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REVIEW ARTICLE

BIOINFORMATICS

IN-SILICO STUDIES OF MICRORNA IN *GLYCINE MAX* AND *BRASSICA NAPUS***S.DUBEY***

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ABSTRACT

MicroRNAs (miRNAs) are very small non-coding molecules of RNA. These are gene products of about 19-25 nucleotides in length which are evolutionarily conserved molecules and expressed in a wide variety of organisms from plants, viruses and animals. MicroRNAs play an important regulatory role in post-transcriptional gene modification. These are derived from larger hairpin RNA precursor molecules and are more conserved in the secondary structure rather than the primary structure.

KEYWORDS

Cancer, microRNA, non-coding molecules, post-transcriptional gene modification.

INTRODUCTION

RNA genes are genes which do not encode a functional protein-product and called as non-coding genes which produce final product as ribonucleic acid. Non-coding RNA ranges from transfer RNAs to some regulatory RNAs¹¹. These regulatory RNAs are ~19-25 nucleotides in length, known as microRNAs (miRNAs). In 1993, firstly discovered regulatory RNA gene was seen during nematode larval (*Caenorhabditis elegans*) development, named as *lin-4* gene, controls the timing of *Caenorhabditis elegans* larval development. This gene does not code for protein but produces a pair of small RNAs⁴. This *lin-4* RNA is acknowledged as the founding member of tiny regulatory RNAs called microRNAs or miRNAs (Lagos-Quintana et al., 2001). After the discovery of the *lin-4* gene, in 2000, new regulatory gene was discovered which was named as *let-7*, another gene in the *Caenorhabditis elegans*, encoded a second ~22 nucleotide regulatory RNA. Thus the term microRNA was used to refer to the small temporal RNAs and all the other tiny RNAs with similar features but unknown functions⁶.

The difference between plant and animal miRNAs is that the targets of plants miRNAs can be realistically predicted by identifying mRNAs (mRNAs are targets of miRNAs) with near complementarities and the most differences are in the sequence of miRNA stem loops not in mature miRNA; the plant predicted fold backs in stem loop are much more variable in size and typically larger than those of animals³.

Recently discovered miRNA functions include control of cell proliferation, cell death, and fat metabolism in flies, neural patterning in nematodes, modulation of hematopoietic

lineage differentiation in mammals^{9,10}, and control of leaf and flower development, apoptosis in plants. In plants, miRNA also regulate diverse genes and pathways, such as development, hormone signaling, stress response and trans-acting siRNAs^{7,8}. There are evidences that miRNAs block translation initiation, as Argonaute proteins bound to miRNAs and their target mRNAs accumulate in processing bodies (P-bodies), are known sites of mRNA degradation¹².

The miRNAs and their precursor sequences were downloaded from the central online repository for microRNA, i.e., miRBase release 12.0. This set contains 8619 miRNA entries from 87 species including Homo sapiens, flies, plants, animals and viruses also^{7,8}. Identification of microRNAs is an important requirement for understanding the mechanisms of post-transcriptional regulation. We have presented here a computational approach for genome wide prediction of *Brassica napus* and *Glycine max* microRNAs and their targets. Homologs of microRNAs of these two species have also been identified using BLAST against microRNA database. Homology provides a great understanding of conserveness within several other species.

MATERIALS AND METHODS

1 Data sources:

1.1. MiRBase:

MiRBase (<http://microrna.sanger.ac.uk/>) is the new home of microRNA data on the web, providing data previously accessible from the miRNA Registry. The current release (12.0) contains 8619 miRNA loci from 87 species including Homo sapiens, flies, plants, animals and viruses also.

- The miRBase Registry continues to provide gene hunters with unique names for novel microRNA genes prior to publication of results.
- The miRBase Targets Database is a new resource of predicted miRNA targets in animals.
- The miRBase Sequences provides miRNA sequence data, annotation, references and links to other resources for all published miRNAs.

Both hairpin and mature sequences are available for searching using BLAST and SSEARCH, and entries can also be retrieved by name, keyword, references and annotation. All sequence and annotation data are also available for download^{7,8}.

1.2. EST sources

Expressed Sequence Tag of desired plant species, i.e. *Brassica napus* and *Glycine max* are retrieved from NCBI website (<http://blast.ncbi.nlm.nih.gov/Blast/>).

NCBI(National Center for Biotechnology Information) Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in computational biology, develops software tools for analyzing genome data,

ESTs are short sequences obtained from cDNA clones and serve as short identifiers of full-length genes. ESTs reflect the abundance of the corresponding mRNA in the cell and mRNAs serve as targets for miRNA.

METHODOLOGY:

1.1 Identification of microRNA targets:

Retrieval of microRNA sequences from miRBase database: MiRBase current release (12.0) contains 87 species including Homo sapiens, flies, plants, animals and viruses also. Among 87 species, 21 are

plant species. *Brassica napus* and *Glycine max* are considered for our present work. There are 45 mature microRNAs of *Brassica napus* and 69 mature microRNAs of *Glycine max* present in database. Mature microRNA sequences of *Brassica napus* and *Glycine max* are downloaded from miRBase database (<http://microrna.sanger.ac.uk/>) which is considered as repository of microRNA sequences of different species.

BLAST against EST Sequences:

BLAST was performed with microRNA sequences of desired plant species against their EST sequences. The BLAST program was developed by Stephen Altschul of NCBI in 1990 and has since become one of the most popular programs for sequence analysis. The objective of performing BLAST is to find high-scoring ungapped segments among related sequences^{13,14}. The existence of such segments above a given threshold indicates pairwise similarity beyond random chance, which helps to discriminate related sequences from unrelated sequences in a database¹.

Hits with threshold bit score 36.1 and E-value less than 1 have been considered. Resultant sequences are considered as potential targets for microRNA.

1.2 Identification of affected proteins:

As potential targets are identified using BLAST against EST sequences, these targets encode specific protein whose translation is being suppressed due to binding of microRNA with corresponding mRNAs.

In order to identify the affected proteins with their functions we had convert target sequence (nucleotide sequence) into protein query. For this purpose BLASTX, which uses nucleotide sequences as queries and translate them in all six reading frames to produce translated protein sequences, was used. These translated protein sequences

further used as protein query for protein sequence Database.

In order to get more specified consequences target sequences with threshold bit score 40.1 and E-value less than 1 was selected and BLASTX was performed for these selected target sequences against SwissProt Database (highly annotated protein database). Hits with highest bit score and lowest E-value should be considered.

microRNA sequences in miRBase Database. MicroRNAs of plant species with bit score more than 100 have been selected as homologs of target microRNAs.

RESULT AND DISCUSSION

1.1 Identification of microRNA targets:

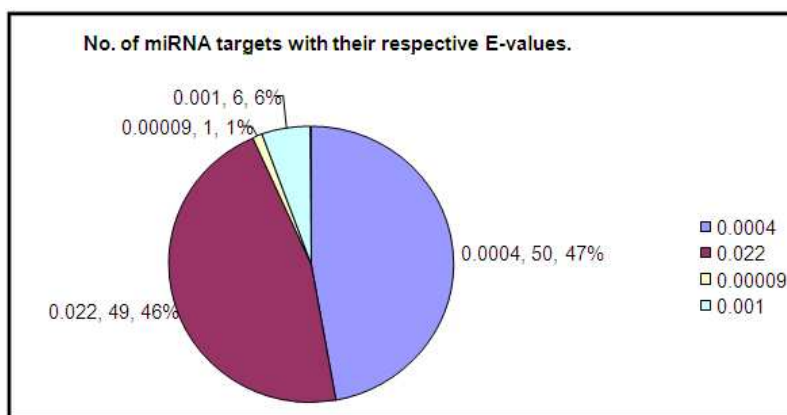
On the basis of sequence similarity exploration, we found 106 potential microRNA targets for 26 mature microRNA sequences of *Brassica napus*, among 45 mature microRNA sequences, published in database.

1.3 Identification of microRNA homologs:

To identify microRNA homologs of desired species, microRNAs of these are taken as input for sequence similarity search against

Figure 1

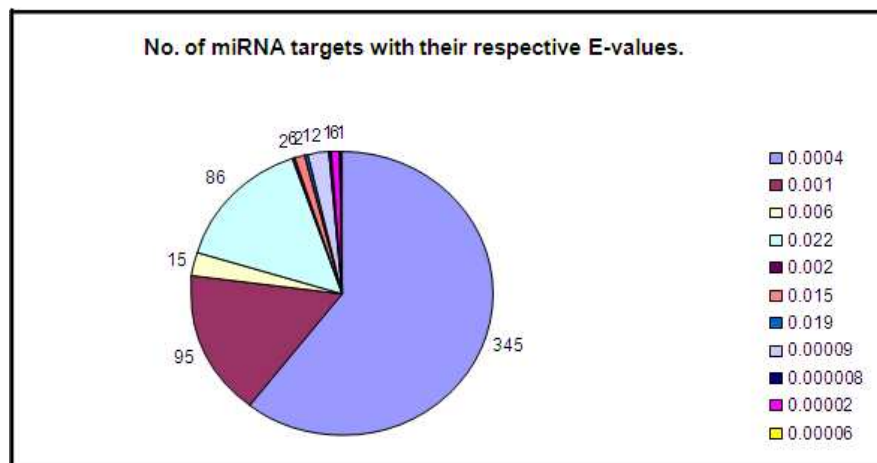
Pie chart showing no. of microRNA targets with their respective E-values for *Brassica napus*.



These targets share very high similarities with microRNA and shows E-value ranging from 0.022 to 0.0004. Among 106 microRNA targets of *Brassica napus*, 47% of targets are showing E-value of 0.0004 and 46% is showing E-value of 0.022 (Fig. 1).

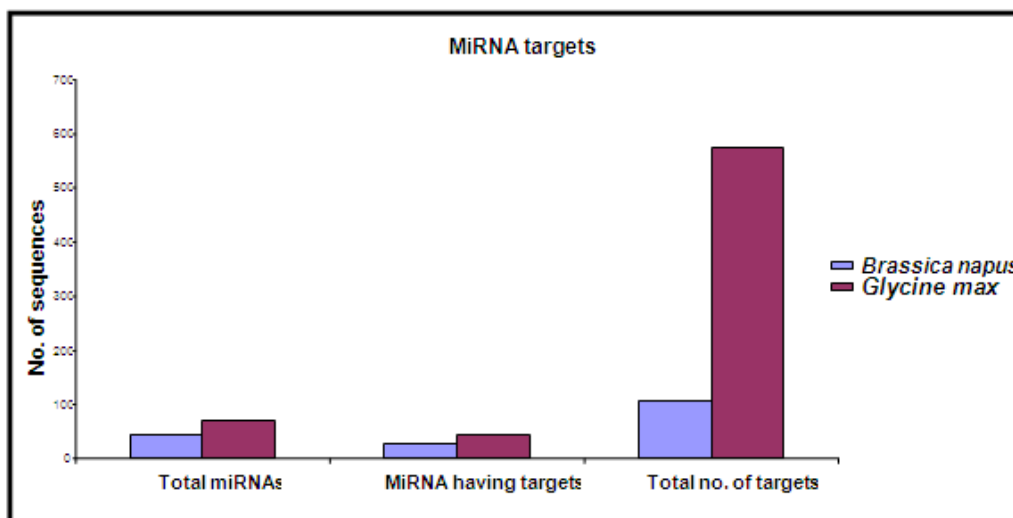
For *Glycine max* we found 573 targets for 44 mature microRNA sequences among 69 mature microRNA sequences published in database. These targets are also showing significant sequence similarities with E-value

Figure 2
Pie chart showing no. of microRNA targets with their respective E-values for *Glycine max*.



Among 573 microRNA targets of *Glycine max*, 61% of targets are showing E-value of 0.0004 and 17% are showing E-value of 0.001 (Fig. 2). Now, it was found that most of the microRNA with their respective target sequence shared similarities with very less E value which is significant and provide accuracy.

Figure 3
microRNA and targets of *Brassica napus* and *Glycine max*.



1.2 Identification of affected proteins:

In case of *Brassica napus*, concerning bit score (40 and above) and E-value we got 69 among 106 target sequences. From these 69 sequences, only 11 targets encode specified protein. In case of *Glycine max* we got 458

targets sequences using suitable statistical parameter i.e. concerning bit score (40 and above) and E-value. Most of the targets encode for *Maturase K (Intron maturase)* and *Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)*. Probably, *Maturase K*

assists in splicing of its own and other chloroplast group II introns. *PsaA* proteins bind P700, the primary electron donor as well as the electron acceptor of photosystem I (PSI). These proteins are among those

protein whose formation is terminated or altered by the action of microRNA binding and interfere RNA splicing and photosynthesis respectively. (Shown in Table 1 and 2.)

Table 1
MicroRNA sequences of Brassica napus with their respective proteins

MicroRNA sequences	Target sequence	Protein function
bna-miR156a MIMAT0004445	gb FG577558.1	Isocitrate lyase
	gb EV197905.1	none
	gb EE558005.1	none
	gb CD835236.1	none
bna-miR159 MIMAT0005635	gb EV097219.1	none
	gb EV097138.1	none
	gb EE543548.1	none
	gb EE462565.1	none
bna-miR167a MIMAT0005626	gb FG569613.1	none
	gb EV055825.1	none
	gb EV043346.1	none
	gb EV042229.1	none
	gb EV134163.1	none
	gb EV133982.1	none
	gb EV096598.1	Mitochondrial ribosomal protein S3
	gb ES910254.1	none
	gb DY023882.1	none
gb EG019793.1	none	
bna-miR167b MIMAT0005627	gb FG569613.1	none
	gb EV055825.1	none
	gb EV043346.1	none
	gb EV042229.1	none
	gb EV134163.1	none
	gb EV133982.1	none
	gb EV096598.1	Mitochondrial ribosomal protein S3
	gb ES910254.1	none
	gb DY023882.1	none
gb EG019793.1	none	
bna-miR167c	gb FG569613.1	none

MIMAT0005628		
	gb EV055825.1	none
	gb EV043346.1	none
	gb EV042229.1	none
	gb EV134163.1	none
	gb EV133982.1	none
	gb EV096598.1	Mitochondrial ribosomal protein S3
	gb ES910254.1	no significant similarity found
	gb DY023882.1	none
	gb EG019793.1	none
bna-miR168		
MIMAT0005625	gb EV056342.1	none
	gb DW997698.1	none
bna-miR171a		
MIMAT0005605	gb ES902868.1	none
bna-miR171b		
MIMAT0005606	gb EE433179.1	none
bna-miR171c		
MIMAT0005607	gb EE433179.1	none
bna-miR171d		
MIMAT0005608	gb EE433179.1	none
bna-miR171e		
MIMAT0005609	gb EE433179.1	none
bna-miR171f		
MIMAT0005610	gb EE433179.1	none
	gb ES902868.1	none
bna-miR171g		
MIMAT0005611	gb DW997698.1	none
	gb ES902868.1	none
bna-miR390a		
MIMAT0005602	gb DW997698.1	none
bna-miR390b		
MIMAT0005603	gb EE544982.1	none
bna-miR390c		
MIMAT0005604	gb EE544982.1	none
bna-miR396a		
MIMAT0004448	gb EE544982.1	none
bna-miR399		
MIMAT0004449	gb BQ704984.1	none
bna-miR824		
MIMAT0005599	gb CX190537.1	none
	gb EV221249.1	none
	gb EV220978.1	none
	gb EV219067.1	RecName: Full=Deoxyhypusine synthase

gb EV188420.1	no significant similarity found
gb EV098093.1	RecName: Full=Deoxyhypusine synthase
gb EV098027.1	RecName: Full=Deoxyhypusine synthase
gb EV097069.1	RecName: Full=Deoxyhypusine synthase
gb EV096987.1	RecName: Full=Deoxyhypusine synthase
gb ES913789.1	none
gb ES904005.1	none
gb ES903874.1	none
gb EE411731.1	no significant similarity found
gb CD837287.1	no significant similarity found

Table 2
MicroRNA sequences of Glycine max with their respective proteins

MicroRNA sequences	Target sequence	Protein function
gma-miR156a MIMAT0001686	gb BE807821.1	absent
gma-miR156b MIMAT0001692	gb FK569365.1	Alternative oxidase 2, mitochondrial precursor
	gb FK562177.1	absent
	gb FK521923.1	Probable phytol kinase 3, chloroplast precursor
	gb FK521248.1	Probable phytol kinase 3, chloroplast precursor
	gb FK365696.1	none
	gb CX708501.1	monogalactosyldiacylglycerol synthase
	gb CO985582.1	aspartic proteinase 5
	gb CO985196.1	none
	gb CO984565.1	none
	gb CO981736.1	Putative membrane protein ycf1 (RF1)
	gb CO980857.1	none
	gb BM731193.1	Full=Probable monogalactosyldiacylglycerol synthase, chloroplastic
	gb BM093898.1	Heat shock protein STI (Stress-inducible protein)
	gb BM092276.1	none
	gb BI470983.1	none
	gb BG651519.1	none
	gb BG650023.1	none
	gb BG507682.1	none
	gb BF596468.1	2S albumin precursor (GM2S-1)
	gb BE806824.1	Cytochrome c oxidase subunit 3
	gb BE329522.1	Glycinin G3 precursor [Contains: Glycinin A subunit; Glycinin B subunit]
	gb AW734915.1	Translation initiation factor IF-1, chloroplast precursor
	gb FK641165.1	none



	gb FK632844.1 	none
	gb FK633061.1 	none
	gb FK608123.1 	none
	gb FK579038.1 	none
	gb FK524278.1 	none
	gb FK516739.1 	none
	gb FK513427.1 	none
	gb FK488231.1 	none
	gb FK470180.1 	none
	gb FK460728.1 	none
	gb FK461068.1 	none
	gb FK442203.1 	none
	gb FK271762.1 	none
	gb CO983287.1 	Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb CO983096.1 	Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb CO980399.1 	none
	gb BM731329.1 	Seed lipoxygenase
	gb BI425943.1 	Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb BG650778.1 	Cytochrome c oxidase subunit 3
	gb BE057288.1 	none
gma-miR156c MIMAT0001674	gb FK664361.1 	none
	gb FK666902.1 	Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK664478.1 	Maturase K (Intron maturase)
	gb FK658463.1 	Maturase K (Intron maturase) ,
	-	Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK658266.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A) ,Proteasome subunit alpha type-5
	gb FK654794.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK648238.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK643635.1 	none
	gb FK647043.1 	none
	gb FK635811.1 	Maturase K (Intron maturase)
	gb FK641518.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK630972.1 	Maturase K (Intron maturase) ,Photosystem I P700

	chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK623706.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK616409.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK607700.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK610097.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Proteasome subunit alpha type-5
<u>gb FK604699.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK596477.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK585638.1 </u>	Maturase K (Intron maturase)
<u>gb FK584753.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK573175.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK574709.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK565917.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK565831.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK564959.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK556149.1 </u>	none
<u>gb FK549500.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK549682.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK547607.1 </u>	Maturase K (Intron maturase)
<u>gb FK534216.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK530811.1 </u>	Maturase K (Intron maturase)
<u>gb FK528782.1 </u>	none
<u>gb FK526264.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK524146.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK517527.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Inducible nitrate reductase [NADH] 2 (NR),

Inducible nitrate reductase [NADH] 1

<u>gb FK511401.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Omega-3 fatty acid desaturase, endoplasmic reticulum;Omega-3 fatty acid desaturase, chloroplast precursor
<u>gb FK506985.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK496213.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK495453.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK496336.1 </u>	Maturase K (Intron maturase)
<u>gb FK495104.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Cytochrome c biogenesis protein ccsA
<u>gb FK499257.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK493516.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK483340.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK481097.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK440078.1 </u>	Maturase K (Intron maturase), Proteasome subunit alpha type-5 (20S proteasome alpha subunit E) (20S proteasome subunit alpha-5)
<u>gb FK430240.1 </u>	none
<u>gb FK432773.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK428368.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK425300.1 </u>	Maturase K (Intron maturase)
<u>gb FK422694.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK418393.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK402969.1 </u>	Beta-conglycinin, alpha chain precursor
<u>gb FK403918.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK393884.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Basic 7S globulin 2 precursor (SBg7S) (Bg) [Contains: Basic 7S globulin 2 high kDa subunit; Basic 7S globulin 2 low

	kDa subunit]
gb FK392010.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), RecName: Full=UDP-sugar pyrophosphorylase 1
gb FK377570.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb FK367385.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb FK369718.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), DNA-binding protein DRP90, Cytochrome P450 78A3
gb FK352183.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb FK345759.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb FK339646.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb FK318835.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Inducible nitrate reductase [NADH] 2 (NR), Inducible nitrate reductase [NADH] 1
gb FK311332.1 	none
gb FK303979.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Phosphoenolpyruvate carboxylase, housekeeping isozyyme (PEPCase) (PEPC 1), Phosphoenolpyruvate carboxylase (PEPCase) (PEPC)
gb FK296761.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), DNA-binding protein DRP90
gb FK290121.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb FK278055.1 	no
gb FK273860.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb CX706284.1 	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
gb CX701955.1 	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
gb BI971210.1 	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit;

Glycinin B3 subunit]	
<u>gb BI699573.1 </u>	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
<u>gb BE821022.1 </u>	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
<u>gb BE611678.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Nodulin 26B precursor (N-26B)
<u>gb BE210632.1 </u>	Translation initiation factor IF-1, chloroplast precursor Early nodulin 75 precursor (N-75) (NGM-75), Translation initiation factor IF-1, chloroplast precursor
<u>gb AW756919.1 </u>	Translation initiation factor IF-1, chloroplast precursor
<u>gb AW459710.1 </u>	Maturase K (Intron maturase)
<u>gb EV277456.1 </u>	none
<u>gma-miR156d MIMAT0001672</u>	<u>gb FK664361.1 </u> none
<u>gb FK666902.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), RecName: Full=Cytochrome P450 71D9
<u>gb FK664478.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK658463.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK658266.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Proteasome subunit alpha type-5 (20S proteasome alpha subunit E) (20S proteasome subunit alpha-5)
<u>gb FK654794.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK648238.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK643635.1 </u>	none
<u>gb FK647043.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK635811.1 </u>	Maturase K (Intron maturase)
<u>gb FK641518.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK630972.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK623706.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK616409.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)



<u>gb FK607700.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK610097.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Proteasome subunit alpha type-5
<u>gb FK604699.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK596477.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Proteasome subunit alpha type-5
<u>gb FK585638.1 </u>	Maturase K (Intron maturase)
<u>gb FK584753.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK573175.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK574709.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK565917.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK565831.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK564959.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK556149.1 </u>	none
<u>gb FK549500.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK549682.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK547607.1 </u>	Maturase K (Intron maturase)
<u>gb FK534216.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK530811.1 </u>	Maturase K (Intron maturase)
<u>gb FK528782.1 </u>	none
<u>gb FK526264.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK524146.1 </u>	Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Maturase K (Intron maturase)
<u>gb FK517527.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Inducible nitrate reductase [NADH] 2 (NR), Inducible nitrate reductase [NADH] 1
<u>gb FK511401.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Omega-3 fatty acid desaturase, endoplasmic reticulum, Omega-3 fatty acid desaturase, chloroplast precursor

<u>gb FK506985.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK496213.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK495453.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK496336.1 </u>	Maturase K (Intron maturase)
<u>gb FK495104.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Cytochrome c biogenesis protein ccsA
<u>gb FK499257.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK493516.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK483340.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK481097.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK440078.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK430240.1 </u>	none
<u>gb FK432773.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK428368.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK425300.1 </u>	Maturase K (Intron maturase)
<u>gb FK422694.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK418393.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK402969.1 </u>	Beta-conglycinin, alpha chain precursor
<u>gb FK403918.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK393884.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Basic 7S globulin 2 precursor (SBg7S) (Bg) [Contains: Basic 7S globulin 2 high kDa subunit; Basic 7S globulin 2 low kDa subunit]
<u>gb FK392010.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A) , RecName: Full=UDP-sugar pyrophosphorylase 1
<u>gb FK377570.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK367385.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)

<u>gb FK369718.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), DNA-binding protein DRP90, Cytochrome P450 78A3
<u>gb FK352183.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK345759.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK339646.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK318835.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Inducible nitrate reductase [NADH] 2, RecName: Full=Inducible nitrate reductase [NADH] 1
<u>gb FK311332.1 </u>	none
<u>gb FK303979.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Phosphoenolpyruvate carboxylase, housekeeping isozyyme (PEPCase) (PEPC 1), Phosphoenolpyruvate carboxylase (PEPCase) (PEPC)
<u>gb FK296761.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), DNA-binding protein DRP90
<u>gb FK290121.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK278055.1 </u>	none
<u>gb FK273860.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb CX706284.1 </u>	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
<u>gb CX701955.1 </u>	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
<u>gb BI971210.1 </u>	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
<u>gb BI699573.1 </u>	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
<u>gb BE821022.1 </u>	Maturase K (Intron maturase), Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit]
<u>gb BE611678.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Nodulin 26B precursor (N-26B)

	gb BE210632.1 	translation initiation factor IF-1, chloroplast precursor
	gb AW756919.1 	Early nodulin 75 precursor (N-75) (NGM-75),
	gb AW459710.1 	Translation initiation factor IF-1, chloroplast precursor
	gb EV277456.1 	Maturase K (Intron maturase)
	gb EV277456.1 	none
gma-miR156e MIMAT0001673	gb FK664361.1 	none
	gb FK666902.1 	Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Maturase K (Intron maturase)
	gb FK664478.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK658463.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK658266.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Proteasome subunit alpha type-5
	gb FK654794.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK648238.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK643635.1 	none
	gb FK647043.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK635811.1 	Maturase K (Intron maturase)
	gb FK641518.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK630972.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK623706.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK616409.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK607700.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK610097.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A),Proteasome subunit alpha type-5
	gb FK604699.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK596477.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
	gb FK585638.1 	Maturase K (Intron maturase)
	gb FK584753.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)



<u>gb FK573175.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK574709.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK565917.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK565831.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK564959.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK556149.1 </u>	none
<u>gb FK549500.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK549682.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK547607.1 </u>	Maturase K (Intron maturase)
<u>gb FK534216.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK530811.1 </u>	Maturase K (Intron maturase)
<u>gb FK528782.1 </u>	none
<u>gb FK526264.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK524146.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK517527.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Inducible nitrate reductase [NADH] 2, RecName: Full=Inducible nitrate reductase [NADH] 1
<u>gb FK511401.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Omega-3 fatty acid desaturase, endoplasmic reticulum, Omega-3 fatty acid desaturase, chloroplast precursor
<u>gb FK506985.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK496213.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK495453.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK496336.1 </u>	Maturase K (Intron maturase)
<u>gb FK495104.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Cytochrome c biogenesis protein ccsA
<u>gb FK499257.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)

<u>gb FK493516.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK483340.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK481097.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK440078.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK430240.1 </u>	none
<u>gb FK432773.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK428368.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK425300.1 </u>	Maturase K (Intron maturase)
<u>gb FK422694.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK418393.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK402969.1 </u>	Beta-conglycinin, alpha chain precursor
<u>gb FK403918.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK393884.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Basic 7S globulin 2 precursor (SBg7S) (Bg) [Contains: Basic 7S globulin 2 high kDa subunit; Basic 7S globulin 2 low kDa subunit]
<u>gb FK392010.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), RecName: Full=UDP-sugar pyrophosphorylase 1
<u>gb FK377570.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK367385.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK369718.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), DNA-binding protein DRP90, Cytochrome P450 78A3
<u>gb FK352183.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK345759.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK339646.1 </u>	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
<u>gb FK318835.1 </u>	Maturase K (Intron maturase), Inducible nitrate reductase [NADH] 2 (NR), RecName: Full=Inducible nitrate reductase [NADH] 1;

	Short=NR, Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb FK311332.1 	none
gb FK303979.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), Phosphoenolpyruvate carboxylase, housekeeping isozyeme (PEPCase)(PEPC 1), Phosphoenolpyruvate carboxylase (PEPCase) (PEPC)
gb FK296761.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A), DNA-binding protein DRP90
gb FK290121.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb FK278055.1 	none
gb FK273860.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb CX706284.1 	Maturase K (Intron maturase),Glycinin G4 precursor
gb CX701955.1 	Maturase K (Intron maturase),Glycinin G4 precursor
gb BI971210.1 	Maturase K (Intron maturase),Glycinin G4 precursor
gb BI699573.1 	Maturase K (Intron maturase),Glycinin G4 precursor
gb BE821022.1 	Maturase K (Intron maturase),Glycinin G4 precursor
gb BE611678.1 	Maturase K (Intron maturase) ,Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A)
gb BE210632.1 	Translation initiation factor IF-1, chloroplast precursor Early nodulin 75 precursor (N-75) (NGM-75), Translation initiation factor IF-1, chloroplast precursor
gb AW756919.1 	Translation initiation factor IF-1, chloroplast precursor
gb AW459710.1 	Maturase K (Intron maturase)
gb EV277456.1 	none
gma-miR159 MIMAT0001675	gb BM893181.1 none
gma-miR159a MIMAT0001675	gb BM893181.1 none
gma-miR159b MIMAT0007351	gb EH223241.1 G/HBF-1 protein [Glycine max],heat shock transcription factor 29
	gb BQ453148.1 none
	gb EV278015.1 none
	gb FK015843.1 none
gma-miR159c MIMAT0007352	gb FK015843.1 none
	gb EV278015.1 none
	gb EH223241.1 G/HBF-1 protein [Glycine max],heat shock transcription factor 29
	gb BQ453148.1 none



gma-miR160 MIMAT0001676	gb CA801322.1 	none
	gb BU760860.1 	Probable phytol kinase 2, chloroplast precursor
	gb BG882856.1 	Probable phytol kinase 2, chloroplast precursor
	gb FK641283.1 	none
		RecName: Full=Purple acid phosphatase; AltName: Full=Zinc(II) purple acid phosphatase; Flags: Precursor
	gb CF808592.1 	
	gb BM887596.1 	none
	gb AI900826.1 	none
	gb AI794655.1 	none
gma-miR162 MIMAT0007353	gb BU081804.1 	none
	gb BI785837.1 	none
		Uricase-2 isozyme 2 (Uricase II isozyme 2) (Urate oxidase) (Nodulin 35) (N-35) (Non-symbiotic uricase),NAD(P)H-quinone oxidoreductase chain 5, chloroplast (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5)
gma-miR166a MIMAT0001677	gb FK648257.1 	
	gb FK528727.1 	none
		Uricase-2 isozyme 2 (Uricase II isozyme 2) (Urate oxidase) (Nodulin 35) (N-35) (Non-symbiotic uricase),NAD(P)H-quinone oxidoreductase chain 5, chloroplast (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5)
	gb FK520130.1 	
		Uricase-2 isozyme 2 (Uricase II isozyme 2) (Urate oxidase) (Nodulin 35) (N-35) (Non-symbiotic uricase),NAD(P)H-quinone oxidoreductase chain 5, chloroplast (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5)
	gb FK301064.1 	
		NAD(P)H-quinone oxidoreductase chain 5, chloroplast (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5)
	gb FK277357.1 	
	gb FG993975.1 	none
	gb EV280596.1 	none
		Uricase-2 isozyme 2 (Uricase II isozyme 2) (Urate oxidase) (Nodulin 35) (N-35) (Non-symbiotic uricase)
	gb EV266011.1 	
	gb CD405934.1 	none
	gb CD391899.1 	none
	gb CA819984.1 	none

	gb BQ785760.1 	none
	gb BM308126.1 	RecName: Full=Seed lipoxygenase-1; Short=L-1
	gb BM092635.1 	none
	gb BI893541.1 	none
	gb FK007014.1 	none
	gb FK007013.1 	none
	gb EV267001.1 	none
	gb CO985884.1 	none
	gb BI972515.1 	none
	gb BG316028.1 	none
		Uricase-2 isozyme 2 (Uricase II isozyme 2) (Urate oxidase) (Nodulin 35) (N-35) (Non-symbiotic uricase),NAD(P)H-quinone oxidoreductase chain 5, chloroplast (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5)
gma-miR166b MIMAT0001678	gb FK648257.1 	
	gb FK528727.1 	none
		Uricase-2 isozyme 2 (Uricase II isozyme 2) (Urate oxidase) (Nodulin 35) (N-35) (Non-symbiotic uricase),NAD(P)H-quinone oxidoreductase chain 5, chloroplast (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5)
	gb FK520130.1 	
		Uricase-2 isozyme 2 (Uricase II isozyme 2) (Urate oxidase) (Nodulin 35) (N-35) (Non-symbiotic uricase),NAD(P)H-quinone oxidoreductase chain 5, chloroplast (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5)
	gb FK301064.1 	
		NAD(P)H-quinone oxidoreductase chain 5, chloroplast (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5)
	gb FK277357.1 	
	gb FG993975.1 	none
	gb EV280596.1 	none
		Uricase-2 isozyme 2 (Uricase II isozyme 2) (Urate oxidase) (Nodulin 35) (N-35) (Non-symbiotic uricase)
	gb EV266011.1 	
	gb CD405934.1 	none
	gb CD391899.1 	none
	gb CA819984.1 	none
	gb BQ785760.1 	none
	gb BM308126.1 	RecName: Full=Seed lipoxygenase-1; Short=L-1
	gb BM092635.1 	none
	gb BI893541.1 	none



	gb FK007014.1 	none
	gb FK007013.1 	none
	gb EV267001.1 	none
	gb CO985884.1 	none
	gb BI972515.1 	none
	gb BG316028.1 	none
gma-miR167a MIMAT0001679	gb FK023040.1 	none
	gb FK014649.1 	none
	gb CX711679.1 	none
	gb CO984488.1 	none
	gb BI095235.1 	Elongation factor Tu, chloroplast precursor (EF-Tu)
	gb FK008682.1 	none
	gb CN472374.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb CN472374.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb CD411229.1 	none
	gb BU548271.1 	none
	gb BQ629383.1 	none
	gb BM892909.1 	none
	gb BG510970.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb BG509097.1 	none
	gb AW472145.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb AW318298.1 	Inducible nitrate reductase [NADH] 2 (NR)
gma-miR167b MIMAT0001680	gb FK023040.1 	none
	gb FK014649.1 	none
	gb CX711679.1 	none
	gb CO984488.1 	none
	gb BI095235.1 	Elongation factor Tu, chloroplast precursor (EF-Tu)
	gb FK008682.1 	none
	gb CN472374.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb CK768366.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb CD411229.1 	none
	gb BU548271.1 	none
	gb BQ629383.1 	none
	gb BM892909.1 	none
	gb BG510970.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb BG509097.1 	none
	gb AW472145.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb AW318298.1 	Inducible nitrate reductase [NADH] 2 (NR)
gma-miR167c MIMAT0007355	gb FK008682.1 	none
	gb CN472374.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb CK768366.1 	Inducible nitrate reductase [NADH] 2 (NR)

	gb CD411229.1 	none
	gb BU548271.1 	none
	gb BQ629383.1 	none
	gb BM892909.1 	none
	gb BG510970.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb BG509097.1 	none
	gb AW472145.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb AW318298.1 	Inducible nitrate reductase [NADH] 2 (NR)
	gb FK023040.1 	none
	gb FK014649.1 	none
	gb CX711679.1 	none
	gb CO984488.1 	none
	gb BI095235.1 	Elongation factor Tu, chloroplast precursor (EF-Tu)
gma-miR168 MIMAT0001681	gb BE661028.1 	none
	gb BE659175.1 	none
	gb AW424354.1 	none
gma-miR169a MIMAT0001693	gb CA953278.1 	Beta-conglycinin, alpha' chain precursor Photosystem II P680 chlorophyll A apoprotein (CP-47 protein)
	gb AW596073.1 	none
	gb BF595231.1 	none
	gb AW201497.1 	none
gma-miR169b MIMAT0007356	gb BF595231.1 	none
	gb AW201497.1 	none
	gb CA953278.1 	Beta-conglycinin, alpha' chain precursor Photosystem II P680 chlorophyll A apoprotein (CP-47 protein)
	gb AW596073.1 	none
gma-miR169c MIMAT0007357	gb BF595231.1 	none
	gb AW201497.1 	none
gma-miR171a MIMAT0007358	gb CA937914.1 	Protein ycf2
gma-miR172a MIMAT0001682	gb BU084569.1 	none
	gb BI320499.1 	none
gma-miR172b MIMAT0001683	gb BU084569.1 	none
	gb BI320499.1 	none
gma-miR319a MIMAT0001684	gb BQ630517.1 	none
	gb BQ630503.1 	none
	gb BE475558.1 	none

gma-miR319b MIMAT0001685	gb BQ630517.1 	none
	gb BQ630503.1 	none
	gb BE475558.1 	none
gma-miR319c MIMAT0001691	gb BG237979.1 	none
gma-miR396a MIMAT0001687	gb FK019312.1 	none
	gb CA853579.1 	none
	gb CA784869.1 	none
	gb CO982379.1 	none
	gb BM521827.1 	Protein ycf2, Nodulin 26B precursor (N-26B)
	gb BG405077.1 	Protein ycf2
gma-miR396b MIMAT0001688	gb CO982379.1 	none
	gb BM521827.1 	Protein ycf2
	gb BG405077.1 	Protein ycf2
	gb FK019312.1 	none
	gb CA853579.1 	none
	gb CA784869.1 	none
gma-miR398a MIMAT0001689	gb CB063312.1 	none
	gb CA937628.1 	Cytochrome P450 77A3
gma-miR398b	gb CB063312.1 	none
	gb CA937628.1 	Cytochrome P450 77A3
gma-miR482 MIMAT0007364	gb CA935176.1 	none
gma-miR1507 MIMAT0007365	gb FK637099.1 	none
	gb FK014653.1 	none
	gb FK008348.1 	none
	gb FK008347.1 	none
	gb CX711875.1 	none
	gb BU083814.1 	none
	gb BU083714.1 	none
	gb BM092446.1 	none
	gb BI967632.1 	none
	gb BI321829.1 	none
	gb AW350017.1 	none
gma-miR1508 MIMAT0007366	gb FG998704.1 	none
	gb FG994738.1 	none
	gb BM887194.1 	none
	gb AW508363.1 	none

gma-miR1509 MIMAT0007367	gb BI785214.1 	none
gma-miR1510 MIMAT0007368	gb BF009798.1 	Vacuolar-processing enzyme precursor(VPE),Photosystem II 44 kDa reaction center protein (P6 protein) (CP43)
	gb AW569234.1 	Vacuolar-processing enzyme precursor(VPE)
	gb CB063582.1 	none
	gb FK015547.1 	none
gma-miR1511 MIMAT0007369	gb AW101147.1 	none
gma-miR1518 MIMAT0007377	gb FG986663.1 	Early nodulin 70,Sucrose synthase (Sucrose-UDP glucosyltransferase) (Nodulin-100)
	gb EV273643.1 	Early nodulin 70
gma-miR1520d MIMAT0007379	gb BU544883.1 	none

1.3 Identification of microRNA homologs:

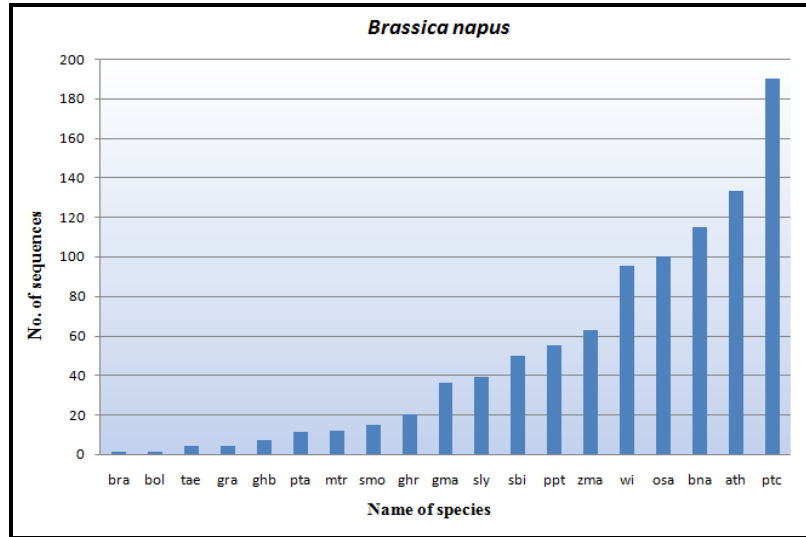
In case of *Brassica napus*, 45 microRNA targets are having total 951 homologs in different plant species. Some of the plant species are *Glycine max*, *Oryza sativa*, *Zea mays*, *Sorghum bicolor*, *Populus trichocarpa*, *Vitis vinifera*, *Solanum lycopersicum*, *Medicago truncatula*, *Pinus taeda*, *Physcomitrella patens*, *Selaginella moellendorffii*, *Solanum lycopersicum* and many more including *B. napus* itself.

In case of *Glycine max* 22 microRNA targets are having total 418 homologs in species like *Physcomitrella patens*, *Triticum aestivum*, *Sorghum bicolor*, *Gossypium hirsutum*, *Vitis*

vinifera, *Oryza sativa*, *Brassica napus* and many more.

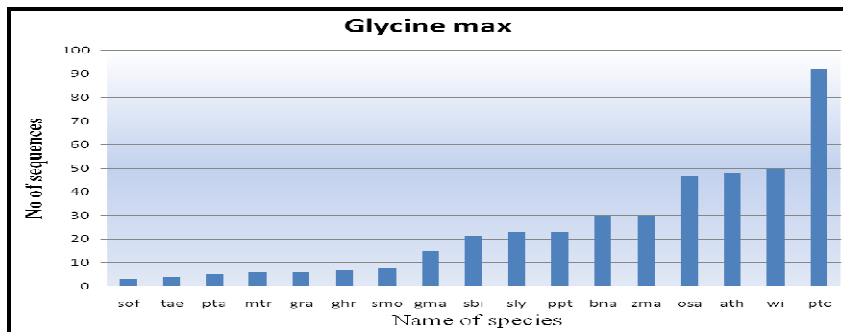
Overall number of microRNA homologs for *Brassica napus* are 951 and 190 microRNA sequences are found as microRNA homologs for *Populus trichocarpa* and species like *Triticum aestivum*, *Saccharum officinarum*, *Brassica oleracea* and *Gossypium rammindii* does not share considerable homology. Hence microRNAs of *Brassica napus* are more conserved with in *Populus trichocarpa*. MicroRNAs of *Arabidopsis thaliana*, *Oryza sativa* and *Vitis vinifera* are also showing homology with *Brassica napus* (Fig. 4).

Figure 4
Graph showing homologs for microRNA sequences of *Brassica napus*



Overall number of microRNA homologs for *Glycine max* is 418 and 92 microRNA sequences are showing homology with microRNA of species *Populus trichocarpa*. Therefore microRNAs of *Glycine max* are more conserved with in *Populus trichocarpa*. MicroRNAs of *Arabidopsis thaliana*, *Oryza sativa*, *Vitis vinifera*, *Zea mays* and *Brassica napus* are also showing homology with *Brassica napus* (Fig. 5).

Figure 5
Graph showing homologs for microRNA sequences of *Glycine max*.



It is remarkable that both *Brassica napus* and *Glycine max* share maximum similarity with *Populus trichocarpa*. In case of *Brassica napus*, species *Brassica oleracea* and *Brassica rapa* and in case of *Gycine max*, species *Triticum aestivum* and *Saccharum officinarum* share minimum homology with their respective species.

CONCLUSION

As according to goal of our work, microRNA targets for microRNA sequences of *Brassica napus* and *Glycine max* have been identified. We got 106 microRNA targets for *Brassica napus* and 573 targets for *Glycine max*. The

broad range of putative microRNA targets indicates that microRNAs participate in the regulation of variety of biological processes. The most affected proteins which are terminated or altered via complementary base pair interactions are Maturase K (Intron maturase) and Photosystem I P700 chlorophyll a apoprotein A1 (PsaA) (PSI-A). Homologs of *Brassica napus* (951 in no.) and *Glycine max* (418 in no.) microRNA have also been identified

with numerous species such as *Oryza sativa*, *Zea mays*, *Sorghum bicolor*, *Populus trichocarpa*, *Vitis vinifera*, *Solanum lycopersicum*, *Medicago truncatula*, *Pinus taeda*, *Physcomitrella patens*, *Selaginella moellendorffii*, *Solanum lycopersicum*. Results indicate that microRNA of *Brassica napus* are more evolutionary conserved than *Glycine max* as later one shows less sequence homology with microRNAs of other species.

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