

Short Communication

A study on banana miRNA and its application in resistance to *Fusarium wilt*

Song Shun^{1,2,3}, Huang Dongmei¹, Xu Yi^{1,2,3}, Guo Gang¹, Li Yujia^{1,2} and Jin Zhiqiang^{1,2,3*}¹Haikou Experimental Station, Chinese Academy of Tropical Agricultural Sciences, Hainan 570101, China.²Hainan Key Laboratory of Banana Genetic Improvement, Hainan 570101, China.³Haikou Key Laboratory of Banana Biology, Hainan 570101, China.

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MicroRNAs refer to a class of short noncoding RNAs (containing about 22 to 24 nucleotides) widely found in eukaryotes, which function in post-transcriptional regulation of target gene expression via base pairing with specified sequences within target mRNAs to cleave target mRNAs or to repress their translation. This paper mainly introduces the research progress of banana miRNA in biological study of resistance to *Fusarium wilt* by means of bioinformatics, hoping to develop miRNA application in resistance to *F. wilt* of banana.

Key words: Plant miRNA, target gene, bananas.

INTRODUCTION

Being the world's largest trade and consumption fruit, banana (*Musa nana* Lour.) is planted in more than 130 countries worldwide. Banana wilt disease is a soil-borne fungal disease caused by *Fusarium oxysporum* f. sp. Cubense (FOC) and is the most powerful destructive agricultural disease. FOC has four physical races within which FOC1 and FOC4 are the main threats in Chinese banana planting area. FOC1 attacks Gros Michel, Musa AAB and dwarf banana; FOC4 can infect virtually all types of bananas, including Cavendish (mainly Musa AAA in China), Gros Michel, dwarf banana and *musa balbisiana* etc. (Persley, 1987), causing the most serious harm.

Since banana is polyploidy cultivar with high infertility that makes it difficult to crossbreed, virus free seed cane is a significant measure to prevent banana from wilt disease. In recent years, healthy banana seeds cultivated

through tissue culture techniques have prevent wilt disease from further spread in the help of reasonable field management technology. So far, there are still no cost-effective cure measures at home and abroad. *Fusarium* is a typical soil-borne disease of vascular system, going through the process of spores adsorption, degradation of physical defense of host, signal recognition and transduction, gene expression and production of various of types of chemicals (Michielse et al., 2009; Liu, 2011) before killing a banana. Its long term ability to infect and complex pathogenic process (Rosita et al., 2008) make the pathogenesis complex and diverse. iRNA are a class of small non-coding single-stranded RNA involved in post-transcriptional regulation of mRNA. Mature miRNA is about 20 to 24nt, which is derived from regions of single-stranded RNA that fold back on themselves to form short hairpins.

*Corresponding author. E-mail: 18689846976@163.com.

miRNA is involved in numerous plant life activity (Cuperus et al., 2011; Thiebaut et al., 2012), including the formation of the organization (Bonnet et al., 2004), leaf growth (Chuck et al., 2007a), male and female differentiation (Chuck et al., 2007b) as well as male or female infertility (Millar and Gubler, 2005) and other processes. These studies suggest that miRNA expression can be induced by environmental stress; meanwhile, their target genes are response to stress-related genes. All these indicate that miRNA plays an important gene-regulatory role in plant stress resistance (Phillips et al., 2007).

miRNA features and miRNA in fruit trees

In plants, miRNA post-transcriptional regulation is realized by base pairing with the target mRNA that causes target mRNA degradation or inhibiting its translation, in other words, negative regulation. Mature miRNA is about 21nt that may be the smallest known thermodynamically stable length needed during mRNA expression. miRNA is specific for either gene regulation. And the shorter the transcription length is, the smaller the transcription error is, which makes regulation more effective. miRNA regulation is specific to transcribed product, which avoids signal transmission and formation of the protein product, besides, this regulation can be quickly and reversibly adjusted. Interaction, including synergistic inhibition and feedback inhibition between miRNA and mRNA makes it possible to do variety of real-time and fast fine regulation in complex and systematic biological processes. This kind of network structure allows the plant to respond quickly to stimuli from internal and external environment so as to survive at minimum costs. MiRNAs play important roles in the control of plant development, flowering timing, metabolism and stress response (Zeng et al., 2009). In addition, the majority of miRNAs are highly conserved, time-ordered and tissue specific (Sunkar and Jagadeeswaran, 2008). Currently, there are two ways to access to miRNAs: first, directly clone small RNA from the RNA, and then exclude small RNA that does not coincide with miRNA structure according to bioinformatics; second, obtain miRNA and its expression level through sequencing technique, then verify through experiment (Barakat et al., 2007). Though clone is direct, reliable, targeted and specific, it is difficult to capture the miRNA with low expression. With the improvement of sequencing technology and sequencing flux, obtaining miRNA through sequencing technology is gradually increasing (Chen et al., 2010). Third, obtain miRNA by predicting, reclassification and excluding from conservative ETS sequences via bioinformatic analysis (Chai et al., 2015).

miRNA of some mode plants and major field crops are mostly and thoroughly studied (Sunkar and Jagadeeswaran 2008). In recent years, research reports relating fruit tree are increasing year by year. Some

highly conserved miRNAs in certain model plants are purposefully chosen to go through BLAST analysis on other plant's ESTs sequences. There are study reports on miRNA in several fruit trees, such as grapes, strawberries and citrus trees. Luo et al. (2013) has downloaded 774 400 ESTs from 32 kinds of fruit trees including apple, orange, grape, banana, kiwi, peach, apricots and other fruit trees and tried to find homologous miRNA by homology search based on bioinformatics, which has ground-breaking significance in the growth and development of fruit trees based on miRNA and in the epigenetic study. He predicted miRNA via bioinformatics and searched for miRNAs in the EST of 32 fruit trees registered in the NCBI database before finding 110 miRNA precursor sequences from 774400 ESTs and encoding 116 mature sequences and classifying them. He found 28, 16, 13, 11 and 10 miRNAs in citrus, apples, bananas, kiwi and peach trees, separately.

Intense relationship between miRNA and bacteria in plant

After it was invaded by fungi, miRNA can quickly involved in physiological processes related to plant disease resistance. Some play a role by regulating the expression of target genes of plants and some can adjust the expression of bacteria genome invading plant in more diverse ways. For example, miRNA393 can be induced by pathogens flagellin of bacterial speck disease in tomato to inhibit the expression of growth hormone receptor (TIR1, AFB2 and AFB3) in gene target, blocking growth hormone response pathways (Navarro et al., 2006) and inhibiting the growth of bacterial virus in host plant; after *Arabidopsis* was infected by non-toxic strains of tomato pathogenic variant of *Pseudomonas syringae*, expression of miRNA398 induced by pathogen was inhibited, which thereby induced the target to increase the level of CSD so as to involve in plant defense response against pathogens (Jagadeeswaran et al., 2009), after it was infected by cucumber mosaic virus, tomato demonstrated 89 different miRNA expressions, which have different influences on different miRNAs expression patterns.

Further verification of expression relationship between 7 miRNAs and 5 mRNA showed that during the interaction between virus and host, virus regulated host gene expression via miRNA and led to corresponding symptoms (Feng, 2009). Study on differential expression of miRNA of sheath blight tolerance in maize obtained 39 resistance-related miRNAs, finding that some defense-related miRNA participated in the growth of corn and in the response process of sheath blight stress and played an important role. By inoculating *exserohilum turcicum* in maize leaves to induce denfense-related miRNA expression, Song (2011) discovered four new miRNAs: miR530, miR811, miR829 and miR845. Further study showed that three miRNAs (miR811, miR829 and miR845)

and miR408 specifically responded to pathogen and then was induced to express. After annotating their functions, they get out those four target genes responding to and inducing miRNAs to express were very important genes involved in physiological processes, such as metabolism, morphological and physiological adaptation, in plants seedling growth period. miRNAs function in negative way after transcription. Experiment also showed significant expression differences between miR811 and miR829, suggesting a very close relationship with the disease course.

Screening miRNA related to *Fusarium* wilt resistance in banana

So far there are no related research reports concerning miRNA regulatory mechanism and response against fungal invasion in banana at home and abroad. Domestic research on banana miRNA is still in its infancy. It is original and feasible to explore related metabolic pathways and important genes via miRNA under the circumstance that pathogenesis of banana wilt disease and disease resistance mechanisms are not clear. In 2013, scientists use genome-sequencing results of banana A and banana B to forecast small RNA of a group of banana. Conservative miRNAs in genome A and B have similar expression level, however, the new miRNA expressions are different in the two genomes. There are a number of specific miRNA expression or significantly different expression levels. And wherein the protein family regulated by target gene of mba-miR15 was related to biotic stress of sugarcane.

CONCLUSION

Separating miRNA and their target genes and revealing their functions as well as accurate grasping of regulatory mechanism during the resistance process against abiotic stress in plants are the important parts in the field of disease-resistant miRNA.

Conflict of Interest

The authors declared that they have no conflicts of interest to this work.

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