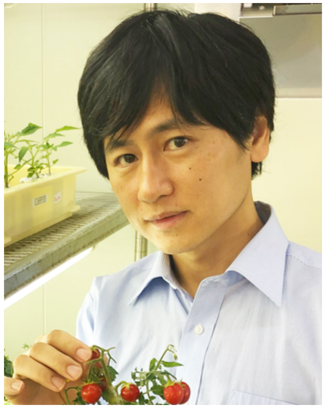
Breakthrough technologies to accelerate breeding and strain improvement in biological production for a sustainable society

Maximizing breeding efficiency by developing digital-transforming breeding technologies



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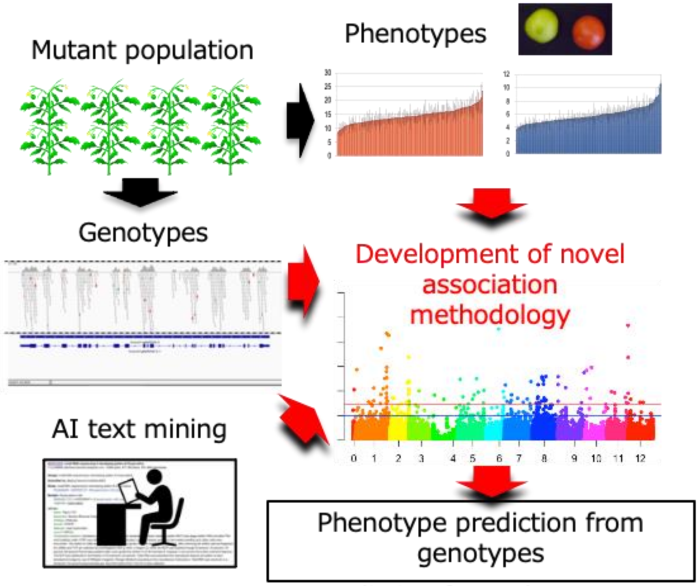
Summary :

Efficiency of plant breeding depends heavily on the genes and genotypes that are modified for achieving the desired traits by the breeders. Currently, plant breeding relies on classical genetic approaches such as QTL analysis. However, these methods require a lot of labor and time to acquire genetic information. Therefore, it is necessary to establish a technological infrastructure to rapidly and efficiently obtain genetic and genotypic information for plant breeding. In this study, we will collect DNA mutation information from the large-scale mutagenesis lines of the dwarf tomato cultivar Micro-Tom, as well as phenotypic information, including fruit metabolite data, of the mutants. Additionally, we will collect the known information on genes using text mining. We aim to establish a novel association methodology which links DNA mutation information with phenotypic information. Our study will facilitate the development and confirmation of a system that can transform phenotypic information into genotypic information and vice versa.



Mutant population

Phenotypes

Genotypes

Development of novel association methodology

AI text mining

Phenotype prediction from genotypes

- ・genotype prediction from phenotypes
- ・acceleration of breeding