast genome resulting variegated leaves in *Fallopia japonica*

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**[Introduction]**

In nature, there are many plants forming variegated leaves. It is known that these plants are mainly caused by the mutation in the chloroplast, which hinders the formation of chlorophyll. "*Fallopia japonica*", an endemic plant originated in Northeast Asia such as Korea, Japan, and China is the representative example. Because this plant has many beneficial effects, it can be used as not only edible plant but also medicinal resource. *F. japonica* with the variegated leaves can be found easily in nature, as calling "Patterned *F. japonica*". In this study, the sequences obtained through NGS (Next generation sequencing) platform from *F.japonica* leaves were assembled and the complete genome sequence was analyzed to elucidate the reason of this phenomenon.

**[Materials and Methods]**

*F.japonica* showing variegated leaves was provided by Hantaek Botanical Garden. One patterned F. japonica plant has all of three leaf types : green leaves, white leaves, mixed leaves. In order to compare the chloroplast genome of each leaf, DNA was extracted from the green leaf and white leaf, respectively. Sequencing was performed using the Illumina MiSeq platform. Sequencing data was assembled based on *Tatami buckwheat* as a reference sequence using CLC genome assembler 4.6 (CLC Inc., Aarhus, Denmark). The sequences of the chloroplast genomes obtained from each leaf were aligned and compared each other by MAFFT web program. Analysis of protein structure model was performed to investigate the effect of nucleotide variation among the chloroplast genomes on gene activity. SWISS-MODEL was used for model the protein structures based on template structures (subunit of PDB ID, 4MEX) obtained from www.rcsb.org. The modeled structures were visualized with PyMol.

**[Results and Discussions]**

The chloroplast genome sequences of green and white leaves were completed with a length of 163,386bp, identically. The structure of the chloroplast genome is divided into 4 compartments as LSC of 87531bp, SSC of 13,555bp, and a pair of IR regions of 31,150bp in length. Only a single nucleotide polymorphism (SNP) was identified between the two complete chloroplast genome sequences, located in the coding region of rpoC2, a subunit gene of plastid encoded RNA polymerase (PEP). It was predicted that PEP couldn't be formed properly due to the SNP mutation interrupting the process of photosystem formation. Consequently, the mutated leaf might have the chloroplast without chlorophyll. In the protein structure model, this SNP caused the substitution of histidine (H) to proline (P) in white leaf. Thus, it appears that the hydrogen bond between the changed amino acid and the adjacent amino acid is removed and the $\alpha$ -helix structure is destroyed, leading to misfolding or different folding of the protein structure. The result of this research will extend our understanding about the effects of chloroplast genome mutation on plants.

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