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*Corresponding author:

Madiha Zaynab;

Email:

madiha.zaynab14@gmail.com

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Plants Defense System Resist against the Pathogen Attack: Transcription Factors in Focus

Mahpara Fatima¹, Safdar Abbas³, Zaheer Ahmad⁴, Yasir Sharif¹, Muhammad Umair³, Khalida Bahadar⁵, Madiha Zaynab^{2*}

¹College of Crop Science, ²College of Life Sciences, Fujian Agriculture and Forestry University, Fuzhou 350002, PR. China.

³Department of Biochemistry Quide-e-Azam University, Islamabad, Pakistan.

⁴Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan.

⁵PARC Institutes of Advanced Studies in Agriculture, NARC, Islamabad, Pakistan.

Abstract

Transcription factors play important roles to drive different pathways by regulating gene expression. Apart from gene expression regulation, these TFs also have vital importance in plant immune system. Both PTI and ETI mode if immunity is important for plants but ETI has a central role in the defense system of a plant. ETI activates the hypersensitive response in which programmed/localized cell death is involved which ranked ETI quantitatively stronger than PTI which is effective in host resistance defense mechanism. Phytohormone such as salicylic acid, jasmonate, abscisic acid and ethylene and their components interact each other either positively or negatively. Their role in plant defense response has been documented.

Keywords: Transcription factors, plant immune system, hypersensitive response.



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INTRODUCTION

Transcription factors (TFs) mediate cellular responses through recognizing specific *cis*-regulatory DNA sequences at the promoters of their target genes. Plants defense system needs to be competent to resist against the pathogen attack. A precise defense system is mandatory by plants that can harmonize with both growth and development to boost ecological survival. Innate immune system of plants comprises of pattern-triggered immunity (PTI) and effector-triggered immunity (ETI) (Jones and Dangl, 2006). Innate immune signaling is activated when individual pathogen effectors are recognized by disease resistance (R) proteins, resulting in effector-triggered immunity (ETI). Pattern recognition receptors (PRRs) on host cell recognize pathogen associated molecular patterns (PAMPs) and endogenous damage-associated molecular patterns (DAMPs) and this recognition activates PTI mode of immunity (Boller and Felix, 2009; Macho and Zipfel, 2014). In ETI mode of immunity host cell recognizes pathogen virulence molecule on the surface of pathogen (Zebell and Dong, 2015). Both PTI and ETI mode, immunity is important for plants but ETI has central role in defense system of a plant. ETI activates hypersensitive response in which programmed/localized cell death is involved which ranked ETI quantitatively stronger than PTI, effective in host resistance defense mechanism (Spoel and Dong, 2012). PTI, adapted microorganisms acquired the ability to deliver effector proteins inside host cells, resulting in enhanced virulence. Pathogen attack induces gene expression changes in host cells and recent studies unleashed the role of some pathways specific transcription factors in immune system of plants (Buscaill and Rivas, 2014; Tsuda and Somssich, 2015). This review will discuss role of transcriptional machinery in plant immunity and how pathogen induces changes in gene expression upon their attack.

Transcriptional control of defense-related hormone signaling

Phytohormones and their components interact each other either positively or negatively (Pieterse *et al.*, 2012). White (1979) reported first time that when plant is treated with Salicylic acids (SA), it gets immunity against viral infection, in case of tobacco and tomato, fungus, in case of wheat. SA is reported to induce pathogenesis-related proteins (PR) augment immune response against pathogen attack. Salicylic acid is phenolic phytohormone and plays vital role in activation of plant defense system against pathogen attack. Systemic acquired resistance (SAR) is one of the best-studied signal transduction pathways involved in this complex resistance response, of which salicylic acid is a key signaling component. It induces SAR mode of defense against microbial biotrophs (Mettraux *et al.*, 1990; Gaffney *et al.*, 1993; Lawton *et al.*, 1995; Vlot

et al., 2009; Falcioni *et al.*, 2013). Jasmonate, a plant hormone, has a vital role in plant immune system especially against pathogen and abiotic stress. JAZ protein has a central role in JA-Ile pathway and it acts as ON-OFF switch. In the absence of jasmonate it binds with transcription factors and inhibits their activity. Upon its proteasomal degradation, TFs like MYC 2, 3, and 4 TF get activated which regulate the gene expression to combat stress (Chini *et al.*, 2007; Fonseca *et al.*, 2009; Pauwels *et al.*, 2010). In 2014, Fonseca and coworkers suggested that in JA-Ile pathway complex competition between activator and repressor determine the fate of JA transcriptional response. Priming is a phenomenon in which plants become immune to pathogen attack and they showed stronger response upon secondary infection (Jung *et al.*, 2009). Priming is of two types in plants; SAR occurs in the distal parts of plants upon localized infection and induced systemic resistance (ISR) is triggered by nonpathogenic bacteria. Phytohormone cytokinin is involved in cell division, grain yield, nutrient mobilization and leaf longevity (Kim *et al.*, 2006; Choi and Hwang, 2007; Matsumoto-Kitano *et al.*, 2008; Zhao *et al.*, 2010). In plant immunity, role of cytokinin's is known but the mechanism underlying is yet to be described. Accumulation of cytokinins in (*Nicotiana tabacum*) plants infers tolerance against drought stress. However, recent work has revealed that plant-originated cytokinin's with salicylic acid (SA) signaling augment plant immunity (Rivero *et al.*, 2007; Robert-Seilanianz *et al.*, 2007). Ethylene is a gaseous plant hormone and perceived by five membrane bounded receptors. Ethylene is reported to play an important role in basal immune system of plants against pathogen attack (Wang *et al.*, 2002; Balaji *et al.*, 2008; Mantelin *et al.*, 2009; Fudali *et al.*, 2013; Wubben *et al.*, 2001). Rhizobacteria play an important role in plant defense and could be promising sources of biocontrol agents (Iqbal and Ashraf, 2017).

Transcription factor families related to plant immunity

WRKY family members are present only in plants but few transcription factors of WRKY family has been reported in slime mold and unicellular protist genome (Rushton *et al.*, 2010). In *Arabidopsis thaliana* >70 and in rice >100 member of WRKY has been documented (Rushton *et al.*, 2010). Role of WRKY family members has been well recognized in plant immunity (Pandey and Somssich, 2009).

Arabidopsis has 74 members of basic domain leucine zipper (bZIP) family which can be classified in 10 groups. Two groups (C and D) play a vital role in immune system. bZIPs bind to DNA motif ACGT as homo or heterodimers. Group D is further divided into three clades. Clades I consist of TTGA1 and AtTGA4, while AtTGA2 and AtTGA5 falls in clades II. Clades III comprises of AtTGA3 and AtTGA7 and all three clades coordinate SA signaling

pathways. Along with SA signaling pathways these three clades provide plants with immunity against biotrophic pathogens. AtTGA2, 5 and 6 has been documented as essential players in systemic acquired resistance (SAR) and they regulate host detoxification pathways as well (Jakoby *et al.*, 2002; Gatz, 2013; Zander *et al.*, 2014).

Few members of bHLH have been documented to have role in plant immunity. Arabidopsis has 162 and rice has 167 members of TF family. DNA binding motif consists of hexamer sequence CANNTG. In *Arabidopsis thaliana* AtMYC2/Ja1/JIN1 regulates the plant defense system in coordination with salicylic acid (SA) (Carretero-Paulet *et al.*, 2010).

Arabidopsis thaliana has 100 genes while rice contains 150 genes for NAC family transcription factors. The NAC acronym is derived from three earliest characterized proteins with a domain (the NAC domain): NAM (no apical meristem), ATAF1/2 (*Arabidopsis* transcription activator factor 1/2) and CUC2 na(cup-shaped cotyledon). Mostly members of NAC family are involved in protection of plants from abiotic stresses like drought and high salinity and their DNA binding motif consist of CATGTG. Few NAC members in *Arabidopsis* like AtANAC019, AtANAC055 and AtANAC072 and in barely HvATAF1 have been reported as important immune components (Jensen *et al.*, 2008; Nakashima *et al.*, 2012; Nuruzzaman *et al.*, 2013).

Myb proto-oncogene protein is a member of the MYB (myeloblastosis) family of transcription factors. MYB transcription factors family has been known as an important member of plants immune system. In *Arabidopsis* and rice genome more than 160 genes has been reported which belong to MYB family. In plants as compared to animals MYBs protein subfamily contains distinctive R2R3 MYB domain and this domain further can be categorized into two classes on the basis of their DNA binding sequences i.e. (T/C)AAC(T/G)G and G(G/T) T(A/T)G(G/T)T (Stracke *et al.*, 2001; Dubos *et al.*, 2010; Buscaill and Rivas, 2014).

CONCLUSION

Transcription factors play important roles to drive different pathways by regulating gene expression. Apart from gene expression regulation, these TFs also have vital importance in plant immune system. Still there are several basic issues which need precise answer. Most of studies to understand the role of these TFs in imparting immunity to plants and to make plant able to combat disease have been conducted in control growth condition. So, data for large scale application is still poor. For developing effective disease management, an in-depth study is required to understand how TFs interact with each other or other components of their pathway and how they interact with pathogen induced changes under combined biotic and abiotic stress.

CONFLICT OF INTEREST

The authors declare that no competing interests exist.

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