Analysis of microRNA Regulated Seed Biology Networks in Arabidopsis

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ABSTRACT

Seed maturation and embryogenesis in plants are crucial event for food production of all human beings. Delayed seed maturation and abnormal embryo formation of food crops degrade the quality and quantity of food grains. By performing comparative gene analysis of different microarray experiments in different stages of embryogenesis in Arabidopsis thaliana, using as model plant, here the authors identified a gene coexpression module in preglobular stage. In this module, different genes have been studied which are over-expressed during embryogenesis related with several KEGG metabolic pathways. Analysing the gene cluster evolved from network we concluded that microRNA regulates gene expression of two genes. One of them NRMP6, a metal ion transporter protein gene and second one SKS8, has copper ion binding activity, are regulated by miR167A/B. Since these two genes are also expressed during embryogenesis of other food crops e.g. rice tomato etc, so the microRNAs regulation on gene expression during embryogenesis can be extrapolated for other economically important seeds.

Keywords: Gene Expression Regulation by miRNA, miRNA, miRNA-mRNA Hybridization, NRMP6, Regulation of Coexpression Gene Network, SKS8

INTRODUCTION

Embryogenesis is the process where a total plant grows from a single cell, known as zygote, through a series of cell division and cell elongation processes. In Arabidopsis thaliana, embryogenesis is a continuous process containing three major phases, described as early, mid, and late. Cell growth, cell differentiation and morphogenesis are three basic steps during embryogenesis. Computational analysis shows that different genes are over-expressed during embryogenesis related with several KEGG metabolic pathways. The large-scale microarray datasets of Arabidopsis thaliana for these genes involved in embryogenesis have been analysed in seed biology (Basu et

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Gene regulatory network involving cis-regulatory elements for Arabidopsis genes have been discussed earlier (Ruan et al, 2011, Basu et al, 2014). The role of microRNAs, a family of small, non-coding RNAs, in regulation of gene expression in various developmental and physiological processes e.g. in cell elongation, differentiation in root and shoot tumor suppression, in both plant and animal genomes has been discovered (Rhoades et al, 2002, He et al, 2004, He et al, 2007). Although the first endogenous 22-nt RNAs and translational repression of the mRNA targets in larval development were identified in the nematode *Caenorhabditis elegans* (Reinhart et al. 2000), the similar mechanism for post transcriptional regulation is observed in plant. Mature microRNAs (miRNAs) formation is a two-step processes to produce ~22-nucleotide small RNAs. In first step, microRNA genes are transcribed by RNA polymerase II as large primary transcripts (pri-microRNA). Initial cleavage of pri-microRNA is catalysed by and processed by a protein complex containing the RNase III enzyme Drosha, to form an approximately 70 nucleotide precursor microRNA (pre-microRNA) in nucleus (Denli et al, 2004). This precursor is subsequently transported to the cytoplasm where it is processed by a second RNase III enzyme, DICER, a nuclease involved in the RNA interference (RNAi) pathway of animals (Bernstein et al. 2001), to form a mature microRNA of approximately 22 nucleotides (Figure 1).

The mature microRNA is then incorporated into a ribonuclear particle to form the RNA-induced silencing complex, RISC, which mediates gene silencing (Reinhart et al, 2002) through mRNA degradation of target gene. Applications of this kind of gene regulation in gene regulatory network have been analyzed in different plants e.g. pineapple, *Arabidopsis* (Yusuf et al, 2015),

*Figure 1. Formation of a mature microRNA of approximately 22 nucleotides*
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