

# In Silico screening of Putative miRNAs and their Targets from a Common Mangrove *Bruguiera gymnorrhiza*



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## Abstract

Micro RNAs, the non-coding single stranded molecules with 18-22 nucleotide sequences, have established its enormous involvement in biological processes including stress response. As the mangrove species restoration program are being conducted world-wide for their protecting and producing nature, investigation on miRNA would be a significant approach towards understanding the small RNA mediated gene regulation leading to plant adaptation. But insufficient molecular data of salt responsive genes and miRNAs have triggered to the present work which might enrich knowledge on adaptability with the rapid salinization of the habitat. The present work elucidate that the target genes for the two miRNAs bg-miR1029 and bg-miR5021 in *Bruguiera gymnorrhiza* are involved in major stress response characteristics. Experimental validation and characterization of these two miRNAs and their predicted target genes along the salinity gradient is yet to be validated.

**Keywords:** *Bruguiera gymnorrhiza*; miRNA; miRNA target; RNA secondary structure; Salt response

## Introduction

Micro RNAs are small (~22 nt), single-stranded, and non-coding RNA molecules. The RNA Pol II mediates the transcription of capped and polyadenylated miRNA precursors (pri-miRNA). Mature miRNAs regulate a wide array of biological processes like development, metabolism, stress response, pathogen defense etc. [1,2]. Its mode of action involves its integration into the RNA-induced silencing complex (RISC) [3], which controls gene expression by hindering translation or by corrupting coding mRNAs through complementing with the target mRNAs [4,5]. More precisely, miRNAs cleave the target genes to prevent gene expression in plants [6]. Several recent findings are in congruence with the fact that miRNAs have significant role on the plant adaptability to salt stress [7-10].

Mangrove is a specialized group of plant community, growing in the coastal estuarine environments of the tropical and subtropical world, thrive under constant abiotic extremities [11]. They provide the coastal ecology with the first line of defense against the coastal calamity like sea storms, Hurricanes, Tsunamis etc. The enormous productive and protective

ecosystem that mangrove provide to both coastal environment and inhabitants, can be conservatively assessed to be worth about US\$186 million per year [12]. Mangroves have to expose regularly with periodic inundation, physiological stress, high salinity, high temperature and higher UV index [13]. As a result environmental factors (increased salinity level, inundation frequency, sea level rise and global warming) and anthropogenic activities (unplanned poaching, reclamation of mangrove area and siltation of river bed leading to less fresh water discharge in the estuary), mangrove forests all over the world are declining at an alarming level [14]. During the period of 1980-1990 this loss was estimated at 2.0% per year and within 1990-2000, 0.7% per year [12]. Mangrove restoration and conservation programs have been taken up by many countries, but it could be a fruitful effort if the genetic information of the plant species could be amalgamated, which is quiet meager [15].

In the present study, putative miRNAs precursor sequences has been fished out with their potential targets in a mangrove species *Bruguiera gymnorrhiza*. The genetic information of

this taxa have been evaluated in many countries and hence prediction of miRNA loci can be used as a resourceful technique towards understanding its better salt adaptability [16] through molecular basis. As miRNA regulates gene expression through cleaving its targeted mRNA, the present work is pointing to the identification of miRNAs and their targets leading to understanding their possible roles in plant growth and development. The new miRNAs identified in this study would be worthwhile in understanding the complexity of miRNA-mediated genes network in various stress adaptability.

## Materials and Method

### Retrieval of data

Available 8442 known plant miRNA sequences were acquired from the publicly available miRNA database, miRBase [17]. The redundant sequences were eliminated using PRINSEQ version 0.20.4 [18]. The remaining 4766 miRNA sequences were used to search their homologs in the EST database of *Bruguiera gymnorrhiza*. The available EST database of NCBI (National Centre for Biotechnology Information) are used for this study.

### Identification of potential miRNAs in *Bruguiera gymnorrhiza*

The sequences of all the above mentioned 4766 miRNA sequences were subjected to BLAST (Basic Local Alignment Search Tool), available on NCBI website, for alignment against the publicly available *Bruguiera gymnorrhiza* EST database. The nucleotide match size between query and database was set to 15 with expectation value 0.01, match sequence less than this values are not taken into account. After checking redundancy, the selected ESTs are subjected to blastx [19] against NCBI non-redundant protein sequence collection to eliminate sequences which are protein-coding. RNAs such as tRNA, rRNA, snRNA, or snoRNA were eradicated by subjecting the ESTs to BLAST against NCBI nucleotide collection.

### Prediction of RNA secondary structures

The selected candidates were then assessed for secondary structure using the mfold Web Server [20]. The default parameters were used for this study. Potential miRNAs were identified based on the following criteria - a) the position of the miRNA is on hairpin, b) minimum number of residues in miRNA should be 15, c) the maximum number of unpaired residues should be 6, d) the maximum number of G-U pairs in miRNA should be 5, e) the maximum size for a bulge in miRNA sequence should be 5nt, f) the negative minimal folding free energy (MFE) should be low, and g) the minimal folding free energy index (MFEI) should be high. Minimal folding free energy index (MFEI) = [(MFE/length of the RNA sequence) \*100] / (G+C %).

### Prediction of potential miRNA targets

Potential targets for the predicted miRNAs from *Bruguiera gymnorrhiza* were analyzed using psRNATarget web server

2017 version [21]. Since no miRNAs have been reported from *Bruguiera gymnorrhiza* till now, potential target was searched against the database of *Arabidopsis thaliana*.

## Result and Discussion

Previously reported 8442 mature miRNA sequences were used in this study to find their homologs in *Bruguiera gymnorrhiza*, a mangrove species. Since their discovery, miRNAs have emerged as principal regulators in plant growth and development. miRNAs role in plant stress responses have arisen after the discovery that miR398 target genes have known role in stress responses [22]. In that context we have predicted the miRNAs utilizing *Bruguiera gymnorrhiza* expressed sequence tag database.

The redundancy check decreased the total number of miRNA sequences to 4766. These sequences were used as query to find out their homologs present in the *Bruguiera gymnorrhiza* EST database. BLAST result produced a total of 272 hits. These were the ESTs which aligned with the query miRNA sequences (Table 1). These ESTs were further subjected to BLAST to eliminate the protein coding sequences and non-coding RNAs. We finally got 14 sequences potential to be miRNA. RNA secondary structure predicting software mfold was used for this study. In the predicted structure the nucleotides that were homologous to the miRNAs were selected and inspected for the above mentioned 7 criterions. The criterion got matched for two ESTs. They were named as bg-miR1029 and bg-miR5021. Both of the sequences were 17 nucleotides long (Table 2). The software generated secondary structure (Figure 1) show -99.67 Kcal/mol minimal folding free energy (MFE) and -13.96 minimal folding free energy index (MFEI). Second one (Figure 1) show -41.1Kcal/mol minimal folding free energy (MFE) and - 8.34 minimal folding free energy index (MFEI).

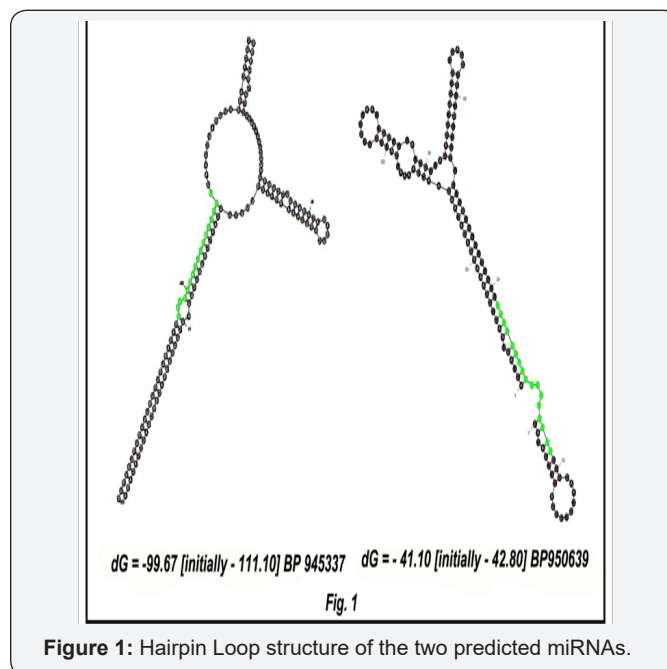


Figure 1: Hairpin Loop structure of the two predicted miRNAs.

Table 1 : Predicted Target sequences for the two miRNAs.

miRNA_Acc.	Target_Acc.	Expectation	UPES	miRNA_start	miRNA_end	Target_start	Target_end	miRNA_aligned_Fragment	Target_aligned_Fragment	Inhibition	Target_Desc.	Multiplicity
hg-miR5021	AT2G28100.1	0	-1	1	20	160	179	UGACAAGACAAGAAAGAAAA	UUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols: ATP1UC1, FUC1   alpha-L-fucosidase 1   chr2:11974663-11976600 FORWARD LENGTH=1772	1
hg-miR5021	AT1G30650.1	0	-1	1	20	91	110	UGACAAGACAAGAAAGAAAA	CUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols: WRKY14, ATWRKY14, AR411   WRKY DNA-binding protein 14   chr1:10868303-10871297 FORWARD LENGTH=1926	1
hg-miR5021	AT4G36950.1	1	-1	1	20	29	48	UGACAAGACAAGAAAGAAAA	UUUUCUUCUUCUUCUUCUCU	Cleavage	Symbols: MAPKK21   mitogen-activated protein kinase kinase 21   chr4:17422572-17423901 REVERSE LENGTH=1330	1
hg-miR5021	AT1G70900.1	1	-1	1	20	6	25	UGACAAGACAAGAAAGAAAA	UUUUCUUCUUCUUCUUCUC	Cleavage	Symbols:   unknown protein; BEST Arabidopsis thaliana match is: unknown protein (TAIR:AT1G23110.4). Has 57 Blast hits to 57 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink)   chr1:26731813-26733875 FORWARD LENGTH=1191	1
hg-miR5021	AT3G22950.1	1	-1	1	20	94	113	UGACAAGACAAGAAAGAAAA	UUUUCUUCUUCUUCUUCUCU	Cleavage	Symbols: ATARRC1, ARFC1   ADP-ribosylation factor C1   chr3:8136182-8138084 REVERSE LENGTH=989	1
hg-miR5021	AT3G22950.2	1	-1	1	20	94	113	UGACAAGACAAGAAAGAAAA	UUUUCUUCUUCUUCUUCUCU	Cleavage	Symbols: ARFC1   ADP-ribosylation factor C1   chr3:8136181-8138084 REVERSE LENGTH=973	1
hg-miR5021	AT1G28420.1	1	-1	1	20	111	130	UGACAAGACAAGAAAGAAAA	GUUUCUUCUUCUUCUUCUCU	Cleavage	Symbols: HB-1   homeobox-1   chr1:9979802-9987638 FORWARD LENGTH=5430	1
hg-miR5021	AT15G6240.2	1	-1	1	20	322	341	UGACAAGACAAGAAAGAAAA	CUUUCUUCUUCUUCUUCUC	Cleavage	Symbols:   INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hapless 8 (TAIR:AT15G6250.1).   chr5:22759805-22764587 REVERSE LENGTH=3532	1

hg-miR5021	AT5656240.1	1	-1	1	20	311	330	UCGACGAAAGGAAAGAAAGAAAA	CUUUCUUUCUUUCUUUCUCC	Cleavage	Symbol:   BEST Arabidopsis thaliana protein match is: hapless 8 (TAIR:AT5G56250.1). Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI Blast).   chr5:22759803-22764576 REVERSE LENGTH=3520	1
hg-miR5021	AT5657870.1	1	-1	1	20	43	62	UCGACGAAAGGAAAGAAAGAAAA	ACUUUCUUUCUUUCUUUCUCA	Cleavage	Symbol: eIFiso4G1   MIF4G domain-containing protein / MA3 domain-containing protein   chr5:23439500-23443781 FORWARD LENGTH=2946	1
hg-miR5021	AT5657870.2	1	-1	1	20	45	64	UCGACGAAAGGAAAGAAAGAAAA	ACUUUCUUUCUUUCUUUCUCA	Cleavage	Symbol: eIFiso4G1   MIF4G domain-containing protein / MA3 domain-containing protein   chr5:23439498-23443781 FORWARD LENGTH=2936	1
hg-miR5021	AT2641900.1	1	-1	1	20	45	64	UCGACGAAAGGAAAGAAAGAAAA	AUUUCUUUCUUUCUUUCUCU	Cleavage	Symbol:   CCH-type zinc finger protein with ARM repeat domain   chr2:17490405-17493922 FORWARD LENGTH=2887	1
hg-miR5021	AT5667030.1	1	-1	1	20	26	45	UCGACGAAAGGAAAGAAAGAAAA	AUUUCUUUCUUUCUUUCUCU	Cleavage	Symbol: ABA1, LOS6, NPQ2, ATABA1, ZEP, IBS3, ATZEP1 zeaxanthin epoxidase (ZEP) (ABA1)   chr5:26753510-26757236 REVERSE LENGTH=2385	1
hg-miR5021	AT5667030.2	1	-1	1	20	26	45	UCGACGAAAGGAAAGAAAGAAAA	AUUUCUUUCUUUCUUUCUCU	Cleavage	Symbol: ABA1, LOS6, NPQ2, ATABA1, ZEP, IBS3, ATZEP1 zeaxanthin epoxidase (ZEP) (ABA1)   chr5:26753522-26757236 REVERSE LENGTH=2377	1
hg-miR5021	AT3612080.1	1	-1	1	20	20	39	UCGACGAAAGGAAAGAAAGAAAA	AUUUCUUUCUUUCUUUCUCU	Cleavage	Symbol: emb27381   GTP-binding family protein   chr3:3847792-3852138 FORWARD LENGTH=2209	1
hg-miR5021	AT3612080.2	1	-1	1	20	20	39	UCGACGAAAGGAAAGAAAGAAAA	AUUUCUUUCUUUCUUUCUCU	Cleavage	Symbol: emb27381   GTP-binding family protein   chr3:3847792-3852138 FORWARD LENGTH=2205	1
hg-miR5021	AT2619600.1	1	-1	1	20	154	173	UCGACGAAAGGAAAGAAAGAAAA	CUUUCUUUCUUUCUUUCUCC	Cleavage	Symbol: ATRK4A, KEA4   K+ efflux antiporter 4   chr2:8479198-8483830 FORWARD LENGTH=2204	1
hg-miR5021	AT2619450.1	1	-1	1	20	14	33	UCGACGAAAGGAAAGAAAGAAAA	CUUUCUUUCUUUCUUUCUCU	Cleavage	Symbol: TAG1, ASI1, ABX45, DCA17, RDS1, ATFDGAT   membrane bound O-acetyl transferase (MBOAT) family protein   chr2:8426206-8429736 FORWARD LENGTH=2074	1
hg-miR5021	AT3621070.1	1	-1	1	20	43	62	UCGACGAAAGGAAAGAAAGAAAA	CUUUCUUUCUUUCUUUCUCU	Cleavage	Symbol: NADK1, ATNADK-1   NAD kinase 1   chr3:7380191-7383980 REVERSE LENGTH=1942	1
hg-miR5021	AT3621070.2	1	-1	1	20	43	62	UCGACGAAAGGAAAGAAAGAAAA	CUUUCUUUCUUUCUUUCUCU	Cleavage	Symbol: NADK1   NAD kinase 1   chr3:7380191-7383980 REVERSE LENGTH=1924	1

hg-miR5021	AT1667410.1	1	-1	1	20	57	76	UGACGAAGAGAAAGAAAGAAA	CUUUUCUUCUUUCUUUCUUUCUU	Cleavage	Symbols:   Exostosis family protein   chr1:25251193-25253667 REVERSE LENGTH=1805	1
hg-miR5021	AT5667420.1	1	-1	1	20	494	513	UGACGAAGAGAAAGAAAGAAA	CUUUUCUUCUUUCUUUCUUUCUC	Cleavage	Symbols: LBD37, ASL39   LOB domain-containing protein 37   chr5:26904289-26906026 REVERSE LENGTH=1651	1
hg-miR5021	AT3625110.1	1	-1	1	20	174	193	UGACGAAGAGAAAGAAAGAAA	GUUUUCUUCUUUCUUUCUUUC	Cleavage	Symbols: AtFAtA, FAtA   fatA acyl-ACP thioesterase   chr3:9146271-9148486 REVERSE LENGTH=1620	1
hg-miR5021	AT3648070.1	1	-1	1	20	43	62	UGACGAAGAGAAAGAAAGAAA	GUUUUCUUCUUUCUUUCUUUCU	Cleavage	Symbols:   RING/U-box superfamily protein   chr3:1775071-17752416 FORWARD LENGTH=1565	1
hg-miR5021	AT2627770.1	1	-1	1	20	141	160	UGACGAAGAGAAAGAAAGAAA	CAUUCUUCUUUCUUUCUUUCUCA	Cleavage	Symbols:   Plant protein of unknown function (DUF868)   chr2:11832809-11834369 REVERSE LENGTH=1561	1
hg-miR5021	AT4632590.1	1	-1	1	20	202	221	UGACGAAGAGAAAGAAAGAAA	UCUUUCUUCUUUCUUUCUUUCUCA	Cleavage	Symbols:   2Fe-2S ferredoxin-like superfamily protein   chr4:15721324-15722908 FORWARD LENGTH=747	1
hg-miR5021	AT4632590.3	1	-1	1	20	202	221	UGACGAAGAGAAAGAAAGAAA	UCUUUCUUCUUUCUUUCUUUCUCA	Cleavage	Symbols:   2Fe-2S ferredoxin-like superfamily protein   chr4:15721324-15722869 FORWARD LENGTH=724	1
hg-miR5021	AT4632590.4	1	-1	1	20	202	221	UGACGAAGAGAAAGAAAGAAA	UCUUUCUUCUUUCUUUCUUUCUCA	Cleavage	Symbols:   2Fe-2S ferredoxin-like superfamily protein   chr4:15721324-15722869 FORWARD LENGTH=712	1
hg-miR5021	AT3648070.2	1	-1	1	20	42	61	UGACGAAGAGAAAGAAAGAAA	GUUUUCUUCUUUCUUUCUUUCU	Cleavage	Symbols:   RING/U-box superfamily protein   chr3:17750712-17752761 FORWARD LENGTH=1307	1
hg-miR5021	AT4632590.2	1	-1	1	20	183	202	UGACGAAGAGAAAGAAAGAAA	UCUUUCUUCUUUCUUUCUUUCUCA	Cleavage	Symbols:   2Fe-2S ferredoxin-like superfamily protein   chr4:15721343-15722822 FORWARD LENGTH=646	1
hg-miR5021	AT1628070.1	1	-1	1	20	33	52	UGACGAAGAGAAAGAAAGAAA	GUUUUCUUCUUUCUUUCUUUCUCC	Cleavage	Symbols:   unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TMRAT2C33510.1); Has 85 Blast hits to 77 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 85; Viruses - 0; Other Eukaryotes - 0 (source: NCBI Blnk)   chr1:9782996-9783998 FORWARD LENGTH=751	1
hg-miR5021	AT1614200.1	1.5	-1	1	20	20	39	UGACGAAGAGAAAGAAAGAAA	UUUUUCUUCUUUCUUUCUUUCUUA	Cleavage	Symbols:   RING/U-box superfamily protein   chr1:4854384-4855200 REVERSE LENGTH=817	1

bg-miR5021	AT3G21320.1	15	-1	1	20	291	310	UGAGAAGAAGCAAGCAAAA	CUUUUCUUCUUCUUCUUCUA	Cleavage	Symbols:   BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT2G25930.1); Has 63 Blast hits to 58 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink);   chr-3:7499053-7501841 REVERSE LENGTH=2419	1
bg-miR5021	AT1G55570.1	15	-1	1	20	1982	2001	UGAGAAGAAGCAAGCAAAA	UUUUUCUUCUUCUUCUUCUA	Cleavage	Symbols: sks12   SKUS similar-12   chr1:2075767-20760076 FORWARD LENGTH=2088	1
bg-miR5021	AT2G18910.1	15	-1	1	20	128	147	UGAGAAGAAGCAAGCAAAA	CUUUUCUUCUUCUUCUUCUA	Cleavage	Symbols:   hydroxyproline-rich glycoprotein family protein   chr2:8192708-8194338 REVERSE LENGTH=911	1
bg-miR5021	AT3G51550.1	2	-1	1	20	177	197	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols: FER   Malectin/receptor-like protein kinase family protein   chr3:19117584-19120881 REVERSE LENGTH=3123	1
bg-miR5021	AT4G05020.2	2	-1	1	20	85	105	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols: NDB2   NAD(P)H dehydrogenase B2   chr4:2572621-2576595 FORWARD LENGTH=2364	1
bg-miR5021	AT4G05020.1	2	-1	1	20	85	105	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols: NDB2   NAD(P)H dehydrogenase B2   chr4:2572621-2576595 FORWARD LENGTH=2253	1
bg-miR5021	AT5G24670.2	2	-1	1	20	140	160	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols:   Cytidine/deoxycytidylate deaminase family protein   chr5:8447954-8451078 FORWARD LENGTH=1800	1
bg-miR5021	AT3G06660.1	2	-1	1	20	110	130	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols:   PAPA-1-like family protein / zinc finger (HIT type) family protein   chr3:2102402-2104906 FORWARD LENGTH=1755	1
bg-miR5021	AT1G73740.1	2	-1	1	20	29	49	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols:   UDP-Glycosyltransferase superfamily protein   chr1:27734279-27736189 FORWARD LENGTH=649	1
bg-miR5021	AT5G26670.1	2	-1	1	20	25	45	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols:   Pectinacetyltransferase family protein   chr5:9318282-9320987 FORWARD LENGTH=1596	1
bg-miR5021	AT5G18760.1	2	-1	1	20	173	193	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols:   RING/U-box superfamily protein   chr5:6258295-6260929 REVERSE LENGTH=1550	1
bg-miR5021	AT5G26670.2	2	-1	1	20	27	47	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols:   Pectinacetyltransferase family protein   chr5:9318280-9320991 FORWARD LENGTH=1519	1
bg-miR5021	AT1G53650.1	2	-1	1	20	55	75	UGAGAAGAAGCAAGCAAAA	UUUCUUCUUCUUCUUCUUCUA	Cleavage	Symbols: CID8   CTC-interacting domain 8   chr1:200729029-20031566 REVERSE LENGTH=1501	1



hg-miR5021	AT4G35790.3	2.5	-1	1	20	248	267	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols: ATP1LDELT, PUDELTA   phospholipase D delta   chr4:1695518-16960170 REVERSE LENGTH=3264	1
hg-miR5021	AT4G35790.1	2.5	-1	1	20	248	267	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols: ATP1LDELT, PUDELTA   phospholipase D delta   chr4:1695518-16960170 REVERSE LENGTH=3158	1
hg-miR5021	AT4G35790.2	2.5	-1	1	20	248	267	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols: ATP1LDELT, PUDELTA   phospholipase D delta   chr4:1695518-16960170 REVERSE LENGTH=3125	1
hg-miR5021	AT3G22150.1	2.5	-1	1	20	53	72	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols:   Tetra-tricopeptide repeat (TPR)-like superfamily protein   chr3:7812944-7815928 FORWARD LENGTH=2985	1
hg-miR5021	AT3G13460.1	2.5	-1	1	20	218	237	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols: ECT2   evolutionarily conserved C-terminal region 2   chr3:4384714-4388525 REVERSE LENGTH=2869	1
hg-miR5021	AT3G13460.3	2.5	-1	1	20	194	213	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols: ECT2   evolutionarily conserved C-terminal region 2   chr3:4384714-4388501 REVERSE LENGTH=2847	1
hg-miR5021	AT3G13460.4	2.5	-1	1	20	170	189	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols: ECT2   evolutionarily conserved C-terminal region 2   chr3:4384714-4388477 REVERSE LENGTH=2818	1
hg-miR5021	AT3G13460.2	2.5	-1	1	20	170	189	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols: ECT2   evolutionarily conserved C-terminal region 2   chr3:4384714-4388477 REVERSE LENGTH=2812	1
hg-miR5021	AT1G03190.1	2.5	-1	1	20	25	44	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols: ATPXD, UVH6   RAD3-like DNA-binding helicase protein   chr1:775527-780027 FORWARD LENGTH=2578	1
hg-miR5021	AT3G07810.1	2.5	-1	1	20	204	223	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols:   RNA-binding (RRM/ RBD/RNP motifs) family protein   chr3:2492273-2495750 FORWARD LENGTH=2518	1
hg-miR5021	AT3G07810.2	2.5	-1	1	20	184	203	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols:   RNA-binding (RRM/ RBD/RNP motifs) family protein   chr3:2492293-2495750 FORWARD LENGTH=2451	1
hg-miR5021	AT2G16750.1	2.5	-1	1	20	2140	2159	UGAGAAGCAGAGAGAGAAAA	UUUUUCUUCUUCUUUCUUUC	Cleavage	Symbols:   Protein kinase protein with adenine nucleotide alpha hydrolases-like domain   chr2:7271012-7274693 FORWARD LENGTH=2428	1



hg-miR5021	AT3G20770.1	2.5	-1	1	20	70	89	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols: EIN3, AEN13   Ethylene insensitive 3 family protein   chr3:7260432-7263352 REVERSE LENGTH=2413	1
hg-miR5021	AT4G32250.3	2.5	-1	1	20	1	22	UGAGAACAAGAAAGAAA-AA	UUCCUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Protein kinase superfamily protein   chr4:15570044-15573323 REVERSE LENGTH=2223	1
hg-miR5021	AT3G6080.1	2.5	-1	1	20	239	258	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Plant protein of unknown function (DUF641)   chr3:22429960-22432042 FORWARD LENGTH=2083	1
hg-miR5021	AT3G6370.1	2.5	-1	1	20	1883	1902	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   O-fucosyltransferase family protein   chr3:9656744-9659935 FORWARD LENGTH=2010	1
hg-miR5021	AT2G40520.4	2.5	-1	1	20	1831	1850	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Nucleotidyltransferase family protein   chr2:16923318-16925914 FORWARD LENGTH=1971	1
hg-miR5021	AT2G40520.1	2.5	-1	1	20	1777	1796	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Nucleotidyltransferase family protein   chr2:16923068-16925914 FORWARD LENGTH=1917	1
hg-miR5021	AT2G40520.2	2.5	-1	1	20	1767	1786	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Nucleotidyltransferase family protein   chr2:16922587-16925914 FORWARD LENGTH=1907	1
hg-miR5021	AT3G50910.1	2.5	-1	1	20	104	123	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66480.1); Has 76 Blast hits to 75 proteins in 28 species: Archae - 0; Bacteria - 10; Metazoa - 7; Fungi - 2; Plants - 49; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink)   chr3:18919513-18922238 FORWARD LENGTH=1861	1
hg-miR5021	AT2G40520.3	2.5	-1	1	20	1691	1710	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Nucleotidyltransferase family protein   chr2:16923350-16925914 FORWARD LENGTH=1851	1
hg-miR5021	AT3G48160.2	2.5	-1	1	20	1530	1549	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols: DEL1, E2L3, E2PE   DP-E2P-like 1   chr3:17783331-17786099 FORWARD LENGTH=1775	2
hg-miR5021	AT1G17940.1	2.5	-1	1	20	63	82	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Endosomal targeting BR01-like domain-containing protein   chr1:6169341-6173222 REVERSE LENGTH=1734	1
hg-miR5021	AT2G01290.1	2.5	-1	1	20	18	37	UCAGAACAAGAGAGAAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols: RP12   ribose-5-phosphate isomerase 2   chr2:148919-150382 REVERSE LENGTH=1464	1

hg-miR5021	AT1G05800.1	2.5	-1	1	20	176	197	UGACAAGAGAAGCAAGAAA-AA	UUCCUUCUUCUUCUUCUUCUCA	Cleavage	Symbols: DCL   alpha/beta-Hydrolases superfamily protein   chr1:1741204-1742619 FORWARD LENGTH=1416	1
hg-miR5021	AT3G10260.3	2.5	-1	1	20	151	170	UGACAAGAGAAGCAAGAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Reticulon family protein   chr3:3171222-3172959 REVERSE LENGTH=1386	1
hg-miR5021	AT5G38220.3	2.5	-1	1	20	9	28	UGACAAGAGAAGCAAGAAA	UUUUUCUUCUUCUUCUUCUUCU	Cleavage	Symbols:   alpha/beta-Hydrolases superfamily protein   chr5:15268827-15271386 FORWARD LENGTH=1361	1
hg-miR5021	AT3G15140.1	2.5	-1	1	20	224	243	UGACAAGAGAAGCAAGAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Polynucleotide transferase, ribonuclease H-like superfamily protein   chr3:5099532-5101781 REVERSE LENGTH=1258	1
hg-miR5021	AT1G16060.1	2.5	-1	1	20	27	46	UGACAAGAGAAGCAAGAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols: ADAP   ARIA-interacting double AP2 domain protein   chr1:5508507-5511735 FORWARD LENGTH=1220	1
hg-miR5021	AT3G10260.1	2.5	-1	1	20	158	177	UGACAAGAGAAGCAAGAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols:   Reticulon family protein   chr3:3171222-3172966 REVERSE LENGTH=1130	1
hg-miR5021	AT5G25810.1	2.5	-1	1	20	528	547	UGACAAGAGAAGCAAGAAA	UUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols: try   Integrase-type DNA-binding superfamily protein   chr5:8986771-8987787 REVERSE LENGTH=1017	1
hg-miR5021	AT4G38600.1	2.5	-1	1	20	121	140	UGACAAGAGAAGCAAGAAA	CUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols: KAK   UPL3   HEAT repeat:HECT-domain (ubiquitin-transferase)   chr4:18041031-18049292 REVERSE LENGTH=6139	2
hg-miR5021	AT4G38600.2	2.5	-1	1	20	81	100	UGACAAGAGAAGCAAGAAA	CUUUUCUUCUUCUUCUUCUUC	Cleavage	Symbols: KAK   UPL3   HEAT repeat:HECT-domain (ubiquitin-transferase)   chr4:18041031-18049252 REVERSE LENGTH=5954	2
hg-miR5021	AT5G66440.1	2.5	-1	1	20	4	23	UGACAAGAGAAGCAAGAAA	UUUUUCUUCUUCUUCUUCUUCU	Cleavage	Symbols:   unknown protein: BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G34560.1) Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI Blnk)   chr5:26530235-26531097 REVERSE LENGTH=863	1

hg-miR5021	AT5G10946.1	2.5	-1	1	20	20	39	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUUC	Cleavage	<p>  Symbols:   unknown protein; FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLINK).   chr5:3455607-3457306 REVERSE LENGTH=833</p>	1
hg-miR5021	AT1G51355.1	2.5	-1	1	20	552	571	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUUC	Cleavage	<p>  Symbols:   unknown protein; FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G20898.1); Has 52 Blast hits to 52 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).   chr1:19041397-19042146 FORWARD LENGTH=750</p>	1
hg-miR5021	AT5G49680.2	2.5	-1	1	20	640	659	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUCA	Cleavage	<p>  Symbols:   Golgi-body localisation protein domain; RNA pol II promoter Pmp27 protein domain   chr5:20176385-20188307 FORWARD LENGTH=7764</p>	1
hg-miR5021	AT4G32600.1	2.5	-1	1	20	155	174	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUC	Cleavage	<p>  Symbols:   RING/U-box superfamily protein   chr4:15723434-15726109 FORWARD LENGTH=2027</p>	1
hg-miR5021	AT2G47820.1	2.5	-1	1	20	58	77	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUG	Cleavage	<p>  Symbols:   unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G09040.1); Has 628 Blast hits to 543 proteins in 149 species: Archae - 0; Bacteria - 106; Metazoa - 145; Fungi - 69; Plants - 97; Viruses - 10; Other Eukaryotes - 201 (source: NCBI BLINK).   chr2:19587408-19590822 FORWARD LENGTH=2845</p>	1
hg-miR5021	AT5G40300.1	2.5	-1	1	20	397	416	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUAC	Cleavage	<p>  Symbols:   Uncharacterised protein family (DUP0497)   chr5:16110688-16112968 FORWARD LENGTH=1170</p>	1
hg-miR5021	AT1G77680.1	2.5	-1	1	20	80	99	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUA	Cleavage	<p>  Symbols:   Ribonuclease II/R family protein   chr1:29191834-29196287 REVERSE LENGTH=3846</p>	1
hg-miR5021	AT3G25660.1	2.5	-1	1	20	1908	1927	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUG	Cleavage	<p>  Symbols:   Amidase family protein   chr3:9339423-9342204 REVERSE LENGTH=1991</p>	1
hg-miR5021	AT2G21320.1	2.5	-1	1	20	31	50	UCGACGAGCAAGCAAGAAAA	UUUUUCUUCUUUUUUUUUUUC	Cleavage	<p>  Symbols:   B-box zinc finger family protein   chr2:9126263-9127843 FORWARD LENGTH=949</p>	1

bg-miR5021	ATTG04310.1	2.5	-1	1	20	212	231	UCGAGAAAGACAGAAAGAAAA	UCUUCUUCUUCUUCUUCUUA	Cleavage	Symbols: ERS2   ethylene response sensor 2   chr1:1154764-1157711 REVERSE LENGTH=2470	1
bg-miR5021	ATTG69060.1	2.5	-1	1	20	42	61	UCGAGAAAGACAGAAAGAAAA	UCUUCUUCUUCUUCUUCUUA	Cleavage	Symbols:   Chaperone domain superfamily protein   chr1:25964468-25967450 FORWARD LENGTH=2309	1
bg-miR5021	ATTG20970.1	3	-1	1	20	59	79	UG- ACAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols:   FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological process unknown; LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: guard cell, cultured cell; BEST Arabidopsis thaliana protein match is: proton pump interactor 1 (TAIR:AT4G27500.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 [source: NCBI BLink]   chr1:17313946-7319574 FORWARD LENGTH=4673	1
bg-miR5021	ATTG19170.1	3	-1	1	20	115	135	UG- ACAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols: SUP3   subtilisin-like serine protease 3   chr2:8314005-8318596 REVERSE LENGTH=2906	1
bg-miR5021	ATTG33980.2	3	-1	1	20	54	74	UG- ACAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols: ATUPF3, UPF3   Sng-4/UPF3 family protein   chr1:12351593-12355023 FORWARD LENGTH=2126	1
bg-miR5021	ATTG33980.1	3	-1	1	20	54	74	UG- ACAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols: ATUPF3, UPF3   Sng-4/UPF3 family protein   chr1:12351593-12355023 FORWARD LENGTH=2120	1
bg-miR5021	AT5G25040.2	3	-1	1	20	14	34	UG- ACAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols:   Major facilitator superfamily protein   chr5:8621954-8624337 FORWARD LENGTH=2017	1
bg-miR5021	AT5G25040.3	3	-1	1	20	14	34	UG- ACAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols:   Major facilitator superfamily protein   chr5:8621954-8624337 FORWARD LENGTH=1845	1
bg-miR5021	AT5G25040.1	3	-1	1	20	14	34	UG- ACAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols:   Major facilitator superfamily protein   chr5:8621954-8624337 FORWARD LENGTH=1837	1
bg-miR5021	AT3G16850.1	3	-1	1	20	81	101	UGA- CAAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols:   Pectin lyase-like superfamily protein   chr3:5748570-5751297 FORWARD LENGTH=1806	1
bg-miR5021	ATZG01735.1	3	-1	1	20	106	126	UGA- GAAGAGAAAGAAAGAAAA	UUUUUCUUCUUCUUCUUCUCA	Cleavage	Symbols: RIE1   RING-finger protein for embryogenesis   chr2:3244472-326094 FORWARD LENGTH=1306	1





bg-miR5021	AT3G49160.1	3	-1	1	20	84	104	UGAGACGAGAAAGAAAGAA- AA	UUUCUUUCUUUCUUUCUUUCUCC	Cleavage	Symbols:   pyruvate kinase family protein   chr:3:18221994-18224885 REVERSE LENGTH=2445	1
bg-miR5021	AT4G37890.1	3	-1	1	20	369	389	UG- ACGAGAAAGAAAGAAAGAA	GUUUUCUUUCUUUCUUUCUACACA	Cleavage	Symbols:   EDAA40   Zinc finger (C3H4+-type RING finger) family protein   chr:4:17812736-17815084 REVERSE LENGTH=2349	1
bg-miR5021	AT2G23300.1	3	-1	1	20	46	66	UGAGACGAGAAAGAAAGAA- AA	UUUCUUUCUUUCUUUCUUUCU	Cleavage	Symbols:   Leucine-rich repeat protein kinase family protein   chr:2:9914608-9917130 FORWARD LENGTH=2322	1
bg-miR5021	AT3G15095.1	3	-1	1	20	168	188	UGAGACGAGAAAGAAAGAA- AA	UUUCUUUCUUUCUUUCUUUCUCC	Cleavage	Symbols:   unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 9762 Blast hits to 6439 proteins in 764 species: Archae - 77; Bacteria - 1339; Metazoa - 3211; Fungi - 718; Plants - 437; Viruses - 131; Other Eukaryotes - 3849 (source: NCBI BLink);   chr:3:5081780-5084081 FORWARD LENGTH=2302	1
bg-miR5021	AT4G37890.2	3	-1	1	20	380	400	UG- ACGAGAAAGAAAGAAAGAA	GUUUUCUUUCUUUCUUUCUACACA	Cleavage	Symbols:   EDAA40   Zinc finger (C3H4+-type RING finger) family protein   chr:4:17812736-17815095 REVERSE LENGTH=2276	1
bg-miR5021	AT2G27030.2	3	-1	1	20	21	41	UGAGACGAGAAAGAAAGAA- AA	UUUCUUUCUUUCUUUCUUUCU	Cleavage	Symbols:   CAM5   calmodulin 5   chr:2:11532007-11534272 FORWARD LENGTH=2266	1
bg-miR5021	AT5G64816.2	3	-1	1	20	481	501	UGAGACGAGAAAGAAAGAA- AA	UUUCUUUCUUUCUUUCUUUCUG	Cleavage	Symbols:   unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink);   chr:5:25913000-25914027 FORWARD LENGTH=659	1
bg-miR5021	AT3G27580.2	3	-1	1	20	58	78	UGAGACGAGAAAGAAAGAA- AA	UUUCUUUCUUUCUUUCUUUCU	Cleavage	Symbols:   ATPK7   Protein kinase superfamily protein   chr:3:10217430-10219900 REVERSE LENGTH=2163	1
bg-miR5021	AT5G12120.1	3	-1	1	20	32	52	UGAGACGAGAAAGAAAGAA- AA	UUUCUUUCUUUCUUUCUUUCUCC	Cleavage	Symbols:   Ubiquitin-associated/translation elongation factor EF1B protein   chr:5:3916048-3918659 REVERSE LENGTH=2154	1
bg-miR1029	AT1G28610.2	2.5	-1	1	20	1323	1342	UCUCUCUCACACCAACCAUAC	GUUUUCUUUCUUUCUUUCUACACA	Translation	Symbols:   GDSL-like Lipase/Acylhydrolase superfamily protein   chr:1:10053617-10055731 REVERSE LENGTH=1478	1
bg-miR1029	AT1G28610.1	2.5	-1	1	20	1377	1396	UCUCUCUCACACCAACCAUAC	GUUUUCUUUCUUUCUUUCUACACA	Translation	Symbols:   GDSL-like Lipase/Acylhydrolase superfamily protein   chr:1:10053617-10055681 REVERSE LENGTH=1532	1

bg-miR1029	AT1G28610.2	2.5	-1	1	20	1323	1342	UCUCUCUCAAACAACCAUAC	GUAUUUUUUUUUAGAGAGAGA	Translation	Symbols:   GDSL-like Lipase/ Acylhydrolase superfamily protein   chr1:10053617-10055731 REVERSE LENGTH=1478	1
bg-miR1029	AT1G28610.1	2.5	-1	1	20	1377	1396	UCUCUCUCAAACAACCAUAC	GUAUUUUUUUUUAGAGAGAGA	Translation	Symbols:   GDSL-like Lipase/ Acylhydrolase superfamily protein   chr1:10053617-10055681 REVERSE LENGTH=1532	1
bg-miR1029	Potri.013G114400.3	2.5	-1	1	20	1048	1067	UCUCUCUCAAACAACCAUAC	GAAUGGUUGUUUAAAAGAGA	Cleavage	pacid=26995417 locus=Potri.013G114400 ID=Potri.013G114400.v3.0 annot-version=v3.0	1
bg-miR1029	Potri.013G114400.2	2.5	-1	1	20	1048	1067	UCUCUCUCAAACAACCAUAC	GAAUGGUUGUUUAAAAGAGA	Cleavage	pacid=26995416 locus=Potri.013G114400 ID=Potri.013G114400.v3.0 annot-version=v3.0	1
bg-miR1029	Potri.013G114400.1	2.5	-1	1	20	1051	1070	UCUCUCUCAAACAACCAUAC	GAAUGGUUGUUUAAAAGAGA	Cleavage	pacid=26995415 locus=Potri.013G114400 ID=Potri.013G114400.v3.0 annot-version=v3.0	1
bg-miR1029	Potri.013G114400.5	2.5	-1	1	20	1054	1073	UCUCUCUCAAACAACCAUAC	GAAUGGUUGUUUAAAAGAGA	Cleavage	pacid=26995419 locus=Potri.013G114400 ID=Potri.013G114400.v3.0 annot-version=v3.0	1
bg-miR1029	Potri.013G114400.4	2.5	-1	1	20	1286	1305	UCUCUCUCAAACAACCAUAC	GAAUGGUUGUUUAAAAGAGA	Cleavage	pacid=26995418 locus=Potri.013G114400 ID=Potri.013G114400.v3.0 annot-version=v3.0	1
bg-miR1029	Potri.001G438100.1	2.5	-1	1	20	87	106	UCUCUCUCAAACAACCAUAC	CUAUGGAUGGUUUUAGAGAGA	Cleavage	pacid=27047900 locus=Potri.001G438100 ID=Potri.001G438100.v3.0 annot-version=v3.0	1
bg-miR1029	AM822656	2.5	-1	1	20	109	128	UCUCUCUCAAACAACCAUAC	CUACGGUUGGAUAGAGAGAGA	Translation	similar to UniRef100_A6YB88 Cluster: Pax3/7; nr1; Platynereis dumerilii Rep: Pax3/7 - Platynereis dumerilii (Dumeril's clam worm), partial (9%)	1
bg-miR1029	EH665658	2.5	-1	1	20	389	408	UCUCUCUCAAACAACCAUAC	CUUUUGGUGGUUAGAGAGAGA	Cleavage	similar to UniRef100_Q9M7J4 Cluster: MAR-binding filament-like protein 1-1; nr1; Nicotiana tabacum Rep: MAR-binding filament-like protein 1-1 - Nicotiana tabacum (Common tobacco), partial (11%)	1



Web server psRNA Target was used to predict the target genes for these two miRNAs. The cDNA library of *Arabidopsis thaliana* was used for this study, as cDNA library of *Bruguiera gymnorhiza* was not available; and being a genetically well studied model organism *Arabidopsis thaliana* can give the most accurate prediction. Default parameters were set for this study. The specificity of target binding for these two miRNAs might provide some useful information towards understanding the stress response. bg-miR5021 showed a total of 146 hits (Table 1). Target genes for this miRNA include NAD kinase1, fatA acyl- ACP thioesterase, Calmodulin S, Topoisomerase, Circadian clock associated 1, Pectin-lyase like siperfamily protein, NADPH dehydrogenase B, Ferredoxin – like superfamily protein among others. All of these genes have some role in growth and development of plants. The binding of the miRNAs to these genes results in despaired activity. On the other hand some of these genes have plant stress responsive activities. Ca<sup>2+</sup>-dependent protein kinases (CDPKs) and sucrose non-fermentation 1 (SNF1)-related kinases (SnRKs) regulate stress responsive gene expression which include ABA-responsive transcription factors and LEA genes [23]. Several protein kinases involved in stress tolerance are stimulated by ABA, which have a immense role in stress response [24]. Calmodulin (CaM) is a major Ca<sup>2+</sup>-sensing protein, involved in transduction of Ca<sup>2+</sup> signals. CaM undergoes conformational change after interacting with Ca<sup>2+</sup> and stimulates the activities of a diverse range of CaM-binding proteins. Most important role played by CaM is in adaptation to adverse environmental conditions [25]. bg-miR1029 showed a total of 12 hits, which includes GDSL-like Lipase/Acylhydrolase superfamily protein among others.

The salinity is increasing all over the globe, this rapid salinization may pose serious threat to the growth and development of the plants [26]. Genes and miRNAs involved in salinity stress have been identified to some extent [27]. But the molecular data of salt responsive genes and miRNAs available currently is very limited. Genome wide molecular level study on the halophytes and mangroves could provide clear insight for coping with the rapid salinization all along the globe. Hence the present work predicted that the target genes for the two miRNAs bg-miR1029 and bg-miR5021, include some genes very important for plant growth and development, as well as plant stress responses. Experimental validation and characterization of these two miRNAs expression and their predicted target genes along the salinity gradient would give us more clear understanding of adaptability within saline atmosphere for the species *Bruguiera gymnorhiza*.

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