

# Genetic Breeding Analysis for Polyploid Species and Development of Cultivar Discrimination Technology

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## Abstract

In the past decades, NGS (Next-generation sequencing) technology has been accelerating genomic and genetic studies in many crop species. We are engaged in genetic and breeding research by using NGS technology. There are two topics of our research as shown below.

### 1. Genetic Breeding Analysis for Polyploid Species

There are many polyploid species in crops, such as potato (*Solanum tuberosum*; tetraploid, 4x), alfalfa (*Medicago sativa*; tetraploid, 4x), bread wheat (*Triticum aestivum*; hexaploid, 6x), sweetpotato (*Ipomoea batatas* (L.) Lam.; hexaploid, 6x) and strawberry (*Fragaria x ananassa*; octoploid, 8x). Our research has been mainly conducted on the hexaploid crop species called sweetpotato. Sweetpotato is one of the most important crop species in the world. However, genetic analysis and marker-assisted breeding programs in sweetpotato have been challenging because this crop has a complex genomic structure derived from highly heterozygous, hexaploids ( $2n = 6x = 90$ ), huge genome (~3Gb), outcrossing nature, and so on. In such a situation, we could identify genomic regions controlling agricultural traits such as nematode resistance, weevil resistance, and yield by performing QTL analysis and GWAS<sup>1), 2)</sup>. Besides, we developed a PCR-based DNA marker for screening resistant plants to the nematode with a high ratio<sup>1)</sup>.

### 2. Development of Cultivar Discrimination Technology

In many crop species, the development of a rapid and precise cultivar discrimination system has been needed for plant breeding and patent protection of plant cultivars and agricultural products. Recently, we developed retrotransposon-based DNA markers for cultivar discrimination in several crop species such as strawberry, sweetpotato, apple, azuki beans, and wheat. As retrotransposon insertions with high copy numbers are dispersed throughout the genome and are inherited genetically, insertion polymorphisms among crop cultivars have been used as molecular markers. We identified a large number of retrotransposon insertion sites at the genome-wide scale in many cultivars with the NGS platform, which enabled us to reveal the genetic relationships among the cultivars and acquire a number of molecular markers for cultivar screening<sup>3)</sup>.

### Literature cited (\*Corresponding author)

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