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Bioinformatics insights into microRNA mediated gene regulation in *Triticum aestivum* during multiple fungal diseases

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ABSTRACT

MicroRNAs are a class of non-coding RNAs known for their vital role in post transcriptional gene regulation during growth, development, and stress responses. Several miRNAs have been reported as regulators of plant-pathogen interaction. Recent studies have identified a number of miRNAs that play important roles in common wheat upon fungal invasion. But the existence of any common miRNA mediated pathways that act for multiple wheat-fungal diseases (based on infection types) was not known. This study aims to check whether any miRNAs are acting in common for wheat upon biotrophic and hemi biotrophic fungal infections. miRNAs were obtained from miRBase database and wheat ESTs were retrieved from Komugy wheat database. Wheat miRNAs and targets were predicted and functionally annotated using computational approaches. We identified and comparatively analysed miRNAs and their targets in resistant and susceptible hosts of common wheat in response to powdery mildew, leaf rust and blast diseases. We identified miRNAs from eighteen families in response to these fungal infections and observed that their functionality strongly depends on the specificity of hosts. In addition to target multiplicity, selective gene targeting by multiple miRNAs of different families was observed. This may point out the importance of regulating these targets in hosts, at specific conditions. Selective gene targeting might be established as one of the tight gene regulatory mechanisms in plants, similar to co-functional miRNAs reported in animals. Investigation of miRNA responses preferred by different hosts revealed that miRNAs enhance plant resistance in resistant hosts and attenuate immune responses in susceptible hosts. To the best of our knowledge, this study is the foremost report on comparative analysis of miRNA mediated gene regulation in wheat during multiple fungal diseases. It also indicates the possibility of co-functional miRNAs in plants.

1. Introduction

Pathogenic fungi remain as major threats to global food security, as around 85% of plant diseases are caused by fungi or fungal like organisms. Based on their interaction with host plants, fungal diseases can be divided into necrotrophic, biotrophic and hemibiotrophic (Oliver and Ipcho, 2004). Unlike necrotrophic pathogens which kill and feed on dead tissues, biotrophic and hemibiotrophic fungi are in need of more complex and advanced plans of action to cope up with the living host's immunity (Ruhe et al., 2016). Fungi interacting with living entities display their potentiality in altering plant metabolism to obtain nutrients for their survival and colonization (Manck-Götzenberger and Requena, 2016).

Encounter with such challenging pathogenic interactions predisposes plants to evolve with various mechanisms to alter plant immune system. Activation of the plant immune system can ensue two layers of responses; PTI (PAMP triggered immunity), after recognising the PAMPs (Pathogen associated molecular pattern) and ETI (effector triggered immunity), in response to the interaction between pathogen derived effectors and corresponding receptors in hosts (if available) (Hou et al., 2011). Reprogramming of plant metabolism is a method of strengthening immune responses and can occur through non-coding RNA mediated gene regulation (Gupta et al., 2018). Recent studies have marked miRNAs, a class of endogenous small non-coding RNAs, as key regulators of gene expression during plant-pathogen interaction. miRNAs post-transcriptionally regulate gene expression either by mRNA cleavage or by translational inhibition (Rhoades et al., 2002). Role of miRNAs in activating plant immune responses upon pathogen infection is well established. miRNAs were manifested as verified partakers of PTI in hormone crosstalk and that of ETI in R gene mediated

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Abbreviations: miRNAs, micro RNAs; EST, Expressed Sequence Tag; BLAST, Basic Local Alignment Search Tool; GO, Gene Ontology; KEGG, The Kyoto Encyclopedia of Genes and Genomes; E-value, expectation value; MFE, Minimal Folding Energy; MFEI, Minimal Folding Energy Index; UPE, Unpaired Energy

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