IOSR Journal of Biotechnology and Biochemistry (IOSR-JBB)
ISSN: 2455-264X, Volume 8, Issue 6 Nov. – Dec. 2022), PP 07-13
www.iosrjournals.org

Expression analysis of Aldehyde Dehydrogenase (GDI_E_37) gene in groundnut under different abiotic stress

G.S.Ranganayakulu[1*] S. GiridharaKumar[2] and Chinta Sudhakar[3]
[1.] *Dept of Botany, Rayalaseema University, Kurnool, AP. India.*
[2]*Regional Plant Resource Centre, ODISSA.*
[3] *Department Botany, Sri Krishnadevaraya University, Anantapur-515003,*
Corresponding author [1]*Dr. G.S.Ranganayakulu, Assistant Professor, Dept of Botany, Rayalaseema University, Kurnool-518002, A.P, INDIA.*

Abstract: *Abiotic stresses such as drought, salt and temperature stresses are limiting factors for crop productivity in arid and semi-arid regions and influences many aspects of plant growth and development. Aldehyde dehydrogenases (ALDHs) are a family of enzymes that are involved in plant metabolism and contribute to aldehyde homeostasis in plants when exposed to abiotic stress and involved in detoxification processes to eliminate toxic aldehydes. To gain a better understanding of the abiotic stress responses at molecular level, we carried out a genomic analysis of stress-responsive genes/transcripts in drought-tolerant cultivar K-134. As a first step toward characterization of stress-responsive genes, previously we constructed, analyzed and classified subtracted cDNA library from drought tolerant groundnut cultivar (K-134). In this present study we analyzed expression profiles of aldehyde dehydrogenase (GDI_E_37) under different abiotic stress levels. Our result showed that aldehyde dehydrogenase (GDI_E_37) was expressed differentially under different abiotic stress conditions. However it was expressed maximum at severe stress conditions over the controls. Results and discussions were discussed in this paper.*

Key words: *Abiotic stress, aldehydes, stress tolerance, Soil moisture level (SML), Groundnut*

Date of Submission: 01-11-2022 Date of Acceptance: 12-11-2022

I. Introduction:

Agriculture is a major user of water resources in many regions of the world. Generally plants are frequently encounter unfavorable conditions such as drought, salinity, high temperature, freezing, nutrition deficiency and chilling, which adversely affect their growth, development, and productivity. Among the abiotic stresses drought is one of the most important stress constraints to global agricultural production. More than 10% of arable land is affected by drought and salinity [1]. With increasing aridity and growing population, water will become an even scarce commodity in the near future. Development of superior high yielding crops led to green revolution in the past has tremendously boosted agricultural productivity worldwide. However, world population will touch the eight billion more in about 25 years from now. As per the United Nations prediction by 2020 we will need 40 per cent more grains than what we produced today [2]. Therefore understanding the plant tolerance to drought is a fundamental research to meet food demands of increasing population and to cope with drastic climatic conditions.

Abiotic stresses such as drought, salt, heat, cold and temperature stresses are major limiting factors which cause severe changes in the morphological, physiological, biochemical and molecular changes that adversely affect plant growth and productivity [3, 4]. Among all abiotic stresses drought is a major factor that limits crop production, it can be simply defined as a period of below normal precipitation that limits plant productivity in a natural or agricultural system [5]. Plants experience drought stresses either when the water supplies to roots become difficult or when the transpiration rate becomes very high. These conditions often coincide under arid and semi-arid regions. Crops which are generally cultivated in these regions dependent on current rainfall rate and suffer from intermittent drought stress during vegetative or reproductive growth period. Plants are varying tremendously in their ability to withstand abiotic stresses, both between species and within populations of a single species [1] and have developed different adaptive mechanisms to meet the adverse environmental conditions. Plants often exhibit avoidance and tolerance characters to resist drought stress. One of the important avoidance characters of crop plants exhibit is deep root system that penetrate the water table [6], besides, leaf reflectance characters to decrease heat load, including fleshy leaves, thick cuticles or pubescence, biosynthesis of epicuticular wax, sunken stomata, and other stomatal variations to regulate the

transpiration through stomata [7]. n addition plants are well adapted and have developed several biochemical and molecular mechanism to deal with various environmental cues. Signaling cascades and cellular pathways leading to the production of proteins, molecular chaperons, ROS scavenging systems, accumulation of compatible solutes in response to stress [3] . One of the major molecular responses plants exhibit to water deficit is altered gene expression. Significant progress has been made in studying the plants systems to understanding the role of various genes, transcription factors, cellular macromolecules and the components of the signal transduction cascades during stress [8].

Several studies have been reported that a number of genes to be induced by various abiotic stresses such as drought, high-salinity, and low temperature, and their products are thought to be function in stress tolerance and response [9, 10]. The molecular and transgenic studies have revealed [11, 12, 13] that the identification of novel genes, determination of their expression patterns in response to the drought stress, and an improved understanding of their functions in stress adaptation will provide us the basis of effective engineering strategies to improve stress tolerance in crop plants [14]. Therefore, the potential stress tolerance can be achieved by the isolation of novel stress responsive genes from stress tolerant crop species and cloned into susceptible species to improve the stress tolerance level of susceptible species.

Aldehyde dehydrogenase (ALDH) enzymes are belong to a family of NAD (P)+ dependent enzymes, that have substrate specificity and catalyse the oxidation of various aldehydes to the corresponding carboxylic acids, thus reducing the peroxidation of lipids. ALDH genes are considered to be 'aldehyde scavengers' to eliminate surplus aldehydes [15, 16]. Aldehyde molecules are common intermediates in most cellular pathways such as carbohydrate, amino acid, protein, lipid or steroid metabolism [17, 16]. Lipid peroxidation resulting in the loss of membrane integrity or modification of proteins subsequently causing cellular and developmental arrest [18, 19, 20]. On the other hand, recent findings suggest that some aldehydes may also have a signaling function [21]. The accumulation of aldehydes leads to the production of reactive oxygen species (ROS) such as singlet oxygen, hydroxyl radical, superoxide and H2O2 [22, 23]. They are involved in stress adaptation to abiotic and biotic environments and regulate aldehyde homeostasis under stress conditions. Various plant ALDH genes have been reported to be activated by environmental stress such as dehydration, salinity or excessive light [24, 15, 25]. Stress related members of ALDH genes have been investigated in Arabidopsis [26]. Several studies reported aldehydes dehydroginases (ALDH3F1, ALDH3I1 or ALDH7B4 genes) were involved in stress tolerant mechanism in plants by a reduction of H2O2 and malondialdehyde (MDA) [27]. The involvement of ALDH genes in stress tolerance was corroborated by the analysis of Arabidopsis ALDH T-DNA knock-out (KO) mutants was reported in stress tolerant *Arabidopsis* [28]. In the present study we analyzed expression profiles of aldehyde dehydrogenase (GDI_E_37) gene under various abiotic stresses such as water, salt and heat stress.

II. Material And Methods:

2.1. Experimental Design and Plant material:

Seeds of groundnut (*Arachis hypogaea* L.) cultivars namely (cultivar K-134 and (cultivar JL-24) were procured from Andhra Pradesh Agricultural Experimental Station Kadiri, Anantapur district. Seeds were surface sterilized with 0.1% (w/v) sodium hypo chlorite solution for 5 minutes, thoroughly rinsed with distilled water, germinated in plastic pots containing 2 kg of soil: sand (2:1) mixture and allowed to grow for nineteen days. The pots were maintained in the departmental botanic garden under natural photoperiod (10-12 hours; temperature 28 ± 4^0C). Nineteen-day-old groundnut plants were subjected to a progressive water stress by withholding water. Plant soil water status (per cent soil moisture level) was measured at regular intervals by gravimetric method to obtain required soil moisture levels (100, 50 and 25% SMLs).

2.2. Total RNA Isolation and Subtractive hybridization:

Total RNA was isolated from the control (100 % SML) and stressed (25% SML) leaf samples according to the protocol described by Datta et al., (1989). Then Subtractive hybridization was performed between biotinylated control single stranded cDNA and stressed mRNA [29]. Then the cDNA library was constructed by subtractive hybridization between control cDNA and stressed mRNA. First strand cDNA synthesis was performed with subtracted mRNA. Subtractive mRNA was used as template and primed with Oligo dT designed with a "GAGA" sequence to protect the *Xho*I restriction enzyme. First strand cDNA was synthesised using lambda UNI-ZAP XR cDNA synthesis kit (Stratagene, USA) components and incubated at 42^oC for 1 hour in the presence of template, primer, dNTPs, reaction buffer and enzyme (strata script) reverse transcriptase as per the instruction manual.

Primer for first strand cDNA synthesis

5'-GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTTT-3'- GA"
XhoI poly (dT)

The second stand of the cDNA is made using the random priming of the first strand cDNA by RNA primers produced by limited digestion of the mRNA template by *E. coli* RNase H followed by transcription with *E. coli* DNA polymerase I at 16°C for 2.5 hours.The subtracted pool was made into dscDNA and cloned and packaged into Uni-ZAP XR vector according to the packaging instructions (Stratagene, USA).

2.3. cDNA sequencing, data base and homology analysis using bioinformatics approach:

The 3'end of cDNA sequence was determined using DYEnamic ET Dye terminator kit (Amersham Pharmacia, Uppsala, Sweden) and ABI 3700 automated sequencer (Perkin Elmer, USA). Sequences are processed using the NCBI developed vector screening programme (http://www.ncbi.nlm.nih.gov/VecScreen/VecScreen.html) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Based on the qualified sequences, the predicted amino acid sequences were used to search for similar peptide sequences in public databases NCBI (National Center for Biotechnology Information, Bethesda, USA) using the BLASTX algorithm http://www.ncbi.nlm.nih.gov [30] and default parameters of the program were used in all cases. The similarity scores between the cDNA clones and known sequences were represented by the BLASTX probability E-values. The cDNAs were classified according to the E-values generated in the BLAST searches. Largest open reading frame was determined using ORF finder program (www.ncbi.nlm.nin.gov/gorf.html) and used for multiple homology analysis. Nearly six proteins for each insert that were showing homology were aligned with each other using multiple alignment program *clustalW* (www.ebi.ac.uk/clustalw). Homology searching tools revels that the EST clone aldehyde dehydrogenase (GDI_E_37) was shown homology with stress related genes in other plant species. So we selected aldehyde dehydrogenase (GDI_E_37) gene for their expression analysis under different abiotic stress conditions.

2.4. Expression analysis of aldehyde dehydrogenase (GDI_E_37) under various abiotic stresses through northern blot:

19-day-old pot grown groundnut plants were subjected to different abiotic stresses such as drought (until soil moisture levels reached to 50 and 25%), Salt stress was imposed to the seedlings by supplementing 50 and 100 mM of NaCl solution to the plants for three days and Heat stress was imposed by keeping the plants at 45^{0C} and 55^{0C} for 8 hours. RNA was isolated from all stress treated leaf samples by [31]. The samples were flash frozen in liquid nitrogen and stored at -80^{0}C for further use. For expression analysis total RNA (20 µg) was separated by electrophoresis in denaturing formaldehyde 1% (w/v) agarose gels [31] and then transferred to Hybond-N+ nylon membrane (Amersham Pharmacia Biotech, Uppsala, Sweden). Plasmid containing GDI_E_37 (aldehyde dehydrogenase) insert was selected from our cDNA library. Inserts were released from the plasmid DNA and Probe (GDI_E_37) was amplified with T3 and T7 primers in the presence of p32dCTP radio label. Hybridization was carried out at 55^{0C} for 12-16 hours. After washing, membrane was exposed to X-ray film.

III. Results:

The major objective of the present investigation is molecular cloning, characterization and expression of stress responsive genes from a stress tolerant crop species groundnut (A*rachis hypogaea* L. cultivar K-134) under water stress. Hence, the expression patterns of subtracted cDNA clones were analyzed by northern blot analysis. In this particular objective we took and studied expression analysis of aldehyde dehydrogenase (GDI_E_37) gene under different abiotic stress conditions.

3.1. Cloning and sequencing of drought stress-induced aldehyde dehydrogenase (GDI_E_37) gene from groundnut.

Since we aimed to identify differentially expressed drought-induced genes in drought-tolerant groundnut cultivar (K-134), cDNA subtraction protocol was followed. A subtracted cDNA library was constructed with poly (A) RNA isolated from drought stressed (25% SML) (since the known stress-responsive genes Gdi-15 and Elip were shown maximum expression at 25% SML) and unstressed (100%SML) leaf samples by subtractive hybridization as described earlier. The length of the subtracted cDNA products visibly ranged from 400 to 2,000 bp (not shown). From the subtracted cDNA library, we selected 200 clones randomly and sequenced from their 50 ends. After removing of vector backbone, 120 high-quality EST sequences were generated. The EST sequences generated from this subtracted cDNA library were analyzed against the current GenBank database using the BLASTX algorithm. Drought induced genes, named as GDI, representing groundnut drought stress induced were deposited in the public domain through NCBI dbEST division database (Genbank). Sequence homology search via NCBI database revealed that the clone (GDI_E_37) had shown

significant homology with aldehyde dehydrogenase gene in *Brassica rapa L*. so the EST (GDI_E_37) identified as putative aldehyde dehydrogenase with this accession number (EC391300) figure.1.

Figure 1. Nucleotide sequence, deduced amino acid sequence of putative aldehyde dehydrogenase (GDI_E_37) and its homology analysis
Nucleotide sequence of GDI_E_37

GCTGGAGCTCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCGGGCTGCAGGAATTCGGCA
CGAGGGAATTTGCTCCAAAACTGATAAATGCTTTGAAAGAAGAGTTGAAGCAATTCTTTGGCGAA
GATCGATGGAATCAAAAGACATGTCTCGTATTGTGTCCCCGACCCAGTTTTCGCGGCTGGTGAAGC
TCTTGGATGAAGATAAAGTATCTGACAAAATTGTTTTTGGAGGTCAGAGGGATGAGATGAAACTA
AAGATTGCACCAACTATCATATTGGATGTTCCAGATGATGCAATGGTGATGCAAGAAGAGATATTT
GGGCCAATAATGCCAATCATCACTGTAGAAAACATAGAAGATAGCTTTGGCATAATCAAATCTAA
GCCAAAACCTCTTGCTGCTTATCTCTTTACAAACAATGAGCAGTTAAAGAAGGCATATGTGGAAAA
TATATCTTCTGGAGGGATGCTCATCAATGACACTGTCATACATGTTGCGACTCGTGGTTTGCCTTTT
GGAGGAGTTGAAGAAAGTGGAATGGGATGTTACCACGGGAAGTTCTCTTTTGATAGTTTCAGCCAT
AAGAAGTCTGTCCTCTATAGAAGTTTTGATGCAGATTCATCCTTAAGGTTCCCTCCATATACACCCG
AGAAGGAAAAATTGTTGAAGGCCATTTTCAGTGGCAACATTATTCGCATAATTCTTACTTTGCTTG
GATGGTCTTAGATTAGAATAAACGCATATACAAGGAACATCC

Translated product (+1 frame: 136 to 735)

MESKDMSRIVSPTQFSRLVKLLDEDKVSDKIVFGGQRDEMKLKIAPTIILDVPDDAMVMQEEIFGPIPIIT
VENIEDSFGIIKSKPKPLAAYLFTNNEQLKKAYVENISSGGMLINDTVIHVATRGLPFGGVEESGMGCYH
GKFSFDSFSHKKSVLYRSFDADSSLRFPPYTPEKEKLLKAIFSGNIIRIILTLLGWS

Multiple sequence alignment

```
gi|7270374    ITTKDFASKLIDALKTELETFFGQNALESKDLSRIVNSFHFKRLESMLKENGVANKIVHG 60
gi|83701643   ----------------------------LKSKDVSRIVNSFHFKRLESMMKENGVANKIVHG 34
gi|77553820   ITTKSFAPKLLEALEKVLEKFYGRDPLRSSDLSRIVNSNHFNRLKKLMDDENVSDKIVFG
60
GDI_E_37  FGTREFAPKLINALKEELKQFFGEDRWNQKTCLVLCPRPSFRGWSSWMKIKYLTKLFLEV
60
                               ...   :    *.  .. :. : ::. ::

gi|7270374    GRITEDKLKISPTILLDVPEASSMMQEEIFGPLLPIITVQKIEDGFQVIRSKPKPLAAYL 120
gi|83701643   GQTMEDKLKISPTILVDVPEESSMMQEEIFGPLLPVITVSKIEDGFQVIRSKPKPLAAYL 94
gi|77553820   GQRDEHQLKIAPTIFMDVPLDSGIMKEEIFGPLLPIITVDKIHESFALINSMTKALAAYL 120
GDI_E_37
RGMRNRLHQLSYWMFQMMQWCKKRYLGQCQSSLKTKIALASNLSQNLLLLISLQTMSSRR 120
                 :  ::: :: :  .    : ..* . *:: . .  ::   :.:::

gi|7270374    FTNNKELEKQFVQDVSAGGITINDTVLHVTVKDLPFGGVGESGIGAYHGKFSYETFSHKK
180
gi|83701643
FTDNKVLQNRFVENVSAGGMGINETVLHVTLKDLPFGGVGESGIGAYHGKFSYETFSHKK 154
gi|77553820
FTKDSKLQEQYEAAISAGGMLVNDTAVHLTNQYLPFGGVGESGMGAYHGRFSFEAFSHKK 180
GDI_E_37      HMWKIYLLEG-CSSMTLSYMLRLVVCLLEELKKVEWDVTTGSSLLIVSAIRSLSSI---- 175
          . .  * :    :: . :   . :   : : :. .  *.:   .  * .::

gi|7270374    GVLYRSFSGDADLRYPPYTPKKKMVLKALLSSNIFAAILAFFGFS 225
gi|83701643   GVLYRSFDGDSDLRYPPYTPEKKRVLKALLSSDIFGAILAFFGFS 199
gi|77553820   AVLVRRFAGEAAARYPPYSPAKLKILRGVLKGNLGAMIKAILGF- 224
GDI_E_37      EVLMQIHPG------SLHIHPRRKNCRPFSVATLFAFLLCLDG-- 212
           ** : . *     . :  :   : .  . : . : .: *
```

gi|7270374 : putative aldehyde dehydrogenase [*Arabidopsis thaliana*]

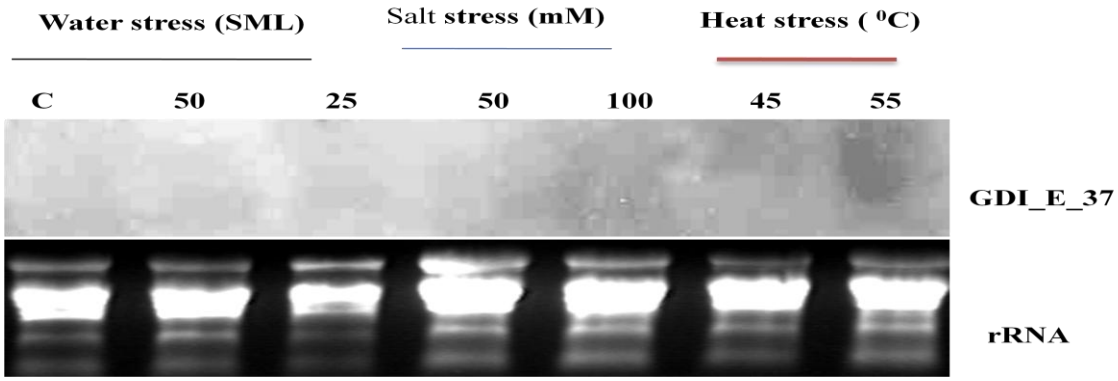
gi|83701643 : putative aldehyde dehydrogenase [*Brassica rapa*]
gi|77553820 : aldehyde dehydrogenase, putative [*Oryza sativa*]

Determination of nucleotide sequence, deduction amino acid sequence and homology analysis of GDI_E_37

3.2. Expression analysis of Aldehyde dehydrogenase (ALDH) under different abiotic stress conditions through Northern blot analysis.

The important molecular response of plants to stress is expression of stress-responsive genes. In this way in the present study we analyzed expression analysis of Aldehyde dehydrogenase (GDI_E_37) under different abiotic stress conditions by Northern blot analysis. Total RNA obtained from leaves of control (100% SML) and various abiotic stress treatments such as water stress (at 50 and 25% SML), NaCl stress (50 and 100 mM), and heat stress (45^0C and 55^0C for 12 h) and transferred on to nylon membranes and hybridized with labeled selected clone (GDI_E_37) such as EC391300 (Aldehyde dehydrogenase). Northern blot analysis revealed that Aldehyde dehydrogenase gene was upregulated with increasing specific stress conditions and share common gene expression due to water, NaCl and temperature stresses studied (Fig. 2).

Figure 2*. Northern expression analysis pattern of groundnut drought induced aldehyde dehydrogenase (GDI_E_37) under different abiotic conditions .Total RNA isolated from leaves of 19-day-old groundnut plants under control (C) and different abiotic stress treatments water stress (Control, 50 and 25 (SML); Salt stress 50 and 100 mM; Heat stress (45^0C and 55^0C for 12 h) was resolved on gel and transferred onto nylon membrane. Blots were hybridized with ^{32}P labeled cDNA probe. rRNA used as loading control as shown in the panels below each blot.*



IV. Discussion:

Aldehyde dehydrogenases (ALDHs) play a major role in the detoxification processes of aldehydes generated in plants when exposed to abiotic stress. Aldehyde molecules are common intermediates in most cellular pathways such as carbohydrate, amino acid, protein, lipid or steroid metabolism [17, 16]. However, when produced in excessive amounts, they can have detrimental effects on cellular metabolism because of their chemical reactivity [32]. Aldehydes can cause genotoxic effects (i.e. chromosomal aberrations and DNA adducts) [33, 34, 35], lipid peroxidation resulting in the loss of membrane integrity or modification of proteins subsequently causing cellular and developmental arrest [32, 36, 18, 37]. On the other hand, recent findings suggest that some aldehydes may also have a signaling function [38]. Therefore, maintaining the in vivo concentration of reactive aldehydes at well-balanced, non-toxic levels is crucial for organisms.

Several workers reported that the roles of ALDHs in various organisms [39, 40, 41]. The first plant ALDH3 genes were isolated from the desiccation-tolerant resurrection plant *Craterostigma plantagineum* (Cp-ALDH) and *A. thaliana* (ALDH3I1 and ALDH3H1) [41]. After then several plant ALDH genes have been reported to be activated by environmental stress such as dehydration, salinity or excessive light by [24]. Accumulation of aldehydes in plants in response to abiotic stress to leads the production of reactive oxygen species (ROS) such as singlet oxygen, hydroxyl radical, superoxide and H2O2 [23]. Under excessive generation of ROS, the capacity of the electron transport chain exceeds the consumption of reduction equivalents delivered to the stroma side of the chloroplastic thylakoid membranes leading to oxidative stress/damage [42]. The molecular relationship of all ALDH genes was examined recently in *Arabidopsis thaliana* [27]. The over expression of ALDH3I1 in transgenic *Arabidopsis* against abiotic stress was reported [19]. Above all works support that Aldehyde dehydrogenase (ALDHs) genes were upregulated with abiotic stress. Similarly our study clearly indicates that the Aldehyde dehydrogenase (GDI_E_37) was expressed with increasing stress than control samples. More over it was expressed maximum at 25% soil moisture level and higher salt (100mM) and

heat stress levels (55^{o}c). These results will lead to better understanding of the biological functions of the aldehyde dehydrogenase in plants under abiotic stresses.

References:

[1]. Bray EA, Bailey-Serres J, Weretilnyk E. Responses to abiotic stresses. In: *Biochemistry and Molecular Biology of Plants*. Gruissem, W., Buchnnan, B. and Jones, R. (Eds.). American Society of Plant Physiologists, Rockville, MD. 2000; 1158-1249.

[2]. Chrispeels MJ. Biotechnology and the poor. Plant Physiology. 2000; 124: 3-6.

[3]. Wang W, Vinocur B, Altman A. Plant responses to drought salinity and extreme temperatures: towards genetic engineering for stress tolerance. Planta, 2003; 218: 1-14.

[4]. Valliyodan B, Nguyen HT. Understanding regulatory networks and engineering for enhanced drought tolerance in plants. *Current Opinion in Plant Biology*, 2006; 9:189-95.

[5]. Kramer PJ, Boyer JS. Water relations of plants and soils. Academic press, San Diego, USA. 1995;1- 495.

[6]. Westgate ME, Boyer JS. Osmotic adjustment and the inhibition of leaf, root, stem and silk growth at low water potentials in maize. Planta. 1985;164:540-549.

[7]. Chaves MM, Maroco JP, Pereira JS. Understanding plant responses to drought - from genes to the whole plant. Functional Plant Biology. 2003; 30: 239-264.

[8]. Xiong L, Schumaker KS, Zhu JK. Cell signaling during cold, drought, and salt stress. Plant Cell, 2002; 14: 165-183.

[9]. Shinozaki K, Yamaguchi-Shinozaki, K. 2000. Molecular responses to dehydration and low temperature: differences and cross-talk between two stress signaling pathways. *Current Opinion in Plant Biology*, 3: 217-223.

[10]. Chandraobulreddy P, Sriranganayakulu G, Thippeswamy M, Sudhakar Reddy P, Reddy MK and Chinta Sudhakar *Identification of stress-induced genes from the drought tolerant semi-arid legume crop horsegram (Macrotyloma uniflorum (Lam.) Verdc.) through analysis of subtracted expressed sequence tags*. Plant Science, 2008. *175 (3)372-38.*

[11]. Bajaj S, Targolli J, Liu LF, Ho THD, Wu R. Transgenic approaches to increase dehydration stress tolerance in plants. Molecular Breeding, 1999; 5: 493-503.

[12]. Hasegawa PM, Bressan RA, Zhu JK, Bohnert HJ. Plant cellular and molecular responses to high salinity. Annual Review of Plant Physiology and Plant Molecular Biology. 2000; 51: 463-499.

[13]. Zhang JX, Klueva NY, Wang Z, Wu R, Ho TH, Nguyen HT, Ho THD. Genetic engineering for abiotic stress resistance in crop plants. In Vitro Cellular & Developmental Biology-Plant, 2000; 36: 108-114.

[14]. Cushman JC, Bohnert HJ. Genomic approaches to plant stress tolerance. Current Opinion in Plant Biology. 2000; 3: 117-124.

[15]. Sunkar R, Bartels D, Kirch Hans H. Over expression of a stress-inducible aldehyde dehydrogenase gene from *Arabidopsis thaliana* in transgenic plants improves stress tolerance. Plant Journal. 2003; 35: 452-464.

[16]. Kirch HH, Bartels D, Wei Y, Schnable PS, Wood AJ. The ALDH gene superfamily of Arabidopsis. Trends in Plant Science 2004; 9:371–377

[17]. Yoshida A, Rzhetsky A, Hsu LC, Chang C. Human aldehyde dehydrogenase gene family. European Journal of Biochemistry. 1998; 251:549–557.

[18]. Chen TH, Murata N. Enhancement of tolerance of abiotic stress by metabolic engineering of betaines and other compatible solutes. Current Opinion in Plant Biology.2002; 5: 250–257.

[19]. Simeon OK, Christine K, Andrea D, Hans-hubert K, Dorothea B. Over-expression of different aldehyde dehydrogenase genes in Arabidopsis thaliana confers tolerance to abiotic stress and protects plants against lipid peroxidation and oxidative stress, Plant, Cell and Environment. 2006; 29:1033–1048.

[20]. 20. Junyi Z, Tagnon D, Missihoun, Dorothea Bartels. The role of Arabidopsis aldehyde dehydrogenase genes in response to high temperature and stress combinations, Journal of Experimental Botany. 2017; 68(15):4295–4308.

[21]. Singh S, Brocker C, Koppaka V, Chen Y, Jackson BC, Matsumoto A, Thompson DC, Vasiliou V. Aldehyde dehydrogenases in cellular responses to oxidative/electrophilic stress. Free Radical Biology & Medicine. 2013; 56:89–101.

[22]. Lamb C, Dixon RA. The oxidative burst in plant disease resistance. Annual Review of Plant Physiology and Plant Molecular Biology 1997; 48; 251–275.

[23]. Bolwell GP. Role of active oxygen species and NO in plant defense responses. Current Opinion in Plant Biology. 1999; 2:287–294.

[24]. Bouché N, Fait A, Bouchez D, Møller SG, Fromm H. Mitochondrial succinic-semialdehyde dehydrogenase of the γaminobutyrate shunt is required to restrict levels of reactive oxygen intermediates in plants. Proceedings of the National Academy of Sciences of the USA 100. 2003; 6843–6848.

[25]. Veeranagamallaiah G, Sriranganayakulu G, Thippeswamy M, Chandra ObulReddy P, Sivakumar M, EswaraNarayana Reddy K, Pandurangaiah M, Sridevi V, Annapurnadevi A, Chinta Sudhakar . Aldose reductase expression contributes in sorbitol accumulation and 4-hydroxynon-2-enol detoxification in foxtail millet (Setaria italica *L.) cultivars with different salt stress tolerance*, Plant Growth Regulation. 2009;59:137-143.

[26]. Stiti N, Missihoun TD, Kotchoni SO, Kirch HH, Bartels D. Aldehyde dehydrogenases in Arabidopsis thaliana: biochemical requirements, metabolic pathways, and functional analysis. Frontiers in Plant Science. 2011; 2:65.

[27]. Kirch HH, Bartels D, Wei Y, Schnable PS, Wood AJ. The ALDH gene super family of Arabidopsis. Trends in Plant Science. 2004;9: 371-377.

[28]. Missihoun TD, Kirch HH, Bartels D. T-DNA insertion mutants reveal complex expression patterns of the aldehyde dehydrogenase 3H1 locus in Arabidopsis thaliana. Journal of Experimental Botany. 2012; 63:3887–3898.

[29]. Mishra RN, Ramesha A, Kaul T, Nair S, Sopory SK, Reddy MK. A modified cDNA subtraction to identify full-length differentially expressed genes from any given system: an alternate to DNA chip technology. Analytical Biochemistry. 2005; 345:149-159.

[30]. Datta K, Schmiit A, Marces A. Characterization of two Soybean repetitive proline rich proteins and a cognate cDNA from germinated axes. Plant Cell. 1989;1: 9445-952.

[31]. Sambrook J, Fritsch EF, Maniatas T. Molecular cloning-A laboratory mannual. 2nd Eds. New York: Cold Spring Habor press. 1989.

[32]. Lindahl R. Aldehyde dehydrogenases and their role in carcinogenesis. Critical Review in Biochemistry and Molecular Biology. 1992;27:283–355.

[33]. Subramaniam R, Roediger F, Jordan B, Mattson PM., Keller JN, Waeg G, Butterfield DA. The lipid peroxidation product, 4-hydroxy-2-trans nonenal, alters the conformation of cortical synaptosomal membrane-proteins. Journal of Neurochemistry.1997;69:1161–1169.

[34]. Comporti M. Lipid peroxidation and biogenic aldehydes: from the identification of 4-hydroxynonenal to further achievements in biopathology. Free Radical Research. 1998; 28:623–635.

[35]. Wacker M, Wanek P, Eder E. Detection of 1,N-2-propanodeoxyguanosine adducts of trans-4-hydroxy-2-nonenal after gavages of trans-4-hydroxy-2-nonenal or induction of lipidperoxidation with carbon-tetrachloride in F344 rats. Chemico Biology Interaction. 2001; 137:269–283.
[36]. Chen HJC, Gonzalez FJ, Shou MG, Chung FL. 2,3- Epoxy-4-hydroxynonenal, a potential lipid peroxidation product for etheno adduct formation, is not a substrate of human epoxide hydrolase. Carcinogenesis. 1998; 19:939–943.
[37]. Chen X, Zeng Q, Wood AJ. ALDH7B6 encodes a turgor-responsive aldehyde dehydrogenase homologue that is constitutively expressed in Tortula ruralis gametophytes. Bryologists. 2002; 105:177–184.
[38]. Weber H, Chételat A, Reymond P, Farmer E. Selective and powerful stress gene expression in Arabidopsis in response to malondialdehyde. Plant Journal. 2004;37:877–888
[39]. Barclay KD, McKersie BD. Peroxidation reactions in plant membranes – effects of free fatty acids. Lipids.1994;29:877–882.
[40]. Deuschle K, Funck D, Hellmann H, Däschner K, Binder S, WB. A nuclear gene encoding mitochondrial Δ1 -pyrroline-5-carboxylate dehydrogenase and its potential role in protection from proline toxicity. Plant Journal. 2001;27:345– 355.
[41]. Kirch HH, Nair A, Bartels D. Novel ABA- and dehydration-inducible aldehyde dehydrogenase genes isolated from the resurrection plant Craterostigma plantagineum and Arabidopsis thaliana. Plant Journal. 2001;28:555–560.
[42]. Niyogi KK, Bjorkman O, Grossman AR.The role of specific xanthophylls in photoprotection. Proceedings of the National Academy of Sciences of the USA. 1997;94:14162–14167.

G.S.Ranganayakulu, et. al. "Expression analysis of Aldehyde Dehydrogenase (GDI_E_37) gene in groundnut under different abiotic stress." *IOSR Journal of Biotechnology and Biochemistry (IOSR-JBB)*, 8(6), (2022): pp. 07-13.