

Small RNAs of Horticultural Crops and their Functional Implications

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Plant small non-coding RNAs (ncRNAs) constitute an key player in gene regulation as an effector molecule of several biological aspects such as growth, development, metabolism, response to environmental stressors, maintenance of genome integrity etc. The three main small RNA players of importance are microRNAs (miRNAs), small interfering RNA (siRNAs) and phased siRNAs (phasiRNAs) (Yu et al., 2019). The diverse yet vital roles of plant small RNAs, especially miRNAs, in various developmental processes such as growth, stress response, temporal transitions, etc are delineated .

The repertoire of small RNAs in horticultural crops and its role in developmental functions and the mechanistic roles they orchestrate is discussed. Originally, the focus of research on small RNAs were in Arabidopsis, a model crop and later shifted to field and horticultural crops. Unraveling of genome sequences of many horticultural crops have greatly aided in this process of characterization of miRNAs. However, with the major jump in success of latest DNA sequencing technologies, the diversity and functional roles, including gene regulatory functions played by this small RNAs of horticultural crops have received a major focus (Fig. 1).

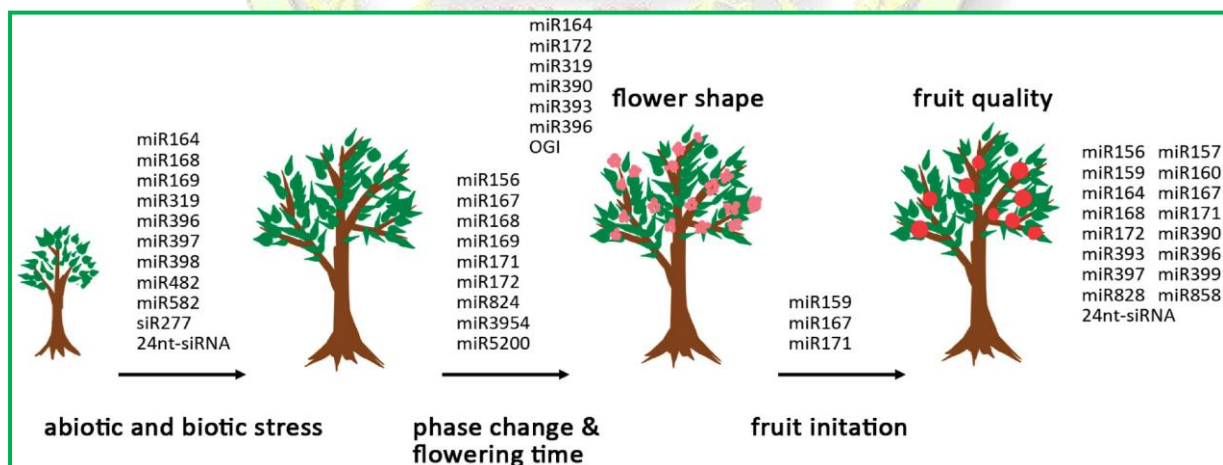


Fig. 1. Role of small RNAs in various developmental stages of horticultural crops (Adapted from Wang et al., 2020)

Small RNAs characterized in horticultural crops

Small RNAs have been characterized in horticultural crops like flower crops (Chrysanthemum); vegetables (tomato, *Brassica rapa* L. ssp. *Pekinensis*), fruits crops such as

apple, banana, citrus, pear, persimmon etc.. Analysis of miRNAs (micro RNAs) of diverse plant species suggests that conserved miRNAs such as miR156, miR162, miR164, miR166, and miR172 are found in horticultural species apple, kiwi fruit and pear (Guo et al., 2020). However, some miRNAs are specific to group of plants eg. miR528 which is a core regulator of reactive oxygen species (ROS) homeostasis is found in monocots.

On the other hand, PHAS-derived phasiRNAs, and tasiRNAs (TAS1 and TAS2) derived due to the activity of miR173 are specific to *Arabidopsis*. Similarly, miR390 and miR828 are known to cleave TAS3 and TAS4, respectively to yield ARF-tasiRNAs, which is involved in flower and fruit development and MYB-tasiRNAs controlling the secondary metabolite synthetic pathway namely phenylpropanoid pathway with profound implications for novel horticultural and consumer traits such as flavor, pigmentation, and texture. In citrus a species-specific miR3954 is involved in the generation of phasiRNAs that has serious implications for flowering time (Liu et al., 2017). Functional role of the miRNAs in horticultural crops is briefed in Table 1.

Table 1. Functional role of miRNAs characterized in horticultural crops

Crop	miRNA	Target transcripts	Developmental role(s)
Apple	miR172	AP2	Fruit size reduction
	miR169a, mir160e, miR167bg,	ARF TFs	Resistance to fire blight disease
	mdm-siR277-1 and mdm-siR277-2 (siRNAs) produced from MdhprRNA277	5 R-genes	Leaf spot resistance
Banana	miR 397 miR 171	HSP 70 HSP 90	Thermo tolerance
	miR528	Polyphenol oxidase	ROS metabolism regulation
	mac-novmiR20	ARF	fruit development and ripening
<i>Citrus sinensis</i>	miR3954	NAC TF and non-coding RNA transcripts (lncRNAs, Cs1 g 09600 and Cs1 g 09635)	Regulation of flowering
Grape vine	miR159, miR319	MYB TF	Vegetative to reproductive phase transition and stress responsive
	miRNA159 (VvmiR159a, VvmiR159b, Vv miR159c)	GAMYBTF	Flowering, seedless grapes development
Kiwi fruit	miR164	AdNAC6 and AdNAC7	Fruit development
<i>Prunus persica</i> (peach) and Rose	miR172	AP2-type ortholog in rosaceae TARGET OF EAT (TOE)	Commercially valued double flowers development
<i>Pyrus bretschneideri</i>	Pbr-miR397a	laccase (LAC)	Reduced lignin and stone cell number in fruit
Radish	494 known miRNAs and 220 novel miRNAs	-	Development of tap roots
Tomato	miR157	LeSPL-CNR	Fruit ripening
	miR172	AP2a	Altered fruit shape, carotenoid accumulation and

			orange ripe fruits
	miR858	SIMYB7-like and SIMYB48-like	Regulation of anthocyanin biosynthesis
	miR390	SIARF2A and SIARF2B	Affects fruit ripening
	miR159	SIGAMYB1/2	Affects fruit set
	miR482	NBS-LRRs	Resistance to <i>P. infestans</i>
	miR1917	SICTR4 splice variants (SICTR4sv)	Ethylene biosynthesis
Strawberry	24-nt siRNA	DNA methylation via RdDM pathway	Fruit ripening
	miR172	RAP1	Tuberization
Potato	miR156	StSPL3, StSPL6, StSPL9, StSPL13, and StLIGULELESS 1	Regulation of potato development
	miR475	Thioredoxin	
	miR160	StARF10	SAR against <i>Phytophthora infestans</i>
	miR156, miR162	SPL TF	Storage root initiation and development
Sweet potato	190 known microRNAs (miRNAs) and 191 novel miRNAs	-	Chilling stress tolerance
	ib-miR156	SPL TF	Anthocyanin biosynthesis
	IbmiR162	IbDCL1	Chilling and heat stress response
Cassava	miR156, miR157, miR159, miR160, miR414, mir473	Multiple TFs	Stress and development responses
	mir172, miR319, miR395, miR396, miR397	Multiple TFs and growth factors	Starch metabolism
Tea	CsmiR156	SPL	Regulation of catechins biosynthesis
	miR7814	<i>CHS1</i>	
	miR5264	<i>ANR2</i>	
	mir2673	TFs	Auxin signaling
Coconut	miR156, miR164, miR166, miR167,	transcript of squamosa promoter binding-like protein, allene oxide synthase	<i>In vitro</i> embryogenesis
Coffee	16 miRNAs (<i>C. arabica</i>) and 20 (<i>C. canephora</i>)	-	Hormonal and stress responses

Conclusion

The widespread occurrence of sRNAs in most developmental processes of food crop growth indicates their role as crucial regulators of agricultural traits. Small RNAs are involved in suppression of target gene expression and also in regulating complex gene regulatory mechanisms. Small RNAs broadens their biological significance and offer novel tools for modifying agriculturally important traits.

References

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