Recognizable Proof of Moderated Mirnas And Their Bioreceptortargets In Jatropha Curcas

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Abstract- *Jatropha curcas L. has a place to family Euphorbiaceae, Jatropha curcas could be a important multipurpose edit, generally it was utilized as medication for wounds and takes off utilized as drinks against jungle fever, jatropha plants utilized to control soil corruption, lighten disintegration, desertification and increase soil ripeness, in any case, in final decades there's more consideration to utilize jatropha oil for deliver biodiesel*

Jatropha curcas is effortlessly engendered by seeds or stem cutting, it is tolerant for dry spell for longtime, it is develop well with tre ated wastewater, too, it can be developed on minimal arrive.

Jatropha curcas seed have about 32-40% valuable oil utilized to create biofuel, subsequently, it may well be the source for biodiesel generation especially in dry and semiarid districts.

I. INTRODUCTION

Jatropha curcas, negligible lands, treated wastewater, biodiesel. Presentation Jatropha curcas a woody bush, it is one of family Euphorbiaceae, it is most widely specie across different regions all over the world due to its quality.

It has numerous names in several locales just like the physic nut, goat nuts, (pinhãomanso in Brazil), Barbados nut, cleansing nut,vexspurge, or fair Jatropha , past investigates appeared that jatropha is local to Central and South America .

Jatropha curcas is fitting for development beneath unfavorable conditions, like dry season, moo supplement supply and saltiness , moreover, jatropha may be a appropriate arrangement for biofuel generation from development inundated with treated wastewater .

Jatropha considered a multipurpose plant, it has been utilized in conventional human medication and for veterinary medication for over a long period of time , it can diminish soil corruption, desertification, and deforestation .

There are more curiously approximately jatropha from the final decades utilize jatropha oil as a primary source for biodiesel generation rather than eatable crops , moreover, it is to combat desertification and decrease soil disintegration in bone-dry locales.

Jatropha has incredible abdicate potential and can be develops well beneath stretch conditions, and it is claimed to be dry season safe and can be developed beneath saltiness and on negligible lands conditions.

The eminent imperative of Jatropha curcas L. as biofuel edit, due to its seeds bearing 32 to 40% oil substance, that can be essentially changed over into bio-diesel, thus, it has tall potential to be utilized in biodiesel generation

Biodiesel gotten from jatropha provides international standards, jatropha had awesome flexibility to bone-dry and semi-arid situations ,prober for no man's land recovery, illustrative natural push, supporting socio-economic , brief development period and being unpalatable to grazers, too.

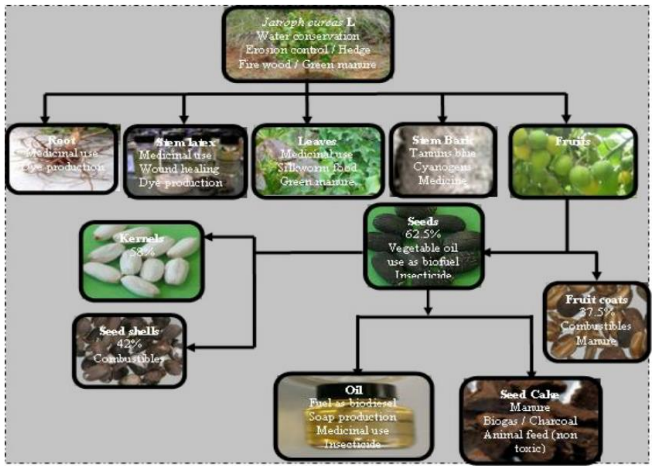
Jatropha curcas is additionally being considered for utilize as a carbon sequestration plant in bone-dry districts .

Jatropha oil cake is wealthy in NPK and can be utilized as natural fertilizers.

Jatropha has been risen to ranchers in bone-dry and semi-arid locales as a promising renewable vitality edit, and a modern financial edit for destitute soil or minimal lands, and itis sweet adjustment

The physiological characteristics of jatropha, related with its financial imminent put it into an alternative biofuel plant for parched and
semiarid districts .

For all the above-mentioned preferences and applications J. curcas remains a favorite feedstockfor deliver bio-diesel and exceedingly alluring for developing on negligible lands.



BOTANICAL:

Jatropha (Jatropha curcas L.) could be a deciduous oilseedm shrub, Jatropha sort one of Joannesieaetribe, as a part of Crotonoideae within the Euphorbiaceae family; local to tropical America , and develop .

Jatropha (more than 8 a long time ancient) reach to 7 -13 meter stature (Fig. 1), the takes off are green, thick and the length is 8.55 cm long and width approximately 5 cm, with heart-shaped, with long
neck reach to 11 cm long.

Jatropha has little greenish yellow blossoms, and the natural products are green at to begin with organize and yellow to brown on maturing.

Natural product contains frequently 2 -3 oval dark seeds, the seed contains kernels and shells, kernel contain protein (22%-28%and tall oil substance (extending from 32% -40%) agreeing to the developing conditions and genotype [18].

Blooming and fertilization:

Jatropha curcasis a monoecious plant.

Inflorescences create on terminals of branches and contain both the male and female blossoms, male blossoms encompassed central female flower .

J. curcas create little greenish yellow blossoms, as a rule, the blossomsare unisexual, as it were many male blossoms are delivered in each inflorescence, all blossoms were open at the same time (both female and male) subsequently.

Cross-pollination might be between blooms from the same plants or from other plants, female blossoms and buds are to some degree larger than the male blossoms, soil moister and legitimate temperature considered as advancing variables for Jatropha to have two crops amid the year .

Beneath Egyptian conditions jatrophacurcas blossoming twice time in the year, to begin with one in April, the moment one gathered in December .

Fruiting and seed Development:

The natural products are around 2.5 cm long and contain three dark seeds, it is reach to total measure after 90 days from fertilization date around, isolated to 30- 45 days after fertilization .

Yellow natural product organize (develop 45-60 days) be that as it may, matured organize begin after 60 days roughly [21].

Abdicate and Trim generation:

There are different variables influencing edit generation of J. curcas, the overall abdicate can be made strides through productive utilize for water necessities and fertilizers, subsequently, water deficiency and destitute supply of nutrients at basic dev elopment organize appears to be the key figure diminished the trim generation [22].

Moreover, the number of branches shaped and fundamental spike length considered major components in expanding the number of natural products and influences the full number of capsules, seed surrender, and seed oil substance.

Methods :

Here,weutilized afew bioinformatics assets todetect p reserved miRNAs inJ. curcas. The schematic workflow for distinguishing miRNAs is portrayed in Fig.1.

Sequence collection and computer program informationEST arrangements were considered for th e genome based identifications of microRNAs. The recommended EST sequences of Jatropha (ID txid180498) were collected from the NCBI Genbank nucleotide database .

To discover conceivable miRNAs within the J. curcas, totally available miRNAs of the bunch viridiplantae Chloro-phyta, Coniferophyta, Embryophyta, and Magnolio-phyta) were recovered from the mirBase.

All the excesor rehashed arrangements from both mi RNAs and ESTsequences were at that point disposed of by CD HIT by keeping the esteem of grouping character cut off to 1.

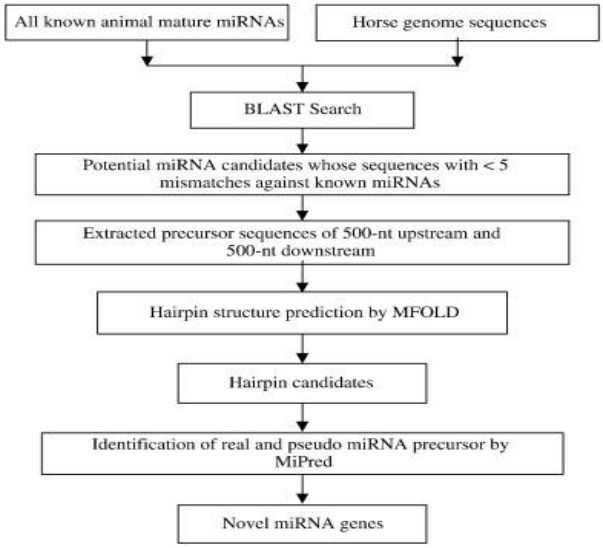
Thescreened develop miRNAs of viridiplantae were utilizedas inquiry arrangements for homology look against the ESTsof J. curcas by utilizing BLASTn of NCBI database 2021) by setting up the parameters to default.

As it were the top result for each Impact was chosen for encourage analysis.

Oncemore , the ESTs from the beat hit of BLASTn w eresubjectedto excess check by utilizing CD HIT. Theobtained ESTs were at that point adjusted against nr database of BLASTx (accessed on July 1, 2021) for dispensing with protein coding sequences and as it were the non protein coding groupingswere chosen to finalize the potential forerunner miRNA(pre-miRNAs) by considering the miRNA antecedent determinant properties.

Identification of pre-miRNAs and putative miRNAs The non-protein coding ESTs were at that point analyzed in mirEval 2.0 to decide the pre miRNA candidates. All the candidates had a length of 85 nucleotides by default in mirEval.

Fig.1 Schematic workflow for the proof of novel miRNAs in br J. curcas



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genome was **chosen** for others and the **expectation** of the strand **arrangement** was set to **unique** .

Antecedent miRNA was **recognized concurring** . The mis-matches among the putative miRNAs and all the previously known miRNAswere **decided** by the **nearby impact**carried out in miRBase database.

Prediction of hair-loop **auxiliary** structure and naming of pre-miRNAs and **unused** miRNA Precursor miRNA **groupings** were **at that point tried** for the secondary structure **forecasts** by **utilizing freely** avail all the parameters were set to the default value.

The candidate miRNAs were chosen based on the criteria **recommended** that **permit** us tolargely **diminish wro ng** positive **comesabout** for **distinguishing** miRNAs [36]. ΔG values (kcal/mol) were **given amid** thepredictionof **auxiliary** structure in MFOL D which cabe **valuable** forcalculating their negative **negligibl e** free ener-gies (MFEs).

Balanced negligible collapsing vitality AMFEand **n egligible collapsing** free **vitality list** MFEI weremeasured as the **expected auxiliary** structure **ought to** have higher **negligible** negative MFEI and MFE . AMFE isdefined as the MFE of a 100-nucleotide length. MFEI for all single pre-miRNAs were calculate

MEF AMFE = X 100 Length of precursor sequence

The MFEI of **auxiliary** structure was calculated **utilizing** the **takingafter** equationTo **discover** the r elated miRNA families of **recognized** mi-RNAs, the putative **groupings** were locally **Impacted** in themiRBase database.

Recently recognized miRNAs were named **taking after** the **classification portrayed** by Grif-fiths-Jones et al. Prediction and **useful investigation** of **recently distinguished** miRNAs targets.

In this **ponder** , we **connected** a homology based **look** method for **deciding** the potential targets of identi-fied miRNAs.

Since of the **restricted quality accessibility** ofJ.curcaswe **util ized**Arabidopsisas a reference **life form**for **deciding** the targets of the candidate miRNAs.

The **recently recognized develop** miRNAs were **utilized** as **i nquiry**againsttheA.thalianaDFCI **quality record** AGI **dischar ge** 15and A. thaliana TAIR10, cDNA, **evacuated** miRNA **quality**

All the parameters in psRNATarget for target **expectation** were kept in default **but** the **taking after** 1 The HSP size was kept **inside** 18, and 2 central **bungle** fortranslational **restraint** was 9 11 nucleotides. The targetproteins, **atomic capacities** an d **natural prepare**in J. curcas were analyzed by **looking** the mRNA IDs in 2021).

The **distinguished focused on qualities** of jcu miR11155c 3p, jcu-miR7805-3p and jcu-miR8786 were **organized utilizing)** as most of the target **qualities** of those three miRNAs were found **related** with diesel **generation** ,stress **resistance** , and h ormonal **direction** .

It **gives** a number of co expressed **qualities pertinent** to target **qualities** to make the **administrative systems** more complete.

Phylogenetic **investigation** of **anticipated** miRNAs and **appr oval**of **distinguished** miRNAs.

The related families of**recently distinguished** novel miRNAs were collected from miRBase by **grouping look** and collated with the putative miRNAs to carry out a phylogenetic **investigation** in Clustal Omega, which utilizes seeded **direct** trees and **Well** profile profile **strategies**to **creat e grouping arrangements** between three ormore **groupings**.

At that point , the **grouping** similarities were **seen** and phylogenetic tree was con-structed in MEGA X **program utilizing** the **separate** based method . As the miRNAs **have to be** be non protein coding, all the putative miRNAs of Jatropha were analyzed for their non-protein coding properties **within the**BLASTx program.

Results:

Acquisition ofJ. Curcas ESTs and reference set of miRNAsA **add up to** number of 46,865 ESTs ofJ. Curcas were **extricated** from the NCBI nucleotide database For the reference set of miRNAs, a **add up to** of 6746 mature miRNAs of plant eudicotyledons, **having a place** to the 20 plant families were collected from the publicly **accessible** miRbase database Supplementary **record**2).

Analysis **within the** CD HIT server **expelled** 4491 **excess** ESTs, **holding** 42,374 ESTs without **rehashed arrangements** for **assist think**

These ESTs will be the potential homologs for finding the target miRNAs.

On the other hand,3514 **develop** miRNA **arrangements** were et al. selected from 6746 eudicotyledons miRNAs after the removal of **repetition** Supplementary **record**.

Screening for non coding miRNA candidates :

Homology-based **look** of the non redundant eudicoty- ledons miRNAs were carried out in BLASTn against 42,374 ESTs of J. curcas by considering all the default parameters.

Each miRNA **inquiry come about** in a **beat** hit against the non-redundant ESTs in BLASTn **investigation** . SixmiRNA **questions** did not **discov er** any homologs against the ESTs and **in this way** the BLASTn **comes about** in 3508 **arrangements** of Jatropha ESTs from homology **look** with the reference miRNAs.

By this approach 3508 potential miRNA containing ESTs were **gotten** . **Assist excess** checks by CD-HIT **come about** in 2880 non repeated ESTs which were kept for **advance examination** Supplementary **record** 5.

Fromthe
BLASTx **examination** of ESTs, **almost** 389 non coding ESTswere **gotten** which are to be **explored** as potentialmiRNA **forerunner groupings** Supplementary

Target **forecast** and **useful investigation** of **recently**identified J. curcas miRNAs Based on their **idealize** or **about culminate** complementaritywith their target **groupings** in Arabidopsis , the 12 putative miRNAs were **found** to be **locked in** in **focusing on** 893 **qualities** . **Additionally** , **inside** ourfiltration **method** , we **found** that 93 of **the overall** 893 targets have **obscure capacities within the show** plant A. thaliana.

The miRNA family 'miR5658' has **the foremost** individual target **qualities** 211 , **whereas** the family miR9741 has **as it were** 16 targets.

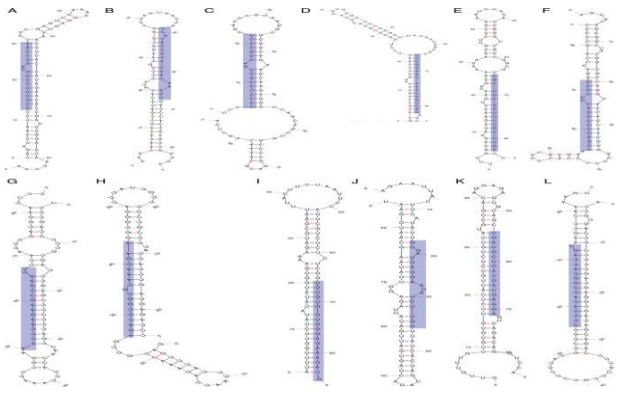
On the other hand, the number of **quality** targets for the rest of themiRNA families - miR5277 (89), miR7121 (73), miR1534 (34), miR6149-3p (95), miR11155c-3p (134), miR4249 (58), miR7805-3p (60), miR8786 (56), miR3520-5p (43), and miR2112-3p (24) were **moreover anticipated**

Distinguishing
proof of both pre miRNAs and putative miRNAs

In J. curcas different pre-defined criteria were **taken after** to **get** pre-miRNAs from 389 non-coding ESTs .

By careful **assessment** based on **jumbles** , lengths etc. described **prior** , these numbers were **diminished** to a **add up to** br of 21 pre miRNAs as candidates of Jatropha miRNAs

All br the pre miRNAs were 85 nucleotides in length as pre br br dicted by mirEval with default parameters



Newly formed miRNAS in Jatropha carcus

Properties	Jatropha Curcas Biodiesel (Foidl et al., 1996)	Jatropha Curcas biodiesel (Sarin et al., 2007)	Jatropha Curcas biodiesel (Dharma et al., 2017)	Mineral Diesel	EN 14214 (Tsoutsos et al., 2019)
Density (kg/m³) at 15 °C	879	–	876.2	840 ± 1.732	860-900
Kinematic Viscosity at 40 °C (cSt)	4.84	4.16	4.57	2.44 ± 0.27	3.4-5.0
Pour Point (°C)	3 ± 1	–	2	6 ± 1	NA
Flash Point (°C)	191	163	125.5	71 ± 3	Min. 101
Corradson Carbon residue (%, w/w)	0.01	< 0.01	–	0.1 ± 0.0	Max. 0.05
Oxidation stability (h)	–	3.23	14.01	–	Min. 6 h
Acid value (mg KOH/gm)	0.24	0.48	0.46	–	Max 0.5
Sulphated ash (%, w/w)	0.014	0.002		0.01 ± 0.0	Max. 0.02
Calorific Value (MJ/kg)	38.5	–	39.46	45.343	–
Sulphur (% w/w)	< 0.001	0.004	–	0.25	Max. 0.05
Carbon (% w/w)	77.1	–	–	86.83	–
Hydrogen (% w/w)	11.81	–	–	12.72	–
Oxygen (% w/w)	10.97	–	–	1.19	–
Cetane No.	51-52	57.1	59 (Cetane index)	49-55	Min 51
Free glycerol (% mass)	0.015	0.01		–	Max 0.020
Total glycerol (% mass)	0.088	0.02		–	Max 0.250

Properties of newly formed miRNA

MicroRNAs have **gotten to be imperative** candidates for **inquire about** as they act as **quality controllers** in **numerous** plants Finding new miRNAs **gives** a novel **understanding** to **get it** thei regulatory **parts** and **capacities** .

The **accessibility** of EST sequences of J. curcas made the **distinguishing proof** of conserved miRNAs **generally** straight forward. In plants, it is believed that **there's** at **slightest** one miRNA per 10,000 ESTs, implying that the **least recurrence** of **finding** a miRNA from ESTs is 0.01% .

Looking of potentialmiRNAs **utilizing** in silico approach **with in the** EST **groupings** of J. curcas**uncovered** 12 putative miRNAs **having a place** to 12 **person** miRNA families .

Comparable ponder was performed by Vishwakarma and Jadeja where they **recognized diverse** miRNAs than **our own** with a lowernumber (05) of miRNA families as well as lower number of targets (78).

To **foresee unused** miRNAs from ESTs, we considered conservancy nature of **arrangements** and ability **to make fastener auxiliary** structure of the potential pre-miRNAs .

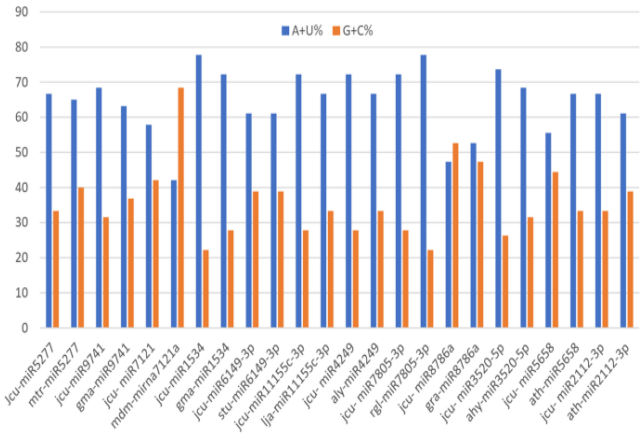
Since collapsing of pre miRNAs into stem-loop **clip** structure **may be a imperative arrange** in miRNA maturation.

On the other hand, a stem-loop **fastener** structure **isn't as it were** a **recognizing highlight** of miRNAsbut **too** other RNAs such as mRNA, rRNA, and tRNAcan have comparable **clip** structures.

In this way , criteria like MFE, AMFE, and MFEI for **clarifying unused** miRNAswere **investigated** to **maintain a strategic distance from deceiving** categorization of other RNAs as miRNA candidates.

The lower the MFE **esteem** , the **auxiliary** structure of the **coordinating arrangements** is more thermodynamically **steady**.

Hence , we have selected the pre-miRNA candidates having MFE values **extended** between 23.70 to−15.80 kcal/mol and **inside**
the **recommended esteem** of other **detailed** pre miRNAs, and also have lower values than **numerous** of the tRNA and ribosomal RNA .



Fig; Over all nucleotide compound

miRNA	Sequence	Length	small RNA library (leaf/seed)	No of clones	Precursor in other plants GenBank Access No	ΔG	known miRNAs in other species
JcumiR001	UGUCGCGAUGGUAAUUCAACC	21	leaf and seed	6 and 2	Hevea brasiliensis DQ306824.1	-23.2	
JcumiR002	GAUCGCGUGGCCUAAUGGA	19	leaf and seed	26 and 2	Vitis vinifera AM463399	-30.4	
JcumiR003	UCCUCUGAGCUAGGCAAUG	19	leaf	1	Jatropha curcas EZ413062.1	-31.1	
JcumiR004	UGAUUGAGCCGUGCCAAUAUC	21	leaf	1	Oryza sative AY551250.1	-54.5	
JcumiR005	GUCGUUGUAGUAUAGUGGU	19	leaf and seed	12 and 5	Populus trichocarpapa AC209103	-27.6	
JcumiR006	GGCAUGGGCGAUAUGGGCAAG	21	leaf	2	Strongylocentrotus purpuratus XM_001189429	-37.8	
JcumiR007	AUCAAAAGGGUUGGUAUUGCUC CU	24	leaf	1	Euphorbia genistoides AM048819	-23.3	
JcumiR008	GAUGCUGGUGUUCGGCUA	19	leaf	2	Medicago truncatu AC156629	-18.1	
JcumiR009	AUUCGGCUCAAUCCUUUUAG	20	leaf	1	Jatropha curcas FJ695500.1	-21.1	
JcumiR010	GGAAACAGAAUUGGCGGCUU	20	leaf	1	Arabidopsis thaliana AL161537	-30.11	
JcumiR011	UGGUUCAAGGCGUAGCAUUGG	21	leaf	3	Vitis vinifera AM477478	-28.57	
JcumiR012	GAAUGUUGUCUGGUUCAAGG	20	leaf	1	Oryza sativa HM139377.1	-58.7	Precursor of Osa-miR166e
JcumiR013	GAAUUAUAGGUGUUGAAUAUG GU	23	leaf	1	Populus trichocarpapa AC213088	-18.6	
JcumiR014	UGGUAGAGCGGUCGGCUGU	19	leaf	1	Phaseolusvulgari EU196765	-44.1	
JcumiR015	UGAGGUAGUAGGUUGUAUAGU	21	leaf	2	Rattus norvegicus NR_037385.1	-34.2	Rattus norvegicus mir-3596a
JcumiR016	UCGCACACAUGUCAGACUCCCC	22	leaf	2	Mimulus guttatusAC182572	-38.2	
JcumiR017	UCCACUGCGCUAUGCGGUC	19	leaf	2	Oryza sativa AY946832	-40.05	Osa mir457 precursor
JcumiR018	CCGGCAAGUCAUCCUUGGCUG	21	leaf	1	Oryza sativa AY551241	-69.06	Osa mirRNA 169c gene
JcumiR019	GGGGAUGUAGCUCAAAUGGUAG AG	24	leaf	5	Oryza sativa AK288811.1	-48.7	
JcumiR020	UCGAAAAUUCAACGCAAGC	19	leaf	1	Oryza sativa AL607000.3	-49.8	
JcumiR021	UUCCCGUUUCCGCCCAACUCA	21	leaf	1	Vitis vinifera AM436815	-38.08	
JcumiR022	GGGUGCGAUCAUACCAGCAC	20	leaf and seed	2 and 7	Vitis vinifera AM48227	-44.84	
JcumiR023	GGGGGGUCCCAGUCCCGAAC	20	leaf	3	Arachis duranensis	-66.9	

Fig ; Newly identified miRNA in Jatropha carcus

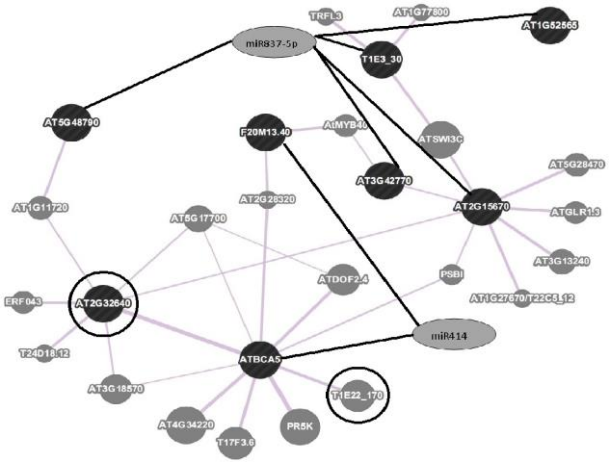


Fig ; Co-expression of genes

conclusion :

The **discoveries** of the **show thinkabout** provide **un used experiences** into the miRNAs of J. curcas.

Insilico **distinguishingproof** of 12 putative miRNAs **together with**their **conceivable** targets will **help** in future **investigate** o nfurther understanding of their **part** in **different perspectives** of **organic forms** such as defense **components** , hormone biosynthesis, **flag** transduction, lipid and **greasy corrosive ge neration** in Jatropha.

The identified miRNA in Jatropha **appeared greatest** similarities with their **particular** miRNA homologs, and thefunctional **examin ation uncovered** that the miRNAs **seem** potentially target **different natural** and metabolic processes with near-perfect complementarity.

It is clearly **apparent** that the **distinguishing proof** of more miRNAs is **however** to be done.

Be that as it may , **test** validation as well as expression **examination** of computationallyidentifiedmiRNAs **should** be performed to **legitimize**their **anticipated** unctions.
AbbreviationsmiRNAs-MicroRNAs

EST -Expressed **Grouping** Tags

MFEs -Minimal free energies

AMFE -Adjusted **negligible collapsing** energy

MFEI -Minimal **Collapsing** Free **Vitality** Index

SIGE -

Sigma E br PEP br Plastid encoded RNA polymerase br PLD ALPHA1 br Phospholipase D alpha

REFERENCES

[1] Openshaw K (2000) A review of Jatropha curcas: an oil plant of unfulfilled promise. Biomass Bioenergy 19(1):1–15

[2] Singh YN, Ikahihifo T, Panuve M, Slatter C (1984) Folk medicine in Tonga. A study on the use of herbal medicines for obstetric and gynaecologicalconditions and disorders. J Ethnopharmacol 12(3):305–329

[3] Staubmann Schubert-Zsilavecz M, Hiermann A, Kartnig T (1999) A complex of 5-hydroxypyrrolidin-2-one and pyrimidine-2, 4-dione isolated from Jatropha curcas. Phytochemistry 50(2):337–338

[4] Igbinosa OO, Igbinosa EO, Aiyegoro OA (2009) Antimicrobial activity and phytochemical screening of stem bark extracts from Jatropha curcas(Linn). Afr J Pharm Pharmacol 3(2):058–062

[5] Becker K, Makkar HP (1998) Effects of phorbol esters in carp (CyprinusCarpio L). Vet Hum Toxicol 40(2):82–86

[6] King AJ, He W, Cuevas JA, Freudenberger M, Ramiaramanana D, Graham IA (2009) Potential of Jatrophacurcas as a source of renewable oil and animal feed. J Exp Bot 60(10):2897–2905

[7] Achten WM, Verchot L, Franken YJ, Mathijs E, Singh VP, Aerts R, MuysB (2008) Jatropha bio-diesel production and use. Biomass Bioenergy32(12):1063–1084

[8] Pandey VC, Singh K, Singh JS, Kumar A, Singh B, Singh RP (2012) Jatropha curcas: a potential biofuel plant for sustainable environmental development. Renewable Sustain Energy Rev 16(5):2870–2883

[9] Tiwari AK, Kumar A, Raheman H (2007) Biodiesel production from jatropha oil (Jatropha curcas) with high free fatty acids: an optimized process. Biomass Bioenergy 31(8):569–575

[10] Rahman KM, Mashud M, Roknuzzaman M, Al Galib A (2010) Biodiesel from Jatropha oil as an alternative fuel for diesel engine. Int J Mech Mechatron (IJMME-IJENS) 10(3):1–6

[11] Zhang B, Pan X, Cannon CH, Cobb GP, Anderson TA (2006) Conservation and divergence of plant microRNA genes. Plant J 46(2):243–259

[12] Zamore PD, Haley B (2005) Ribo-gnome: the big world of small RNAs. Science 309(5740):1519–1524

[13] Zhang B, Wang Q, Pan X (2007) MicroRNAs and their regulatory roles in animals and plants. J Cell Physiol 210(2):279–289

[14] Hawkins PG, Morris KV (2008) RNA and transcriptional modulation of gene expression. Cell Cycle 7(5):602–607

[15] Tan Y, Zhang B, Wu T, Skogerbø G, Zhu X, Guo X, He S, Chen R (2009) Transcriptional inhibiton of Hoxd4 expression by miRNA-10a in human breast cancer cells. BMC MolBiol 10(1