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### **Extended Abstract**

# Exploring miRNAs for Developing Disease Resistant Crop

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#### Introduction

Climate change and environmental pressures have a significant impact on global crop production and require growing crops that can withstand many climate changes and environmental disruptions, such as irregular water supply leading to drought or waterlogging, excessive salinization of the soil, extreme and variable temperatures, ultraviolet radiation and much biotic stress. Plant have complex molecular mechanisms to cope with these dynamic environmental change; one of the most common and useful mechanism is reprogramming expressions stress-responsive genes. Plant miRNAs (miRNAs) have become vital post-transcriptional and translational gene expression regulators to modulate stress effects.

Recent research set their critical roles in epigenetic regulation of stress / adaptive reactions, as well as in ensuring the stability of the plant genome. Some stress-sensitive miRNAs identified from various crops and miRNA-based RNA interference (RNAi) turns into a technology of choice for improving crop traits and providing a phenotypic and genotypic solution. Here present a promising review of the study of miRNAs as potent targets for crops that can withstand multi-stress environments using function loss/enhancement approaches.

This review also shed light on the potential role of plant miRNAs play in genome-stability and their emergence as a potent target for genome-editing. Current knowledge on plant miRNAs, their biogenesis, function, their targets and latest developments in bioinformatics approaches for plant miRNAs focus though recent reviews discussing the individual miRNAs responsive to single stress factors primarily, however, considering the practical limitation of this approach, the particular emphasis given in this review on miRNAs involved in responses and adaptation of plants to multi-stress environments including at epigenetic and epigenomic levels.

The expanding populace of the world and their food requests requires centered endeavors for the improvement of harvest plants to guarantee reasonable food creation. Control of mRNA transcript wealth by means of miRNA control gives an extraordinary system to adjusting differential plant quality articulation and miRNAs are along these lines developing as the cutting edge focuses for hereditary building for development of the agronomic properties of harvests. Nonetheless, a more profound comprehension of its latent capacity and the systems included will encourage the plan of appropriate techniques to acquire the attractive attributes with least exchange offs in the altered yields. In such manner, this audit features the different jobs of preserved and recently recognized miRNAs in different food and mechanical harvests and ongoing advances made in the employments of miRNAs to improve plants of agronomically significance to altogether upgrade crop yields and increment resistance to different natural pressure operators of biotic-or abiotic birthplace.

Previous test concentrates in Arabidopsis and different plants have indicated that miRNAs are associated with numerous natural procedures where they assume essential job being developed and development, support of genome respectability, signal transduction, hormone flagging pathways, hormone homeostasis, intrinsic insusceptibility, and reaction to various ecological abiotic and biotic anxieties (Navarro et al., 2006; Sun, 2012; Xie et al., 2014; Zhang and Wang, 2015). Parts of the administrative jobs of plant miRNAs during advancement, in the versatile reaction to stresses and in the miRNA pathway itself have been checked on (Mallory and Vaucheret, 2006) and more keeps on being accounted for.

For instance, our ongoing topical investigation uncovered that miRNAs can be used to reconstruct cell digestion following the impression of organism related sub-atomic example (MAMP) particles during pathogen assault in plants, prompting dynamic changes to the microtranscriptome related with differential transcriptional guideline on the side of insusceptibility and basal obstruction (Djami-Tchatchou and Dubery, 2015). Investigation of Tables 1–3 shows the expansive extent of miRNA impacts, intermittently focused at TFs, themselves controllers of quality articulation.

Another as often as possible happening objective is quality transcripts encoding proteins or compounds engaged with digestion. Practical examination of miRNAs showed their significance in numerous natural and metabolic procedures in monetarily significant harvests. Numerous examinations revealed that miRNAs are among the most significant quality controllers (riboregulators) which control plant development, advancement and reaction to abiotic and biotic worry in plants. In this manner, miRNA-based hereditary adjustment innovation is one of the most encouraging arrangements which can add to agrarian profitability so as to deliver unrivaled harvest cultivars.