



# ROLE OF MICRO RNA IN PLANT STRESS AND DEVELOPMENTAL PROCESSES: A REVIEW ARTICLE

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**Abstract:** Numerous issues are involved in the growth and development process of plants such as environmental stresses, pathogen attack, etc. which disrupts their normal life cycle. Due to all these disturbances, a decline in the agricultural yield has been seen. Micro RNAs are small non-coding, endogenous nucleotide belongs to the class of small RNA; which functions to regulate the gene at post-transcriptional level in the plant. They are stress bio-regulators which plays significant regulatory roles in the stress conditions and biological development of plant by reducing their workload. The study aims to identify the involvement of different miRNAs and their major targets in multiple abiotic stresses like salinity, drought, temperature, etc. and in several developmental processes including development of root, leaf, flower, fruit, phase transitions in plants, etc. By targeting their particular gene transcripts, miRNA plays their functional roles in several plants.

**Keywords-** MicroRNA, plant, stress, developmental processes, transcription factors, high throughput sequencing, post-transcriptional.

## I. INTRODUCTION

Ribonucleic-acids or RNAs are one of the most essential components of life which not only serves as mediators between protein and genes in the process of central dogma but also acts as regulators of life processes in direct way like in form of regulatory RNAs and ribozymes. The RNA is divided into two classes: coding RNAs and non-coding RNAs (You et al., 2017; Dong et al., 2022). Small ribonucleic-acids or sRNAs are generally 20-30 nucleotides long non-coding, low weight molecules, recognized as significant regulators in plants involved in various biological functions such as oxidation-reduction, transport process, transpiration and response to stress (Gao et al., 2012; Guleria et al., 2011; Liu et al., 2015; Lu et al., 2015; Jeyaraj et al., 2017; Huen et al., 2018; Jiang et al., 2020). In plant kingdom small RNAs are classified in miRNAs, piRNAs, tasiRNAs, siRNAs, etc. among which micro RNAs (miRNAs) is a more abundant major class (Ding et al., 2012; Guleria et al., 2011; Jeyaraj et al., 2017; You et al., 2017; Bao et al., 2018; Jiang et al., 2020).

Micro RNAs or mi RNAs are transcribed by the enzyme RNA polymerase type II which are a class of small endogenous 20-24 nucleotides long, non-coding RNAs found in eukaryotes; acts as silencing and regulating gene at transcriptional and post transcriptional level without majorly altering at mRNA level (Bertolini et al., 2012; Liu et al., 2014; Barciszewska-Pacak et al., 2015; Alptekin et al., 2016; Meena et al.,

2017; Wu et al., 2018; Chen et al., 2020; Samad et al., 2020; Campo et al., 2021; Meher et al., 2022; Xu et al., 2022). MicroRNAs are processed by Dicer-like protein (Dicer-like enzyme) from stem-loop sections of long primary transcripts in plants (Gao et al., 2012; Wu et al., 2014; Wei et al., 2015; Pirro et al., 2019). The genes for miRNA are usually found in the intergenic region. A number of miRNAs are clustered in genome, thus their biogenesis occurs in nucleus (Djami-Tchatchou et al., 2017). MicroRNAs present in plant cells, affects the gene expression level by showing complementary interaction with their specific mRNA sequences or targets and disrupts the process of transcription thus silences their mRNA target (Liu et al., 2020; Yang et al., 2021).

The regulation of gene by micro RNAs takes place in three different methods which involves: targeting mRNA degradation, translational repression and mRNA decay mediated by miRNA. The miRNA can bind to transcripts of genes which are targeted based on their pairing mechanism i.e., perfect or almost perfect which leads to the endo-nucleolytic cleavage-induced degradation of that mRNA or translational inhibition. The rate of translational inhibition is determined by the number of micro RNA binding sites on the target mRNA, more the sites for binding, more is the efficiency of translational repression (Ding et al., 2012; Guleria et al., 2011; Hou et al., 2017; Yadav et al., 2021; Yang et al., 2021). In plants, microRNAs are highly complementary to the target mRNA, they show cleavage as their major action mode (Dong et al., 2022). Micro RNAs bind to the complementary molecule of the messenger RNA (mRNA) and behaves as negative regulators to gene expression by means of translational repression or endo-nucleolytic cleavage of the similar mRNA targets (Aslam et al., 2020; Samad et al., 2020). When the pairing of target sequence and miRNA sequence is imperfect then translational repression without cleaving the mRNA occurs. The cleavage initiates removal of poly-A tail which leads to destabilization of target microRNAs and decay of mRNA (Guleria et al., 2011; Djami-Tchatchou et al., 2017; Lopez-Galiano et al., 2019).

The mature microRNA is responsible for mediating the sequence-specific and post-transcriptional repression of the mRNA targets (Wang and Guo, 2015). Heterosilencing is the term used for gene silencing mediated by the miRNA as the genes which are regulated by the miRNA and the gene which synthesizes the miRNA are both different. The RNAs from which micro RNAs are derived posses imperfect base paired hairpin like structure (Guleria et al., 2012; Chung et al., 2020; Jiang et al., 2020; Samad et al., 2020; Yang et al., 2021). Epigenetic modifications like methylation of histone and DNA for controlling their targets may also cause by the miRNAs (Li et al., 2019). Micro RNAs are believed to signify as an evolutionary primordial constituent of gene regulation because of their highly conserved sequences across the eukaryotes (Yang et al., 2021).

Micro RNAs are responsible for playing vital role in physiological as well as developmental processes. miRNAs plays key role in not only plant growth and development but also in environmental stress conditions, protein degradation, signal transduction, defense response and pathogen infection (Liu et al., 2014; Wang and Guo, 2015; Yuan et al., 2015; Li et al., 2017; Wang et al., 2017; Bao et al., 2018; Li et al., 2019; Dong et al., 2020; Sun et al., 2020; Campo et al., 2021; Yang et al., 2021; Xu et al., 2022; Xue et al., 2022).

## II. MICRO RNA REGULATION IN STRESS CONDITIONS

Any type of change in the environment or any external issue which is capable of generating a negative impact in plant's normal growth and development process is known as stress inducer (Sanz-Carbonell et al., 2019). Unfavorable climatic conditions are responsible in creating various stresses like temperature (hot and cold), salinity, drought, nutritional supplements, heavy metal toxicity, light, oxidative, biotic, etc. among the plants which declines the growth, development and agricultural yield, miRNAs plays significant regulatory roles in all these stresses (Bertolini et al., 2012; Tripathi et al., 2015; Alptekin et al., 2016; Meena et al., 2017; Franke et al., 2018; Chen et al., 2020; Dong et al., 2020; Jatan et al., 2020; Sharma et al., 2021; Gul et al., 2022; Meher et al., 2022). Among all these conditions; heat, cold, salinity and drought are the most studied abiotic stresses from which plants cannot easily escape due to their sessile nature (Tripathi et al., 2015).

There have been several stress-responsive microRNAs described in plants, which are exposed to abiotic (temperature, light, drought, etc.) and biotic stresses (viral, bacterial, fungal, etc.) both. Tissue, types of genotype and kind of stress are the factors upon which the miRNA response towards various stress is depended (Sanz-Carbonell et al., 2019; Meher et al., 2022). MiRNAs can be regarded as bio-regulators of stress which are responded by the plants as they are capable of regulating the expression of genes responsible for producing stress (Zhou et al., 2013; Meher et al., 2022). The gene expression is regulated by miRNAs which involves translational inhibition of the targets into proteins which further leads to repression. During stress conditions the expression of gene targets are directly altered or indirectly the expression of hormones or transcription factors can be targeted (Alptekin et al., 2016). At the time of stress conditions, increase in miRNA expression is responsible for de-regulating the negative regulators of the stress whereas decrease in the miRNA expression leads to accretion of the positive regulators of stress (Aslam et al., 2020). MiRNAs can be repressed or induced under the stress conditions (Guleria et al., 2011).

There have been extensive studies in the area of plant responses to salinity and drought stress as both of them shows many similarities and in order to understand the physiological and molecular mechanisms of the plant adaptation. In case of these stresses, plants experiences scarcity of water which alters their cell growth and photosynthesis and also induces the osmotic regulation in order to maintain the cell turgor and current water uptake whereas in salinity condition the concentrations of sodium and chlorine ion increases in the cells which leads to damage, turgidity and toxicity (Zhou et al., 2013; Yuan et al., 2015).

## 2.1 DROUGHT

Stress due to drought is one of the most important abiotic stresses which a plant faces, as the response due to this stress involves a complex signal transduction mechanism. The stress leads to decline in the crop production (Bakhshi et al., 2016). Insufficiency of water (drought) due to less rainfall negatively affects growth and development of the plant by modulating hormonal levels, nutrient uptake, photosynthesis, etc. which frequently results in dehydration of tissue (Tripathi et al., 2015). In rice, miR166 and miR169 were found to play significant role in the drought resistance, on the contrary in Arabidopsis; the miRNA was down-regulated by drought (Tripathi et al., 2015; Li et al., 2020). In stress due to drought, miR160 plays major role in the plant (Cheah et al., 2015). The drought tolerance response is down regulated by miR169 at post-transcriptional level by targeting NF-YA2 target, in Arabidopsis (Zhang et al., 2017). Several miRNAs like miR159, miR164, miR167, miR398 and miR408 respond to water scarcity (Ren et al., 2022).

## 2.2 TEMPERATURE (HEAT/COLD)

Temperature includes both cold and heat, is a severe stress which makes extreme and direct impact on the plants (Yadav et al., 2021). Heat or high temperature is responsible for changing the membrane fluidity, cellular state, organelle properties and composition of lipid. This stress is responsible for negatively affecting the plant growth and also flower development by reducing fertility and floral number (Tripathi et al., 2015; Yadav et al., 2021). Stress due to low temperature or cold includes both chilling and freezing cold shocks which reduces plant's metabolic rate, causes flower abortion and affects seed filling (Tripathi et al., 2015; Yadav et al., 2021). In case of stress due to cold, plants suffers from chlorosis, necrosis, reproductive issues, shows poor germination, wilting of leaves and early death (Aslam et al., 2020). At the time of stress due to temperature change the miRNAs acts as post-transcriptional regulators in various plants being directly involved in cold and heat stress adaptation (Alptekin et al., 2016). MiR156 plays crucial role in stress due to high temperature or heat while miR172 regulates certain genes such as AP2 and its expression under high temperature stress is considerably inhibited. Several miRNAs like miR398, miR396, miR393, miR159 and miR166 are also related with heat stress (Chen et al., 2020; Campos et al., 2023). Various miRNAs responsive to cold stress such as miR167, miR319 and miR1425 were identified and said to play significant role in modulating expression of the responsible or target genes during cold conditions (Djami-Tchatchou et al., 2017).

## 2.3 SALINITY

Salinity or salt stress is the most complicated among all abiotic stresses as in this condition both osmotic stress which is a kind of secondary stress and ionic actions are invoked which increases its toxicity (Parmar et al., 2020; Yadav et al., 2021). In plants, salt stress affects root elongation and height. Due to high salinity in rice, MiR169 was found to be stimulated (Tripathi et al., 2015).

## 2.4 NUTRIENTS

In plants, phosphate is very crucial inorganic nutrient which is necessary for the development of root and efficiency. MiR827 plays major role in homeostasis of P by targeting the expression of NLA, in Arabidopsis. Phosphate intake is enhanced in Arabidopsis by up-regulation of miR399 (Islam et al., 2022). In sulfate response miR395 and in response due to phosphate starvation, miR399 is involved (Tripathi et al., 2015; Chung et al., 2016).

## 2.5 MiRNA RESPONSE TO MULTIPLE STRESSES

Among all the members in miRNA family, miR319 and miR528 are known to respond to several stresses in different plants including cold, salt stress, drought, nitrate starvation and up-regulation by dehydration in maize, phalaenopsis orchid, rice, creeping bentgrass, Arabidopsis and sugarcane plant (Zhou et al., 2013; Yuan et al., 2015). Involvement of miR394 was found in response to salinity and drought stress (Goswami et al., 2020). In response to drought, nitrate availability and salinity stress, miR393 is the responsible microRNA (Cheah et al., 2015; Jatan et al., 2020). For maize, tomato and Medicago truncatula, miR169 responses to drought tolerance while the same microRNA in sugarcane responses to salinity stress tolerance. MiR156, miR167, miR169, miR172 and miR408 are responsible for cold stress in following plants: tea, rice and tomato while miR397 and miR820 controls heat stress or high temperature in rice (Gao et al., 2012; Djami-Tchatchou et al., 2017).

**Table 1: miRNAs involved in stress related processes**

miRNA	TARGET GENE	FUNCTION	PLANT SP.	REFERENCES
miR156	SBP/SPL, multicystatin gene, LTP, MYB	Drought, disease resistance, stress memory, heat stress tolerance	Barley, cowpea, peanut, switch grass, Arabidopsis	Djami-Tchatchou et al., 2017; Chen et al., 2019; Campos et al., 2023
miR159	ARF	Enhanced drought tolerance, drought stress	Cowpea	Djami-Tchatchou et al., 2017; Ren et al., 2022
miR160	-	Drought stress	Cowpea	Cheah et al., 2015; Djami-Tchatchou et al., 2017
miR164	NAC	Drought stress response, drought tolerance	Sugarcane, Cassava, Medicago	Gao et al., 2012; Djami-Tchatchou et al., 2017; Ren et al., 2022
miR166	PHABULOSA, Homeodomain containing protein4, LRR	Salinity stress, heavy metal stress, disease resistance, drought resistance, drought stress	Potato, Medicago, rice, cowpea, peanut, tobacco	Djami-Tchatchou et al., 2017; Goswami et al., 2020; Li et al., 2020; Yadav et

				al., 2021
miR167	ARF	Cold stress, drought stress, enhanced drought tolerance, defense against pathogen, stress response	Rice, cowpea, Arabidopsis	Djami-Tchatchou et al., 2017; Dong et al., 2022; Ren et al., 2022
miR169	NF-YA, ARF, HAP12-CCAAT-box transcription factor, NFY	Drought stress response, drought tolerance, cold/drought stress resistance, salt stress tolerance	Arabidopsis, Medicago, maize, tomato, sugarcane, sorghum, tobacco	Gao et al., 2012; Djami-Tchatchou et al., 2017; Zhang et al., 2017; Ren et al., 2022
miR172	AP2 family	Salt tolerance		Dong et al., 2022
miR319	-	Drought, salt, cold stress	Arabidopsis, maize, rice, potato, barley	Zhou et al., 2013
miR393	Auxin receptor gene (AFB), ARF, NY-YA, TIP, DBP, GRR-1 like protein	Drought response, cold/drought stress, salt stress, water scarcity, nitrate availability	Rice, tomato, coffee	Cheah et al., 2015; Djami-Tchatchou et al., 2017; Jatan et al., 2020
miR394	-	Salinity and drought stress		Goswami et al., 2020
miR395	SULTR 2, APS	Sulphate metabolism, sulphate starvation response	-	Meng et al., 2010; Tripathi et al., 2015; Chung et al., 2016
miR396	GRF	Drought and salinity	Arabidopsis	
miR397	L-ascorbate oxidase, ARF, NF-YA	Heat stress response, cold/drought stress response	Switch grass	Djami-Tchatchou et al., 2017
miR398	Serine/threonine kinase like gene	Salinity stress tolerance, drought stress	Rice, tomato	Djami-Tchatchou et al., 2017
miR399	UBC 24 enzyme, inorganic pyrophosphatase2, phosphatase transporter, PHO2	Phosphate deficiency, drought stress response, phosphate starvation response, P homeostasis, P signaling	Sugarcane	Djami-Tchatchou et al., 2017; Ren et al., 2022
miR408	Plastocyanin-like	Cold stress, drought stress	Arabidopsis, rice, sorghum, sugarcane, barley	Meng et al., 2010; Tripathi et al., 2015; Chung et al., 2016; Djami-Tchatchou et al., 2017; Tian et al., 2018
miR528			Tea plant	Djami-Tchatchou et al., 2017; Ren et al., 2022

	-	Salt and drought stress, low temperature response, N starvation	et al.,2022
miR820	DRM2	Maize, sugarcane, rice, creeping bentgrass	Yuan et al.,2015
miR827	NLA	High temperature, salinity response	Djami-Tchatchou et al., 2017
		P homeostasis	Islam et al., 2022
		Arabidopsis	

**Abb:** DBP- DNA binding protein; NLA- Nitrogen limitation adaptation; TIP- Transport inhibitor like-protein; miR- micro RNA

### III. MICRO RNA IN DEVELOPMENT OF DIFFERENT PARTS OF PLANT

Most of the plants possess more than 100 miRNA gene mainly located in the intergenic regions all over the genome (Rogersa and Chen, 2013). MiRNAs are said to play regulatory role in numerous plants and are significant for development of plant involving phase transition, pattern formation, cell differentiation, organ polarity, senescence, developmental timing, tissue differentiation, leaf morphogenesis, vegetative, root, floral, fruit and proper embryonic development. Several miRNAs plays several roles in different types of plants may acting as helpers in reducing the load of natural plant defense against pathogens (Guleria et al., 2011; Zhou et al., 2013; Wang and Guo, 2015; Tripathi et al., 2015; Hou et al., 2017; Bao et al., 2018; Chung et al., 2020; Dong et al., 2020; Jiang et al., 2020; Samad et al., 2020; Xue et al., 2022).

#### 3.1 INVOLVEMENT OF miRNAs IN NUMEROUS BIOLOGICAL PROCESSES

Single miRNA may involve in regulation of several aspects of growth and development of the plant by interacting with other target/miRNA or targeting dissimilar mRNAs like involvement of miR159 in leaf development, floral time control, determination of seed shape and size, respectively (Wang and Guo, 2015; Li et al., 2017; Campos et al., 2023). Involvement of miR390, miR160 and miR167 in embryo, root, seed, stem, floral organ and leaf development by targeting certain genes transcripts of Auxin Response Factor (ARF) (Liu et al., 2014; Wang and Guo, 2015; Li et al., 2017; Zhang et al., 2017; Lian et al., 2018; Dong et al., 2022).

In Arabidopsis, maize and other plants, regulation of growth phase transition or vegetative phase change (juvenile-adult) is done by miR156 by targeting SPL transcription factor and the same is also responsible for delay in flowering (Xie et al., 2012; Lin et al., 2013; Cheah et al., 2015; Wei et al., 2015; Zhang et al., 2015; Jeyaraj et al., 2017; Sun et al., 2018; Chung et al., 2020; Liu et al., 2020; Sun et al., 2021). The microRNA naming miR396 is responsible for negatively regulating the weight and size of tomato fruit and leaf cell proliferation in rice, Arabidopsis and Medicago (Zhang et al., 2017; Dong et al., 2022). MiR156 regulates various processes like development of root, leaf and fruit, embryonic pattern formation, anthocyanin biosynthesis and fertility process (Zhang et al., 2015; Sun et al., 2021).

#### 3.2 FLOWER DEVELOPMENT

Flowering is very essential process for any plant as it is related to the growth cycle. Various studies have shown the significant role of miRNA in flower development (Li et al., 2022). Several miRNAs have found to be concerned in various flowering stages of the plant along with their target genes (Ren et al., 2022). miR393 and miR172 responses to early flowering, high tillering, floral development and phase change in maize, barley, potato, rice and cotton (Djami-Tchatchou et al., 2017; Dong et al., 2022).

miR164 plays important role in initiation of organ from meristematic tissues and also down-regulates the responsible gene CUC (cup-shaped cotyledon) expression, during flower development post-transcriptionally in a plant called Arabidopsis, whereas miR156, miR159, miR172 and miR824 plays vital roles in floral transition through targeting certain transcripts and are also involved in flowering time regulation by age-

dependent pathway (Gao et al., 2012; Guleria et al., 2011; Niu et al., 2015; Wang and Guo, 2015; Zhang et al., 2015; Ge et al., 2016; Li et al., 2017; Silva et al., 2019; Hou et al., 2020; Sun et al., 2021; Yu et al., 2021; Dong et al., 2022; Li et al., 2022).

Flower development is influenced by several miRNAs by targeting their specific transcription factors like MiR159, miR167 and miR319 targets MYB33 (leads to delay in flowering), Auxin Response Factor (ARF) and TCP family, respectively (Ge et al., 2016; Li et al., 2022). In floral development of the plant, miR398, miR396, miR393, miR159 and miR166 are responsible for playing important role (Djami-Tchatchou et al., 2017; Carbone et al., 2019; Li et al., 2020; Campos et al., 2023). Identity of floral organ and flowering time is influenced by miR172 in Arabidopsis and other plants by AP2 and down regulation of TOE1 and TOE2, respectively, whereas in maize the miRNA is responsible for playing key role in maintenance of juvenility (Wu et al., 2014; Chung et al., 2016; Yang et al., 2016; Chung et al., 2020; Sun et al., 2020; Dong et al., 2022).

### 3.3 FRUIT DEVELOPMENT

Various miRNAs are involved in the development of fruit and maturation process in variety of fruits like melon, strawberry, papaya, pear, date palm, grape, peach, apple, pomegranate, tomato, banana, sweet orange, blueberry, etc. due to the high throughput sequencing technology in miRNA-related research (Hou et al., 2017; Zhang et al., 2017; Dong et al., 2020; Samad et al., 2020).

In tomato, miR172, miR156 and miR157 were revealed to control the process of ripening by targeting CNR which is a ripening regulator, likewise miR159, in strawberries, acts as a ripening regulator via targeting Fa-GAMYB which plays vital role in development to ripening of the strawberry (Karlova et al., 2013; Wu et al., 2014; Bi et al., 2015; Djami-Tchatchou et al., 2017; Hou et al., 2017; Zhang et al., 2017; Carbone et al., 2019; Chung et al., 2020).

MiR156, miR159, miR160, miR166, miR167, miR172 in peanut, tea, apple, potato, etc. controls plant growth and development and also fruit development in grapevine (Djami-Tchatchou et al., 2017; Tiwari et al., 2020). In tomato, fruit development is regulated by miR168 by targeting SLAGO1 gene (Liu et al., 2020).

### 3.4 ROOT DEVELOPMENT

Function of microRNAs related to root growth regulation has been studied in several plants like, Arabidopsis, banana, rice, maize, etc. (Goswami et al., 2020). MiR393 is responsible for suppressing root growth by targeting AFB3 in Arabidopsis plant and also play crucial role in regulation of lateral root growth, root development and root architecture (Li et al., 2017; Goswami et al., 2020; Jatan et al., 2020; Dong et al., 2022; Xue et al., 2022). miR160, miR164, miR167, and miR390 are the miRNA families which are involved in the formation of root cap, root tip and primary root growth and development of lateral root (Lin et al., 2013; Chung et al., 2016; Goswami et al., 2020).

MiR166 is involved in lateral root growth, vascular patterning of root, development of root and nodule by regulating the expression of specific transcription factor in several plants like soybean, Medicago, Arabidopsis, etc. (Jatan et al., 2020; Yadav et al., 2021; Dong et al., 2022). Root architecture is controlled by miR169 by targeting NF-YA2 (Zhang et al., 2017). Primary root growth is promoted by miR163 (Chung et al., 2016). miR395, miR398 and miR399 are involved in nutritional metabolism of roots (Lian et al., 2018). MiR164 and miR160 in barley, Arabidopsis, maize, rice, Medicago, tobacco, orange etc. is responsible for controlling lateral root and root development (Djami-Tchatchou et al., 2017; Yang et al., 2021; Dong et al., 2022).

### 3.5 LEAF DEVELOPMENT

Leaf growth begins from the peripheral region of the shoot apical meristem and later progresses in a 3-d manner (Zhang et al., 2018). MicroRNAs which regulate the development of leaf in Arabidopsis include miR159, miR164, miR165/166 and miR319. Leaf phenotype is maintained by miR159 which regulates MYB and miR319 which targets TCP transcription factors (Naqvi et al., 2010).

Development of leaf, leaf fate and morphogenesis is regulated by miR319 and miR165 by targeting the specific gene transcripts TCP family and HD-ZIP III genes, respectively (Wang and Guo, 2015; Zhang et al., 2017; Zhang et al., 2018; Yu et al., 2021; Dong et al., 2022). Senescence of leaf is promoted when there is a gradual decrease in miR164 (Xie et al., 2012). MiR156 plays important role in development of leaf by negatively regulating SPB or SPL (Squamosa promoter binding like protein) transcription factors in Arabidopsis and maize (Cheah et al., 2015; Dong et al., 2022).

MiR319 positively regulates the leaf senescence in Arabidopsis, bentgrass and tomato; by means of jasmonic acid biosynthesis pathway which results to less accretion of jasmonic acid thus delays the leaf senescence in the bentgrass, and also mediates leaf shape changes in the plant by targeting transcription factors TCP (Zhou et al., 2013; Gupta and Nath, 2015; Yuan et al., 2015; Li et al., 2017; Dong et al., 2022).

**Table 2: microRNAs involved in developmental processes of plant**

MiRNA	TARGET	FUNCTION	PLANT SP.	REFERENCES
miR156	SPB/SPL, MIKC gene, CNR	Promotes flowering, leaf, root, fruit development, embryonic pattern formation, juvenile-adult phase transition, anthocyanin biosynthesis, fertility process, flowering time regulation, floral transition, regulates fruit ripening in tomato	Arabidopsis, maize, tomato	Gao et al., 2012; Bi et al., 2015; Cheah et al., 2015; Wang and Guo, 2015; Zhang et al., 2015; Sun et al., 2018; Tian et al., 2018; Chung et al., 2020; Dong et al., 2022
miR157	CNR	Regulates fruit ripening	Tomato	Bi et al., 2015; Hou et al., 2017; Carbone et al., 2019
miR159	MYB	Seed, leaf, flower development, phase change (vegetative-reproductive), maintaining leaf phenotype, flowering time control, floral transition, receptacle development (strawberry)	Arabidopsis, grapevine, apple, strawberry	Naqvi et al., 2010; Wu et al., 2014; Wang and Guo, 2015; Djami-Tchatchou et al., 2017; Li et al., 2017; Hou et al., 2017; Carbone et al., 2019; Dong et al., 2022
miR160	ARF,NAC1, ASP gene	Leaf, root development, root cap formation, lateral root development, primary root growth, root architecture	Arabidopsis, Medicago, maize, potato, orange, sweet potato	Meng et al., 2010; Djami-Tchatchou et al., 2017; Li et al., 2017; Zhang et al., 2017; Dong et al., 2022
miR163	PXMT1	Primary root growth, flowering time regulation	-	Gao et al., 2012; Chung et al., 2016
miR164	NAC family, ARF	Leaf, flower development, lateral root development, root cap formation, leaf growth and differentiation	Arabidopsis, rice, maize, tobacco, barley, soybean, sweet potato	Xie et al., 2012; Djami-Tchatchou et al., 2017; Yu et al., 2021; Dong et al., 2022
miR165	HD-ZIP III	Lateral root growth, root absorption, leaf morphology, floral development	Arabidopsis, apple, soybean, orange	Djami-Tchatchou et al., 2017; Kouhi et al., 2020; Li et al., 2020; Dong et al., 2022



miR166	ARF, HD-ZIP III,	Seed development, lateral root growth, leaf, root development	Arabidopsis, Medicago, apple, soybean	Naqvi et al., 2010; Djami-Tchatchou et al., 2017; Jatan et al., 2020; Yadav et al., 2021; Dong et al., 2022
miR167	ARF	Lateral root development, leaf, root, stem, flower development, regulates flowering time, floral organ development	Arabidopsis, sweet potato, apple, rice	Lin et al., 2013; Wang and Guo, 2015; Djami-Tchatchou et al., 2017; Dong et al., 2022
miR168	SIAGO1	Fruit development, phase transition	Tomato	Liu et al., 2020
miR169	CBF, NF-YA family	Root architecture	Arabidopsis, maize	Zhang et al., 2017; Dong et al., 2022
miR171	SCL	Phase transition, flowering time	Arabidopsis, barley	Naqvi et al., 2010; Dong et al., 2022
miR172	AP2 family, SPL, MIKC	Flower opening, flower development, phase change, regulates flowering, fruit ripening (tomato), flowering time regulation, floral identity	Arabidopsis, maize, rice, potato, barley, cotton, tomato	Naqvi et al., 2010; Karlova et al., 2013; Niu et al., 2015; Djami-Tchatchou et al., 2017; Tian et al., 2018; Kouhi et al., 2020; Dong et al., 2022
miR173	ABI5	Receptacle development	Strawberry	Hou et al., 2017
miR319	MYB, TCP	Leaf development and senescence, phase change (vegetative-reproductive), leaf shape change,	Arabidopsis, tomato, grapevine, cotton, creeping bentgrass	Zhou et al., 2013; Yuan et al., 2015; Djami-Tchatchou et al., 2017; Li et al., 2017; Dong et al., 2022
miR390	TAS3, TAS3-ARF	Lateral root growth, root cap formation, root (in rice) and lateral root development, leaf morphology	Arabidopsis, tomato, rice	Meng et al., 2010; Lin et al., 2013; Djami-Tchatchou et al., 2017; Dong et al., 2022
miR393	TIR1, AFB	Lateral root growth, root development, root architecture	Arabidopsis	Li et al., 2017; Goswami et al., 2020; Dong et al., 2022, Xue et al., 2022
miR394	LCR		Arabidopsis	Dong et al., 2022
miR396	GRF, GIF	Leaf inclination and architecture	Medicago, Arabidopsis, barley, rice	Djami-Tchatchou et al., 2017; Yu et al., 2021; Dong et al., 2022
miR398	ARF, NAC	Cell proliferation in leaf, seed development, leaf growth and differentiation	Sweet potato	Gao et al., 2012; Djami-Tchatchou et al., 2017
miR399	PHO2	Root development, flowering time regulation	-	Meng et al., 2010
miR824	Agamous-like genes	Potential role in root development	Arabidopsis	Wang and Guo, 2015

## Floral transition

**Abb:** ASP- Auxin signal pathway, HD-ZIP- Homeodomain-leucine zipper, CNR- Colorless non- ripening, GRF- Growth regulating factor, GIF- GRF interacting factor, AP2- apetala2, SCL- Scarecrow-like, TAS- Trans-acting SIRNA, ARF- Auxin responsive factor, AFB- Auxin signaling F-box proteins, TIR- Transport inhibitor response, SPL- Squamosa-promoter binding protein like

#### IV. CONCLUSION

Growth and development of plant is very important for their life. Certain abiotic stresses affect the normal condition of the plant, represses its growth, weakens their natural defense mechanism, declines yield and may cause plant death. Micro RNA plays crucial role in plant's development and in stress conditions by regulating certain and specific gene transcription factors. There are several miRNAs which are involved in playing multiple roles in stress; like, miR319, miR393, miR394 and miR528 as well as biological development such as miR156, miR159, miR160, miR167 and miR390. Major target gene and families expressed are ARFs, TCPs, NF-YAs, SPL/SBP, MYBs, HD-ZIP, NAC family, etc. The review shows the microRNA action mechanism, their regulatory role in plants and impact in stress situations.

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