

Study of patterns of MYB transcription factors in different plants to study their potential use towards stress tolerance adaptation

Deepshikha Kaushik^{1*}, Saroj Rani², Aanchal Gupta²

¹Centre for Bioinformatics, Maharshi Dayanand University, Rohtak- 124001 (Haryana)

²Department of UIBT, Chandigarh University, Mohali- 140413 (Punjab)

Corresponding author's email: drdeepshikha.rp.cbinfo@mdurohtak.ac.in

ABSTRACT

Transcription factors play an important role in plant's adaptation towards biotic and abiotic stress. They can quickly detect cascades of signals that occur in external environmental conditions, and can further transmit those signals within a specified time for plants respond to the environment. TFs are predicted in different plants to study their structural properties, origin, evolution and gene function. This review primarily focuses on MYB TFs available in public databases to understand their interaction with biotic and abiotic stress factors, causing an increase in plant's adaptation.

Keywords: Abiotic and biotic stress, database, MYB, NAC

INTRODUCTION

Plants have to show adaptation towards environmental problems like drought, salinity, temperature, and pathogenic stress during their growth. Plant stresses, biological and physical, can affect a plant during various stages of its development, and instead of one multiple stress affect a plant together (Chinnusamy *et al.* 2004). Global climate debilitation will eventually lead to increased prevalence of drought, heat wave and also an increased salt accumulation in fields (Easterling *et al.* 2000). Plants continue to survive with these stresses, and they evolve themselves to adapt the complex rapid responses, but result is often a decreased crop yield. Global warming and future climate change allow researchers to understand plant responses related with the activation of various signaling cascades. There is a need to increase focus on each gene expression study in response to increase crop yield (Baillio *et al.* 2019).

TF genes also have been engineered for improvement of stress tolerance in model plants. They are further studied to understand their potential use in improving tolerance of multiple crops' stress under natural conditions of field (Wang *et al.* 2016).

Table 1 List of major transcription factors (WRKY, NAC, MYB, AP2/ERF) of *Solanum lycopersicum* and different *Saccharum* species, their number present in NCBI database.

S.No.	Taxon	Transcription Factors			
		WRKY	NAC	MYB	AP2/ERF
1	<i>Solanum lycopersicum</i>	129	129	508	11
2	<i>Saccharum officinarum</i>	3	2	8	0
3	<i>Saccharum hybrid cultivar</i>	15	21	138	1
4	<i>Saccharum fulvum</i>	1	1	0	0
5	<i>Saccharum spontaneum</i>	4	0	2	0
6	<i>Saccharum barberi</i>	0	0	3	0
7	<i>Saccharum robustum</i>	0	0	1	0
8	<i>Saccharum elegans</i>	0	0	1	0
9	<i>Saccharum rufipilum</i>	0	0	1	0
10	<i>Saccharum sp. GP-2012</i>	0	0	1	0

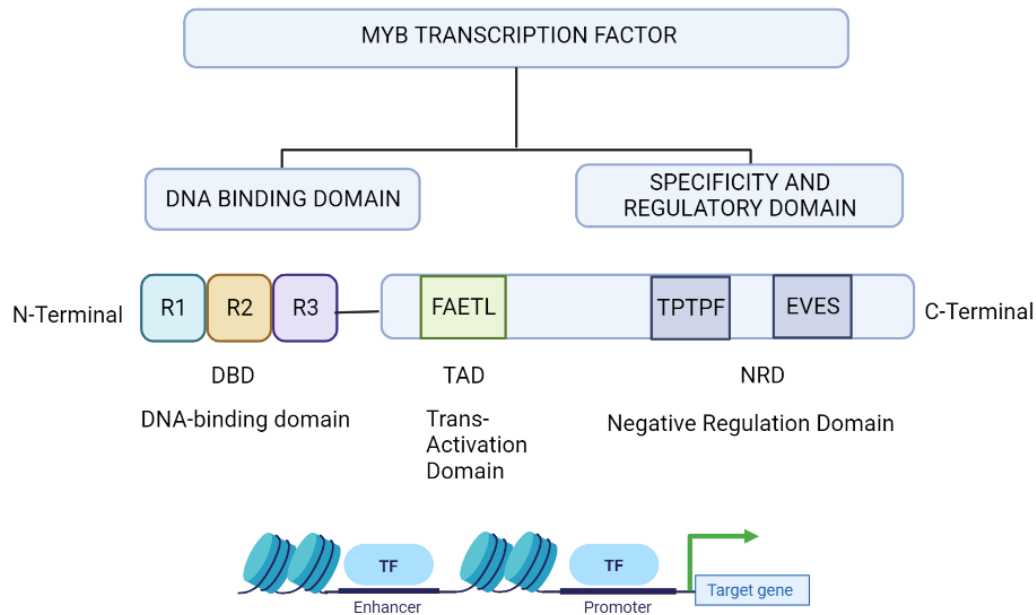
Researchers have significantly improved sugarcane varieties to develop energy wands cane varieties that can accumulate up to 18 percent sucrose in the stem. Similarly in tomato varieties, TFs are proven to signify a crucial part in process of seed development and ripening of fruit whereas gene silencing in some studies has led to delayed ripening and inhibition of carotenoid accumulation. Table 1 shows major transcription factor data for WRKY, NAC, MYB and AP2/ERF present at NCBI.

MYB TRANSCRIPTION FACTOR

MYB transcription factor named after its conserved domain, is present in Eukaryotes. v-Myb oncogene of AMV (avian myeloblastosis virus) is the initially derived MYB gene (Klempnauer *et al.* 1982) and various such genes have been predicted in different plants, fungi, slime molds and animals since then. The structure and function of MYB TFs are conserved in plants in contrast to yeasts and animals. Twenty-four R2R3MYB TFs were identified in *Solanum lycopersicum* in recent research. They showed that MYB49 gene's overexpression increases tomato's resistance towards *P. infestans* and also enhances crop's resistance towards drought and saline stress; thereby proving MYB49 as a regulator that can protect chloroplast and control damage of cell membrane (Cui *et al.* 2018).

DECIPHERING STRUCTURAL INFORMATION

A common and important characteristic of MYB protein consists of the DNA-binding domain (MYB domain), that in plants usually comprised of one to four imperfect repeats. Every repeat is comprising near about 52 amino acid residues, and spans across the major groove of DNA. It is a helix with three tryptophan residues that are consistently spaced within the hydrophobic core that leads to recognition of specific DNA sequence HTH structure (Ogata *et al.* 1996). Structure and function of MYB are shown diagrammatically in Fig 1. COLORED1 (C1) was the first gene to be identified that codes for a plant MYB domain protein, which leads to the production of anthocyanin in the aleurone layer of maize kernels (*Zea mays*) (Paz-Ares *et al.* 1987). Different MYB proteins are present in crops such that they can act specific part individually. It has been shown to function during different biological processes, that include regulation of metabolism, seed and flower development, defense, cell fate, identity and stress.



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Fig 1. Diagrammatic representation of structure and function of c-MYB Transcription factor.

FUNCTIONAL ADAPTATIONS TOWARDS ABIOTIC AND BIOTIC STRESS

Because crops are sedentary, they have exposure to different environmental strains. Various genes and proteins show regulation during abiotic stress, and prove that transcription factors are essential. It is considered among the largest TF groups of plants that are necessary for responses against abiotic stress (Dubos *et al.* 2008). Important among all abiotic stresses are droughts which hamper plant's vegetative and reproductive development adversely and decrease crop yield. Genome-wide transcriptome and microarray analysis show that many genes containing MYB proteins, and the MYB-binding elements are present in *Arabidopsis thaliana*, *Gossypium herbaceum*, *Zea mays*, *Macrotiloma uniflorum*, *Mars pumila*, *Musa*, *Populus euphratica*, and *Glycinmax* (Davey *et al.* 2009; Gollacket *et al.* 2011; Pereira *et al.* 2011; Ranjan *et al.* 2012; Bhardwaj *et al.* 2013).

In response to abiotic stimuli, a vast number of MYB gene are either activated or suppressed. But the underlying process is still a mystery. It has just recently come to light that short RNAs frequently target MYB family members implicated in responses for abiotic stress. AtMYB113 and lbMYB that involved in the production of anthocyanins and the reaction to injury, are directly targeted by microRNA828 (Rajagopalan *et al.* 2006; Lin *et al.* 2012). In addition, microRNA828 causes the synthesis of TAS4-siRNA81(-), which in turn targets the *Arabidopsis* proteins PAP1, PAP2, and MYB113 and creates an auto-regulatory feedback loop with PAP1 in the sugar stress signaling pathway (Luo *et al.* 2012). By focusing on the first intron and causing the lbMYB1 gene to become methylated during injury, sRNA8105 suppresses the production of lbMYB1 (Lin *et al.* 2013). On sequence analysis, it was deduced that the mRNAs are encrypted by most of the MYB genes, and are targets of miRNAs during aluminium stress condition in wild soybean plant. MYB-TF affects ABA-signaling pathways as a response against drought related stress condition in numerous plants, especially *Arabidopsis* species (Baldoni *et al.* 2015).

Fruit ripening event in *Solanum lycopersicum* accompanies simultaneous processes of chlorophyll degradation and carotenoid, flavonoid accumulation. SIMYB72 has transcriptional activation property; its downregulation causes uneven colored fruit production, chlorophyll accumulation and biogenesis of chloroplast in tomato fruits thereby decreasing the amount of lycopene, increasing production of β carotene and flavonoid content. Thus, SIMYB72 can serve as a potential target towards improvement of fruit nutrition in crops (Wu *et al.* 2020).

In a study 127 SIMYB genes were identified from tomato and classified into 18 groups on the basis of domain similarity and phylogeny. Also, the effect of SIMYB overexpression was studied in terms of physiological and metabolic changes for purple tomatoes (Li *et al.* 2016) Another research in tomato showed that anthocyanin accumulation is induced due to SIMYB75 causing an increase in production of ethylene, phenolic and aromatic compounds. SIMYB75 activates promoters of LOXC, AADC2 and TPS genes and its conserved elements for core binding site include MYBPLANT and MYBPZM (Jian *et al.* 2019).

Because of drought stress, MYB are established as active TFs in ABA- signaling pathway in a variety of crops, most notably *Arabidopsis* (Jishaet *et al.* 2015). Due to drought stress, 51% of MYB protein was shown to be elevated (such as AtMYB2/74/102) and 41% were negatively regulated (Katiyar *et al.* 2012). It has been found that overexpressing AtMYB44, which isa member of the R2R3-MYB TF subfamily, increases soybean resistance against drought/salt stress (Seo *et al.* 2012). Similarly, BcMYB1 was substantially increased under salt stress, increased polyethylene glycol concentrations, and water stress in *Boeacrossifolia*. BcMYB1 is another family member of the R2R3-MYB TF. However, in low temperatures, BcMYB1 induction was only negligible (Chen *et al.* 2005).

Besides responding against abiotic-stresses, MYB-TF has been shown to combat biotic stress. As in *Arabidopsis*, AtMYB102 has been found to sensitize them to hit GPA (peach aphid) infestation (Zhu *et al.* 2018). AtMYB96 often act as a key molecular-link among SA and ABA crosstalk and enhance pathogen resistance in *Arabidopsis* (Seo *et al.* 2010). Important microbes that are also beneficial, trigger plant resistance response in which root-specific MYB72 functions as a joining node in *Arabidopsis* signaling (Segarra *et al.* 2009). Excess expression of TaRIM1 caused its increased resistance for *Rhizoctonia cerealis* infection in the transgenic variety of wheat (Shan *et al.* 2016). The Yellow Seed 1 (MYB TF y1), from sorghum, yielded the 3-deoxyanthocyanidin phytoalexin due to the challenge given by *Colletotrichum sublineolum* in varieties of maize (Ibraheemet *et al.* 2015). Furthermore, activation of MYB-TF by insect infestation was also examined in chrysanthemums. The over-expression of CmMYB15 due to accretion of lignin can decrease the growth of aphids (An *et al.* 2019). Likewise, MdMYB30 aid in regulation of wax biosynthesis in apples further improving its disease resistance (Zhang *et al.* 2019). A new MYB-Transcription Factor, CaPHL8, is effective in enhancing immunity against *Ralstoniasolanacerum* infection in pepper plants (Noman *et al.* 2019). VdMYB1, an example of the TF, R2R3-MYB was seen as a defense response activating factor that led to the expression of stilbene

synthase gene 2 (VdSTS2) as a response for the infection that was caused by *Erysiphe necator* in grapevine (Yu *et al.* 2019). Hence, MYB-TF increases the plant's adaptation against various biotic and abiotic stresses.

SUMMARY AND FUTURE PROSPECTS

TFs are extraordinary at transcription-levels because of their abilities like repression or activation of the genes under various stress conditions. Regulation (both positive and negative) of any specific gene involves participation of several TFs. Nearly thousands of TFs (ARF, WRKY, DBB, NAC, SBP, MYB, VOZ, AP2/ERF, etc.) have been recognized in various plants being facilitated by different signaling pathways, but huge TFs are still needed to be identified to deal with biological stress. When NCBI database was explored to discover more TFs, there also we got 129 WRKY, 129 NAC, 508 MYB and 11 AP2/ERF TFs for *Solanum lycopersicum* and 23 WRKY, 24 NAC, 155 MYB and single AP2/ERF TFs when we searched for *Saccharum*. Plant epigenetics can be considered that includes conserved regulatory mechanisms of gene expression, histone modifications, DNA-methylation, chromatin remodeling, noncoding RNAs, which will help to understand the biological processes better towards enhancement of plants environmental response towards stress factors.

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