

RESEARCH

Open Access



Computational analysis of the *AP2/ERF* family in crops genome

Shouhartha Choudhury^{1,2,3*}

Abstract

Background The *Apetala 2/ethylene-responsive factor* family has diverse functions that enhance development and torment resistance in the plant genome. In variation, the *ethylene-responsive factor (ERF)* family of TF's genes is extensive in the crop genome. Generally, the plant-specific ethylene-responsive factor family may be divided by the *dehydration-responsive element-binding (DREB)* subfamily. So, the *AP2/ERF* super-family demonstrated the repeated *AP2 domain* during growth. The sole *AP2 domain* function represents abiotic stress resistance. Also, the *AP2 with B3 domain* enhances during the replication of brassinosteroid.

Objective The study objective is to investigate the *Apetala 2/ethylene-responsive factor* family in a model organism of the *Arabidopsis thaliana* for comparative analysis towards *Solanum lycopersicum* (Tomato), *Brassica juncea* (Indian and Chinese mustard), *Zea mays* L. (Maize) and *Oryza sativa* (Indian and Japanese Rice). So, examinations of the large *AP2/ERF* super-family are mandatory to explore the *Apetala 2 (AP2) family*, *ERF family*, *DREB subfamily*, and *RAV family* involved during growth and abiotic stress stimuli in crops.

Methods Therefore, perform bioinformatics and computational methods to the current knowledge of the *Apetala 2/ethylene-responsive factor* family and their subfamilies in the crop genome. This method may be valuable for functional analysis of particular genes and their families in the plant genome.

Results Observation data provided evidence of the *Apetala 2/ethylene-responsive factor (AP2/ERF)* super-family and their sub-family present in *Arabidopsis thaliana* (Dicots) and compared with *Solanum lycopersicum* (Dicots), *Brassica juncea* (Dicots), *Zea mays* L. (Monocots) and *Oryza sativa* (Monocots). Also, remarks genes in *Oryza sativa*. This report upgraded the *Apetala 2/ethylene-responsive factor (AP2/ERF)* family in the crop genome. So, the analysis documented the conserved domain, motifs, and phylogenetic tree towards Dicots and Monocots species. Those outcomes will be valuable for future studies of the defensive *Apetala 2/ethylene-responsive factor* family in crops.

Conclusion Therefore, the study concluded that the several species-specific TF genes in the *Apetala 2/ethylene-responsive factor (AP2/ERF)* family in *Arabidopsis thaliana* and compared with crop-species of *Solanum lycopersicum*, *Brassica juncea*, *Zea mays* L. and *Oryza sativa*. Those plant-specific genes regulate during growth and abiotic stress control in plants.

Highlights

- The study is significantly associated with crop development.
- The developmental and abiotic stress-responsible gene families observed in different crops.

*Correspondence:

Shouhartha Choudhury

shouharthac@gmail.com; bioinfo11shouhartha@gmail.com

Full list of author information is available at the end of the article



© The Author(s) 2024. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

- The *AP2* family originated during the growing embryo, leaf, and flower.
- The *ERF/DREB* families initiated abiotic stress such as freezing, drought, salt, low oxygen, oxidative, osmotic, heat, heavy metals, and soil salinity.
- Finally, the *RAV* family implicated the solution of brassinosteroid.
- So, the analysis data provided valuable information for the Department of Agriculture Biotechnology.
- Also, the documented data are valuable for the plant database and research.

Keywords *AP2/ERF* superfamily, *ERF/DREB* family, Abiotic stress and development

Introduction

The plant-specific *Apetala 2/ethylene-responsive factor* family genes are predominant in the dicotyledonous and monocotyledonous plant genomes. Also, the *AP2/ERF* (*Apetala 2/ethylene-responsive factor*) family is typically divided into *subfamilies*: (1) The primary *AP2* family, (2) the *ERF/DREB* family, and the last (3) *RAV* family. The *AP2* family illustrated the duplex *AP2 domain* associated with developmental processes like growing embryos, leaves, and flowers in plants. The classical *ERF* family proposed the sole *AP2 domain* plays a core function in the *Apetala 2/ethylene-responsive factor* (*AP2/ERF*) family. So, the defensive *ERF* family and stress-responsive *DREB* subfamily functioned as abiotic stress controls such as freezing, drought, salt, low oxygen, oxidative, osmotic, heat, ABA ethylene, jasmonic acid, and abscisic acids have major upshot on the growth and production of plants. The third *RAV* family proposed a combined function of the *AP2* with the *B3 domain* involved during the reaction of brassinosteroid in the plant genome. Those identified twice *Apetala 2 domain*, sole *Apetala 2 domain*, and combined between *Apetala 2* with *B3 domain* consist of amino acid residues involved in DNA binding [1]. The first *AP2* (*Apetala 2*) domain is reports in a model organism of *Arabidopsis thaliana*. Recent empirical data illustrated the repeated *AP2 domain* regulates during the developmental processes in crop variety (i.e. flower, meristem, leaf, and embryo development) [2–6]. On the other hand, the ethylene-responsive factor (*ERF*) family divides into two main subfamilies: *C-repeat/dehydration-responsive element binding factors* family (*CBF/DREB* family) [7–9]. The plant-specific *AP2 domain* observed as a conserved DNA-binding domain called *ethylene-responsive element binding factors* or *ERFs* (i.e. *ERF1*, *ERF2*, *ERF3*, and *ERF4*) generally binds to the GCC box motifs [10–12]. However, the major *Apetala 2/ethylene-responsive factor* (*AP2/ERF*) family implicates diverse functions like hormonal signal transduction, cellular processes, regulation of metabolism, and

growth processes in plants [6, 8, 13–23]. In December, 2000, the Arabidopsis Genome Initiative (AGI) sequenced the genome of a model plant called *Arabidopsis thaliana* and identified 145 genes in the broad *AP2/ERF* family [8]. Also, particular genes in the supreme *AP2/ERF* family require to determine again. So, we can observe the likelihood of *AP2 domain*-mediated genes play a role and physiological aspect in plant species. Also, a transgenic experiment will be necessary to govern the biological phenomenon of a particular gene in the defensive *AP2/ERF* family in plant genomes. The previous evolutionary study shows that the large *Apetala 2/ethylene-responsive factor* families classified into subfamilies are closely related [24–26]. A comparative and functional study of the particular gene from the *AP2/ERF* (*Apetala 2/ethylene-responsive factor*) family in crop-specific *Arabidopsis thaliana* (Dicots), *Solanum lycopersicum* (Dicots), *Brassica juncea* (Dicots), *Zea mays* L. (Monocots) and *Oryza sativa* (Monocots) is necessary for functional abundance. This process and evaluation of the link between gene families would provide a significant direction for predicting and upgrading the species-specific *transcription factor* genes in the particular genome. The current availability of the draft genome sequences of *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays* L., and *Oryza sativa* allowed comparative and functional analysis between plant genomes, which is valuable for the practical and evolutionary diversity of gene families in the genome. In this work, an establishment and comprehensive investigation of the *Apetala 2/ethylene-responsive factor* family in *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays* L. and *Oryza sativa* attempts. Also, the genes in the *Apetala 2/ethylene-responsive factor* family in the *Arabidopsis thaliana* genome was survey again and also compared with crops of *Solanum lycopersicum*, *Brassica juncea*, *Zea mays* L. and *Oryza sativa*. A comparative and functional study between Dicots (*Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*) and

Table 1 Query sequence

```
>ERF109
AAACACAAACAAAACATCATATTTCAATCTCCAGGTGCTTTACACCAACAGAGTCGCAAGAAAACAAAACAAAACCTCGGATTTAGTTTGACAGAAGAAGGAATC
GAGAGTCGGGTATGCATTATCCTAACAAACAGAACCGAATTCGTCGGAGCTCCAGCCCCAACCCGGTATCAAAGGAGCAGTTGTCACCGGAGCAAGAGCTTTCAGTTA
TTGTCTCTGCTTTGCAACACGTGATCTCAGGGGAAAACGAAACGGCGCCGTGTCAGGGTTTTTCCAGTGACAGCACAGTGATAAGCGCGGGAATGCCTCGGTTGG
ATTAGAGACATTTGCAAGTCTGAGGATCGAAGGATGTCCTCGCTGTAACACTTTTTTCGCGCCAAATCAGAGAATTTGAAAAGAATCATCAACAAGAAGAAGAGATTA
CTAGTAGTAGTAACAGAAGAAGAGAGAGCTCTCCCGTGGCGAAGAAAGCGGAAGGTGGCGGGAAAATCAGGAAGAGGAAGAACAAGAAGAATGGTTACAGAG
GAGTTAGGCAAAGACCTTGGGGAAAATTTGCAGCTGAGATCAGAGATCCTAAAAGACCCACACGTGTTGGCTTGGTACTTTTCGAAACCGCCGAAGATGCGGCTC
GAGCTTATGATCGAGCCGATGGATTCCGTGGGCAAGGGCTAAACTCAACTTCCCTTTGTGGATTACACGTCTTCAGTTTCATCTCTGTTGCTGCTGATGATA
TAGGAGCAAAGGCAAGTCAAGCGCCAGTGTGAGCGCCACAGATTCAGTTGAGCAGAGCAATGGAACGAGGAGGAGGGGATTGCAATATGGAGAGTGATGGA
ATATGATGATGATGATGGATTTGGGAATGGAGATTCCTCAGATTCAGGAAATACAATTGCTGATATGTTCCAGTGATAAATGAGCTCTTTCTGTTGGCGTTTTTGGAG
TTAAGTGAAGAAGAGATTGACACTGTGGCTTTTAAAGTGAACAAGAACAAAGAAAGCATGTAATTAGTAGTCTCATTCTTTTGTGTTGGTCAATCTATGTTTATCTC
ATATAAATCTGAGTTAAACCTATCTGAGGAGAGAGTAAATAAAGAGGTTAAGAAACCAACATTGGCTGTAATTATAACGTAAGTGCAACGTTGTTATAAAGGA
GAAAACATAATTGGTGACAAAAGACATAAAGAAAAGATGCTACTCTACAAAAGCATGCGTGCAGCTATTCGACAAACAATGGCATCTCCAGAGAGGAAATCCG
AGCTCTTGGCTAGTTATCTGTAATGTGAAAACATGAATGTATTGAGTTTATTCTGTAACATTGGAAGCGAAATAAAGGGTTATCAACTGTTACCAA
>ERF109
MHYPNNRTEFVVGAPAPTRYQKEQLSPEQELSVIVSALQHVISGENETAPCQGFSSDSTVISAGMPRLDSDTCQVCRIEGLGCNYFFAPNQRIEKNHQEEITSSNRRRESSP-
VAKKAEGGGKIRKRNKNGYRGRVQRWPKFAAEIRDPKRATRVWLGTETAEDAARAYDRAAIGFRGPRAKLNFPVDYTSVSSPVAADDIGANASASVSATDSVE-
AEQWNGGEDCNMEEWMMMMMDFGNGDSSDSGNTIADMFQ
```

Query gene: (a) Nucleotide and (b) Peptide

Table 2 Summary of the AP2 domain and RRTF1

Species	HMMER	BLAST2	BLAST2GO
<i>Arabidopsis thaliana</i> (Dicots)	224	141	1
<i>Solanum lycopersicum</i> (Dicots)	182	129	2
<i>Brassica juncea</i> (Dicots)	470	391	6
<i>Zea mays L.</i> (Monocots)	327	187	2
<i>Oryza sativa</i> (Monocots)	178	108	1

Summary of the algorithm hits in all species

Monocots (*Zea mays L.* and *Oryza sativa*) perform. So, the study reviewed the comparative and functional genomics of the *Apetala 2/ethylene-responsive factor family* response to growth and abiotic stress response in plants.

Results

The primary sequence demonstrated the formation of nucleotides and peptides in the *ERF109 (RRTF1)* gene in *Arabidopsis thaliana*. The sequence composed of 1386 nucleotides and 268 peptides among 64 peptides bind to the DNA sequence called *AP2 domain* (Table 1).

So, take a closer look at the plant-specific *AP2/ERF family* and analyze genes known so far; those have different composition and functional domains. Also, the observation summarized the total number of *Apetala 2 domains* in a model organism of *Arabidopsis thaliana* and compared it with crops of *Solanum lycopersicum*, *Brassica juncea*, *Zea mays L.*, and *Oryza sativa* (Table 2).

Also, the gene ontology (GO) annotation demonstrated the sequence accuracy of the *RRTF1 (ERF109)* gene in the defensive *AP2/ERF family* in all species (Table 3).

Table 3 Summary of the GO annotation

Gene Id	Gene	Protein	Species
AT4G34410.1	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Arabidopsis thaliana</i>
Solyc10g050970	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Solanum lycopersicum</i>
Solyc01g108240	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Solanum lycopersicum</i>
BjuB05g59080S	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Brassica juncea</i>
BjuA03g05680S	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Brassica juncea</i>
BjuA01g40180S	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Brassica juncea</i>
BjuB02g73640S	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Brassica juncea</i>
BjuA08g14310S	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Brassica juncea</i>
BjuB03g42060S	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Brassica juncea</i>
Zm00001eb100800	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Zea mays L</i>
Zm00001eb038070	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Zea mays L</i>
BGIOSGA030907	<i>ERF109</i>	ethylene-responsive transcription factor <i>ERF109</i>	<i>Oryza sativa</i>

Summary of the GO annotation of *RRTF1 (ERF109)* in all species

Further, the GO annotation of the *RRTF1* gene demonstrated the molecular function, cellular component, and biological process in particular organisms. Also, remark genes in *Oryza sativa* (Indian Rice): Os02g42580, Os02g52880, Os03g02650, Os04g36640, Os04g48330, Os06g42910 and Os12g07030. The repeated gene in the crop of *Oryza sativa*: LOC_Os06g09717.1 was completely identical with OsERF#139 (Os06g09730) and OsERF#010 (Os06g09690), afterward proposed a new gene Id: Os06g09717. So, the crop-specific transcription factor data analysis documented the total *AP2* domain-mediated isoforms in the *AP2* family, *ERF* family, *DREB* subfamily, and *RAV* family between *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays L.* and *Oryza sativa* accordingly. Also, the multiple hits of repeated *AP2* domain, single *AP2* domain, and *B3* domain are listed from all species for sequence alignment. The MSA demonstrated the high consensuses (90%) sequence is

conserved in the *AP2* family, *ERF* family, *DREB* subfamily, and *RAV* family between the plant-specific *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays L.* and *Oryza sativa* (Figs. 1, 2, 3, and 4). In contrast, the *RRTF1* gene was conserved among all species with their sequence-specific motifs (Figs. 5 and 6). The phylogenetic tree demonstrated the molecular evolutionary link between the *RRTF1* genes in the *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays L.* and *Oryza sativa* (Fig. 7). Also, the phylogeny analysis demonstrated the particular clade represented the *AP2* family, *ERF* family, *DREB* sub-family and *RAV* family (Fig. 8). Further, the *RRTF1* (*Redox responsive transcription factor 1*) expression is highly revealed in the flowering stage and minimal in the germinating period of the plants and observed abundant in flower, blade, hypocotyl, lateral root, and cotyledon.

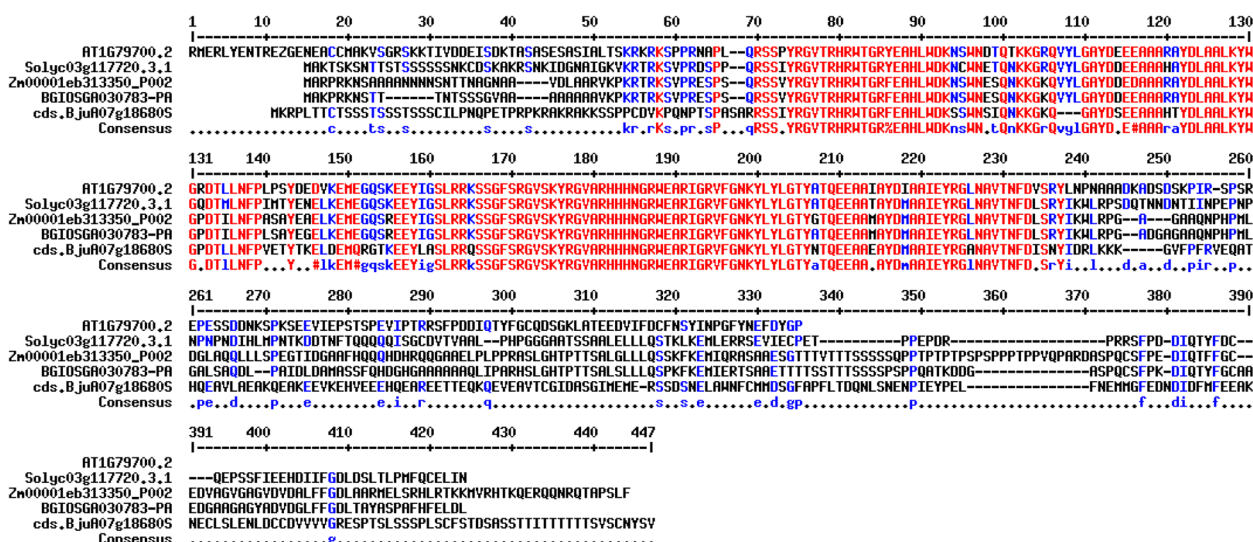


Fig. 1 Conserved repeated *AP2* domain in the *AP2* family

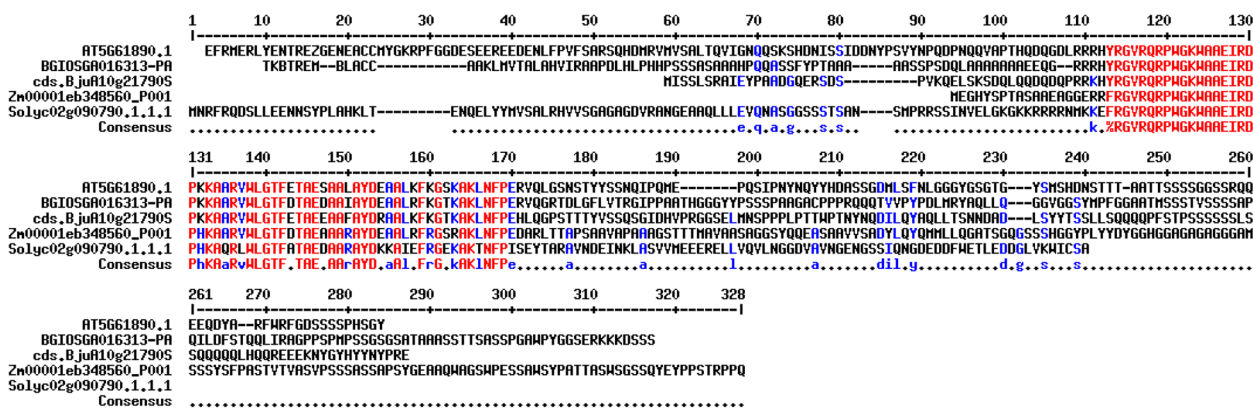


Fig. 2 Conserved single *AP2* domain in the *ERF* family

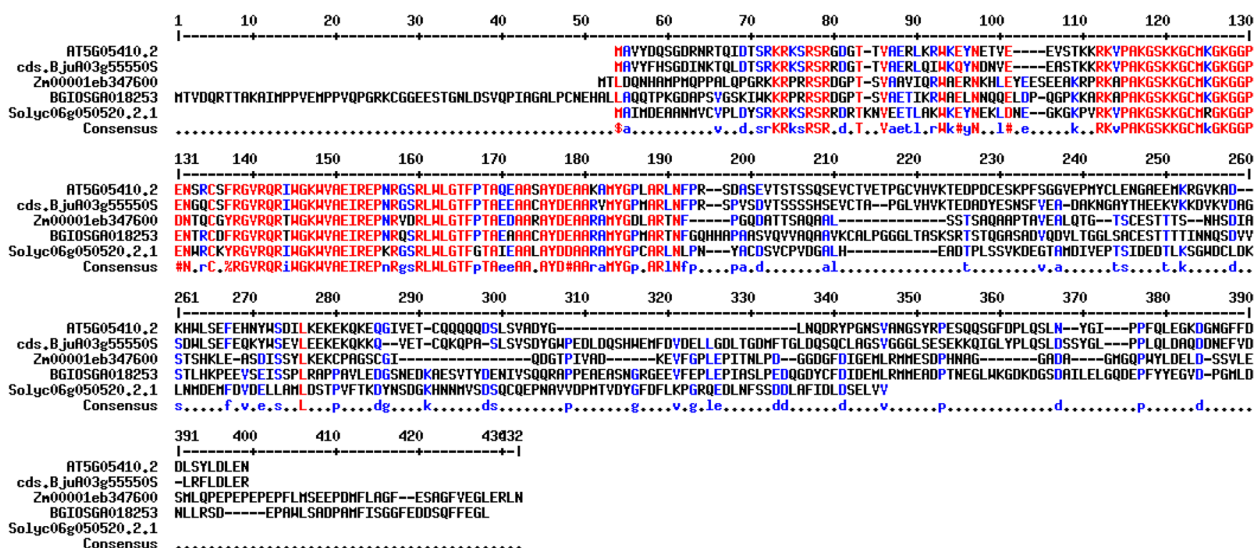


Fig. 3 Conserved single AP2 domain in the DREB subfamily

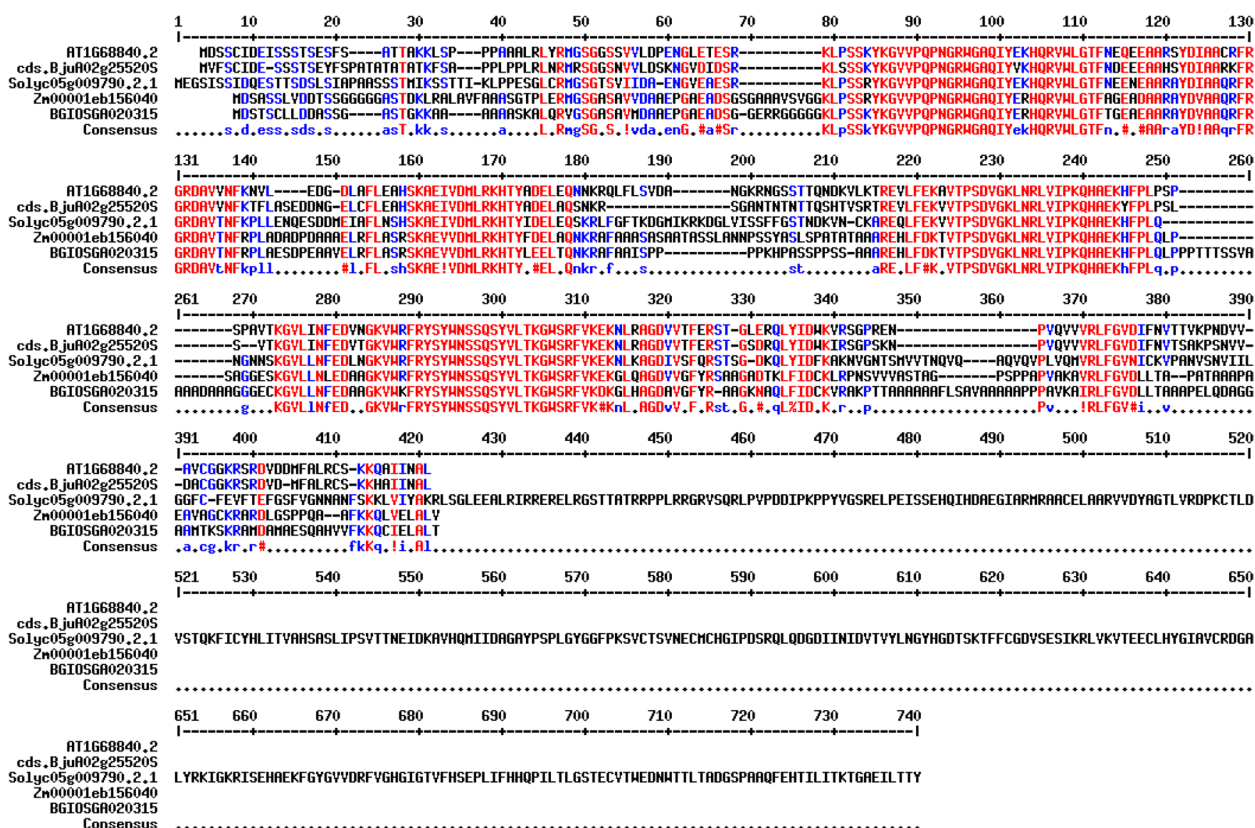


Fig. 4 Conserved AP2 with B3 domain in the RAV family

Discussion

The study demonstrated the *Apetala 2/ethylene-responsive factor* family between *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays L.*, and

Oryza sativa. The earlier empirical data suggested that Sakuma et al. (2002) reported 17, 121, and 6 genes in the *Apetala 2* family, *ethylene-responsive factor* family, and *Related to ABI3 and VPI* family in a superior model

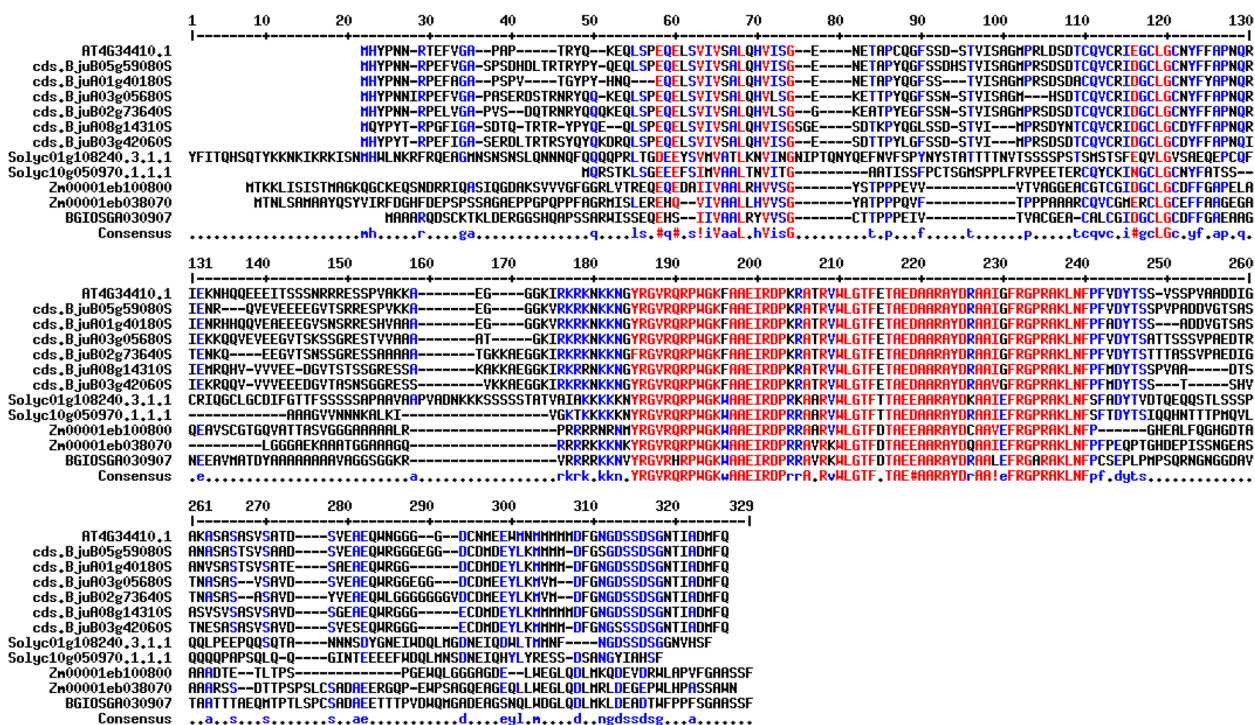


Fig. 5 Conserved AP2 domain in RRTF1

plant of *Arabidopsis thaliana* respectively. Also, the collaboration of Nakano et al. (2006) suggested 18, 122, and 6 AP2 domain-associated isoforms in the *Apetala 2* family, ethylene-responsive factor family, and Related to the ABI3 family in universal *Arabidopsis thaliana* and also compared with 139 specimens in the ethylene-responsive factor family of *Oryza sativa*. This study upgraded the total number of plant-specific genes in the *Apetala 2* (AP2) family, ethylene-responsive factor (ERF) family, DREB subfamily, and RAV (Related to the ABI3) family of the crop-specific *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays* L. and *Oryza sativa* (Table 4). The *Brassica juncea* exhibited the highest number of specific hits, whereas *Oryza sativa* showed the lowest. So, the study forwarded the developmental genes in the AP2 family (i.e. flower, meristem, leaf, and embryo development). In contrast, the abiotic stress-responsive genes in the ERF (ethylene-responsive factor) family and DREB subfamily (i.e. low oxygen, freezing, drought, salt, oxidative, osmotic, heat, ABA ethylene, jasmonic acid, and abscisic acids) (Table 5). At last, the involvement of the RAV family in a brassinosteroid response were observed.

So, the AP2/ERF super-family is necessary to explore the sub-families involved during the growth and survival of crops. A comparative analysis of crops' genomes

is mandatory for agriculture science and development. Also, the crops are manageable through agriculture biotechnology for research and development. In contrast, approximately 80% of crops produce in India. Those crops are economically beneficial around the globe.

Conclusion

The ecosystem depends on a balance among flora and fauna. The living organisms build on the food cycle to manage the Eco-system. Ecologically, plants are the subject of survival organisms. In addition, the crops are vital for a healthy life span. The cultivation of crops proposes the knowledge of agriculture biotechnology. So, the perusal of crop genomes is necessary to observe stress and developmental-responsive genes in particular species. This study summarized genes in the AP2/ERF super-family in different crops-genomes. Those species-specific genes are necessary for the growth and survival of crops. Crops are economically valuable worldwide. Therefore, the study provided extensive knowledge of the agronomic, economic, and ecological traits and possibly other benefits of crops. Also, the documented data provide valuable information in plant databases for agriculture research and development.

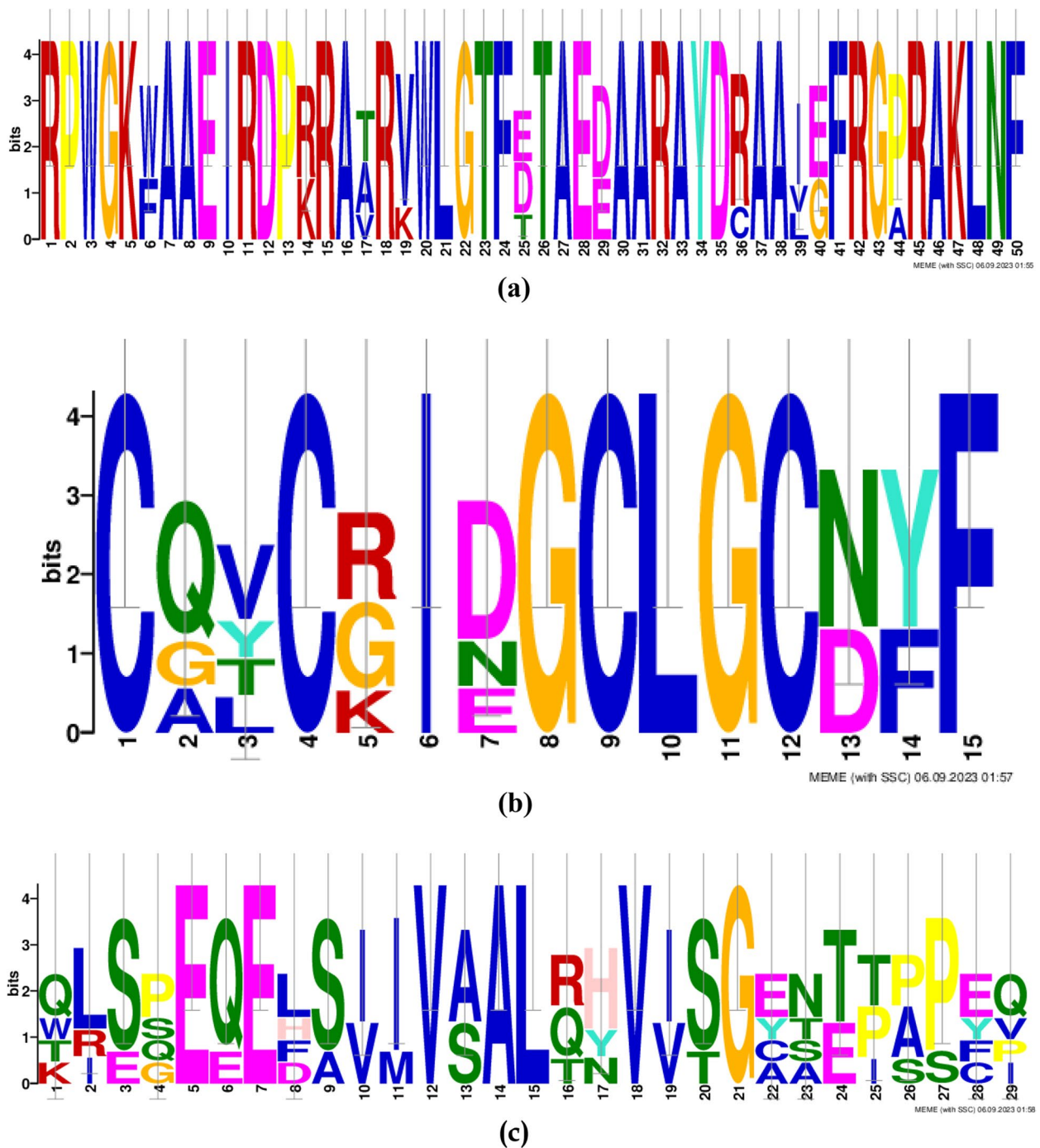


Fig. 6 Sequence motifs in *RRTF1* (a, b, and c)

Methods

Sequences and database

The current draft genome sequences of *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays L.*, and *Oryza sativa* was download from the TAIR

(<https://www.arabidopsis.org/>) and Ensemble (<https://asia.ensembl.org/index.html>) genome database. The *Arabidopsis Information Resource* (TAIR) database provides the option to attain the target sequence of model organisms of *Arabidopsis thaliana*. Also, SMART (<http://smart.embl-heidelberg.de/>) and Pfam (<http://>

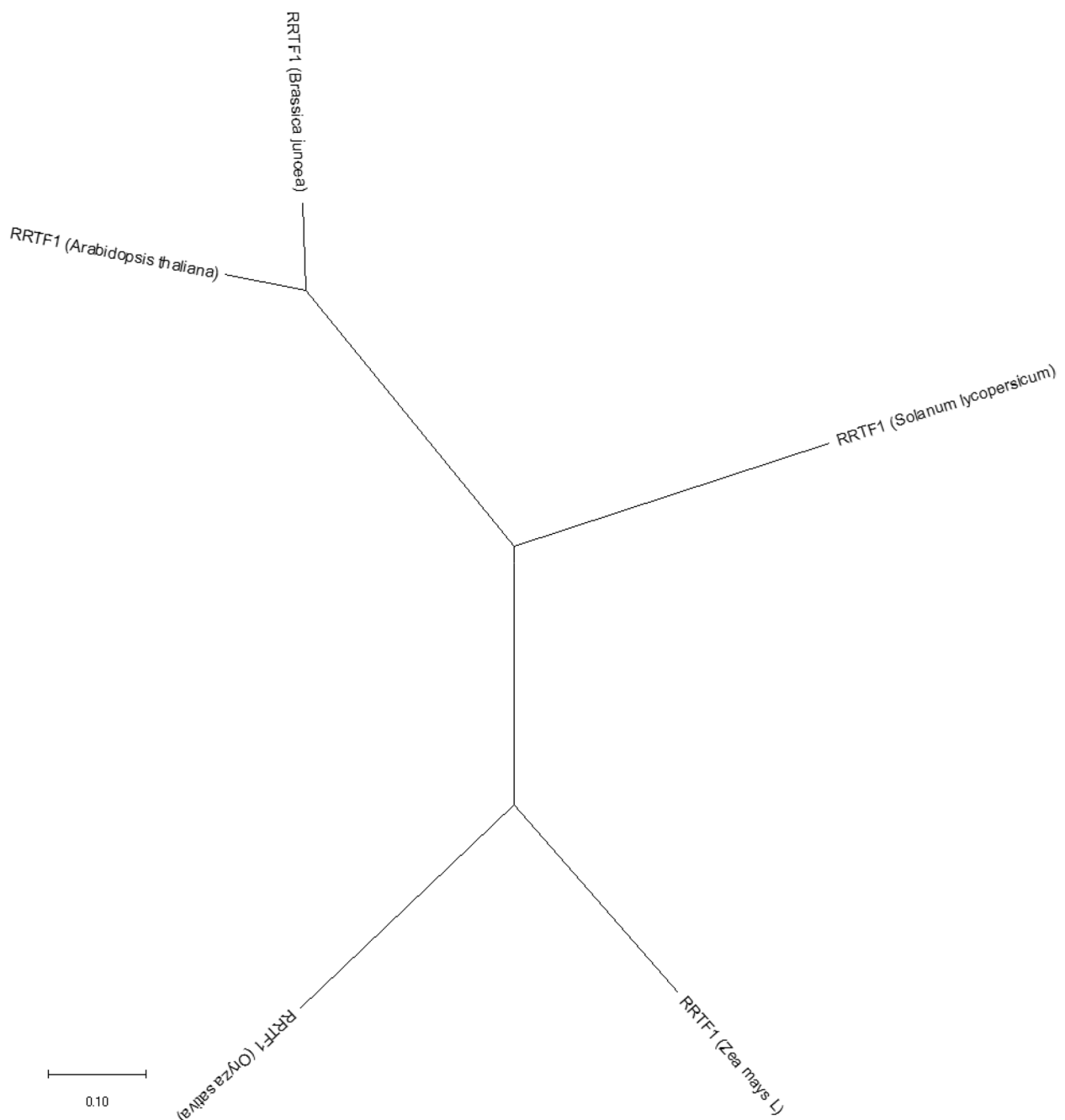


Fig. 7 The molecular evolutionary link of the *RRTF1* among all species

pfam.xfam.org/) retrieves to identify the particular domains in the *AP2/ERF* family.

Standalone tools and gene ontology (GO) annotation

The HMMER algorithm executes by the MSA of the specific domain as a profile search. HMMER is a statistical algorithm that allows MSA (making multiple sequence alignment) of the particular domain as

a profile search. It is an implemented practice of the probabilistic norm called the profile hidden Markov pattern. Standalone BLAST2 performs for homolog genes in both organisms. Also, BLAST2GO performs for the sequence accuracy of a specific transcription factor in the genome. BLAST2GO (BioBam) is a bioinformatics and statistical tool for high-throughput GO annotation of the novel sequence.

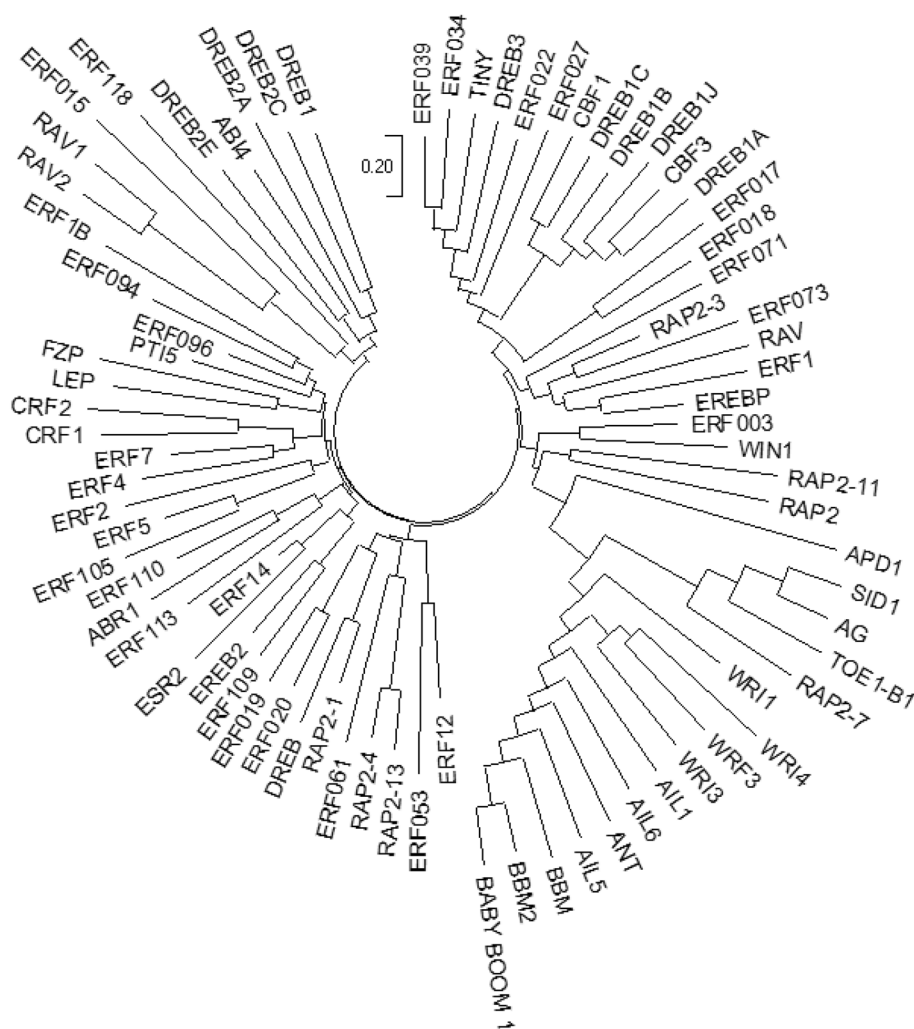


Fig. 8 Evolutionary link between genes in the AP2/ERF family

Table 4 Summary of the AP2/ERF super-family

Classification	<i>Arabidopsis thaliana</i>	<i>Solanum lycopersicum</i>	<i>Brassica juncea</i>	<i>Zea mays L</i>	<i>Oryza sativa</i>
AP2 Family	56	23	24	75	32
ERF Family	134	148	381	219	127
DREB Family	8	4	12	8	5
RAV Family	26	7	53	25	14
Total	224	182	470	327	178

Summary of the (a) AP2 family (b) ERF family (c) DREB sub-family and (d) RAV family

Sequence domain, motif, and phylogeny

Multiple sequence alignment (MSA) systems was used to calculate the average match of the homologous sequences for the identities, similarities, and differences that appear. MSA of multiple hits sequences analysis done by a web-based application MultAlin

(<http://multalin.toulouse.inra.fr/multalin/>) for identification and upgradation of the conserved domain. Also, the MEME suite is commonly known as a computational web-based tool for analysis and even discovery of sequence-specific motifs, so retrieve specific motifs via MEME suite (<https://meme-suite.org/meme/>).

Table 5 Biological Function of genes in the *AP2/ERF* family

Plant Species	Gene	Biological Function
<i>Arabidopsis thaliana</i>	<i>TINY</i>	Negatively regulated development and Positively regulated abiotic stress
<i>Arabidopsis thaliana</i>	<i>RAP2.4</i>	Positively regulated light and ethylene and drought stress response
<i>Arabidopsis thaliana</i>	<i>ERF4</i>	Positively regulated ethylene and ABA response
<i>Arabidopsis thaliana</i>	<i>RAP 2.3</i>	Positively regulated low oxygen, oxidative, and osmotic stress response
<i>Arabidopsis thaliana</i>	<i>ERF53</i>	Positively regulated heat and ABA response
<i>Arabidopsis thaliana</i>	<i>ERF1</i>	Positively regulates salt, drought, and heat stress response
<i>Arabidopsis thaliana</i>	<i>DREB2A</i>	Positively regulated drought, salt, heat, and cold stress response
<i>Arabidopsis thaliana</i>	<i>ERF109</i>	Oxidative stress response (Redox response)
<i>Arabidopsis thaliana</i>	<i>RAP2.4</i>	Positively regulates light- and ethylene-mediated growth regulation
<i>Arabidopsis thaliana</i>	<i>ERF7</i>	Abscisic acid response
<i>Arabidopsis thaliana</i>	<i>WIN1</i>	Wax accumulation
<i>Arabidopsis thaliana</i>	<i>ABR1</i>	Abscisic acid response and sugar signaling
<i>Arabidopsis thaliana</i>	<i>AG</i>	Floral homeotic response
<i>Arabidopsis thaliana</i>	<i>RAV1</i>	Low temperature response

Biological functions of the *AP2/ERF* family in *Arabidopsis thaliana*

Finally, the perusal of the molecular evolutionary link between genes and their particular families in between *Arabidopsis thaliana*, *Solanum lycopersicum*, *Brassica juncea*, *Zea mays L.*, and *Oryza sativa*, performed MEGA7 for constructing a phylogenetic tree by *Neighbor-Joining Methods*.

Acknowledgements

The author was grateful to Assam University, Silchar, Assam, India, for providing the requisite lab facilities during research work.

Dedication

This research paper is a gift to my beloved friend Catherine Tresa Alexander.

Author's contributions

This research paper contains the sole author. The author proposed the idea, experimented, analyzed the data and prepared the manuscript.

Funding

The author did not avail of financial assistance from any source in undertaking the present study.

Availability of data and materials

The data and material may be available on request through the corresponding author of Shouhartha Choudhury (Email Id: shouharthac@gmail.com).

Gene Id 829591

TF Id: AT4G344110.1

<https://www.arabidopsis.org/>

https://www.arabidopsis.org/servlets/Search?type=general&search_action=detail&method=1&show_obsolete=F&name=ERF109&sub_type=gene&SEARCH_EXACT=4&SEARCH_CONTAINS=1

<https://www.arabidopsis.org/servlets/TairObject?id=126772&type=locus>

<http://plants.ensembl.org/index.html>

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Author details

¹Har Gobind Khorana School of Life Sciences, Assam University, Silchar-788011 Assam, India. ²Department of Biotechnology, Assam University, Silchar-788011 Assam, India. ³Department of Life Science and Bioinformatics, Assam University, Silchar-788011 Assam, India.

Received: 2 October 2023 Accepted: 3 January 2024

Published online: 23 January 2024

References

- Lang-Mladek C, et al. Transgenerational inheritance and resetting of stress-induced loss of epigenetic gene silencing in *Arabidopsis*. *Mol Plant*. 2010;3(3):594–602.
- Elliott RC, et al. AINTEGUMENTA, an APETALA2-like gene of *Arabidopsis* with pleiotropic roles in ovule development and floral organ growth. *Plant Cell*. 1996;8(2):155–68.
- Chuck G, Meeley RB, Hake S. The control of maize spikelet meristem fate by the APETALA2 like gene indeterminate spikelet1. *Genes Dev*. 1998;12(8):1145–54.
- Moose SP, Sisco PH. Glossy15, an APETALA2-like gene from maize that regulates leaf epidermal cell identity. *Genes Dev*. 1996;10(23):3018–27.
- Boutillier K, et al. Ectopic expression of BABY BOOM triggers a conversion from vegetative to embryonic growth. *Plant Cell*. 2002;14(8):1737–49.
- Sakuma Y, et al. DNA-binding specificity of the ERF/AP2 domain of *Arabidopsis* DREBs, transcription factors involved in dehydration- and cold-inducible gene expression. *Biochem Biophys Res Commun*. 2002;290(3):998–1009.
- Dubouzet JG, et al. OsDREB genes in rice, *Oryza sativa L.*, encode transcription activators that function in drought-, high-salt- and cold-responsive gene expression. *Plant J*. 2003;33(4):751–63.
- Sakuma Y, et al. Functional analysis of an *Arabidopsis* transcription factor, DREB2A, involved in drought-responsive gene expression. *Plant Cell*. 2006;18(5):1292–309.

9. Fujimoto SY, et al. Arabidopsis ethylene-responsive element binding factors act as transcriptional activators or repressors of GCC box-mediated gene expression. *Plant Cell*. 2000;12(3):393–404.
10. Alonso JM, et al. Genome-wide insertional mutagenesis of Arabidopsis thaliana. *Science*. 2004;301(5633):653–7.
11. Hu YX, et al. Arabidopsis RAV1 is down-regulated by brassinosteroid and may act as a negative regulator during plant development. *Cell Res*. 2004;14(1):8–15.
12. Ohme-Takagi M, Shinshi H. Ethylene-inducible DNA binding proteins that interact with an ethylene-responsive element. *Plant Cell*. 1995;7(2):173–82.
13. Shinshi H, Usami S, Ohme-Takagi M. Identification of an ethylene-responsive region in the promoter of a tobacco class I chitinase gene. *Plant Mol Biol*. 1995;27(5):923–32.
14. Ohme-Takagi M, Suzuki K, Shinshi H. Regulation of ethylene-induced transcription of defense genes. *Plant Cell Physiol*. 2000;41(11):1187–92.
15. Stockinger EJ, Gilmour SJ, Thomashow MF. Arabidopsis thaliana CBF1 encodes an AP2 domain-containing transcriptional activator that binds to the C-repeat/DRE, a cis-acting DNA regulatory element that stimulates transcription in response to low temperature and water deficit. *Proc Natl Acad Sci*. 1997;94(3):1035–40.
16. Liu Q, et al. Two transcription factors, DREB1 and DREB2, with an EREBP/AP2 DNA binding domain separate two cellular signal transduction pathways in drought- and low-temperature-responsive gene expression, respectively, in Arabidopsis. *Plant Cell*. 1998;10(8):1391–406.
17. Van Der Fits L, Memelink J. The jasmonate-inducible AP2/ERF-domain transcription factor ORCA3 activates gene expression via interaction with a jasmonate-responsive promoter element. *Plant J*. 2001;25(1):43–53.
18. Aharoni A, et al. The SHINE clade of AP2 domain transcription factors activates wax biosynthesis, alters cuticle properties, and confers drought tolerance when overexpressed in Arabidopsis. *Plant Cell*. 2004;16(9):2463–80.
19. Broun P. Transcription factors as tools for metabolic engineering in plants. *Curr Opin Plant Biol*. 2004;7(2):202–9.
20. Gong H, et al. Silicon alleviates oxidative damage of wheat plants in pots under drought. *Plant Sci*. 2005;169(2):313–21.
21. Van der Graaff E, et al. Activation tagging of the LEAFY PETIOLE gene affects leaf petiole development in Arabidopsis thaliana. *Development*. 2000;127(22):4971–80.
22. Banno H, et al. Overexpression of Arabidopsis ESR1 induces initiation of shoot regeneration. *Plant Cell*. 2001;13(12):2609–18.
23. Kranz HD, et al. Towards functional characterisation of the members of the R2R3-MYB gene family from Arabidopsis thaliana. *Plant J*. 1998;16(2):263–76.
24. Bailey PC, et al. Update on the basic helix-loop-helix transcription factor gene family in Arabidopsis thaliana. *Plant Cell*. 2003;15(11):2497–502.
25. Reyes JC, Muro-Pastor MI, Florencio FJ. The GATA family of transcription factors in Arabidopsis and rice. *Plant Physiol*. 2004;134(4):1718–32.
26. Nakano T, et al. Genome-wide analysis of the ERF gene family in Arabidopsis and rice. *Plant Physiol*. 2006;140(2):411–32.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.