1 **Discovery of Drought-Responsive Transposable Element-Related Peach miRNAs**

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11 **Running Title:** Transposable Element Related Peach miRNAs

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16 **ABSTRACT**

17 MicroRNAs (miRNA) are small non-coding regulatory RNAs that suppress their specific
 18 target transcripts either by cleavage or inhibition of translation. Transposable element related
 19 miRNAs (TE-miRNA) have been subjected to various studies so far, and some of them were
 20 found to be involved in stress response in plants. Here, small RNA (sRNA) sequencing
 21 libraries generated from drought stress treated peach tissues were utilized to identify TE-
 22 miRNAs. Our computational analysis led to the identification of 63 TE-miRNAs, which were
 23 either locating nearby of any TE (TE-related), or overlapping with a TE (TE-derived).
 24 Furthermore, 13 out of 63 TE-miRNAs were designated as drought-responsive. Expression
 25 pattern of the identified drought-responsive TE-miRNAs are observed as tissue-specific
 26 manner, and their specific target transcripts are mostly related to transcription factors and
 27 growth-associated genes. Our findings suggest that miRNAs in relation with transposable
 28 elements might be key molecular players in the regulation of drought response.

29 **Keywords:** microRNA, repetitive element, TE-miRNA, drought, *Prunus persica*.

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31 INTRODUCTION

32 Transposable elements (TE) are DNA fragments that can move from one position to another
 33 in the host genomes, and they constitute the majority of plant genome (.Deragon et al. 2008).
 34 TEs are divided into two groups in plants, each group includes autonomous and non-
 35 autonomous elements (.Kejnovsky et al. 2012). Class I elements, retrotransposons, ‘copy and
 36 paste’ themselves by reverse transcription. The members of this group are LTR (Long
 37 Terminal Repeat), LINEs (Long Interspersed Elements) and SINEs (Short Interspersed
 38 Elements). LTR type retrotransposons include *copia* and *gypsy* groups, TRIM (Terminal-
 39 repeat Retrotransposons in Miniature) and LARD (Large Retrotransposon Derivatives)
 40 families (.Deragon, Casacuberta and Panaud 2008, Kejnovsky, Hawkins and Feschotte 2012).
 41 Class II elements ‘cut and paste’ themselves by excising from the chromosome and relocating
 42 at a new position. MITEs (Miniature inverted-repeat transposable elements) are the most
 43 common types of class II non-autonomous elements including TIR (Terminal inverted
 44 repeats) and Helitrons (.Lisch 2013, Wicker et al. 2007).

45 TEs play crucial roles in plant genome evolution by activating-deactivating or duplicating
 46 genes or creating entirely new ones because of their mutagenic potential. (.Bennetzen and
 47 Wang 2014). Movement of transposable elements can also leads to evolution of plant miRNA
 48 encoding genes (.Piriyapongsa and Jordan 2008). It was found that various number of miRNA
 49 genes were mobilized by transposable elements in grass genome (.Abrouk et al. 2012). The
 50 previous reports also demonstrated the association between miRNA gene evolution and TEs
 51 in *Arabidopsis thaliana* (.Maher et al. 2006, Piriyapongsa and Jordan 2008, Santiago et al.
 52 2002).

53 MiRNAs are small (19-24 nt long), endogenously expressed non-coding RNAs which
 54 negatively regulate gene expression at post-transcriptional level (.Eldem et al. 2013). Besides
 55 their roles in plant development (.Mallory et al. 2005, Mallory et al. 2004, Palatnik et al.
 56 2003), miRNAs play important roles in stress responses such as drought (.Qin et al. 2011).

As one of the major abiotic factors, drought or water deprivation limits plant growth, crop yield, and quality (.Zhang 2015). The functional regulatory roles of miRNAs in drought stress response were reported in a number of studies conducted on model organisms such as barley (*Hordeum vulgare*) (.Kantar et al. 2010) wheat (*Triticum aestivum*) (.Akdogan et al. 2016), cotton (*Gossypium hirsutum*) (.Xie et al. 2015), switchgrass (*Panicum virgatum*) (.Xie et al. 2014), tobacco (*Nicotiana tabacum*) (.Frazier et al. 2011) and rice (*Oryza sativa*) (.Zhao et al. 2007). Functional studies with miR408 in chickpea (*Cicer arietinum*) (.Hajyzadeh et al. 2015), miR169 in tomato (*Solanum lycopersicum*) (.Zhang et al. 2011) and miR319 in creeping bent grass (*Agrostis stolonifera*) (.Zhou et al. 2013) proved the role of miRNAs in drought regulation TE-related miRNAs have been subjected to several studies so far. All the miRNAs located on repetitive elements in four plant species (*A. thaliana*, *Populus trichocarpa*, *O. sativa*, and *Sorghum bicolor*) were revealed in a previous report by Sun et al. (2012) (.Sun et al. 2012). In another study, TE-miRNAs in rice genome were discovered, and the question how the transposable elements are domesticated into new miRNA genes, was elucidated (.Li et al. 2011). Yongsheng, et al. (2011) identified two short-interfering RNAs (siRNA) as repetitive element derived and found out that these two small RNAs regulate abscisic acid signaling and abiotic stress response positively (.Yan et al. 2011). Therefore, TE-miRNA and drought stress response regulation in plants is one of the novel biological perspectives to be deeply analyzed for further translational applications.

Our group previously introduced drought-responsive set of miRNA sequences and their measurement at genome-wide in peach (*P. persica*) by high-throughput sequencing of control and drought tissues (.Eldem et al. 2012). In this study, we aimed to annotate TE-derived and TE-related peach miRNAs from the previously generated sRNA deep-sequencing libraries, and to identify drought-responsive ones among all TE-derived and TE-related miRNAs.

82 MATERIALS AND METHOD

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84 miRNA identification

85 In this study, sRNA libraries generated in our previous study (.Eldem, Celikkol Akcay,
86 Ozhuner, Bakir, Uranbey and Unver 2012) were utilized to identify TE-related miRNAs. Our
87 sRNA dataset were consisting of four libraries generated from (i) roots of control sample
88 (RC), (ii) roots of drought applied sample (RS), (iii) leaves of control sample (LC), and (iv)
89 leaves of drought applied sample (LS). To identify and count the miRNAs in the libraries, *P.*
90 *persica* genome (assembly: Prupe1_0) in multi-fasta format were downloaded from Ensembl
91 Plants database v31 (<http://plants.ensembl.org>) (.Kersey et al. 2016). Furthermore, *P. persica*
92 mature miRNA sequences was extracted as General Feature Format (GFF) file from miRBase
93 release 21 (<http://www.mirbase.org/>) (.Kozomara and Griffiths-Jones 2014), and our sRNA
94 libraries in fasta format were analyzed using miRDeep2 v2.0.0.7 (.Friedländer et al. 2012)
95 with default parameters. The count values of the identified peach miRNAs were obtained as
96 count per million (CPM) values. In order to detect differentially expressed miRNAs in control
97 and stress libraries, we calculated fold change for each miRNA, and miRNAs with differential
98 expression values ≥ 2 fold-changes we considered as drought responsive.

99 Annotation of TE-derived and TE-related miRNAs

100 To determine genomic locations of the miRNAs identified by miRDeep2, we utilized BLAST
101 tool v2.5.0. Known precursor-miRNA (pre-miRNA) sequences provided in miRDeep2 output
102 were scanned within the peach genome using BLAST tool, and genomic location(s) of each
103 pre-miRNA were determined. Afterwards, TE annotation, available at Ensembl Plants
104 database, were downloaded, and examined whether TEs were co-located or overlapping with
105 Bedtools v2.25.0 (.Quinlan 2014). We considered miRNA sequence as TE-related, if the
106 distance between miRNA and TE was less than 1 kb. If miRNA sequence was overlapping
107 $>50\%$ with any TE, it was classified as TE-derived.

Target transcript prediction and gene ontology analysis

The target transcripts of TE-derived and TE-related miRNAs were predicted by an online miRNA target analysis tool; psRNATarget (<http://plantgrn.noble.org/psRNATarget/>) (Dai and Zhao 2011). All TE-derived and TE-related miRNA sequences were uploaded to psRNATarget web server, and their potential targets were extracted. In order to identify the functional annotation of the targets, Gene Ontology (GO) analysis of the target transcripts was performed with Blast2GO tool (Conesa et al. 2005). The target transcript sequences were loaded to the tool in fasta format. BlastX search was done with a parameter of e value as 1e-10. Then, GO terms of each Blast hit were obtained and these terms were categorized in three GO categories: (i) cellular component, (ii) molecular function, and (iii) biological process. The schematic representation of the methodology is shown in Figure 1.

RESULTS

A total of 214 known miRNAs and 17 novel miRNAs were detected in *P. persica* genome by miRDeep2. Among the identified peach miRNAs that were found in at least one of the libraries, 63 miRNAs were defined as TE-miRNA (either TE-derived or TE-related) by the localization analysis. One of these miRNAs, ppe-MIR6284, was named as TE-derived miRNA. Seventy-two out of 97 nucleotide of this miRNA is in the repeat region named; LTR_Sl_chr_06_1092 according to Ensembl annotation (Figure 2).

A total of 62 miRNAs was detected as TE-related and 58 of them were previously annotated known mRNAs such as miR166, miR171, miR172, miR399, and miR482. Besides, 4 of the 17 novel miRNAs were detected as TE-related (Supplementary Table 1). Most of TE-related miRNAs are in the window with more than one transposable element. We also identified 7 TE-related pre-miRNAs that were not detected in any of four sRNA sequencing libraries; MIR399a, MIR6267c, MIR6288c, MIR6291b, MIR6296, MIR7122a, and MIR828.

The comparative expression measurement analysis indicated that 58 of TE-related miRNAs were not differentially regulated in response to drought (Figure 3). Twelve of TE-related and one TE-derived miRNAs were detected as drought responsive with their differential expression pattern compared to stress treated versus control samples. Following TE-related miRNAs are reported as drought responsive; miR160b, miR162, miR167c, miR169g, miR169l, miR172a-5p, miR172d, miR5225-5p, miR6266a, miR6288c-3p, miR8123-5p, miR827 and miR6284 (Table1). The expression values of miR6284, which is a drought responsive TE-derived miRNA, suppressed in leaves and up-regulated in roots with the fold changes of -2.52 (LC vs LS) and 2.36 (RC vs RS), respectively. The expression levels of most drought responsive TE-related miRNAs have changed in roots rather than leaves. Among them, the expression levels of miR169g and miR169l are seem to be changed in response to drought in roots, the former is related with an LTR, the latter is with a GA repeat. Fold change

of miR162 is significant in roots, and miR6266a has differentially expressed both in leaves and roots.

A total of 346 target transcripts regulated by TE-miRNAs were predicted by psRNAtarget tool (Supplementary Table 2). These were subjected to functional annotation with B2GO resulting a total of 564 GO terms (Supplementary Table 3). Biological process of target transcripts, regulated by TE-miRNAs, is mainly regulation of transcription (Supplementary Table 3). Fifty-five of total 355 biological process hits are relevant to regulation of transcription. Oxidation-reduction process, auxin signaling pathway, phosphorylation, translation and response to stimuli are the other mostly represented processes. Response to stimuli includes; abscisic acid, auxin, oxidative stress, salt stress, water deprivation, osmotic stress responses. In the case of molecular function, the targets generally role in binding, mostly DNA and RNA binding, 62 hits were found as either DNA or RNA binding. Hydrolase and transferase activities, ion binding and kinase activity are also prevalent in total 418 molecular function hits. Membrane, chloroplast and nucleus are the most common locations of the targets. Among all targets, maximum number of GO terms is hit to the sequence DW345250, histidine kinase 1, a target of miR482-5p (Supplementary Table 2). Some of the hits are related with biological process, response to osmotic stress, water deprivation, and seed maturation. As molecular function, the hits are, osmosensor and kinase activity. The target transcripts of drought responsive TE-miRNAs are related with transcription, translation, plant development, auxin and abscisic acid signaling pathways and cell division mostly, in terms of biological process (Supplementary Table 3).

DISCUSSION

In this study we revealed a total 63 TE-miRNAs (either TE-derived or TE-related) in *P. persica* genome, and analyzed their tissue-specific expression pattern in response to drought. We identified *PpeMIR6284* as a TE-derived miRNA gene since a considerable part of (74%) gene sequence is located in the long terminal repeat of a retrotransposon. This finding suggests that, while this retrotransposon translocates by a copy-paste mechanism, it might possibly carry the precursor of miR6284 within the transposon itself.

LTRs are one of the most common types of TEs, which are potentially located in the 1 kb region of TE-related miRNAs. The LTRs or any other TEs co-located with miRNA genes in a 1 kb region, might aid these miRNA genes to move while jumping from one location to the other in the genome. Some members of miR166, miR171, miR172, miR399, miR482 families were detected in the 1 kb region of TEs, thus it might denote that, these families have been affected from translocating events of TEs nearby.

The expression of TE-derived miR6284 in leaves was detected as suppressed 2.5 fold whereas it was upregulated nearly 2.4 fold in root upon drought (Figure 3). Tissue-specific differential regulation of the TE-derived miR6284 was observed in response to drought. Additionally, we discovered that, the expression level of many of the drought responsive TE-miRNAs ($FC > 1.5$) were differentially regulated only in roots. For miR169l, as an example, the root fold change is -3.2 but there is no significant change in the leaf tissue. Only two TE-miRNAs (miR6266a and miR160b) were regulated in leaf with fold changes of -1.7 and 1.6 respectively. On the other hand, 7 of the predicted TE-related miRNA precursor transcripts (MIR399a, MIR6267c, MIR6288c, MIR6291b, MIR6296, MIR7122a and MIR828) were found to be undifferentiated upon drought treatment.

Blast2GO results indicated that most of the TE-miRNA target transcripts are functionally related with transcription mechanism in terms of biological process, and DNA or RNA and

binding as molecular function (Supplementary Table 3). Therefore it can be deduced that; TE-related miRNAs target generally transcription factors. Auxin related processes are also common among the GO terms of target transcripts. Since, it is a plant growth hormone involved in developmental, it can also regulate transcription (.Perrot-Rechenmann 2014). Some of the target transcripts found to be related to developmental processes and cell growth independent of auxin implying that, TE-related miRNAs in peach might target the mRNAs of the genes to regulate the growth and development. TE-miRNAs might also control the process of response to various stimuli including osmotic stress, water deprivation and oxidative stress by targeting the transcripts associate with these mechanisms. Expression analysis and GO outputs indicated that drought responsive TE-related miRNAs might regulate stress tolerance by targeting the genes encoding transcription factors and proteins to control plant development either auxin dependent or independent in tissue specific manner.

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294 **Figure legends;**

295 Figure 1. Flowchart representation of methodology. Blue rectangles represent tools, green
296 ellipses are data used in tools as inputs.

297 Figure 2. 74 nucleotides of overlapping of MIR6284 with the LTR in chromosome 8, plus
298 strand. Blue and orange blocks represent LTR_SI_chr_06_1092 and ppe-MIR6284
299 respectively. The LTR begins at 20,947,395th nucleotide and ends at 20,948,172th nucleotides.
300 ppe-MIR6284 gene is located in between 20,948,100th and 20,948,196th nucleotides of
301 chromosome 8.

302 Figure 3. Heat map of TE-related miRNAs. Drought-responsive TE-miRNAs, which were
303 differentially expressed in root and leaf upon, stress treatment represented.

304 **Supplementary materials;**

305 Supplementary table 1. TE-related miRNAs & TEs in 1kb window

306 Supplementary table 2. TE-miRNA targets

307 Supplementary table 3. Blast2GO table

308 Supplementary table 4. Blast2GO table of the target transcripts of drought responsive TE-
309 miRNAs

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Table 1. Drought responsive TE-miRNAs and their fold changes in four sRNA libraries. FC; Fold Change, LC; Leaf-control, LS; Leaf-stress, RC; Root-control, RS; Root-stress. miR6284, which is written in red, is TE-derived, others are TE-related.

miRNA	FC LC vs LS	FC RC vs RS	Related transposable element
miR160b	1,65	-1,22	(TGGA)n, LTR_Gm_17_5361, (CATATA)n, Bd1_RLC_72
miR162	0,25	-2,96	LTR_Sb_chr_02_1099
miR167c	0,07	-2,35	LTR_AC195581.3_5451, LTR_SI_chr_11_2076, LTR_Gm_14_4344, trep4247
miR169g	0,28	-2,80	LTR_AC187047.4_14371
miR169l	0,23	-3,22	(GA)n
miR172a-5p	0,06	-1,63	trep4247, trep4410, LTR_AC185219.3_1390, trep4410
miR172d	1,06	1,95	RLC_Barbara_3B_045_E05-1, LTR_Sb1_00020_929, trep4411
miR5225-5p	0,06	3,45	LTR_SI_chr_00_49
miR6266a	-1,75	3,69	DTC_unnamedfam16_3B_079_D10-1, LTR_Gm_07_2481, (TG)n, trep3525
miR6284	-2,52	2,37	LTR_SI_chr_06_1092
miR6288c-3p	-0,75	2,48	LTR_SI_chr_05_1081
miR8123-5p	-0,26	-1,63	LTR_Gm_09_3151
miR827	-0,52	-2,44	LTR_Sb_chr_06_655, Gypsy-3_Pru-LTR

Long Terminal Repeat

MIR6241