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Evolutionary Genetics and Genomics

Lineage-Specifically Emerged Genes in Plant Evolution

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Time: 2023. 04. 13 Thu. 10:00
Venue: Auditorium, 1st Floor
Interdisciplinary Research Building
跨領域科技研究大樓1樓演講廳
Host: Dr. Chi-Hon Lee 李奇鴻特聘研究員

~Attendee are suggested to wear mask~
~與會者建議配戴口罩~

Abstract

During the course of plant evolution, genomes acquire novel genetic elements as sources of functional diversities. Recent advance of next generation sequencing revealed much of lineage-specifically emerged genes such as duplicated genes, de-novo alternative splicing isoforms and de-novo small coding genes in plant genomes. However, lineage-specifically duplicated genes might keep redundant functions with original ones. Also, de-novo alternative splicing isoforms and small genes are expressed as RNA, but the RNA products might be just transcription errors. Therefore, I'm trying to identify lineage-specific genes inducing phenotypic diversities in plants. I mainly used the best model organism of plants (*Arabidopsis thaliana*) to understand the adaptive evolution throughout lineage-specifically emerged genes. First, I collected various omics data such as transcriptome, proteome, metabolome, interactome, phenome, etc in *A. thaliana* (Evaluation). Throughout the integration of these omics by bioinformatics analysis, I tried to infer recently emerged genes causing phenotypic changes in evolution (Study & Design). Then, I examined the functional roles of inferred genes by transgenic plants (Construction). This strategy (Evaluation → Study → Design → Construction) is useful to understand the molecular mechanisms of target genes. Here, as sources of phenotypic diversities, I will introduce the evolution of phenotypic variation by three types of newly emerged genes such as gene duplication, alternative splicing isoforms, and small genes (Figure 1).

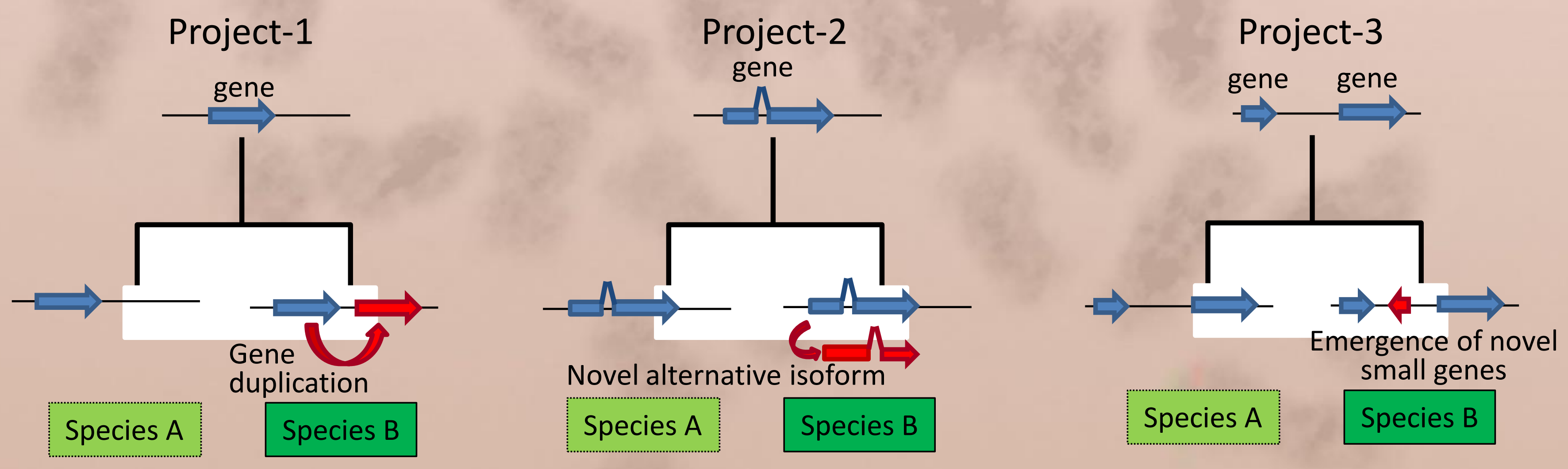

Figure 1. Phenotypic diversities led by three types pf newly emerged genes