

Role of WRKY Transcription Factors in Plant Disease Resistance Breeding

Laxman Singh Rajput^{1&3}, Rajneesh Sharma¹, Kartar Singh*⁴ Sumit Kumar Aggarwal², Sanjeev Kumar³, and Hemant Singh Maheshwari³

¹ICAR-Central Arid Zone Research Institute, Jodhpur, Rajasthan

²ICAR-Indian Institute of Maize Research, Ludhiana, Punjab, India

³ICAR – Indian Institute of Soybean Research, Indore, Madhya Pradesh, India

⁴Regional Station, Jodhpur, ICAR- National Bureau of Plant Genetic Resources, New Delhi

SUMMARY

In response to biotic stresses to plant, the stress-response apparatus is triggered by the innate defense system comprising genes, miRNAs, siRNAs, and particularly, transcription factors (TFs). Within the range of activated various transcription factors, the WRKY TF superfamily encodes the maximum number of regulatory proteins. These WRKY TFs control downstream genes through direct and indirect mechanisms. The WRKY TFs, oriented in the promoter region of genes linked with various types of plant innate immunity, including PAMP-triggered immunity (PTI), effector-triggered immunity (ETI), basal defense, and systemic acquired resistance (SAR). Due to this characteristic molecular coordination, the WRKY TF superfamily has been recognized as a potential target in the management of plant diseases.

INTRODUCTION

In the features of erratic shifts in climate patterns, crop plants are suffering from various biotic stresses. Utilizing genetic resistance emerges as the most lucrative, efficient, and eco friendly strategy for managing these biotic stresses. On the other hand, the constrained genetic diversity within the gene pool poses a obstruction to speedy advancements in the field of plant genetic resistance. Additionally, the constant evolution of new virulent races or biotypes is causing the knockdown of essential resistance genes. Hence, the long-lasting concept of durable resistance has persisted throughout the ages in the management of biotic stresses. In natural condition, plants challenge with a combinations of various biotic and abiotic stresses. Therefore, prioritizing broad-spectrum resistance and developing resilience against multiple forms of stress becomes paramount in mitigating economic yield losses (Rajput et al., 2017; Madhusudhan et al. et al., 2019).

Mechanism to manage phytopathogens:

In times of biotic stress especially plant diseases, particularly among several gene families, regulatory genes presume a critical role in signal transduction, influencing the expression of genes that form the base of various defense pathways. Targeting regulatory proteins, specifically transcription factors (TFs), presents a viable option. Transcription factors directly manage the downstream R genes, making them highly potential candidates for breeding programs aimed at increasing disease resistance. To date, a huge number of transcription factors have undergone identification and structural-functional characterization.

Among these, transcription factor families like WRKY, NAC, Whirly, Apetala2 (AP2), and ethylene-responsive elements (ERF) have been associated to the transcriptional reprogramming of plant defense responses. The members of the WRKY TFs family share a conserved WRKY domain, comprising approximately 60 amino acids featuring a divergent heptapeptide sequence (WRKYGQK). This domain is come with by a Zn²⁺-finger motif responsible for binding to specific cis-regulatory elements within defense related genes, known as W-boxes (TTGAC[C/T]). The W-box, recognized in the promoter regions of genes linked with plants' innate immunity, plays a critical role in various defense mechanisms, including PTI, ETI, and S. These transcription factors (TFs) respond to pathogen-associated molecular patterns (PAMPs) and damage-associated molecular patterns (DAMPs) through interactions with the host's pattern recognition receptor (PRR) proteins. They selectively attach to the cis-elements of defense genes, exerting regulatory control over their expression. Plants showed immediate resistance against plant pathogens upon detecting conserved molecular patterns at the membrane or intracellular levels, this phenomenon known as plant innate immunity or priming.

The majority of plant pathogenic bacteria, fungi, manage to evade this immunity by acquiring the ability to introduce proteinaceous molecules directly into susceptible host cells. In response, a few plants have evolved mechanisms to oppose these proteinaceous molecules by triggering a defense system known as ETI.

Upon the recognition of either proteinaceous molecules or conserved molecular patterns by the plant, a series of events are initiated within the host plant cell. These events includes the influx of Ca^{+2} ions, the generation of reactive oxygen species (ROS) and nitric oxide (NO), in addition to the phosphorylation of G proteins and 14-3-3 proteins. These events conclude in the phosphorylation of signaling molecules such as CDPKs, AGCPK, and MAPK, with MAPK playing a pivotal role in signal transduction. Through ongoing substrate-level phosphorylation, these signaling molecules pass through into the nucleus, where they activate transcription factors (TFs) related to defense mechanisms (Bigeard et al. 2015).

TFs adhere to specific conserved DNA sequences, prompting the induction of genes associated with defense pathways. These genes add to the creation of phytoalexins, pathogenesis-related (PR) proteins, synthesis of salicylic acid (SA), jasmonic acid (JA), or ethylene, as well as the generation of defense-related phenols and enzymes for scavenging reactive oxygen species (ROS). Notable TFs involved in this process encompass WRKY, AP2/ERF, MYB, bZIP, NSC, and MYC (Rajput et al., 2020).

Utilization in plant pathology:

WRKY TFs, particularly WRKY13, have been comprehensively studied and applied in breeding programs deals with plant disease resistance. The overexpression or knockout of WRKY TFs triggers the launch of defense pathways against plant pathogens. In case of rice, overexpression of the WRKY gene OsWRKY13 induces resistance mechanisms, including induced systemic resistance (ISR), against significant pathogens such as *Magnaportha oryzae* and *Xanthomonas oryzae* pv *oryzae* (Rajput et al., 2020). Researcher also find, overexpression and knock-out studies of WRKY have make clear that OsWRKY45 stands out as the most critical WRKY TFs in rice against range of biotic and abiotic stresses. Its overexpression induces defense responses against a spectrum of both abiotic and biotic stresses, including drought, salt, osmotic stress, as well as resistance to the pathogens, *M. oryzae* and *X. oryzae* pv *oryzae* (Qiu and Yu, 2009). Through Virus-Induced Gene Silencing (VIGS) and overexpression studies, it was observed that CaWRKY1 showed over expression after following inoculation with bacterial phytopathogens such as *X. axonopodis* pv. *vesicatoria* and *Pseudomonas syringe* pv. *tabaci*. Oh and colleagues were the first to propose the affirmative regulatory functions of CaWRKY1 and CaWRKY2 against two formidable viruses, namely Tobacco Mosaic Virus and Pepper mild mottle virus, as documented in their particular series of research publications (Oh et al., 2008). Suppression of OsERF922 (AP2/ERF) transcription factor has been shown to resulted in the initiation of phytoalexin, PR proteins, and phenylalanine ammonia lyase (PAL) production in rice upon infection by *M. oryzae* (Kazan 2006). Hence, gaining complete understanding of the functions of varied transcription factor families is very important in resistance breeding efforts, aimed at mitigating crop yield losses caused by various diseases in different crops.

CONCLUSION

In the dominion of plant growth and development, plants meet diverse biotic stresses posed by various phytopathogens. The development in molecular researcher over the recent time has significantly improved our basic understanding of the regulation and functions of WRKY TFs, contribution economic and ecological advantages for plant management. The insights of current information on WRKY TFs can be practical used to create plant ideotypes, depiction them resistant or tolerant to a diversity of phytopathogens, through manipulation of WRKY TFs by overexpression or knockdown. In addition, the deployment of clustered regularly interspaced short palindromic repeats (CRISPR) and their associated genes facilitates the exploitation and functional characterization of positively or negatively controlled WRKY TF genes. Furthermore, identifying the response of WRKY TFs to various abiotic and biotic stresses is crucial; necessitate the harmonization of environmental factors and plant disease defense mechanisms for a comprehensive understanding.

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