

Research progress of MYB transcription factor family in plant stress resistance

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Abstract

The MYB (v-MYB avian myoblast viral oncogene homolog) family of transcription factors is a large class of transcription factors that are widely distributed in eukaryotes and found in nearly all eukaryotes. The MYB protein exhibits the typical structure and function of transcription factors. Its protein molecular structure consists of a highly conserved DNA-binding domain known as the MYB domain, as well as a relatively less conserved transcriptional activation region and negative regulatory region. MYB proteins can regulate plant growth and development, primary and secondary metabolism, and respond to various abiotic stresses such as drought, high temperature, and high salt. In this paper, we summarize the structural characteristics of MYB family transcription factors, as well as their roles in biotic and abiotic stresses. We also elaborate on the progress of relevant research, aiming to provide theoretical insights for better understanding the functions and regulatory mechanisms of all members of the MYB family in plants. Furthermore, we aim to explore the potential utilization of these transcription factor family members in crop improvement.

Keywords: MYB transcription factors; protein structure; plant; stress

Introduction

Plants are vulnerable to long-term adverse environmental disturbances, such as biotic stress caused by diseases, pests, and other organisms; and abiotic stress caused by drought, high salt, heavy metals, extreme temperatures, etc. Among them, drought, salinity, and extreme temperatures are the primary environmental factors that limit agricultural plant productivity and jeopardize crop safety (Chen *et al.*, 2022). The ongoing climate changes further intensify the influence of abiotic stress on plants. In order to withstand both biotic and abiotic stresses, plants have developed diverse defense mechanisms. However, these stresses continue to significantly impact crop quality and yield. Reports indicate that China's major crops, including rice, wheat, and corn, are particularly vulnerable to drought and high salinity soils. It is expected that by 2050, climate change may cause 50% of the land to become severely saline and alkaline (Javed *et al.*, 2020).

Transcription factors (TFs), also known as trans-effectors, regulate the processes of biological life activities and participate in various signal transduction and regulatory processes (Pratyusha and Sarada, 2022). They are key regulatory factors for gene expression in organisms. TFs directly or indirectly bind to cis-acting

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elements to regulate the inhibition or enhancement of target gene transcription efficiency, enabling plants to respond to stress (Ma *et al.*, 2022), and play an important role in plant stress resistance (Inukai *et al.*, 2017). Typical plant transcription factors have four functional regions: a DNA binding region (DBD), a nuclear localization signal, an oligomerization site, and a transcriptional regulatory region (Dubos *et al.*, 2010). Usually, transcription factors can be divided into several families based on the characteristics of DNA binding regions. Among these families, four main categories are related to plant stress resistance: bZIP, WRKY, AP2/ERF, and MYB (Li *et al.*, 2019).

The MYB (*v*-MYB avian myeloblastosis viral oncogene homolog) family is a transcription factor family with diverse functions and a wide distribution (Liu *et al.*, 2008). The first MYB transcription factor cloned from *Gramineae* plants is the *ZmMYBC1* gene (Paz-Ares *et al.*, 1987). This gene primarily regulates the biosynthesis of anthocyanins in corn. The varying number of structural domains in the MYB family gives them different functions. They not only regulate plant growth and development, cell morphology, and physiological metabolism, and other physiological processes (Grotewold *et al.*, 1994), but also participate in the regulation of secondary metabolism, control of cell morphogenesis, and plant nitrogen metabolism (Ambawat *et al.*, 2013).

In this paper, we provide a summary of the fundamental structural characteristics of the MYB transcription factor family and its response to both biotic and abiotic stresses. The aim is to offer theoretical insights for future research on the function and regulatory mechanisms of the MYB transcription factor family, as well as to enhance the utilization of these transcription factors in crop improvement engineering.

Basic structural characteristics of MYB transcription factor family

The MYB transcription factor family has a highly conserved DNA binding domain known as the MYB domain. This domain typically contains incomplete repeats of 1-4 tandem MYB repeat sequences (Rs) at the N-terminus. Each repeating sequence typically contains 50-53 amino acids and encodes three α -helices. The second and third helices form a helix-turn-helix (HTH) structure that binds to larger grooves in DNA (Kranz *et al.*, 1998; Dubos *et al.*, 2010; Rosinski and Atchley, 1998). There are three tryptophan residues in the MYB domain, separated by approximately 18 amino acids, which are crucial for maintaining the hydrophobic structure of the HTH (Baldoni *et al.*, 2015). Tryptophan is sometimes replaced by aromatic or hydrophobic amino acids (Ogata *et al.*, 1996). In most MYB transcription factors, there are transcriptional activation domains rich in acidic amino acids located between the C-terminal and DNA binding domains. These domains can regulate protein activity and play an crucial role in maintaining protein functional diversity (Kranz *et al.*, 1998).

MYB can be divided into the following four categories based on the number and position of repetitive sequences in the MYB domain (Figure 1): 1R-MYB (R1/R2, R3-MYB), 2R-MYB (R2R3-MYB), 3R-MYB (R1R2R3-MYB), and 4R-MYB (R1/R2-MYB) (Wang *et al.*, 2021b). 1R-MYB (MYB-related) is an important telomere-binding factor responsible for maintaining the integrity of chromosome structure and regulating gene transcription (Yu *et al.*, 2000; Romero *et al.*, 1998). 2R-MYB, also known as R2R3-MYB, is the most abundant and functional MYB protein in plants. R2R3-MYB participates in cell differentiation, organogenesis, leaf morphogenesis, hormone response, secondary metabolism, and defense against various stressors (Yu *et al.*, 2023; Yan *et al.*, 2021). 3R-MYB primarily regulates the cell cycle, cell differentiation, and plant tolerance to stress (Haga *et al.*, 2007). 4R-MYB is only found in *Arabidopsis*, grapes, and *Populus tomentosa*, so its functional research has not been fully developed (Wilkins *et al.*, 2009; Du *et al.*, 2013; Matus *et al.*, 2008). In these classifications, the R2R3-MYB transcription factor has been widely studied for its various roles in plants (Li *et al.*, 2019). Currently, with the advancement of research progress and the emergence of whole genome sequencing, a significant number of MYB transcription factor family members have been identified in plants,

including 217 transcription factors found in potatoes (Li *et al.*, 2021); 187 transcription factors were found in radish (Muleke *et al.*, 2021). The expression levels of these MYBs vary among different plant species. They are widely involved in various response mechanisms and play an important regulatory role in combating biotic and abiotic stresses (Ma and Constabel, 2019; Pratyusha and Sarada, 2022; Shimotohno *et al.*, 2021).

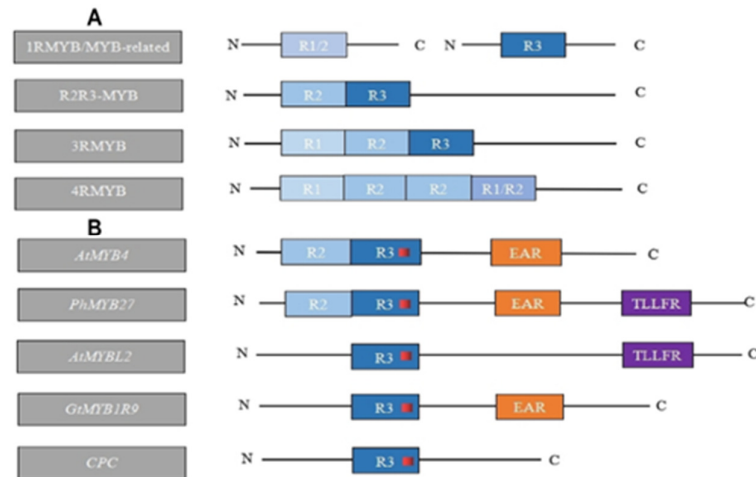


Figure 1. A Classification of MYB TFs in plants; B Structure of several MYB TFs (The red rectangles in the R3 domain represent the basic-helix-loop-helix- binding domain) (Ma and Constabel, 2019)

The role of MYB transcription factors in biotic stress

Biotic stress refers to the collective term for various biological factors that are detrimental to the survival and development of plants (Abe *et al.*, 1997). Usually caused by infections and competition between plants, such as diseases, pests, and weed hazards. In plants, for example, when soybeans can be invaded by *Sphyrmonas fabricius*, tomatoes can be infected by *Botrytis cinerea*, and cucumbers can be infected by powdery mildew (Aoyagi *et al.*, 2014; Liu *et al.*, 2016; Meng *et al.*, 2022), MYB transcription factors are induced in response to pathogen attacks. *AtMYB30* has been confirmed to be induced by reactive oxygen species treatment in *Arabidopsis*. In addition, *AtMYB30* targets lipid transfer protein 1 (LTPG1) and LTPG2, which are anchored by GPI, forming a MYB30-dependent regulatory network that triggers an immune response to bacteria (Mabuchi *et al.*, 2018). Identification of the R2R3-MYB gene *TaRIM1* from transcriptome data and cloning from resistant *Wheat C112633* for positive regulation of tolerance to *Rhizoctonia solani* (Shan *et al.*, 2016).

The MYB transcription factor combats pests by regulating the accumulation of flavonoids and glucosinolates. In *Arabidopsis*, *AtMYB41* can resist external insect invasion by inducing dehydration after injury (Cominelli, 2008). Experimental evidence has shown that in *Brassicaceae*, MYB29 is highly induced under pest treatment, and most genes regulating indole glucosinolate were found to be upregulated in the experiment. Homologous MYB proteins exhibit a high degree of complexity in transcriptional regulation under stimulation (Augustine, 2015).

In addition, as demonstrated by mutation and overexpression studies on eggplants have demonstrated that the *SmMYB44* gene in *Solanum* plants positively regulates the tolerance of *Ralstonia solanacearum* (Qiu *et al.*, 2019). Several other genes, including *AtMYB15*, *AtMYB30*, *AtMYB73*, *MdMYB30*, and *PacMYBA*, have also been identified as positive regulators of *Pst DC3000* stress in transgenic *Arabidopsis* (Kim *et al.*, 2020; Jia *et al.*, 2011; Shen *et al.*, 2017; Zhang *et al.*, 2019; Vaillau *et al.*, 2002). Similarly, three MYB transcription

factors have been found in cotton: *GhMYB4*, *GhMYB36*, and *GhODO1*. These factors enhance *Dahlia*'s tolerance to *verticillium wilt* by regulating several defense mechanisms (Zhu *et al.*, 2022; Liu *et al.*, 2022; Xiao *et al.*, 2021). Unlike many other transcription factors, CaPHL8, a MYB transcription factor in chili peppers, plays a positive regulatory role in the response to *Ralstonia solanacearum* but is not related to high-temperature stress tolerance.

In addition, some MYB transcription factors act as repressors in the interaction between hosts and pathogens. For example, when *Arabidopsis* is stressed by *PstDC3000*, the signaling of jasmonic acid (JA) and salicylic acid (SA) is upregulated in JA/SA insensitive mutants. This indicates that *AtMYB13* is involved in the plant's response to *PstDC3000* stress in the JA/SA independent pathway. Further research reports suggest that the loss of *AtMYB13* function can promote sugar deposition and accelerate cell death, indicating a negative role in immune responses against pathogens (Chen *et al.*, 2013). In summary, MYB transcription factors can enhance the tolerance of plants to pathogen infection, activate or inhibit responses to various stresses, and play a positive role in plant resistance to biotic stress.

The role of MYB transcription factors in abiotic stress

The role of MYB transcription factors under drought stress

Drought stress is one of the primary abiotic stresses in plants, which not only impacts plant growth and development but also jeopardizes crop yield and quality (Li *et al.*, 2019). According to reports, MYB transcription factors can directly or indirectly participate in drought signaling pathways through various mechanisms, with the majority belonging to R2R3-MYB and 3RMYB. Stomatal regulation is one of the important mechanisms for controlling plant water loss (Gupta *et al.*, 2020).

AtMYB60 is the first transcription factor involved in the regulation of stomatal movement (Simeoni *et al.*, 2022). Overexpressed *AtMYB60* plants are sensitive to drought stress (Oh *et al.*, 2011). Under drought stress, most MYB transcription factors are associated with the abscisic acid (ABA) signaling pathway. The regulation of ABA by MYB transcription factors can be divided into three types. The first type is the induced type, which primarily participates in plant responses to abiotic stress by inducing the accumulation of ABA. The expression of the *PttMYB94* gene, which encodes the R2R3MYB transcription factor in *Populus tomentosa*, is induced by dehydration stress. With the enhancement of ABA, the drought resistance of plants will increase (Fang *et al.*, 2020); The second type is mediated, which enhances plant stress tolerance by regulating the size of stomata through ABA mediation. *TaMYB33* in wheat is regulated by ABA-mediated stress response signals and enhances drought tolerance by accumulating intracellular osmoregulatory substances and enhancing the ability of cells to clear reactive oxygen species (Qin *et al.*, 2012); The third type is ABA-dependent, which can confer abiotic stress tolerance by regulating the expression levels of various stress markers in the ABA-dependent pathway. For example, the overexpression of *GaMYB85* in cotton can enhance the accumulation of free proline and chlorophyll in transgenic plants. It can also increase the expression of stress response genes such as *RD22*, *ADH1*, *RD29A*, *P5CS*, and *ABI5*. As a result, the resistance of transgenic plants to drought stress is enhanced (Butt *et al.*, 2017).

However, the expression of the *BcMYB1* gene significantly increased under drought stress, but was very low under exogenous ABA treatment. This indicates that the *BcMYB1* gene is independently involved in the response to drought stress through the ABA pathway (Chen *et al.*, 2005). In addition, the *IbMYB116* gene in barley activates the reactive oxygen species scavenging system through the JA signaling pathway and participates in drought stress responses (Zhou *et al.*, 2019). MYB transcription factors participate in drought tolerance related to leaf permeability by regulating the synthesis of flavonoids and stratum corneum, which are related to leaf permeability (Wang *et al.*, 2021a).

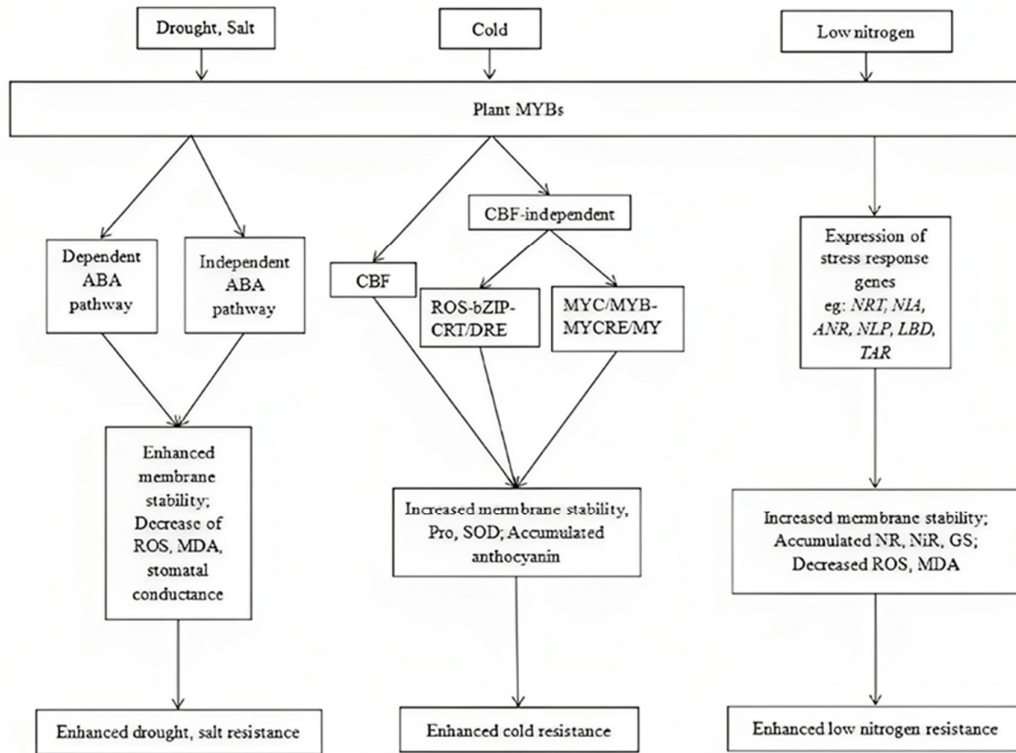


Figure 2. MYB TFs regulate plant drought, salt, cold and low nitrogen pathway (Wang *et al.*, 2021a)

The role of MYB transcription factors under high salt stress

Due to the combined effects of salt and drought stress, which result in water scarcity, certain MYB transcription factors have been found to play a similar role in salt responses. They respond to drought and salt stress through a series of regulatory mechanisms, such as accumulating osmotic regulatory substances to improve osmotic pressure and antioxidant capacity, altering secondary metabolism, and enhancing membrane stability (Abe *et al.*, 1997). The majority of MYB genes involved in salt stress response are R2R3-MYB. Research has shown that a few MYB-related genes and 3RMYB genes are also involved in salt stress regulation. For example, under high salt stress conditions, the levels of reactive oxygen species and malondialdehyde decrease in transgenic *FtMYB13* plants, while protein content and photosynthetic efficiency increase. This improvement in salt tolerance has been observed (Huang *et al.*, 2018). MYB transcription factors can also improve plant salt tolerance by increasing the expression level of stress-related genes. For example, overexpressing *CmMYB2* plants can delay flowering time, increase sensitivity to ABA, and decrease stomatal opening (Shan *et al.*, 2012). Further analysis showed that the expression levels of some stress-related genes, including *RD22*, *RD29A*, *COR47*, and *ABA1*, increased. These results indicate that the overexpression of *CmMYB2* can significantly enhance salt tolerance in plants. Furthermore, *PtrSSR1* gene of *Populus tomentosa* enhances salt tolerance in transgenic plants by regulating lateral root development and ABA signaling (Fang *et al.*, 2017); *AtMYB73* negatively regulates the response of SOS to salt stress in *Arabidopsis* (Kim *et al.*, 2013).

The role of MYB transcription factors under heavy metal stress

Plants have evolved tolerance mechanisms to withstand heavy metal stress over the course of long-term evolution. Research has found that the MYB transcription factor family is involved in the response to metal stress in plants, although most of the research has focused on iron and aluminum stress. Iron is an essential

nutrient element for plant photosynthesis and respiration, and it plays a role in various metabolic processes in plants, including photosynthesis, respiration, and nitrogen fixation. The product encoded by the *MxMYB1* gene in small mallow is a regulatory protein related to plant iron absorption and utilization. It serves as a negative regulator of iron transport and storage (Shen *et al.*, 2008). The *DwMYB2* gene, a R2R3-MYB transcription factor in orchids, can be ectopically expressed in *Arabidopsis*. This expression regulates iron transporter genes and increases *Arabidopsis*' sensitivity to iron deficiency (Chen *et al.*, 2006). Aluminum toxicity is the primary factor that limits plant growth and development in acidic soils. In wild soybeans, the overexpression of *GsMYB7* and *GsMYB10* genes enhances the tolerance of transgenic soybean plants to aluminum acid stress. This finding proves that *GsMYB7* gene is an essential transcription factor for responding to aluminum stress (Zeng *et al.*, 2012). Overexpression of the *RsMYB1* gene, a member of the factor family can enhance the expression of genes related to heavy metal detoxification, such as glutathione gene (*GSH*), phytochelatins (*PCs*), and antioxidant genes (*SOD*, *CAT*, and *POX*). This, in turn, improves the resistance of transgenic plants to heavy metal ions like zinc, copper, and chromium (Ai *et al.*, 2018).

The role of MYB transcription factors under temperature stress

Analysis of the plant transcriptome under temperature stress indicates that many MYB transcription factors are involved in the response to temperature stress (Tian *et al.*, 2013). High temperatures can inhibit plant photosynthesis and respiration, disrupt cellular structure, and consequently affect the stability of various components within cells and the normal progression of various physiological and biochemical reactions. Under high temperature conditions, plants overexpressed with *OsMYB55* showed significantly higher growth compared to wild-type plants, suggesting that *OsMYB55* can enhance the heat tolerance of rice varieties (El-Kereamy *et al.*, 2012). Under high temperature conditions in *Arabidopsis*, the activity of *AtMYB68* in *Arabidopsis* roots significantly increases, and the growth activity of the mutant *myb68* is significantly lower than that of the wild-type, indicating that *AtMYB68* is involved in the plant's response to high temperature tolerance (Deng *et al.*, 2020). The *AtMYB30* gene can bind to the *ANN1* and *ANN4* promoters and inhibit their expression (Liao *et al.*, 2017). Research has found that MYB transcription factors regulated by calcium signaling are also involved in the response mechanism of grape leaves to high temperature stress after heat shock (Liu *et al.*, 2012).

Low temperatures can also cause serious damage to plants, including frostbite. At present, plants have two regulatory pathways for low temperature stress, namely the ABA-dependent and ABA-independent regulatory pathways (Figure 2). ABA independent regulatory pathways can be further divided into CBF-dependent pathways and CBF-independent pathways (Park *et al.*, 2015). Currently, the most popular research topic is the CBF-dependent pathway (Ma *et al.*, 2022). As a negative regulatory factor in response to low temperature stress, *AtMYB15* can bind to the trans-acting element in the CBF gene promoter region, inhibit the expression of CBF, and reduce plant cold resistance (Agarwal *et al.*, 2006). *OsMYBS3* is a positive regulatory factor for cold resistance, which can inhibit the DREB/CBF-dependent cold signaling pathway in rice. This indicates that different pathways play a gradual role in adapting to short-term and long-term cold stress (Su *et al.*, 2010). *AtMYB31* can promote the expression of the CBF gene under low temperature, enhancing plant resistance to low temperature and oxidative stress (Su *et al.*, 2010; Li *et al.*, 2019). Research has found that *MYBS3* participates in the response of rice to low temperature stress by inhibiting the DREB/CBF-dependent cold signaling pathway, which appears to have a role in the transcriptional regulation. Unlike the rapid and transient response of the DREB/CBF signaling pathway to stress, *OsMYBS3* responds slowly to low-temperature stress. Therefore, it can be concluded that there may be a new signaling pathway involved in the short-term and long-term responses of plants to low temperature stress, which complements the DREB/CBF signaling pathway. MYB transcription factors can also assist other transcription factors in inducing the

expression of cold stress genes, thereby enhancing the plant's ability to withstand low temperature stress. *MdMYB308L* can interact with *MdbHLH33*, enhancing the binding ability of *MdCBF2* and *MdDFR* promoters, and improving the cold resistance of apple callus tissue (An *et al.*, 2020).

The MYB transcription factor family is a highly significant and extensive group of transcription factors. Table 1 presents the stress resistance function of various MYB families in different species. This paper not only summarizes the plants' response to drought, high salt, temperature, and heavy metals, but also examines the regulation and expression of these responses under ultraviolet and low nitrogen stresses. Through years of research on the MYB family, it is not only possible to predict the biological functions of unknown MYBs in different species based on the correlation between the structure and My transcription factors (MYB-TFs), but also to provide a theoretical basis for the breeding and improvement of plant varieties (Yu *et al.*, 2023).

Table 1. Research on the function of MYB family in resistance to stress

MYB genes	Functions in plant defense	Species	References
<i>OsFLP</i>	Drought/Salt tolerance	<i>Oryza sativa</i>	(Qu <i>et al.</i> , 2022; Zhang <i>et al.</i> , 2022)
<i>CgMYB1</i>	Low temperature tolerance	<i>Chenopodium</i>	(Zhou <i>et al.</i> , 2023)
<i>MYB68</i>	High temperature tolerance	<i>Arabidopsis thaliana</i>	(Feng <i>et al.</i> , 2004)
<i>GhMYB36</i> <i>GhODO1</i>	<i>Verticillium dahlia</i>	<i>Gossypium hirsutum</i>	(Liu <i>et al.</i> , 2022; Zhu <i>et al.</i> , 2022)
<i>MYB13</i>	Ultraviolet B tolerance	<i>Arabidopsis thaliana</i>	(Qian <i>et al.</i> , 2020)
<i>SiMYB3</i>	low nitrogen tolerance	<i>Setaria italica</i> L.	(Ge <i>et al.</i> , 2019)
<i>RsMYB1</i>	heavy metal ions tolerance	<i>Petunia</i>	(Ai <i>et al.</i> , 2018)
<i>MYB12</i>	Ultraviolet B tolerance	<i>Arabidopsis thaliana</i>	(Zhou, Windhorst <i>et al.</i> , 2023)
<i>GhBM</i>	Ultraviolet B tolerance	<i>G. barbadense</i>	(Abid <i>et al.</i> , 2023)
<i>Myb-7B</i> <i>Myb-7D</i>	Ultraviolet B tolerance	Wheat	(An <i>et al.</i> , 2023)
<i>MYBA1</i>	Ultraviolet B tolerance	Grapes	(Liu <i>et al.</i> , 2023)
<i>CmMYB42</i>	low nitrogen tolerance	<i>Chrysanthemum</i>	(Ma <i>et al.</i> , 2023)
<i>SiMYB30</i>	low nitrogen tolerance	<i>Setaria italica</i> L.	(Zhang <i>et al.</i> , 2023)
<i>MYB113</i> <i>MYB114</i>	low nitrogen tolerance	<i>Arabidopsis thaliana</i>	(Qin <i>et al.</i> , 2022)
<i>CsMYB21</i>	low nitrogen tolerance	Cucumber	(Wang <i>et al.</i> , 2018)

Conclusions

At the same time, the MYB transcription factor serves as a molecular link, integrating various resistance genes and defense signaling pathways, making it essential for plant disease resistance. The structure and defense function of MYB have been widely studied, including the interactions between different defense molecules and signals that help organisms cope with biological stress (Zhang *et al.*, 2023). Although MYB plays a crucial role in plant immunity, its specific molecular function remains unclear. Unlocking the potential molecular mechanism of MYB-mediated immune response is an important step in addressing plant biotic stress.

In addition, so far, although the expression of MYB can be induced by various signals, there are still many doubts about the regulation of these MYBs are regulated during the regulatory process. Meanwhile, due to the diverse functions of most MYBs, it is challenging to uncover the functions and regulatory mechanisms of specific members using traditional molecular biology methods. Therefore, it is crucial to conduct more in-depth research on MYB using new experimental techniques and methods.

Authors' Contributions

Both authors read and approved the final manuscript.

Ethical approval (for researches involving animals or humans)

Not applicable.

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Conflict of Interests

The authors declare that there are no conflicts of interest related to this article.

References

- Abe H, Yamaguchi-Shinozaki K, Urao T, Iwasaki T, Hosokawa D, Shinozaki K (1997). Role of *Arabidopsis* MYC and MYB homologs in drought- and abscisic acid-regulated gene expression. *Plant Cell* 9(10):1859-68. <http://doi.org/10.1105/tpc.9.10.1859>
- Abid MA, Zhou Q, Abbas M, He HY, Meng ZG, Wang Y, ... Liang CZ (2023). Natural variation in *Beauty Mark* is associated with UV-based geographical adaptation in *Gossypium* species. *BMC Biology* 21(1). <http://doi.org/10.1186/s12915-023-01591-5>
- Agarwal M, Hao Y, Kapoor A, Dong CH, Fujii H, Zheng X, Zhu JK (2006). A R2R3 type MYB transcription factor is involved in the cold regulation of CBF genes and in acquired freezing tolerance. *Journal of Biological Chemistry* 281(49):37636-37645. <http://doi.org/10.1074/jbc.M605895200>
- Ai TN, Naing AH, Yun BW, Lim SH, and Kim CK. (2018). Overexpression of *RsMYB1* enhances anthocyanin accumulation and heavy metal stress tolerance in transgenic *Petunia*. *Frontiers in Plant Science* 9:1388. <http://doi.org/10.3389/fpls.2018.01388>
- Ambawat S, Sharma P, Yadav NR, Yadav RC (2013). MYB transcription factor genes as regulators for plant responses: an overview. *Physiology and Molecular Biology of Plants* 19(3):307-321. <http://doi.org/10.1007/s12298-013-0179-1>
- An JP, Wang XF, Zhang XW, Xu HF, Bi SQ, You CX, Hao YJ (2020). An apple MYB transcription factor regulates cold tolerance and anthocyanin accumulation and undergoes MIEL1-mediated degradation. *Plant Biotechnology Journal* 18(2):337-353. <http://doi.org/10.1111/pbi.13201>
- An X, Zhao SQ, Luo XH, Chen CL, Liu TT, Li WL, ... Sun CD (2023). Genome-wide identification and expression analysis of the *regulator of chromosome condensation 1* gene family in wheat (*Triticum aestivum* L.). *Frontiers in Plant Science* 14. <http://doi.org/10.3389/fpls.2023.1124905>
- Aoyagi Luciano N, Lopes-Caitar Valéria S, de Carvalho Mayra CCG, Darben Luana M, Polizel-Podanosqui A, Kuwahara Marcia K, ... Marcelino-Guimarães FC (2014). Genomic and transcriptomic characterization of the transcription

- factor family R2R3-MYB in soybean and its involvement in the resistance responses to *Phakopsora pachyrhizi*. *Plant Science* 229:32-42. <http://doi.org/10.1016/j.plantsci.2014.08.005>
- Baldoni E, Genga A, Cominelli E (2015). Plant MYB Transcription factors: their role in drought response mechanisms. *International Journal of Molecular Sciences* 16(7):15811-15851. <http://doi.org/10.3390/ijms160715811>
- Butt H. I, Yang Z, Gong Q, Chen E, Wang X, Zhao G, ... Li F (2017). *GaMYB85*, an R2R3 MYB gene, in transgenic Arabidopsis plays an important role in drought tolerance. *BMC Plant Biology* 17(1):142. <http://doi.org/10.1186/s12870-017-1078-3>
- Chen Bo-Jun, Wang Yong, Hu Yuan-Lei, Wu Qi, Lin Zhong-Ping (2005). Cloning and characterization of a drought-inducible MYB gene from *Boea crassifolia*. *Plant Science* 168(2):493-500. <http://doi.org/10.1016/j.plantsci.2004.09.013>
- Chen Y, Chen Z, Kang J, Kang D, Gu H, Qin G (2013). *AtMYB14* regulates cold tolerance in Arabidopsis. *Plant Molecular Biology Report* 31(1):87-97. <http://doi.org/10.1007/s11105-012-0481-z>
- Chen YA, Feng PP, Zhang XW, Xie QL, Chen GP, Zhou S, Hu ZL (2022). Silencing of *SlMYB50* affects tolerance to drought and salt stress in tomato. *Plant Physiology and Biochemistry* 193:139-152. <http://doi.org/10.1016/j.plaphy.2022.10.026>
- Chen YH, Wu XM, Ling HQ, Yang WC (2006). Transgenic expression of *DwMYB2* impairs iron transport from root to shoot in Arabidopsis thaliana. *Cell Research* 16(10):830-840. <http://doi.org/10.1038/sj.cr.7310099>
- Ma D, Constabel CP (2019). MYB repressors as regulators of phenylpropanoid metabolism in plants. *Trends in Plant Science* 24(3):275-289. <http://doi.org/10.1016/j.tplants.2018.12.003>
- Deng M, Wang Y, Kuzma M, Chalifoux M, Tremblay L, Yang S, ... Wan J (2020). Activation tagging identifies Arabidopsis transcription factor AtMYB68 for heat and drought tolerance at yield determining reproductive stages. *The Plant Journal* 104(6):1535-1550. <http://doi.org/10.1111/tpj.15019>
- Pratyusha DS, Sarada DVL (2022). MYB transcription factors-master regulators of phenylpropanoid biosynthesis and diverse developmental and stress responses. *Plant Cell Reports* 41(12):2245-2260. <http://doi.org/10.1007/s00299-022-02927-1>
- Du H, Wang YB, Xie Y, Liang Z, Jiang SJ, Zhang SS, ... Tang YX (2013). Genome-wide identification and evolutionary and expression analyses of MYB-related genes in land plants. *DNA Research* 20(5):437-448. <http://doi.org/10.1093/dnares/dst021>
- Dubos C, Stracke R, Grotewold E, Weisshaar B, Martin C, Lepiniec L (2010). MYB transcription factors in *Arabidopsis*. *Trends in Plant Science* 15(10):573-581. <http://doi.org/10.1016/j.tplants.2010.06.005>
- El-Kereamy A, Bi YM, Ranathunge K, Beatty PH, Good AG, Rothstein SJ (2012). The rice R2R3-MYB transcription factor *OsMYB55* is involved in the tolerance to high temperature and modulates amino acid metabolism. *PLoS One* 7(12):e52030. <http://doi.org/10.1371/journal.pone.0052030>
- Fang Q, Jiang T, Xu L, Liu H, Mao H, Wang X, ... Luo K (2017). A salt-stress-regulator from the poplar R2R3 MYB family integrates the regulation of lateral root emergence and ABA signaling to mediate salt stress tolerance in Arabidopsis. *Plant Physiology and Biochemistry* 114:100-110. <http://doi.org/10.1016/j.plaphy.2017.02.018>
- Fang Q, Wang X, Wang H, Tang X, Liu C, Yin H, ... Luo K (2020). The poplar R2R3 MYB transcription factor *PtrMYB94* coordinates with abscisic acid signaling to improve drought tolerance in plants. *Tree Physiology* 40(1):46-59. <http://doi.org/10.1093/treephys/tpz113>
- Feng C, Andreasson E, Maslak A, Mock HP, Mattsson O, Mundy J (2004). *Arabidopsis MYB68* in development and responses to environmental cues. *Plant Science* 167(5):1099-1107. <http://doi.org/10.1016/j.plantsci.2004.06.014>
- Ge L, Dou Y, Li M, Qu P, He Z, Liu Y, ... Ma Y (2019). SiMYB3 in foxtail millet (*Setaria italica*) confers tolerance to low-nitrogen stress by regulating root growth in transgenic plants. *International Journal of Molecular Sciences* 20(22). <http://doi.org/10.3390/ijms20225741>
- Grotewold E, Drummond BJ, Bowen B, Peterson T (1994). The myb-homologous P gene controls phlobaphene pigmentation in maize floral organs by directly activating a flavonoid biosynthetic gene subset. *Cell* 76(3):543-553. [http://doi.org/10.1016/0092-8674\(94\)90117-1](http://doi.org/10.1016/0092-8674(94)90117-1)
- Gupta A, Rico-Medina A, Caño-Delgado AI (2020). The physiology of plant responses to drought. *Science* 368(6488):266-269. <http://doi.org/10.1126/science.aaz7614>

- Yan H, Pei X, Zhang H, Li X, Zhang X, Zhao M, ... Zhao X (2021). MYB-mediated regulation of anthocyanin biosynthesis. *International Journal of Molecular Sciences* 22(6). <http://doi.org/10.3390/ijms22063103>
- Haga N, Kato K, Murase M, Araki S, Kubo M, Demura T, ... Ito M (2007). R1R2R3-Myb proteins positively regulate cytokinesis through activation of KNOLLE transcription in *Arabidopsis thaliana*. *Development* 134(6):1101-1110. <http://doi.org/10.1242/dev.02801>
- Huang Y, Zhao H, Gao F, Yao P, Deng R, Li C, ... Wu Q (2018). A R2R3-MYB transcription factor gene, *FtMYB13*, from Tartary buckwheat improves salt/drought tolerance in *Arabidopsis*. *Plant Physiology and Biochemistry* 132:238-248. <http://doi.org/10.1016/j.plaphy.2018.09.012>
- Inukai S, Kock KH, Bulyk ML (2017). Transcription factor-DNA binding: beyond binding site motifs. *Current Opinion in Genetics & Development* 43:110-119. <http://doi.org/10.1016/j.gde.2017.02.007>
- Javed T, Shabbir R, Ali A, Afzal I, Zaheer U, Gao SJ (2020). Transcription factors in plant stress responses: challenges and potential for sugarcane improvement. *Plants-Basel* 9(4). <http://doi.org/10.3390/plants9040491>
- Jiao JIA, Xing JH, Dong JG, Han JM, Liu JS (2011). Functional Analysis of MYB73 of *Arabidopsis thaliana* Against *Bipolaris oryzae*. *Agricultural Sciences in China* 10(5):721-727. [http://doi.org/10.1016/S1671-2927\(11\)60055-2](http://doi.org/10.1016/S1671-2927(11)60055-2)
- Li J, Han G, Sun C, Sui N (2019). Research advances of MYB transcription factors in plant stress resistance and breeding. *Plant Signaling & Behavior* 14(8):1613131. <http://doi.org/10.1080/15592324.2019.1613131>
- Kim JH, Nguyen NH, Jeong CY, Nguyen NT, Hong SW, Lee H (2013). Loss of the R2R3 MYB, AtMyb73, causes hyper-induction of the *SOS1* and *SOS3* genes in response to high salinity in *Arabidopsis*. *Journal of Plant Physiology* 170(16):1461-1465. <http://doi.org/10.1016/j.jplph.2013.05.011>
- Kim SH, Lam PY, Lee MH, Jeon HS, Tobimatsu Y, Park OK (2020). The *Arabidopsis* R2R3 MYB transcription factor *MYB15* is a key regulator of lignin biosynthesis in effector-triggered immunity. *Frontiers in Plant Science* 11:583153. <http://doi.org/10.3389/fpls.2020.583153>
- Kranz HD, Denekamp M, Greco R, Jin H, Leyva A, Meissner RC, ... Weisshaar B (1998). Towards functional characterisation of the members of the R2R3-MYB gene family from *Arabidopsis thaliana*. *The Plant Journal* 16(2):263-276. <http://doi.org/10.1046/j.1365-313x.1998.00278.x>
- Liu L, Du H, Tang XF, Wu YM, Huang YB, Tang YX (2008). The roles of MYB transcription factors on plant defense responses and its molecular mechanism. *Yi Chuan* 30(10):1265-1271. <http://doi.org/10.3724/sp.j.1005.2008.01265>
- Li M, Lin L, Zhang Y, Sui N (2019). ZmMYB31, a R2R3-MYB transcription factor in maize, positively regulates the expression of CBF genes and enhances resistance to chilling and oxidative stress. *Molecular Biology Reports* 46(4):3937-3944. <http://doi.org/10.1007/s11033-019-04840-5>
- Li YM, Liang J, Zeng XZ, Guo H, Luo YW, Kear P, ... Zhu GT (2021). Genome-wide analysis of MYB gene family in potato provides insights into tissue-specific regulation of anthocyanin biosynthesis. *Horticultural Plant Journal* 7(2):129-141. <http://doi.org/10.1016/j.hpj.2020.12.001>
- Liao C, Zheng Y, Guo Y (2017). MYB30 transcription factor regulates oxidative and heat stress responses through ANNEXIN-mediated cytosolic calcium signaling in *Arabidopsis*. *New Phytologist* 216(1):163-77. <http://doi.org/10.1111/nph.14679>
- Liu GT, Wang JF, Cramer G, Dai ZW, Duan W, Xu HG, ... Li SH (2012). Transcriptomic analysis of grape (*Vitis vinifera* L.) leaves during and after recovery from heat stress. *BMC Plant Biology* 12:174. <http://doi.org/10.1186/1471-2229-12-174>
- Liu T, Chen T, Kan J, Yao Y, Guo D, Yang Y, ... Zhang B (2022). The GhMYB36 transcription factor confers resistance to biotic and abiotic stress by enhancing *PR1* gene expression in plants. *Plant Biotechnology Journal* 20(4):722-735. <http://doi.org/10.1111/pbi.13751>
- Liu WW, Mu HY, Yuan L, Li Y, Li YT, Li SC, ... Wang LJ (2023). VvBBX44 and VvMYBA1 form a regulatory feedback loop to balance anthocyanin biosynthesis in grape. *Horticulture Research* 10(10). <http://doi.org/10.1093/hr/uhad176>
- Liu Z, Luan Y, Li J, Yin Y (2016). Expression of a tomato MYB gene in transgenic tobacco increases resistance to *Fusarium oxysporum* and *Botrytis cinerea*. *European Journal of Plant Pathology* 144(3):607-617. <http://doi.org/10.1007/s10658-015-0799-0>

- Ma R, Yang S, Liu YH, Sun X, Wang WL, Zheng CS (2023). An R2R3-MYB transcription factor *CmMYB42* improves low-nitrogen stress tolerance in *Chrysanthemum*. *Journal of Plant Growth Regulation* 42(9):5600-5614. <http://doi.org/10.1007/s00344-023-10940-1>
- Mabuchi K, Maki H, Itaya T, Suzuki T, Nomoto M, Sakaoka S, ... Tsukagoshi H (2018). MYB30 links ROS signaling, root cell elongation, and plant immune responses. *Proceedings of the National Academy of Science USA* 115(20):E4710-e19. <http://doi.org/10.1073/pnas.1804233115>
- Matus JT, Aquea F, Arce-Johnson P (2008). Analysis of the grape *MYB R2R3* subfamily reveals expanded wine quality-related clades and conserved gene structure organization across *Vitis* and *Arabidopsis* genomes. *BMC Plant Biology* 8(1):83. <http://doi.org/10.1186/1471-2229-8-83>
- Meng X, Yu Y, Song T, Yu Y, Cui N, Ma Z, ... Fan H (2022). Transcriptome sequence analysis of the defense responses of resistant and susceptible cucumber strains to *Podospaera xanthii*. *Frontiers in Plant Science* 13:872218. <http://doi.org/10.3389/fpls.2022.872218>
- Muleke EMM, Yan WANG, Zhang WT, Liang XU, Ying JL, Karanja BK, ... Liu LW (2021). Genome-wide identification and expression profiling of MYB transcription factor genes in radish (*Raphanus sativus* L.). *Journal of Integrative Agriculture* 20(1):120-131. [http://doi.org/10.1016/S2095-3119\(20\)63308-1](http://doi.org/10.1016/S2095-3119(20)63308-1)
- Ogata K, Kanei-Ishii C, Sasaki M, Hatanaka H, Nagadoi A, Enari M, ... Sarai A (1996). The cavity in the hydrophobic core of Myb DNA-binding domain is reserved for DNA recognition and *trans*-activation. *Nature Structural Biology* 3(2):178-187. <http://doi.org/10.1038/nsb0296-178>
- Oh JE, Kwon Y, Kim JH, Noh H, Hong SW, Lee H (2011). A dual role for MYB60 in stomatal regulation and root growth of *Arabidopsis thaliana* under drought stress. *Plant Molecular Biology* 77(1):91-103. <http://doi.org/10.1007/s11103-011-9796-7>
- Park S, Lee CM, Doherty CJ, Gilmour SJ, Kim Y, Thomashow MF (2015). Regulation of the Arabidopsis CBF regulon by a complex low-temperature regulatory network. *Plant Journal* 82(2):193-207. <http://doi.org/10.1111/tpj.12796>
- Paz-Ares J, Ghosal D, Wienand U, Peterson PA, Saedler H (1987). The regulatory *c1* locus of *Zea mays* encodes a protein with homology to *myb* proto-oncogene products and with structural similarities to transcriptional activators. *Embo Journal* 6(12):3553-3558. <http://doi.org/10.1002/j.1460-2075.1987.tb02684.x>
- Qian C, Chen Z, Liu Q, Mao W, Chen Y, Tian W, ... Huang X (2020). Coordinated transcriptional regulation by the UV-B photoreceptor and multiple transcription factors for plant UV-B Responses. *Molecular Plant* 13(5):777-792. <http://doi.org/10.1016/j.molp.2020.02.015>
- Qin J, Zhao CZ, Wang SW, Gao N, Wang XX, Na XF, ... Bi YR (2022). PIF4-PAP1 interaction affects MYB-bHLH-WD40 complex formation and anthocyanin accumulation in *Arabidopsis*. *Journal of Plant Physiology* 268. <http://doi.org/10.1016/j.jplph.2021.153558>
- Qin Y, Wang M, Tian Y, He W, Han L, Xia G (2012). Over-expression of TaMYB33 encoding a novel wheat MYB transcription factor increases salt and drought tolerance in *Arabidopsis*. *Molecular Biology Reports* 39(6):7183-7192. <http://doi.org/10.1007/s11033-012-1550-y>
- Qiu Z, Yan S, Xia B, Jiang J, Yu B, Lei J, ... Cao B (2019). The eggplant transcription factor MYB44 enhances resistance to bacterial wilt by activating the expression of *spermidine synthase*. *Journal of Experimental Botany* 70(19):5343-5354. <http://doi.org/10.1093/jxb/erz259>
- Qu X, Zou J, Wang J, Yang K, Wang X, Le J (2022). A rice R2R3-Type MYB transcription factor OsFLP positively regulates drought stress response via OsNAC. *International Journal for Molecular Science* 23(11). <http://doi.org/10.3390/ijms23115873>
- Fuertes R, Malpica BL, Paz-Ares (1998). More than 80 *R2R3-MYB* regulatory genes in the genome of *Arabidopsis thaliana*. *The Plant Journal* 14(3):273-284. <http://doi.org/10.1046/j.1365-313x.1998.00113.x>
- Rosinski JA, Atchley WR (1998). Molecular evolution of the Myb family of transcription factors: evidence for polyphyletic origin. *Journal of Molecular Evolution* 46:74-83. <http://doi.org/10.1007/pl00006285>
- Rui M, Bowen L, Xi G, Xiao D, Na Y, Xia S, ... Chengshu Z (2022). Biological function and stress response mechanism of MYB transcription factor family genes. *Journal of Plant Growth Regulation* 42(1):83-95. <http://doi.org/10.1007/s00344-021-10557-2>
- Shan H, Chen S, Jiang J, Chen F, Chen Y, Gu C, ... Yang X (2012). Heterologous expression of the chrysanthemum R2R3-MYB transcription factor *CmMYB2* enhances drought and salinity tolerance, increases hypersensitivity to ABA

- and delays flowering in *Arabidopsis thaliana*. *Molecular Biotechnology* 51(2):160-173. <http://doi.org/10.1007/s12033-011-9451-1>
- Shan T, Rong W, Xu H, Du L, Liu X, Zhang Z (2016). The wheat R2R3-MYB transcription factor *TaRIM1* participates in resistance response against the pathogen *Rhizoctonia cerealis* infection through regulating defense genes. *Scientific Reports* 6:28777. <http://doi.org/10.1038/srep28777>
- Shimotohno A, Aki SS, Takahashi N, Umeda M (2021). Regulation of the Plant Cell Cycle in Response to Hormones and the Environment. *Annual Reviews in Plant Biology* 72:273-296. <http://doi.org/10.1146/annurev-arplant-080720-103739>
- Shen J, Xu X, Li T, Cao D, Han Z (2008). An MYB transcription factor from *Malus xiaojinensis* has a potential role in iron nutrition. *Journal of Integrative Plant Biology* 50(10):1300-1306. <http://doi.org/10.1111/j.1744-7909.2008.00761.x>
- Shen X, Guo X, Guo X, Zhao D, Zhao W, Chen J, Li T (2017). PacMYBA, a sweet cherry R2R3-MYB transcription factor, is a positive regulator of salt stress tolerance and pathogen resistance. *Plant Physiology and Biochemistry* 112:302-311. <http://doi.org/10.1016/j.plaphy.2017.01.015>
- Simeoni F, Skiryca A, Simoni L, Castorina G, de Souza LP, Fernie Alisdair R., ... Galbiati M (2022). The AtMYB60 transcription factor regulates stomatal opening by modulating oxylipin synthesis in guard cells. *Scientific Reports* 12(1):533. <http://doi.org/10.1038/s41598-021-04433-y>
- Su CF, Wang YC, Hsieh TH, Lu CA, Tseng TH, Yu SM (2010). A novel MYBS3-dependent pathway confers cold tolerance in rice. *Plant Physiology* 153(1):145-158. <http://doi.org/10.1104/pp.110.153015>
- Tian DQ, Pan XY, Yu YM, Wang WY, Zhang F, Ge YY, ... Liu XJ (2013). De novo characterization of the *Anthurium* transcriptome and analysis of its digital gene expression under cold stress. *BMC Genomics* 14(1):827. <http://doi.org/10.1186/1471-2164-14-827>
- Vailleau F, Daniel X, Tronchet M, Montillet JL, Triantaphylidès C, Roby D (2002). A R2R3-MYB gene, *AtMYB30*, acts as a positive regulator of the hypersensitive cell death program in plants in response to pathogen attack. *Proceedings of the National Academy of Sciences* 99(15):10179-10184. <http://doi.org/10.1073/pnas.152047199>
- Wang C, Wang JW, Tian CY, Fan LX, Wu T (2018). Cloning and functional analysis of low nitrogen tolerance related gene *CsMYB21* in cucumber. *Pakistan Journal of Botany* 50(1):29-34.
- Wang X, Niu Y, Zheng Y (2021a). Multiple functions of MYB transcription factors in abiotic stress responses. *International Journal of Molecular Sciences* 22(11). <http://doi.org/10.3390/ijms22116125>
- Wilkins O, Nahal H, Foong J, Provart NJ, Campbell MM (2009). Expansion and diversification of the *Populus* R2R3-MYB family of transcription factors. *Plant Physiology* 149(2):981-993. <http://doi.org/10.1104/pp.108.132795>
- Xiao S, Hu Q, Shen J, Liu S, Yang Z, Chen K, ... Zhu L (2021). GhMYB4 downregulates lignin biosynthesis and enhances cotton resistance to *Verticillium dahliae*. *Plant Cell Reports* 40(4):735-751. <http://doi.org/10.1007/s00299-021-02672-x>
- Yu EY, Kim SE, Kim JH, Ko JH, Cho MH, Chung IK (2000). Sequence-specific DNA Recognition by the Myb-like Domain of Plant Telomeric Protein *RTBP1*. *Journal of Biological Chemistry* 275(31):24208-24214. <http://doi.org/10.1074/jbc.m003250200>
- Yu Y, Zhang S, Yu Y, Cui N, Yu G, Zhao H, ... Fan H (2023). The pivotal role of MYB transcription factors in plant disease resistance. *Planta* 258(1):16. <http://doi.org/10.1007/s00425-023-04180-6>
- Zeng QY, Yang CY, Ma QB, Li XP, Dong WW, Nian H (2012). Identification of wild soybean miRNAs and their target genes responsive to aluminum stress. *BMC Plant Biology* 12:182. <http://doi.org/10.1186/1471-2229-12-182>
- Zhang C, Zhang J, Liu H, Qu X, Wang J, He Q, ... Le J (2022). Transcriptomic analysis reveals the role of FOURLIPS in response to salt stress in rice. *Plant Molecular Biology* 110(1-2):37-52. <http://doi.org/10.1007/s11103-022-01282-9>
- Zhang YL, Zhang CL, Wang GL, Wang YX, Qi CH, Zhao Q, ... Hao YJ (2019). The R2R3 MYB transcription factor MdMYB30 modulates plant resistance against pathogens by regulating cuticular wax biosynthesis. *BMC Plant Biology* 19(1):362. <http://doi.org/10.1186/s12870-019-1918-4>
- Zhang YS, Xu Y, Xing WT, Wu B, Huang DM, Ma FN, ... Song S (2023). Identification of the passion fruit (*Passiflora edulis* Sims) MYB family in fruit development and abiotic stress, and functional analysis of *PeMYB87* in abiotic stresses. *Frontiers in Plant Science* 14:1124351. <http://doi.org/10.3389/fpls.2023.1124351>

- Zhang YW, He Z, Qi X, Li MM, Liu J, Le S, ... Chen M (2023). Overexpression of MYB-like transcription factor *SiMYB30* from foxtail millet (*Setaria italica* L.) confers tolerance to low nitrogen stress in transgenic rice. *Plant Physiology and Biochemistry* 196:731-738. <http://doi.org/10.1016/j.plaphy.2023.02.025>
- Zhou Y, Zhu H, He S, Zhai H, Zhao N, Xing S, ... Liu Q (2019). A novel sweet potato transcription factor gene *IbMYB116* enhances drought tolerance in transgenic *Arabidopsis*. *Frontiers in Plant Science* 10:1025. <http://doi.org/10.3389/fpls.2019.01025>
- Zhou Z, Windhorst A, Schenke D, Cai DG (2023). RNAseq-based working model for transcriptional regulation of crosstalk between simultaneous abiotic UV-B and biotic stresses in plants. *Genes* 14(2). <http://doi.org/10.3390/genes14020240>
- Zhou Z, Wei X, Lan H (2023). *CgMYB1*, an R2R3-MYB transcription factor, can alleviate abiotic stress in an annual halophyte *Chenopodium glaucum*. *Plant Physiology and Biochemistry* 196:484-496. <http://doi.org/10.1016/j.plaphy.2023.01.055>
- Zhu Y, Hu X, Wang P, Wang H, Ge X, Li F, Hou Y (2022). *GhODO1*, an R2R3-type MYB transcription factor, positively regulates cotton resistance to *Verticillium dahliae* via the lignin biosynthesis and jasmonic acid signaling pathway. *International Journal of Biological Macromolecules* 201:580-591. <http://doi.org/10.1016/j.ijbiomac.2022.01.120>



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