FUNDING PROGRAM FOR NEXT GENERATION WORLD-LEADING RESEARCHERS

Project Title: Functional analysis of the plant epigenome in dominance relationships between alleles	
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1. Background of research

A diploid organism has two copies of each gene in the genome, one inherited from each parent. The expression of two inherited genes is sometimes biased by the effects known as dominance/recessive relationships, which determine the final phenotype of the organism. To explore the mechanisms underlying these relationships, I have examined the monoallelic expression of *S*-locus protein 11 genes (*SP11*), which encode the male determinants of self-incompatibility in *Brassica*. We showed that *SP11* expression was monoallelic in some *S* heterozygotes, and that the promoter regions of recessive *SP11* alleles were specifically targeted to be methylated in the anther tapetum via trans-acting small RNA on the dominant *SP11* alleles.

2. Research objectives

My goal is to elucidate the molecular mechanism of dominant/recessive relationships between alleles in plants in terms of epigenetic regulations using whole genome approaches. The outcome of this research will provide deep insights into the mechanisms of monoallelic gene expression regulated by DNA methylation as well as a deeper understanding of the mechanisms underlying important agricultural traits of F_1 hybrid such as hybrid vigor.

3. Research characteristics (incl. originality and creativity)

Evidence from my studies provide an idea that sRNA could act in trans in heterologous genomes to regulate transcriptional gene silencing via DNA methylation in a target sequence dependent manner. This research is based on our findings on the epigenetic regulation of dominance relationships between self-incompatibility alleles in *Brassica* as described above. I believe that this research will provided novel insights into the widespread phenomenon of monoallelic gene expression in heterologous organisms.

4. Anticipated effects and future applications of research

Heterosis is the phenomenon where crossing two inbred lines can produce descendants with superior genetic foundation, and therefore it is widely used in breeding program. The outcome of this research will provide important and new aspects in regulation of heterosis that will be useful for improved productivity and biomass control.