

## The International Debate on Genome Sequencing in Octoploid Strawberry and its Application to Molecular Breeding

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Strawberry (*Fragaria × ananassa*) was artificially generated in the 16th century Europe by crossing between two octoploid species, *F. chiloensis* and *F. virginiana*. It is cultivated and consumed entire the world. Strawberry is an allo-polyploidy species ( $2n = 8X = 56$ ) with an estimated genome size of  $1C = 708,720$  Mb. The complex structure of the polyploid genome has inhibited advances in genomics and genetic analysis. We have sequenced a Japanese variety 'Reikou' with Illumina platform, and constructed subgenome-specific reference sequences by using DenovoMAGIC. A total of 62 (31 × 2 haplotypes) pseudomolecules were developed based on the linkage map in a total length of 1,125 Mb. The large structure differences among the sub-genomes were identified by comparison with the *F. vesca* genome. By using the constructed pseudomolecules, we have performed RNA-Seq analysis in fruit color. Genomic selection for fruit hardness has also performed with the four strawberry breeding stations, i.e., National Agricultural Research Organization, Tochigi prefecture, Fukuoka prefecture and Chiba prefecture. The conventional GS requires genome wide genotyping for the both training and breeding populations. To decrease the cost and time for geno-

typing in the breeding population, we used Ensemble-based Genetic and Genomic Search (EGGS) that enable to make a model with less number of DNA markers. Genomic, genetic analysis and molecular breeding in polyploidy species is still difficult, however, the advance of NGS technologies as well as novel approaches for data analysis has made the challenge possible.

### Biography:

Sachiko Isobe started her career as a conventional red clover breeder. Currently she is a plant molecular biologist, lab head of Plant Genomics and Genetics of Kazusa DNA Research Institute. The research group has performed genome sequencing and molecular genetics including DNA marker development, linkage map construction, QTL identification and marker assisted selection. More than 30 model and crop species have been targeted such as strawberry, sweetpotato, tomato, *Lotus japonicus*, groundnut, and clovers. Of these, strawberry is one of the main species, and comprehensive analysis has been performed such as genome sequencing, RNA-Seq and Genomic Selection.