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3rd Global Summit on

Plant Science

August 07-09, 2017 | Rome, Italy

Genome-wide screening and functional characterization of long intergenic noncoding RNAs in *Arabidopsis*

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Over the past two decades, animal long noncoding RNAs (lncRNAs) have emerged as important regulators of key biological processes. However, plant lncRNAs remain poorly characterized. Here, we identified 6.5K long intergenic noncoding RNAs (lincRNAs) by analyzing 200 *Arabidopsis* tiling array datasets. Transcriptome profiling revealed that these lincRNAs are expressed at a level between mRNAs and precursors of miRNAs in tissue- or stress-specific manners. Further analysis of transcriptome data in 11 mutants uncovered serrate, cap binding protein 20 (CBP20), and CBP80 as regulators of lincRNA expression and biogenesis. Additionally, these three proteins are needed for splicing of a small group of intron-containing lincRNAs. Following this finding, we characterized the function of *Arabidopsis* lincRNAs, designated ELF18-Induced Long-Noncoding RNA 1 (ELENA1), as a factor enhancing resistance against *Pseudomonas syringae pv. tomato* DC3000. ELENA1 knock-down plants show decreased expression of pathogenesis-related gene 1 (PR1) and the plants are susceptible to pathogens. By contrast, plants over-expressing ELENA1 show elevated PR1 expression after ELF18 treatment and display a pathogen-resistance phenotype. ELENA1 directly interacts with Mediator subunit 19a (MED19a) and affects enrichment of MED19a on the PR1 promoter. These results show that MED19a regulates PR1 expression through ELENA1. Our findings uncover an additional layer of complexity, implicating long-noncoding RNAs in the transcriptional regulation of plant innate immunity.

Biography

Choonkyun Jung is working as a Associate Professor in Seoul National University, Pyeongchang, Republic of Korea

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