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Original article

YABBY Transcription Factors in Chickpea: Evolutionary Footprints and Functional Clues under Drought Stress

Serdar Coşkun [a, *], E. Sümer Aras [a] & İlker Büyük [a]

[a] Department of Biology, Biotechnology Section, Faculty of Science, Ankara University, Ankara, Türkiye

Abstract

Chickpea (*Cicer arietinum* L.) is an important plant species globally due to its economic value and nutritional content. The YABBY gene family plays a significant role in the growth and development of plants. A review of the literature reveals that there has been no prior study conducted on the YABBY gene family in chickpea. Based on this gap, the aim of this study is to perform a comprehensive analysis of the YABBY gene family in chickpea (*C. arietinum* L.) and to evaluate the transcript levels of these genes under drought stress. This study aims to uncover the potential roles of YABBY proteins in drought tolerance. YABBY proteins were identified and classified using chickpea genome data through bioinformatic approaches. Phylogenetic analysis, motif structure, chromosomal localization, and gene structure were examined. The expression levels of YABBY genes under drought stress were visualized in the form of a heat map using in silico techniques. As a result of the analyses, 8 CaYABBY family members were identified in the chickpea (*C. arietinum* L.) genome. These proteins range in length from 97 to 221 amino acids. The isoelectric points (pI) of YABBY proteins range from 5.15 to 9.58, covering both acidic and basic ranges, and their molecular weights vary between 10.90 and 24.62 kDa. CaYABBY gene family could be classified into the INO, YAB5, YAB2, CRC and FYAB3 subgroups. The genomic distribution of YABBY proteins in chickpea (*C. arietinum* L.) is irregular, although they share similar motif structures. According to our RNA-seq data, YABBY proteins may potentially play a role in the molecular adaptation processes of chickpea (*C. arietinum* L.) under drought stress. These results give a good starting point for more research on how chickpeas work and suggest possible ways to make them more resistant to drought by using breeding or genetic methods.

Keywords: Bioinformatics, Chickpea, Genome-wide analysis, YABBY genes

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* **Corresponding author:**

Serdar Coşkun is a doctoral candidate in the Department of Biology at Ankara University in Ankara, Türkiye. His research interests include the Biology, Molecular Biology and Biotechnology. He has lived, worked, and studied in Ankara, Türkiye.
Email: bio.serdarcoskun@gmail.com

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is one of the oldest legumes grown by people, and it's very important in farming around the world. It's especially useful in dry and semi-dry areas because it can pull nitrogen from the air and store it in special bumps on its roots, which helps the plant grow better. The crop completes its vegetative cycle within 60–100 days and is widely consumed due to its high nutritional content, including proteins, carbohydrates, vitamins, and essential minerals such as phosphorus, magnesium, potassium, calcium and iron. Dry chickpea seeds contain approximately 5% fat, 20–25% protein and 50–60% carbohydrates (Alajaji and El-Adawy, 2006; Jukanti et al., 2012). They contain important amino acids like histidine, leucine, isoleucine and lysine, which are necessary for good health (Candela et al., 1997).

Plants often face non-living stressors like lack of water, too much salt, very hot or cold temperatures, which can hurt their growth and how well they produce food. To deal with these stressors, plants use a variety of defense systems, many of which control gene activity. Transcription factors are important parts of these systems, helping plants adjust their gene expression to deal with tough environmental conditions (Buyuk et al., 2019; Yılmaz et al., 2025).

Some transcription factors are only found in plants, and one special group is the YABBY gene family. YABBY proteins belong to a bigger group called zinc finger proteins. They have two key parts that are similar in many species. The first part is at the start of protein structure and is called the C2C2-type zinc finger domain. The second part is at the end of protein structure and is named the YABBY domain. These two parts help the proteins bind to DNA and move to the nucleus (Sawa et al., 1999). In terms of evolution, YABBY genes appear only in seed plants and are connected to the start and development of side structures, especially in forming the upper and lower sides of leaves (Bowman, 2000; Rajani and Sundaresan, 2001).

In angiosperms, five major YABBY subfamilies have been identified: CRC, INO, YABBY5, FIL/YABBY3, YABBY2 (Yamada et al., 2003). In Arabidopsis thaliana, there are sixYABBY genes that have both similar and different functions in shaping plant parts, controlling leaf growth, and guiding flower development. (Sawa et al., 1999; Siegfried et al., 1999; Balasubramanian et al., 2002). Although structurally conserved, these genes exhibit differential expression patterns and functional divergence (Li et al., 2019).

Besides their role in development, YABBY genes are also involved in how plants handle abiotic stresses and respond to hormones. For instance, when OsYABBY1 is overexpressed in rice, it causes the plant to become semi-dwarf by changing how gibberellin (GA) is made and how it works while OsYABBY4 regulates growth through GA pathways (Toriba et al., 2007; Yang et al., 2016). Moreover, ectopic expression of AcYABBY4 from pineapple reduced salt tolerance in Arabidopsis thaliana (Li et

al., 2019), and genome-wide studies in other legumes such as kidney bean and soybean have shown that YABBY genes are involved in drought and salt stress responses (Inal et al., 2017; Zhao et al., 2017).

Although there is increasing evidence that YABBY genes help plants cope with stress, no comprehensive study has been conducted on the YABBY gene family in chickpeas. Since chickpeas are very important for agriculture and are particularly sensitive to drought, it is important to examine these genes in more detail. In this study, we examined all YABBY genes in chickpeas, C. arietinum and analyzed their structures, common patterns, where they are located on chromosomes, and how they are related to each other in terms of evolution. We also checked how these genes are expressed under drought conditions using in silico RNA-seq data. The results provide a better understanding of how YABBY genes can help chickpeas survive drought and lay the groundwork for future research and breeding efforts to make chickpeas more resistant to stress.

MATERIAL and METHOD

Identification of YABBY Gene Family Members in Cicer arietinum

To identify *YABBY* gene family members in *Cicer arietinum*, the Pfam domain accession number PF04690 was retrieved from the Plant Transcription Factor Database. Candidate *C. arietinum* YABBY protein sequences were obtained from the Phytozome v12.1 database (https://phytozome.jgi.doe.gov) using both keyword search with the Pfam ID and Hidden Markov Model (HMM)-based searches. These analyses were performed against the *C. arietinum* genome assembly version 2.0 (Goodstein et al., 2012; Han et al., 2024).

All putative YABBY proteins were subjected to BLASTP analysis using the NCBI non-redundant protein database to annotate hypothetical proteins. Redundant sequences were eliminated using https://web.expasy.org/decrease_redundancy/). The presence of conserved YABBY domains was confirmed using the HMMER tool (http://www.ebi.ac.uk).

Pfam (https://pfam.xfam.org/) the Conserved Domain Database (CDD) of NCBI (https://www.ncbi.nlm.nih.gov/cdd), and the SMART database (http://smart.embl-heidelberg.de). The physical and chemical features of the found proteins, like their size, electric charge, and how stable they are, were calculated using the ProtParam tool (https://web.expasy.org/protparam/).

Chromosomal Localization and Gene Duplication Analysis

The locations of all *CaYABBY* genes on the chromosomes were determined using TBtools v1.098 (Chen et al., 2020). Segmental and tandem duplications were found using the MCScanX tool with its standard settings (Wang et al., 2012). The gene duplication relationships were shown using the genes duplication view feature in TBtools v1.098.

Multiple Sequence Alignment and Phylogenetic Analysis

YABBY protein sequences were done using ClustalW with the standart settings. A phylogenetic analysis was carried out using the Maximum Likelihood method in MEGA version 11.0, and 1000 bootstrap replicates were used. The resulting phylogenetic tree was visualized using the Interactive Tree of Life (iTOL) platform (http://itol.embl.de) (Letunic and Bork, 2011).

Analysis of Domains, Gene Structure and Motifs

Conserved motifs in the YABBY proteins were found using Multiple EM for Motif Elicitation method was used (MEME Suite version v4.11.1; https://meme-suite.org/) (Bailey et al., 2015), and the maximum number of motifs was set to 6. The domain structures and how the genes are organized, including their exons and introns, were shown along with the phylogenetic tree using TBtools v1.098.

Promoter Analysis of CaYABBY Genes

The promoter regions of the *CaYABBY* genes were obtained from the Phytozome v12.1 database and checked for possible cis-acting elements. To find possible regulatory elements, the 1500 base pair regions upstream of the *CaYABBY* gene promoters were taken and checked using the PlantCARE database (Lescot et al., 2002).

In Silico miRNA Target Prediction for CaYABBY Genes

To evaluate potential miRNA-target interactions, known plant miRNAs were obtained from the pmiREN v2.0 database (https://www.pmiren.com/). miRNA target prediction was performed using the psRNATarget online tool (https://www.zhaolab.org/psRNATarget/). Interactions between miRNAs and YABBY genes were shown using Cytoscape version 3.9.1. (Shannon et al., 2003).

RESULTS and DISCUSSION

Identification of YABBY genes in *Cicer arietinum* genome

In this study, we found 8 *YABBY* genes in the *Cicer arietinum* genome after doing detailed bioinformatic analysis. These genes were designated as *CaYABBY*, derived from the abbreviation of the species name (*Cicer arietinum*) and the *YABBY* gene family. The identified *CaYABBY* genes were catalogued in Table 1, which includes their chromosomal locations, start and end positions, protein length (in amino acids), theoretical isoelectric point (pI), molecular weight (kDa).

YABBY genes have been found and studied in various plant species. In different plants, the number of *YABBY* genes identified is as follows: 9 in *Ananas comosus* (Li et al., 2019), 7 in *Vitis vinifera* (Zhang et al., 2019), 16 in *Phyllostachys edulis* (Ma et al., 2021), 17 in *Glycine max* (Zhao et al., 2017), 23 in *Gossypium hirsutum* (Yang et al., 2018), 21 in *Triticum aestivum* (Buttar et al., 2020), 8 in *Phaseolus vulgaris* (Inal et al., 2017), and 9 in *Solanum lycopersicum* (Huang et al., 2013). In our study, 8 *YABBY* genes were discovered in chickpea (*C. arietinum*).

The CaYABBY proteins varied in length, with the shortest one being 97 amino acids long (CaYABBY-05) and the longest measuring 221 amino acids (CaYABBY-04). Correspondingly, their molecular weights varied between 10.90 kDa (CaYABBY-05) and 24.62 kDa (CaYABBY-04). The predicted isoelectric points (pI) of the proteins spanned from 5.15 (CaYABBY-02) to 9.58 (CaYABBY-03), indicating a distribution of both acidic and basic proteins within the CaYABBY family. These early results show how different the *YABBY* gene family is in chickpea and set the stage for more research on its structure and role under usual and stressful situations.

Table 1. *CaYABBY* Gene Family Members Identified in *Cicer arietinum*

ID	Genomic Database Identifier	Chr	Start position (bp)	End Position (bp)	Protein length (aa)	pI	Molecular weight (kDa)
CaYABBY-01	Ca_07101	1	14328962	14334898	186	9.03	20.76
CaYABBY-02	Ca_21472	2	8282616	8285174	217	5.15	24.32
CaYABBY-03	Ca_18533	2	15817121	15818244	178	9.58	19.63
CaYABBY-04	Ca_25981	6	29746004	29749760	221	8.23	24.62
CaYABBY-05	Ca_15210	6	32082506	32088074	97	7.21	10.90
CaYABBY-06	Ca_06681	7	6813077	6815648	193	8.73	21.93
CaYABBY-07	Ca_12379	7	20166114	20169306	183	7.77	20.54
CaYABBY-08	Ca_08692	scaffold1348_1	41416	43920	217	6.61	24.28

pI: isoelectric point

The *CaYABBY* genes were given numbers according to where they are located on the chromosomes. The study showed that the eight *CaYABBY* genes are spread out in an uneven way across four different chromosomes in the *Cicer arietinum* genome. The highest number of *CaYABBY* genes (two genes per chromosome) was found on Chr-02, Chr-06, and Chr-07, whereas only one gene was identified on Chr-01, indicating a non-uniform chromosomal distribution.

Comparative analysis with other plant species reveals both conservation and variability in *YABBY* gene family characteristics. In a study on about wheat (*Triticum aestivum*), researchers found 20 *TaYABBY* genes and these genes were found to spread across 15 of the 21 chromosomes. The proteins made by these genes varied in length, from 164 amino acids (*TaYABBY2D*) to 297 amino acids (*TaYABBY1A* and *TaYABBY1B*). The weight of these proteins ranged from 17.76 kDa to 31.44 kDa. The pH level, or isoelectric point (pI), of these proteins ranges from 5.62 to 9.30. (Hao et al., 2022).

Similarly, eight *YABBY* genes were identified in cucumber (*Cucumis sativus*). These genes encode proteins ranging in length from 173 to 194 amino acids, with predicted molecular weights between 19.2 and 21.5 kDa (Hashmi et al., 2022).

Mazhar et al. (2023), identified seven *StYABBY* genes in potato (*Solanum tuberosum*). The genes that make the StYABBY protein come in different lengths, ranging from 142 to 219 amino acids.

StYABBY proteins was determined to be between 16.15 and 24.48 kDa. StYABBY2 was reported as the smallest protein and StYABBY3 as the longest protein (Mazhar et al., 2023).

When all findings are considered together, it is emphasized that the presence of YABBY proteins shows differences among various plant species. These differences likely reflect the species-specific diversification and functional adaptation of *YABBY* family members during evolution.

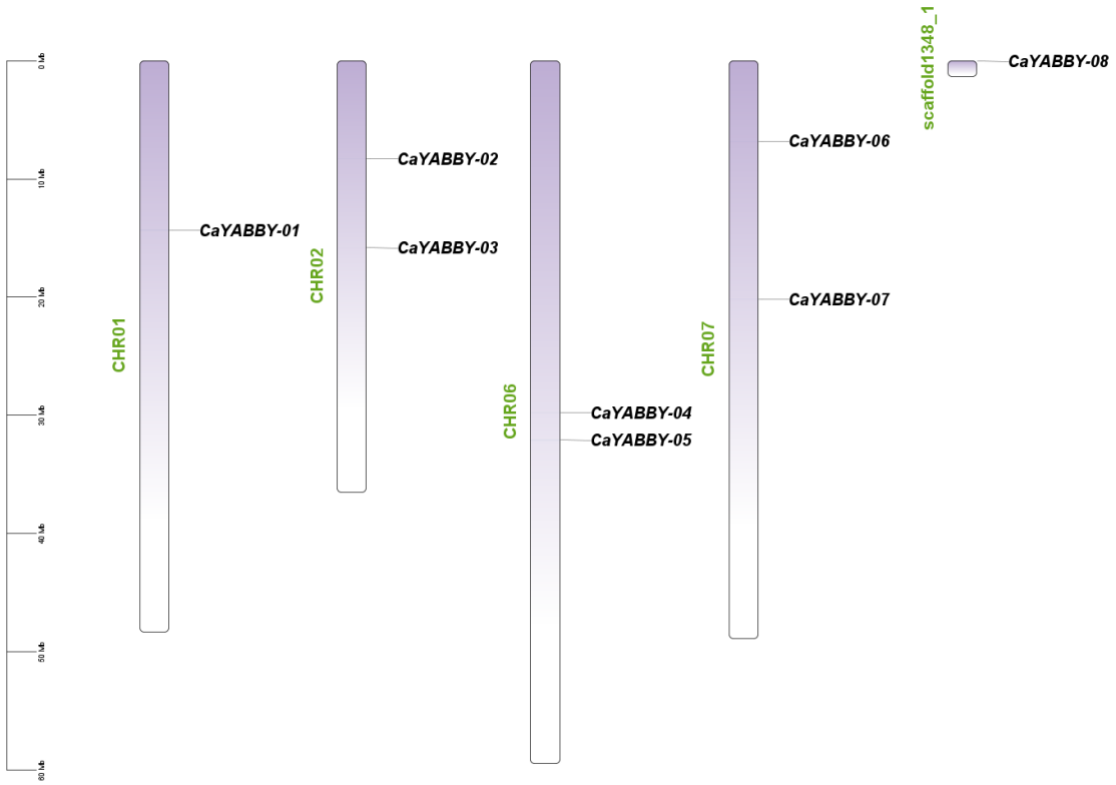

Figure 1. Chromosomal Distribution of *CaYABBY* Genes

Phylogenetic Analysis, Domains, Gene Structure and Promoter Analysis

A phylogenetic analysis was done using protein sequences from Cicer arietinum, Phaseolus vulgaris, Arabidopsis thaliana and Glycine max. Study how closely related the YABBY gene family members are and their shared ancestry. A total of 39 YABBY proteins was divided into five main clades corresponding to the well-known YABBY subfamilies: INO, YAB2, FIL/YAB3 (FYAB3), YAB5, and CRC. Among the analyzed species, C. arietinum and P. vulgaris each contributed 8 YABBY proteins, while A. thaliana and G. max contributed 6 and 17 proteins, respectively.

The INO, YAB2, and FYAB3 clades were the largest, each comprising 9 members. In contrast, the YAB5 group was the smallest, with only 5 members. Specifically, the INO group included 1 member from A. thaliana, 2 from P. vulgaris, 5 from G. max, and 1 from C. arietinum. The YAB2 group comprised 1 protein from A. thaliana, 2 from P. vulgaris, 4 from G. max, and 2 from C. arietinum. Similarly, the FYAB3 group contained 1 A. thaliana, 2 P. vulgaris, 4 G. max, and 2 C.

arietinum members. The YAB5 group, the smallest in size, consisted of 1 protein each from A. thaliana, P. vulgaris, and C. arietinum, and 2 from G. max.

Phylogenetic analysis showed that StYABBY genes in potato (Solanum tuberosum) can be divided into five subgroups: CRC, INO, YAB5, AFO/YAB3 and YAB2, as in A. thaliana. Among these subgroups, in potato (S. tuberosum) AFO/YAB3 is the biggest group with 11 genes, followed by YAB5 with 10 genes, then YAB2 with 8 genes, CRC with 7 genes and INO with 7 genes. (Mazhar et al., 2023). In our study, the largest group was YAB2, FYAB3 and CRC with 2 members, while the smallest group was INO with 1 member.

These results show that the YABBY gene family has remained similar throughout evolution in legume plants and in A. thaliana, while also exhibiting species-specific gene expansion, particularly in G. max. The C. arietinum YABBY genes are found in all five subfamilies, indicating that they have evolved different functions and may play roles in different growth processes and how the plant reacts to stress.

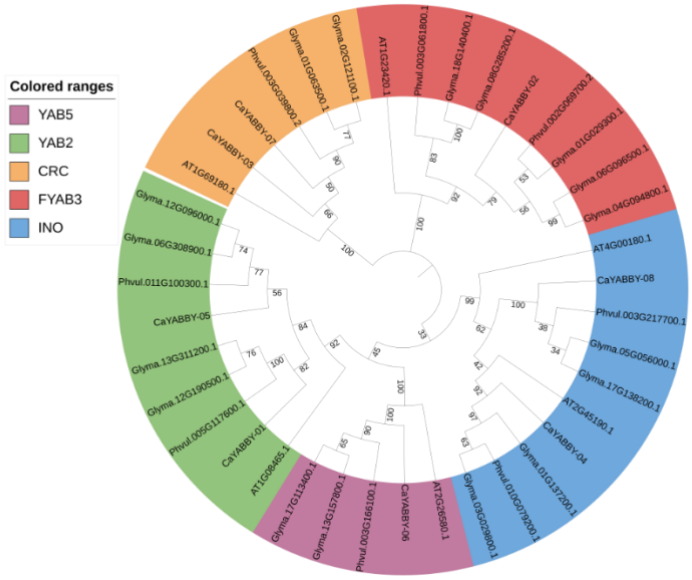

Figure 2. Phylogenetic Analysis of *Cicer arietinum* and selected plant species

To gain deeper insights into the evolutionary relationships and structural divergence within the *YABBY* gene family in *Cicer arietinum*, we performed a comprehensive analysis of conserved motifs, domain architecture, exon-intron gene structures, and phylogenetic relationships of all identified *CaYABBY* genes. Conserved motif analysis was carried out using MEME Suite v4.11.1, which revealed a total of six distinct conserved motifs among the CaYABBY proteins.

Among these, motif 2 was found to be conserved and present in all CaYABBY members, indicating it plays a key role in their function.Interestingly, CaYABBY-02, CaYABBY-03, CaYABBY-06, and CaYABBY-07 contained only Motif 1 and Motif 2, which may indicate a more compact or simplified functional structure compared to other members. The distribution and arrangement of these

motifs were largely consistent with the conserved domain structures predicted by SMART and Pfam, indicating a high level of agreement between motif and domain-based analyses.

Moreover, comparison of motif organization with gene structure and phylogenetic clustering revealed a strong correlation among these parameters. Genes sharing similar motif compositions tended to group together in the phylogenetic tree and exhibited similar exon-intron structures. These results show that the presence of similar motifs in the *CaYABBY* genes might show that they are closely connected through evolution and could also work in similar or related ways.

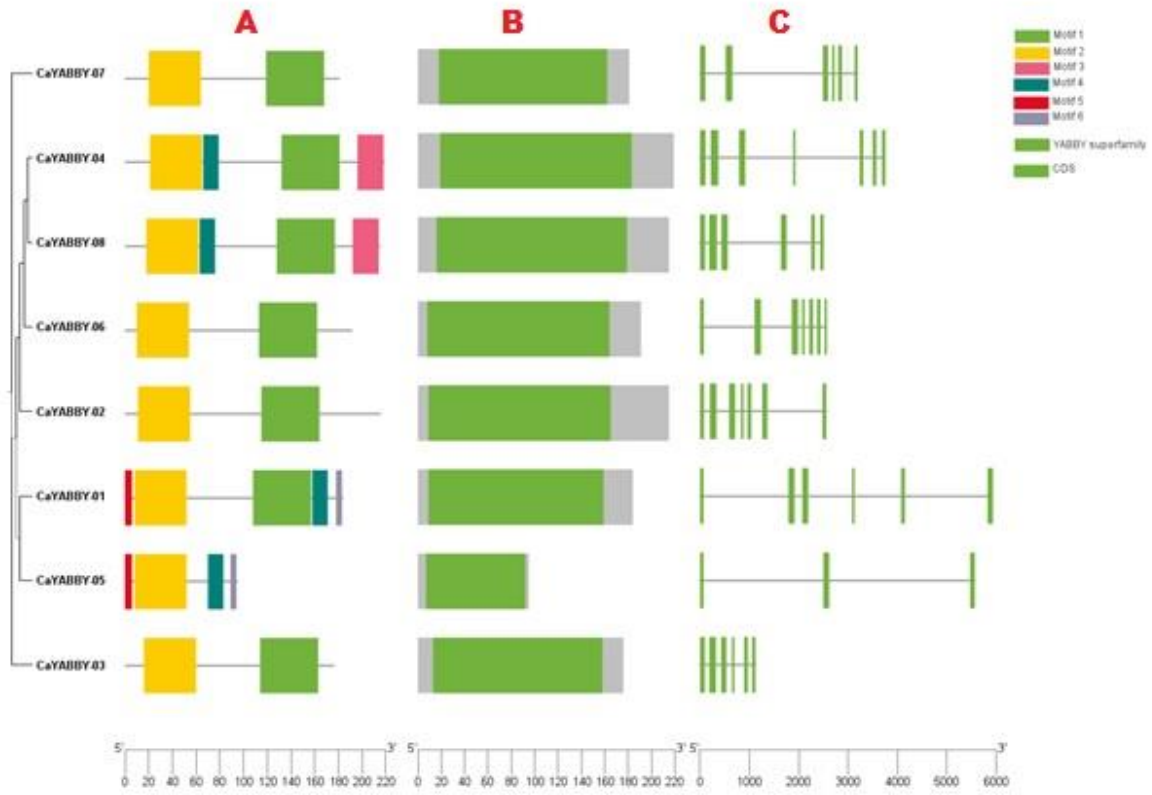

Figure 3. Conserved motifs, YABBY protein domains and *YABBY* genes intron-exon arrangements (*C. arietinum*).

(A) YABBY proteins conserved motifs. The corresponding YABBY proteins contain motif variations with distinct colorations. The arrangement of the motif is in accordance with where they are found in certain protein sequences. (B) A schematic depiction of each *YABBY* genes domain. (C) The *YABBY* genes intron-exon arrangements.

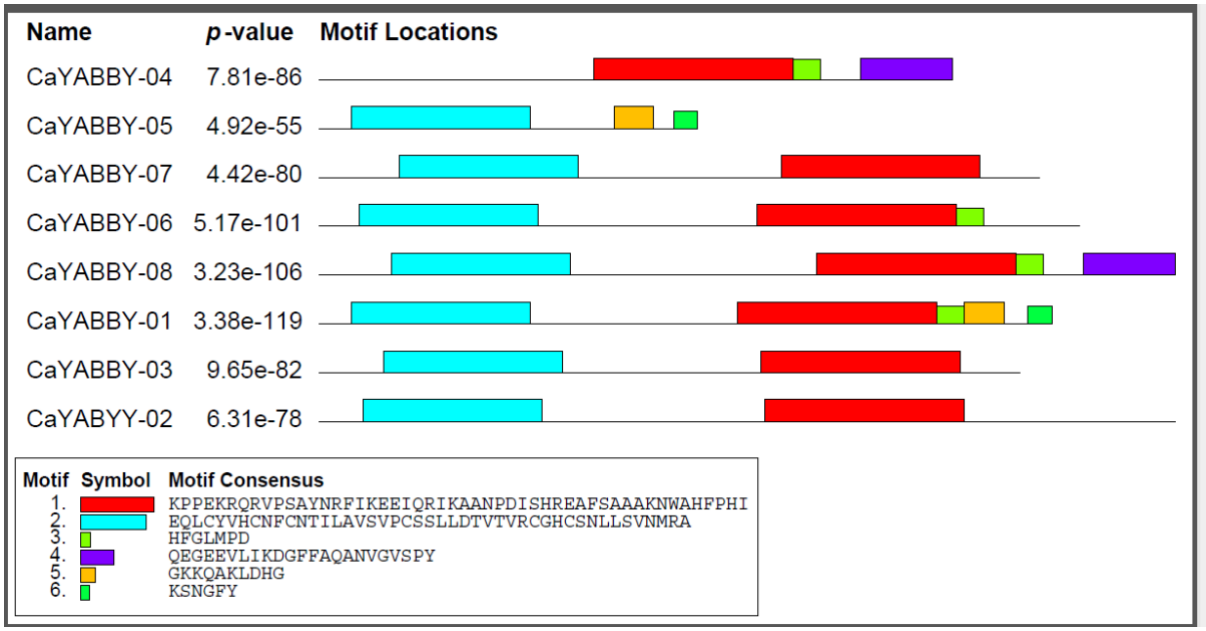

Figure 4. Conserved motifs of CaYABBY proteins from *C*

arietinum. Schematic depiction of 6 conserved motifs in CaYABBY proteins. The MEME online tool was used to identify motifs. Each motif type is denoted using different-colored boxes, and the numbers in the boxes (1–6) signify motifs 1–6. The length and position of each colored box is scaled to size and motif consensus was provided.

The coincidence or consistency of introns and exons in gene structures leads to clues about the structural and functional properties of the common ancestors of the genes it contains. This holistic genomic architecture is important in bioinformatics studies. The number of exons among the analyzed *CaYABBY* genes ranged from 3 to 7, corresponding to 2 to 6 introns. *CaYABBY*-06 and *CaYABBY*-02 contained the highest number of exons (7 exons) and introns (6 introns). *CaYABBY*-05 exhibited the lowest exon number (3 exons) with 2 introns. The remaining genes possessed 5 to 6 exons, resulting in 4 to 5 introns.

The promoter region of a gene is a highly noteworthy factor in the modulating of genetic networks against plant stressors (Yamaguchi-Shinozaki and Shinozaki, 2005). Because of this, scientists studied cis-acting regulatory elements using a computer tool that analyzes promoters. Most of the elements they found were linked to how plants grow and develop, how they react to environmental stress, signals from hormones, responses to light, and places where other proteins attach to control genes.

The promoter regions of the *CaYABBY* genes were obtained from the Phytozome v12.1 database and checked for possible cis-acting elements. The analysis showed that both CGTCA- and TGACG-motifs are present in *CaYABBY* genes, and these cis-elements are known to be involved in how plants respond to methyl jasmonate (MeJA). Additionally, ABRE and TCA elements, known to be responsive to abscisic acid (ABA), salicylic acid (SA), and ethylene hormones, were identified.

Moreover, several stress-related cis-elements previously characterized in *Arabidopsis thaliana* were also detected (Lenka and Kailash 2019). Among them, MYB and MYC binding sites were found at high frequency, suggesting a role in ABA-independent stress signaling. On the research on rice

showed, certain transcription factors such as NAC, AREB/ABF, DREB1/CBF, and DREB2 are involved in helping plants handle abiotic stress. (Chinnusamy et al., 2004; Bartels and Sunkar, 2005; Sunkar et al., 2007), the enrichment of MYB and MYC motifs in *CaYABBY* genes promoters highlights their possible contribution to abiotic stress responses in chickpea.

Synteny analyses among YABBY genes of P. vulgaris and A. thaliana

The evolutionary relationships of the *YABBY* gene family among *Cicer arietinum*, *Arabidopsis thaliana* and *Phaseolus vulgaris* were investigated through synteny analysis. The results revealed a higher degree of similarity between *C. arietinum* and *P. vulgaris*, attributed to a greater number of orthologous gene pairs.

Four pairs of genes that are similar between *C. arietinum* and *A. thaliana* were found, and eight pairs of similar genes were found between *C. arietinum* and *P. vulgaris*. Genomic duplications between *C. arietinum* and *A. thaliana* were limited to two chromosomes (Chr-01 and Chr-02), whereas duplications between *C. arietinum* and *P. vulgaris* were distributed across four chromosomes (Chr-01, Chr-03, Chr-06, and Chr-08) (Figure 5). These findings support the notion that *C. arietinum* diverged from *A. thaliana* earlier in evolutionary history and is more closely related to *P. vulgaris*, consistent with their taxonomical classifications.

In a study conducted to understand gene types and relative conservation sequences between different species diverging from the same ancestral species, 2 pairs of duplication genes occurred between lotus (*Nelumbo nucifera*) and *A. thaliana*. In our study, we found 4 pairs of duplicated genes in *A. thaliana* and 8 pairs of duplicated genes in *P. vulgaris* (Zhao et al., 2023).

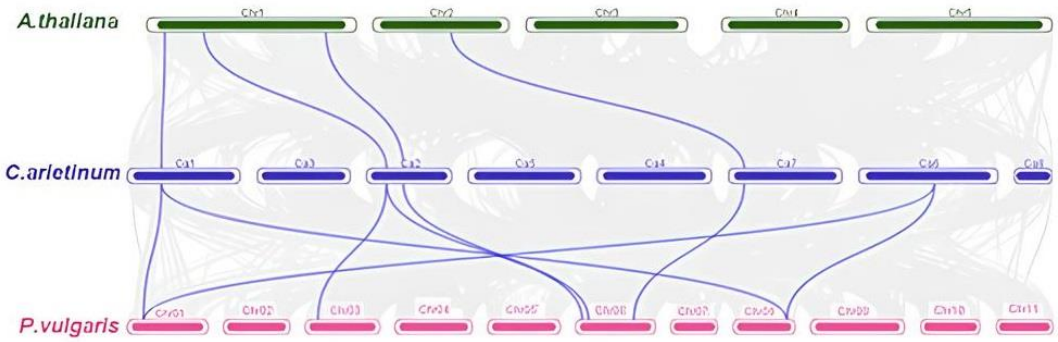

Figure 5. Synteny relationships among *YABBY* genes of *Cicer arietinum*, *Phaseolus vulgaris*, and *Arabidopsis thaliana*

Chromosomal locations of orthologous *YABBY* genes are indicated, with connecting lines representing conserved gene pairs across the three species.

Detection of miRNAs Targeting the CaYABBY Genes

MicroRNAs (miRNAs), small regulatory RNAs ranging from 21 to 24 nucleotides in length, were first identified in 2002 by the research group of David Bartel in the genetic model plant Arabidopsis thaliana (Reinhart et al., 2002). Plant miRNAs are a type of small molecule made naturally by plants. They help control how genes work, which is important for the plant's growth, how it responds to changes in its environment, and how it fights off diseases or harmful conditions (Pegler et al., 2019).

Cicer arietinum, miRNA analysis revealed a 8 miRNAs targeting 6 CaYABBY genes (Figure 6). Among these, the genes CaYABBY-01, CaYABBY-02, CaYABBY-04, CaYABBY-06, CaYABBY-07, and CaYABBY-08 were identified as miRNA targets. Notably, the genes CaYABBY-04 and CaYABBY-02 were most frequently targeted by the identified miRNAs (Figure 6).

Figure 6. Schematic representation of predicted interactions between *CaYABBY* genes and their corresponding miRNAs in *Cicer arietinum*.

Blue boxes indicate miRNAs, and yellow boxes represent the targeted *CaYABBY* genes. Arrows denote predicted regulatory relationships based on sequence complementarity.

The miRNA Car-miR2109, which targets *CaYABBY-02*, is known to be specific to leguminous plants and has been reported to accumulate predominantly in the petals of ethylene-treated flowers (Pei et al., 2013). Another miRNA associated with *CaYABBY-02*, Car-miR747 studies have shown that this gene plays a key role in helping chickpeas deal with high salt levels and lack of water, especially when looking at the full picture of its structure, how it has changed over time, and what it does in the plant (Nehra et al., 2025).

Car-miR408, targeting *CaYABBY-06*, has been implicated in drought tolerance by contributing to copper chloroplast homeostasis in plant leaves, and was also found to delay phenotypic senescence (Hao et al., 2022). These results, together with what this study found, show that *CaYABBY-02* and *CaYABBY-06* might play a role in how chickpea plants handle drought stress, which is an important issue for this type of legume crop.

Moreover, Car-miR164, which targets *CaYABBY-08*, is known to regulate embryonic meristem initiation, control boundary size, and influence cotyledon formation during early plant development (Dong et al., 2022). In addition, Car-miR394, targeting *CaYABBY-04*, has been reported to suppress leaf curl sensitivity in plants (Knauer et al., 2013). When you look at the miRNAs found in this study along with what has been found before, it clearly shows that the *CaYABBY* genes are connected to how plants handle stress and also to important growth processes.

Response of CaYABBY genes to drought stress

Transcriptomic analysis using RNA-seq obtained from the NCBI SRA database (accession: PRJNA15243937) revealed that only a subset of *CaYABBY* genes exhibited (Figure 7). According to the heat map, significant expression changes were observed in *CaYABBY-01*, *CaYABBY-02*, *CaYABBY-04*, and *CaYABBY-08* compared to control conditions. Among these, *CaYABBY-04* showed the highest upregulation, while *CaYABBY-02* exhibited the lowest increase in expression.

No notable changes in transcript levels were detected for *CaYABBY-03*, *CaYABBY-05*, *CaYABBY-06* and *CaYABBY-07*, this means that these genes may not be directly involved in how plants handle drought stress under the conditions that were studied. The upregulation observed in a subset of genes suggests a possible role for these *CaYABBY* members in drought stress adaptation in chickpea.

Supporting evidence from a recent study in balloon flower (*Platycodon grandiflorus*) demonstrated that drought stress changes how *YABBY* genes are expressed in different parts of the plant and as time passes. Among six identified *pgYABBY* genes, three (*pgYABBY-01, pgYABBY-02* and *pgYABBY-05*) showed a marked decrease in expression levels under drought conditions (Kong et al., 2023). These results show that *YABBY* genes react to drought conditions, but how they work might be different depending on the species and the type of tissue.

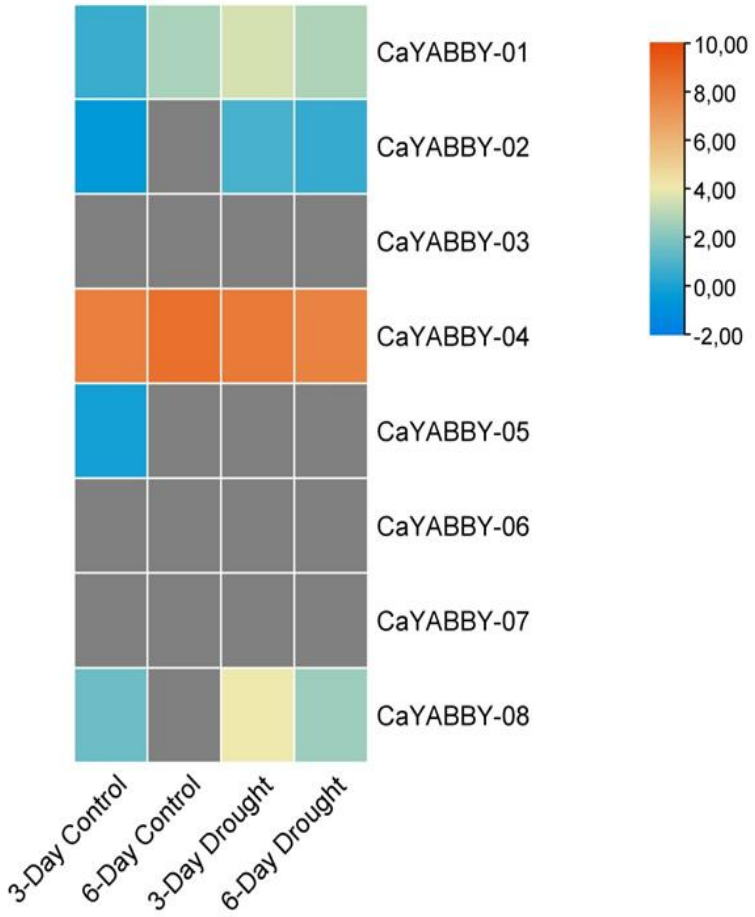

Figure 7. A heatmap showing which *CaYABBY* genes are expressed more or less under normal conditions and during drought stress at 3 and 6 days.

Expression values were derived from RNA-seq data (NCBI SRA: PRJNA15243937). Color gradients indicate relative expression levels, with upregulation shown in orange tones and downregulation in blue tones.

CONCLUSION

This study is the first to look at all the genes in the *YABBY* family across the entire genome of Cicer arietinum, and it has found eight different *CaYABBY* genes. Phylogenetic, structural, and promoter analyses revealed that these genes are evolutionarily conserved and may participate in developmental processes and environmental stress responses. Some *CaYABBY* genes were found to have special sections of DNA that respond to stress and hormones, and they are also targeted by certain microRNAs related to drought, like miR2109, miR747, and miR408. The study on how plants respond to drought showed that the genes *CaYABBY-04*, *CaYABBY-08*, *CaYABBY-02*, and *CaYABBY-01* became more active, which suggests these genes help the plant adjust to stressful conditions. These results offer a good base for future research and efforts to improve chickpeas, especially when it comes to making them more resistant to dry conditions.

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