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## **Genome Sequencing of *Perilla frutescens***

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### **[Introduction]**

*Perilla frutescens* is an annual plant belongs to the mint family, Lamiaceae. It is mainly cultivated throughout East Asia. *Perilla* contains high levels of unsaturated fatty acids (more than 60% of total fatty acid), which is very beneficial to not only human health but a plant oil industry. Hence, interpreting the *Perilla* genome is essential to understand a structural and functional genetics of the oilseed crop.

### **[Materials and Methods]**

*Perilla* cultivar 'Deasildeulkkae' (*P. frutescens*, 2n=4x=40) was used for genome assembly. Fluorescence *in situ* hybridization (FISH) analysis was performed to draw a chromosome specific genetic map and to identify molecular cytogenetic karyotypes.

### **[Results and Discussion]**

FISH showed that *Perilla frutescens* was allotetraploid type compared to autodiploid of *P. citriodora*, wild type. The assembly of genome by PacBio sequencer platforms is on-going and we estimated the genome size of 1.379 Gb using Jellyfish. The genome assembly was merged with PacBio pipelines and about 1,152 Gb was obtained with a contig N50 length of 528,499 bp. Though the process of Hi-C grouping, we analyzed contigs with clustering and ordering/orientation. Contigs were grouped to 20 superscaffolders of the total genome length of 953.4 Mb by Hi-C heatmap. We also identified chloroplast (cp) genome sequences of six cultivars (4x) and three wild (2x) *Perilla* species for analysis of the complete cp genome sequences. The results above will provide useful information of the genome structure to understand the functional genomics of *Perilla*.

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