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Identification and characterization of abiotic stress responsive genes in *Ricinus communis* L. using bioinformatics tools

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Abstract

Bioinformatics is one of the leading fields in biology for genomics research. In the present research bioinformatics analysis of abiotic stress responsive genes investigation was carried out in *Ricinus communis* L. Selected twenty-seven genes of model plant *Arabidopsis thaliana* were searched in *Ricinus communis* L. The investigated genes belonged from salt, heat, cold and drought stress. Genes were find out using insilico analysis. Homology search was applied using a best available tool of NCBI called BLAST. Homology search gave best results up to 97% query coverage (ANAH-like) for the presence of selected model plant genes in *Ricinus communis* L. The query coverage results varied from 2% to 97%. Seven genes ANAH (97%), CSD1 (93%), TAF1 (82%), SOS4 (70%), HOS10 (61%) and MPK3 (61%) expressed high query coverage in R. communis L. Ten genes HVA22 (59%), SOS2 (49%), MYBR1 (45%), HOS31 (49%), STZ (42%), DDF1 (41%), BO1 (41%), LOS4 (39%), CDPK1 (37%) and KIN11 (35%) were somewhat similar. While remaining genes expressed similarity less than 30%. Besides query coverage the investigation of conserved domains showed that these predicted genes exhibited conserved domains similar to that of model plant genes. Phylogenetic analysis of some selected genes confirm the genes existence and gave evolutionary aspect of the gene. The identification of abiotic stress responsive genes makes good contribution to the research on this plant and will help to understand the mechanism to respond the stress in this plant.

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Introduction

Plants are the diverting source of organic compounds, several of which have been used for therapeutic purposes. Here countless ordinary fundamental medications that have been used to treat numerous disease and conditions one of them is *Ricinus communis* L. family euphorbiaceae frequently well-known as 'castor plant' and commonly known as palm of Christ (Jena *et al.,* 2012). The castor oil plant is a fast growing, tricking perennial plant or sporadically a soft forested small tree up to 6 meter or more. This plant was cultured for leaf and flower shades and for oil production (Evans, 2009). Any alteration in the surrounding environment may interrupt homeostasis. Plants initiate specific stress responses when exposed to stress conditions (Atkinson and Urwin, 2012).

The stress resistant genes play vital role to adapt the plant in unpredictable situations. Several plants can endure in cold stress climatic conditions and the mechanism of post transcriptional regulation play vital role in stresses responses (Anderson *et al.,* 1994; Ghebremariam *et al.,* 2013).

The plants frequently encounter numerous abiotic elements water shortage, salinity, temperature, drought and decreased accessibility of fundamental nutrients. Several signalling trails control stress reactions of different plants (Knight and Knight, 2001) thus the appearance of genes is convinced in reaction to changed stress elements (Seki *et al.,* 2001). The different abiotic stresses the two main abiotic stresses, are drought and salinity are more common which negatively affect the plant. Salinity reduce the plant growth, and decrease the water up take which cause reduction in growth rate. The water deficit may cause cellular damages (Seki *et al.,* 2001).

Salt stress leads to changes in growth, production and may threaten to survival. At the physiological level, the number of effects of salt stress specifies the importance of defensive system of the organism from damage by reactive oxygen species (Foyer and Noctor, 2005). Salinity stress is complex response to photosynthesis which indirectly affect the growth inhibition or leaf shedding. Salinity responses will lead to reestablishment of cellular homeostasis and purification. In addition, these stresses alter photosynthesis and cell growth (Yan *et al.,* 2005). Temperture stress is one of the key factor to effect plant yield and leads to advirse climate changes (Rossi *et al.*, 1997). Undesirable outcome of temperture on the world manufacture has testified on wheat, maize and barrley (Sun *et al.*, 2002). However high tempearture stress effect economical loss on agriculture fields and depress the complex nature of plants production (Tuberosa and Salvi, 2006). Drought stress estimated at molecular levels, consequences gained through transcriptional analysis of drought inducible gene appearance in Arabidopsis and rice consuming microarrays, comprising evidence about understanding potential purposes of scarcity inducible genes in stress reaction and lenience (Yamaguchi-Shinozaki and Shinozaki, 2005).

The proposed research is deliberate at the exploration of abiotic stresses responsive genes in *Ricinus communis* L. by using combination of bioinformatics tools. For understanding the abiotic stress mechanism in *Ricinus communis* L. identification of abiotic genes and the characterization of new genes will be a good contribution.

Materials and methods

Different abiotic stress responsive genes like drought, salt, cold in *Ricinus communis* L. were investigated using combination of bioinformatics tools, based on homology search using methodology of Shahid *et al.* (2012). *Ricinus communis* L. existed to examined for abiotic straining receptive genes. Nominated 24 genes of model plants Arabidopsis thaliana. Selected genes presence was then studied in *Ricinus communis* L. *R. communis* was selected after literature review to investigate the abiotic stress responsive genes, as it was not previously explored and have available ESTs. There are 62592 ESTs of Ricinus communis L.

Identification of genes

Different abiotic stress responsive genes were studied, identified and selected that respond to cold, salt and other abiotic stresses in model plant *Arabidopsis thaliana* L. Articles and research papers were studied regarding these abiotic stress responsive genes. These genes were ANAH, CSD1, TAF1, SOS4, HOS10, MPK3, HVA22, SOS2, MYBR1, HOS31, STZ, DDF1, BO1, LOS4, CDPK1, KIN11, SAT32, DRIP1, DREB2A, RAB18, NPH4, CRK1, HSF1, CHLH-GUN5, RD29A, RCI3.

Fetching of model plant genes

Sequences of selected abiotic stress responsive genes that respond to different environmental stresses of model plant Arabidopsis thaliana were fetched. From NCBI complete nucleotide sequences of selected genes were saved in FASTA format. Repeated the procedure for all genes.

Gene's identification through homology search

For homology search one of the new technique tools for relative genomic method is BLAST. To carryout homology search the fetched genes sequences of model plants were subjected to BLASTn (designed by Altschul *et al.,* 1990) against the publicly available genomic and transcriptomic sequences (Expressed sequence tags) of *Ricinus communis* L. at NCBI Genbank. (https://blast.ncbi.nlm.nih.gov/Blast.cgi). From obtained results selected the one with highest query coverage, identity, best evalue. Saved the EST (nucleotide sequence) of that selected one. Searched the presence of all selected genes of model plant in *Ricinus communis* L. repeating the same procedure. The obtained similar sequences were regarded as predicted abiotic stress responsive genes in *Ricinus communis* L.

Conserved domain investigation and comparison

Through conserved domain database (CDD), conserved domains on reference genes of Arabidopsis thaliana and on predicted abiotic stress responsive genes of *Ricinus communis* L. were investigated. CDD is also one of the best tools of NCBI for identification of evolutionary conserved domains. ORF sequences of model genes and predicted genes were subjected to the CDD. The conserved domains were identified and compared. (https://www.ncbi.nlm.nih.gov/cdd).

Phylogeny of identified genes

Cladograms were constructed using multiple sequence comparison by Log-Expectation (MUSCLE), an advance version of Clustal-w for phylogenetic analysis. The gene of model plant, predicted genes of *Ricinus communis* L. and one same gene from other plants were all subjected to MUSCLE for phylogeny. Saved the results and analysed (https://www.ebi.ac.uk/Tools/msa/muscle/).

Results

Recognition of genes

In silico identification of abiotic stress responsive genes was carried out in *Ricinus communis* L. Expressed sequence tags were explored for this purpose. Investigated 62,592 ESTs of *Ricinus communis* L. and identified twenty eight abiotic stress responsive genes.

These genes respond to salt, cold, heat and drought stresses (seven each). Some of these genes responded to more than one stresses called multiple stress responsive genes.

Table 1. ORF features for salt stress responsive genes in *Arabdopsis thaliana* and *Ricinus communis*.

s#	Gene name	mRNA length base pairs		Frame preferred		Frame length base pairs		Amino acids length	
		Ath	R.c	Ath	R.c	Ath	R.c	Ath	R.c
1	CDPK1	2681	912	1+	3+	1638	858	545	285
2	CSD1	873	675	1+	2+	459	459	152	152
3	HVA22A	977	464	2+	1+	534	318	177	105
4	P5CS1	2590	653	3+	2+	2145	225	714	74
5	SAT32	2048	512	1+	3+	1326	147	441	48
6	SOS1	3772	921	3+	1-	3432	615	1143	204
7	SOS2	1890	895	3+	3+	1341	648	446	215
8	SOS4	1562	772	1+	1+	930	663	309	220
9	STZ	1303	856	3+	2+	684	690	227	229

ORF features

For salt stress responsive genes over all frame one and three were preferred. Least preferred frame was frame two. Except one, all frames were positive.

After prediction of ORF the range of genes and their aminoacids comes closer in selected model plant and studied plant *Ricinus communis*. For gene CSD1 both model and selected plants after ORF prediction have same number of nucleotides and aminoacids. Frame +1 was selected highly in drought stress responsive genes. Model plant preferred +3 frame mostly while *R.communis* select +3 only for single gene. Genes DDF1 (+1) and RAb18 (+3) preferred similar frames. Lengths of nucleotides and aminoacids came into somewhat uniform values after ORF prediction.

Similarly ORF was investigated for heat stress responsive genes and compared the results.

There was no similarity between preferred frames. Only single gene NPH4 preferred negative frame. Likewise for cold stress genes only one gene RCI3 in *R.communis* used frame negative. Genes HOS10 (+1) and MPK3 (+3) preferred similar frames in both Rabidopsis thaliana and *Ricinus communis*.

Table 2. ORF features for drought stress responsive genes in *Arabdopsis thaliana* and *Ricinus communis*.

s#	Gene name	mRNA length base pairs		Frame preferred		Frame length base pairs		Amino acids length	
		Ath	R.c	Ath	R.c	Ath	R.c	Ath	R.c
1	TAF1	1653	860	2+	1+	870	741	289	246
2	MYBR1	1985	770	1+	2+	918	681	305	226
3	DDF1	1135	768	1+	1+	630	699	209	222
4	KIN11	1964	887	3+	1+	1539	594	512	197
5	RAB18	881	714	3+	3+	558	450	185	149
6	DREB2A	1651	861	3+	2+	1008	732	335	243
7	DRIP1	2280	748	1+	2+	924	567	307	188

Table 3. ORF features for heat stress responsive genes in *Arabdopsis thaliana* and *Ricinus communis*.

s#	Gene name	mRNA length base pairs		Frame preferred		Frame length base pairs		Amino acids length	
		Ath	R.c	Ath	R.c	Ath	R.c	Ath	R.c
1	ANAH-like	1016	835	3+	1+	483	495	160	164
2	HOS3-1	1450	787	3+	1+	927	720	308	239
3	BOB1	1519	838	1+	2+	915	789	304	262
4	CHLH-GUN5	4753	855	2+	1+	4146	753	1382	250
5	HSF1	1682	503	2+	1+	1488	267	495	88
6	CRK1	2443	758	2+	3+	1731	288	576	95
7	NPH4	4429	936	1+	-3	3495	390	1164	129

Conserved domain identification and comparison

Conserved domains were investigated and then compared on all studied genes of model plant and predicted genes of *R. communis*. Out of twenty eight genes on twenty six genes similar conserved domains were investigated. Irrespective of percentage identity and query coverage the presence of conserved domain showed the existence of these genes in model plant and from these results the genes of model plant can be predicted to be present in *R.communis*.

Homology search

Selected model genes from Arabidopsis thaliana were exposed to similarity search /homology search of certain genes in *Ricinus communis* L. The query coverage fluctuated from 2% to 97 % for all studied genes. The results of homology was categorized as highly similar showing similarity ≥ 60%, moderately similar expressing homology ≥ 30% and finally less similar exhibiting similarity < 30%. Studied salt stress genes expressed homology up to 93%. Two genes CSD1 (93%) and SOS4 (70%) fall in the category having highly similarity. Four salt stress genes HVA22A (59%), SOS2 (49%), STZ (42%) and CDPK1 (37) were moderately similar and only one gene SAT32 (13%) remained in the category of less similarity. Identity of all genes was greater than 65% up to 79% (Table 1). With seven drought stress responsive model genes (Table 2) of Arabidopsis thaliana up to 82% similarity was shown by Ricinus communis L. Single gene expressed high similarity TAF1 (82%). Three genes were moderately similar i.e MYBR1 (45%), DDF1 (41%) and KIN11 (35%). Genes RAB18 (16%), DREB2A (13%) and DRIP1 (3%) were less similar. Seven heat stress responsive genes were predicted in *R.communis* (Table 3). Highest query coverage was up to 97% for gene ANAH-like gene. Two genes were moderately similar HOS3-1 (49%) and BOB1 (41%). Remaining genes CHLH-GUN5 (20%), HSF1 (15%), CRK1 (15%) and NPH4 (12%) came in to the category of less similar genes. Six cold stress responsive genes were investigated in R. communis.

Table 4. ORF features for cold stress responsive genes in *Arabdopsis thaliana* and *Ricinus communis*.

s#	Gene name	mRNA length base pairs		Frame preferred		Frame length base pairs		Amino acids length	
		Ath	R.c	Ath	R.c	Ath	R.c	Ath	R.c
1	COR47	2320	848	1+	2+	798	693	265	230
2	HOS10	675	608	1+	1+	639	495	212	164
3	LOS4	1860	835	3+	1+	1491	777	496	258
4	MPK3	1858	898	3+	3+	1113	789	370	262
5	RCI3	1254	712	1+	-3	981	291	326	96
6	RD29A	2660	863	3+	2+	2133	627	710	208

Table 5. Conserved domain identification and comparison of Salt stress responsive genes in Arabidopsis thaliana and Ricinus communis.

s#	Gene name	Conserved domain Family	
		A.thaliana	*R.communies*
1	CDPK1	Pkc_like superfamily	Pkc_like superfamily
2	CSD1	Cu_Zn superoxide dismutase super-family	Cu_Zn superoxide dismutase super-family
3	HVA22A	TB2_DP1_HVA22 super family	TB2_DP1_HVA22 super family
4	P5CS1	ProB superfamily	ProB superfamily
5	SAT32	IFRD super family	IFRD super family
6	SOS1	Na_H exechanger super family	
7	SOS2	PKc_like super family	PKc_like super family
8	SOS4	ribokinase_pfkB_like super family	ribokinase_pfkB_like super family
9	Stz	zf-C2H2_6 super family	zf-C2H2_6 super family

Three genes COR47 (78%), MPK3, (61%) and HOS10 (61%) were highly similar. One gene LOS4 (39%) was in the category of somewhat similar (Table. 4). Reminig genes RCI3 (29%) and RD29A (2%) were in the category of less similar genes. Overall the identity up to 79%.

Phylogenetic analysis

The Phylogenetic tree which was constructed to showed the different evolutionary relationship between the model plants subjected plant and another plant from dicot family. From each stress one gene was selected with maximum query coverage from salt stress CDPK1 gene was designated and and match with model plant subjected plant and other dicot plant Solanum lycopersicum. The MYBR1 gene is selected from drought stress and COR47 from cold stress and from heat stress HOS3-1 was nominated to construct a cladogram for phylogenetic investigation. The cladogram which was constructed for

Phylogenetic analysis of four abiotic stress gene clearly exposed that in CDPK1 gene the Solanum lycopersicum closely link with Arabidopsis thaliana. In drought stress gene MYBR1 in which model plant and subjected plant was directly link with each other. Both in heat stress and cold stress the subjected plant and another dicot plant narrowly linked to each other rather than model plant.

Table 6. Conserved domain identification and comparison of drought stress responsive genes in Arabidopsis thaliana and Ricinus communis.

s#	Gene name	Conserved domain Family	
		A.thaliana	*R.communies*
1	TAF1	NAM super family	NAM super family
2	MYBR1	SANT super family	SANT super family
3	DDF1	AP2 super family	AP2 super family
4	KIN11	PKc_like super family	PKc_like super family
5	RAB18	Dehydrine super family	Dehydrine super family
6	DREB2A	AP2 super family	AP2 super family
7	DRIP1	RAWUL family	RING_ubox super family

Table 7. Conserved domain identification and comparison of heat stress responsive genes in Arabidopsis thaliana and Ricinus communis.

s#	Gene name	Conserved domain Family	
		A.thaliana	*R.communies*
1	ANAH-like	AANH_like super family	AANH_like super family
2	HOS3-1	ELO super family	ELO super family
3	BOB1	alpha-crystallin-HsPs_p23 like super family	alpha-crystallin-HsPs_p23 like super family
4	CHLH-GUN5	cobN_like super family	cobN_like super family
5	HSF1	HSF_DNA-bind super family	HSF_DNA-bind super family
6	CRK1	PKc_like super family	EFh_PEF super family
7	NPH4	AUX_IAA super family	AUX_IAA super family

Discussion

The present study work was on examinations of different abiotic stress responsive genes in *Ricinus communis* L. by using the bioinformatics tools. In recent research 28 abiotic stress responsive genes were recognized. In abiotic stress the main stress is salt stress. Seven genes of each salt stress, cold, heat and drought were identified.

Table 8. Conserved domain identification and comparison of cold stress responsive genes in Arabidopsis thaliana and Ricinus communis.

s#	Gene name	Conserved domain Family	
		A.thaliana	*R.communies*
1	COR47	Dehydrine super family	Dehydrine super family
2	HOS10	SANT super family	SANT super family
3	LOS4	DEXDc super family	DEXDc super family
4	MPK3	PKc_like super family	PKc_like super family
5	RCI3	plant_peroxidase_like super family	plant_peroxidase_like super family
6	RD29A	CAP160 Super family	NAC super family

It is understand that there is continuously an occurrence of serval abiotic stress slightly than a signal stress in the arena state. The altered abiotic stresses which might happen in combination of phase at a plant expansion stage which is serious issue for decreased the photosynthetic proficiency and compact on yield production (Wang *et al.*, 2004). Ecological factors that caused the main abiotic stress, such as scarcity, salt and heat stress, which directly effects on plant output.

Table 9. Represents Homology of *R.communis* with the salt stress, drought stress, heat stress and cold stress of responsive model genes from *A.thaliana*.

S. No	Gene name	Salt stress		Query coverage%	Idenity%
		A.thaliana	R.communis		
1	CSD1	NM_100757.4	EV521296.1	93%	79%
2	SOS4	NM_001344222.1	GE633159.1	70%	77%
3	HVA22	NM_106112.3	EV520175.1	59%	77%
4	SOS2	NM_122932.5	EE259791.1	49%	77%
5	STZ	NM_102538.3	EG696617.1	42%	69%
6	CDPK1	NM_101746.5	EG696909.1	37%	68%
7	SAT32	NM_202194.3	EE258411.1	13%	71%

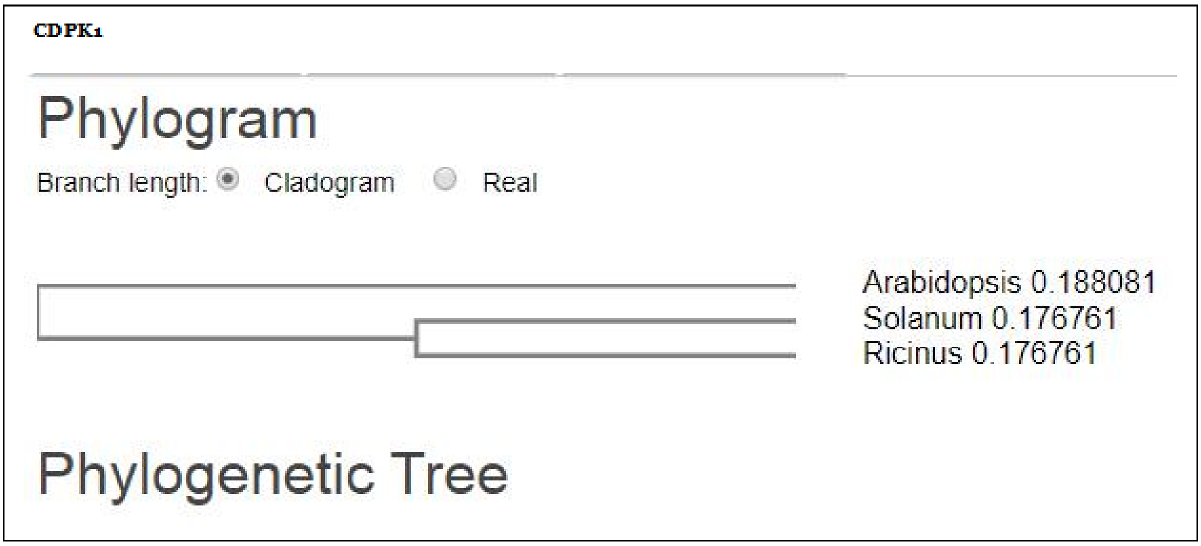
S. No	Gene name	Drought stress		Query coverage%	Idenity%
		A.thaliana	R.communis		
1	TAF1	NM_100054.3	EG661297.1	82%	71%
3	MYBR1	NM_126130.2	GE634981.1	45%	78%
2	DDF1	NM_101131.4	EG701091.1	41%	70%
4	KIN11	NM_202645.3	EG660845.1	35%	83%
5	RAB18	NM_001037085.1	EV521739.1	16%	88%
6	DREB2A	NM_120623.3	GE634915.1	13%	76%
7	DRIP1	NM_202046.2	GE635450.1	3%	86%

S. No	Gene name	Heat stress		Query coverage%	Idenity%
		A.thaliana	R.communis		
1	ANAH-like	NM_115259.5	EV523323.1	97%	75%
2	HOS3-1	NM_001342419.1	EG663325.1	49%	69%
3	BOB1	NM_124719.4	EV523367.1	41%	75%
4	CHLH-GUN5	NM_121366.4	EG664695.1	20%	78%
5	HSF1	NM_117884.3	EG687972.1	15%	75%
6	CRK1	NM_129679.2	EG676546.1	15%	73%
7	NPH4	NM_180716.3	EG683748.1	12%	78%

S. No	Gene name	Cold stress		Query coverage%	Idenity
		A.thaliana	R.communis		
1	COR47	NM_101894.4	GE633307.1	78%	65%
2	HOS10	NM_179418.2	GE634365.1	61%	79%
3	LOS4	NM_115171.3	EV523321.1	39%	70%
4	MPK3	NM_114433.3	EG688551.1	61%	76%
5	RCI3	NM_100405.4	EG663858.1	29%	67%
6	RD29A	NM_12 4610.3	EV523665.1	2%	85%

The abiotic stresses inhibits plant growth by various means initiating instinctive cell death to compressed crop harvest or total crop disaster (Yokota *et al.*, 2002). Current research was basically based on the investigation of genes from EST analysis of selected plant. EST are the direct evidence and confirm the sequences as genes. An imperative genomic method to classify abiotic stress associated gene is constructed on EST garneted from diverse cDNA libraries. For data there is satisfactory experimental model was available for the study of different abiotic stresses. The investigation of complete genome a large set of well categorized transformed is available like (EST), microarray, proteomics data and different protocols.

The significance to select the Ricinus Communis L. plant was that very large number of ESTs were publically available (Rhee *et al.*, 2006). There are 62592 ESTs of *Ricinus communis* L. were reported in genome bank. A comprehensive data on the type of collections and the amount of EST created from each public library is indexed at the (NCBI). After NCBI, recovered particular databases and investigated for their phylogenetic relationship.



CDPK1

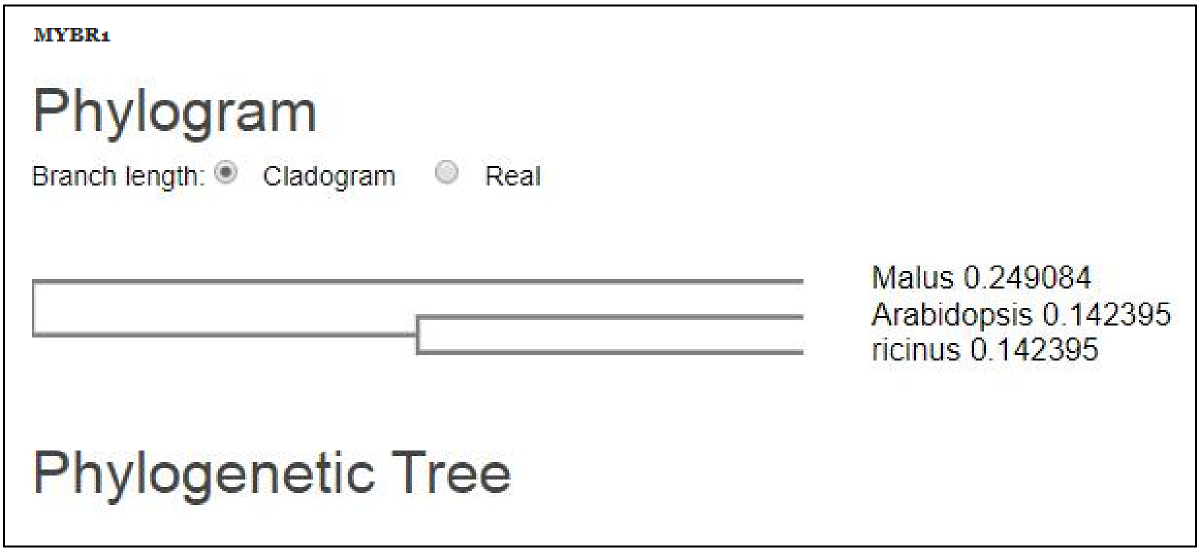
Phylogram

Branch length: ● Cladogram ○ Real

Phylogenetic Tree

Fig. 1. Cladogram for CDPK1 gene showing the closeness of Ricinus communis with solanum lysopersicum as compared to arabidopsis thaliana.

Homology search was performed by using BLASTn. Based on homology searched was performed by Ooka *et al.* (2003) and selected the homologs that cover at least 40% of interval of gene in database. The maximum substantial matches to Arabidopsis thaliana and tomato probes were physically measured by the matches of the query coverage (%) and identity (%) of and the great scoring section pairs were examined (Sun *et al.*, 2002).



MYBR1

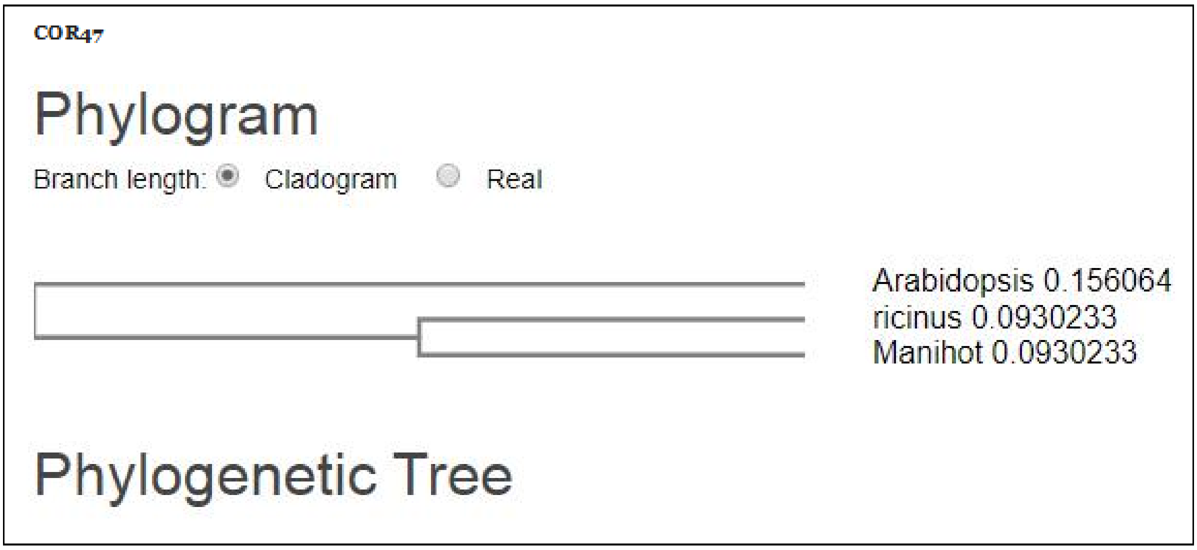
Phylogram

Branch length: ● Cladogram ○ Real

Phylogenetic Tree

Fig. 2. Cladogram for MYBR1 gene showing the closeness Ricinus Communis with Arabidopsis thaliana as compared to malus domestica.

The EST with high homology was expressed in *Ricinus communis* L. In different abiotic stresses the heat stress which showed the highest query coverage % in gene ANAH (97%) and (75%) identity in salt stress the CSD1 gene which presented the 93% query coverage for salt stress genes HVA22A (59%), SOS2 (49%), STZ (42%) and CDPK1 (37) were discreetly alike and only one gene SAT32 (13%) continued in the group of less matched.


COR47

Phylogram

Branch length: ● Cladogram ○ Real

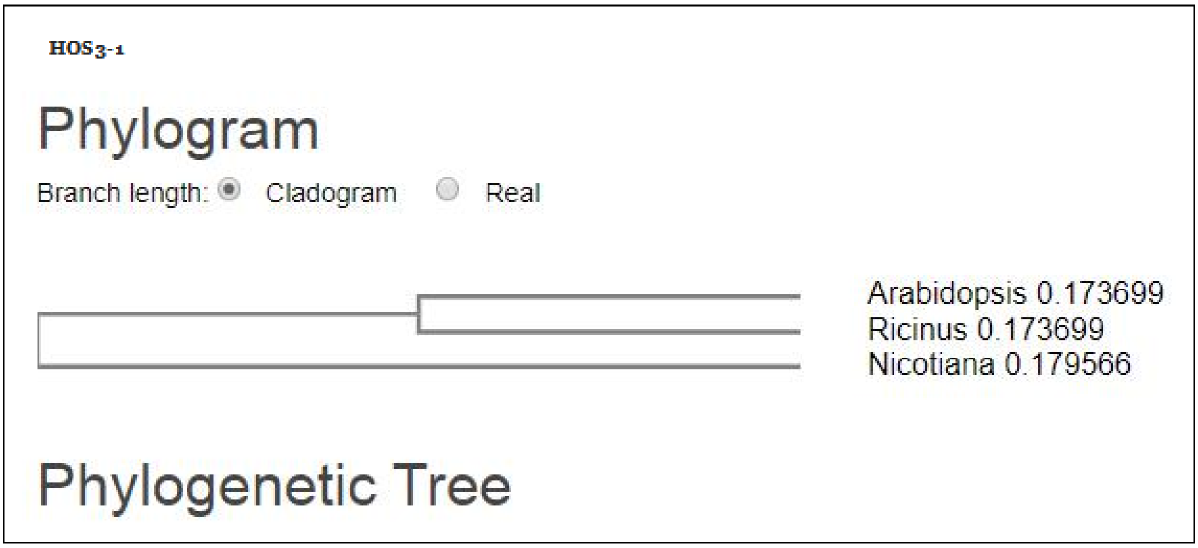
Phylogenetic Tree

Fig. 3. Cladogram for COR47 gene showing the closeness of Ricinus communis with menihot as compared to arabidopsis thaliana.

In cold stress and drought stress the gene in drought stress TAF1 show 82% query coverage and in cold stress the gene COR 47 with maximum query coverage. The consequences are optimistic for presence of these genes in Ricinus communis L. Shahid *et al.* (2012) selected the homology of outcome from 50% to above they determined that they are the homolog gene. The result check through different trials growing gossypium in salt condition and then link the expressed transcript their consequence give the conformation of genes consuming homology from 50% to 94% correspondingly Teigi *et al.* (2004).

Salt stress responsive genes CSD1 and SOS1 in Arabidopsis & Ricinus Communis L. Both comprise the super families of Na+_H+ ion exchanger. In *Arabidopsis thaliana* the sodium and potassium ions were important for growth embarrassment and homeostatic maintains (Rizshki *et al.*, 2002). SOS1 expressed excellent role in plants in response to stress condition of salinity among the three loci of SOS, when compared to other like SOS2, SOS3. SOS1 mutant plants are expressive to the stresses caused by Li+ along with Na+. So, the analysis of mutants showed that type SOS1 work in the same path followed SOS3 and SOS2 (Han *et al.*, 2015). The SOS4 gene was recently isolated. The SOS4 mutations block the initiation of maximum root hairs and damage the tip growth of those that were initiated. The root hair less phenotype of SOS4 mutants was complemented by the wild type SOS4 gene (Rizshki *et al.*, 2002).

The several physiological studies which show that the salt and drought responses of the plants accrue the compactible solutes which is actual necessary to protect the plant cell from damage and play significant role in plant homeostasis (Herimat ,2011). Abiotic stress signals such as wounding, cold, high salinity and drought are known to cause variations in cytosolic Ca2 levels as well as changes in protein phosphorylation (Teigi *et al.,* 2004). Numerous evidence recommend that CDPKs simplify abiotic stress signalling pathways. Transcriptional activation of several different CDPKs by a variety of abiotic stresses has been established in tissues from diverse species (Jamil *et al.,* 2011). The cold stress genes which caused the shunting of plant growth and caused serious damage to plants leaves in Arabidopsis thaliana L. and in the coaster oil bean plant the cold stress gene COR47 which contain the dehydrin superfamily which is uttered throughout the phases of low water content. Maximum members of the dehydrin superfamily are identified during exposure to ecological stresses where the osmotic stress is a reason to the stress mechanism (Strack *et al.*, 2001).


HOS3-1

Phylogram

Branch length: ● Cladogram ○ Real

Arabidopsis 0.173699
Ricinus 0.173699
Nicotiana 0.179566

Phylogenetic Tree

Fig. 4. Cladogram for HOS3-1 gene showing the closeness of Ricinus communis with solanum lysopersicum as compared to nicotiana tabacum.

The heat stress which is the one of reason to effect the plant harvest and cause advirse environment fluctuations (Rossi *et al.*, 1997). The unwanted result of heat stress on the world production has appeared on wheat, and barrley (Lobell & field, 2007) the heat shock protein in *Arabidopsis thalaina* L. and *Ricinus communis* L. the gene HOS10 show similar super family SANT in both model plant and in *Ricinus communis* L. The HOS3 effective as an ABA-inhibitor, measured as germination rate of HOS3 in mutant seeds no slanted seeds were able to grow at higher applications of ABA however the wild-type continuous to propagate at a low degree (Wang *et al.,* 2004). In heat stress the well-known gene HSF1 the heat shock transcription factor (HSFs) are the key heat shock factors flexible to the heat stress response.

They contribute in variable expression of heat shock proteins (HSPs), which are serious in the defence against stress injury and many other essential genetic trainings (Ma *et al.*, 2012). These insilco identification will provide the basis for exploring the mechanism of plants respond to various stresses.

Conclusion

In all abiotic stresses the highest query coverage was noticed in heat stress in gene ANAH 97%. The second maximum coverage was notice in salt stress gene CSD1 93%.in drought stress gene 82% query coverage was noted.in salt and cold stress in two genes 70% and above than query coverage was seen. Examination of different abiotic stress responsive genes in *Ricinus communies* L. showed that most of the genes exposed similar conserved domain both in model plant and subjected plant. One gene from each stress showed the different conserved domain in SOS1, DRIP1, RD29A, and CRK1, in these four gene the altered conserved domains were seen. The genes might be progressive with their time interval and variations came in their sequences which might be helpful in evolutionary studies. The subsequent approvals are proposed below in the light of outcomes is recommended that The effect of abiotic stress situations on distinct parameters concentrating inclusive harvest of Ricinus communies L. might be considered in upcoming future by developing it in abiotic stress like in salt and in cold stress. By examining the records from all abiotic stress mostly from cold stress treated Ricinus communies L. plants more genes may be confirmed in future in expended research. Through wet lab find out the abiotic stress genes which highly effect the most plant yield all over the world. Genes that counter to numeral of stress are great significance like RD29A because the engineering of these genes will support to manage the plants from several type of strains. Mention the analysis of stress transferable factor in extra plants as a large amount of plants quiet required to be traveled for stress receptive genes. Find out those genes through bioinformatics tools which are responsible for plant diseases.

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