



Genome-Wide Characterization of the *ADK* Gene Family and Analysis of Expression Patterns Under Abiotic Stress in Beans

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Abstract

In plants, *Adenylate Kinase (ADK)* genes are essential genetic components that regulate critical processes such as growth, development and response to abiotic and biotic stress factors. In this study, genome-wide identification, bioinformatic analyses and expression profiles of *ADK* genes in *Phaseolus vulgaris* leaf tissue under drought and salt stress were investigated. As a result of the study, 7 *Phvul-ADK* proteins were identified and it was determined that the amino acid lengths of these proteins ranged from 239 to 597 and molecular weights ranged from 26,6 to 66,9 kDa. In addition, it was determined that the number of exons of the genes varied between 3 and 19. Phylogenetic analysis based on *ADK* proteins from *Phaseolus vulgaris*, *Arabidopsis thaliana*, *Hordeum vulgare*, *Oryza sativa* and *Volvox carteri* species revealed that the genes were divided into three different groups. In addition, *Phvul-ADK-2* and *Phvul-ADK-5* genes were found to show segmental duplication in the bean genome. This study is the first comprehensive genome-wide analysis of the *Adenylate Kinase* family in bean and highlights the important roles of the *ADK* gene family in plant development and stress responses. It is evaluated that the findings obtained will provide important contributions to bean breeding studies and stress tolerance research.

Keywords: *P. vulgaris*, *ADK*, drought, genome-wide analysis, salt

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Introduction

Adenylate kinase (ADK) is an enzyme found in almost all organisms and is known as adenylate in cells (Chang and Fu, 2014). This enzyme is responsible for the production of adenosine monophosphate (AMP), one of the four main

mononucleotides that make up ribonucleic acid. AMP is an important compound that regulates energy release in organisms, and this process plays a critical role in regulating metabolic activities (Dzheia et al., 1986; Dzeja and Terzic, 2009). *ADK* plays an important role in plants in growth and development



as well as in adaptation mechanisms to environmental stresses. Furthermore, the cellular localization of ADK in plants varies greatly between species; this localization has been observed in different cellular organelles such as the cytosol, mitochondria, and plastids (Kawai et al., 1992; Chen et al., 1994; Regierer et al., 2002; Carrari et al., 2005).

Phaseolus vulgaris (bean) plays an important role in growth and development processes and is sensitive to various abiotic stress factors, particularly drought and salinity (Beebe et al., 2014; Arteaga et al., 2020). These stress factors negatively affect the morphological, physiological, and biochemical characteristics of the bean plant, leading to yield and quality losses (Lone et al., 2021; Feki et al., 2024). Bean plants have developed complex defense mechanisms to cope with these stress factors. These mechanisms function through gene expression; under stress conditions, relevant genes are activated and help plants adapt to stress conditions (Abuqamar et al., 2009; Ramegowda and Senthil-Kumar, 2015). Therefore, identifying the genes or gene families responsible for stress tolerance in beans is of great importance for developing varieties suitable for environmental changes (Bartels and Sunkar, 2005).

ADK genes have been studied in some plant species such as *Solanum lycopersicum* (tomato), *Gossypium hirsutum* (cotton), *Solanum tuberosum* (potato), *Oryza sativa* (rice), and *Arabidopsis thaliana* (Huang et al., 2024), the function of ADK genes in bean plants has not yet been determined. This study aims to identify and characterize bean ADK genes and understand their role in response to drought and salt stress. Various molecular approaches have been developed to address problems caused by abiotic stress factors. To effectively implement these approaches, the structure and function of the ADK gene family were examined in detail. In this context, the structure and

functions of ADK genes in beans have been identified using bioinformatics tools. As part of the in-silico analyses, the exon-intron structures, chromosomal locations, gene duplications, three-dimensional protein structures, promoter analyses, and gene expression analyses of ADK genes in beans were performed. Additionally, orthologs of ADK genes in plants such as *Phaseolus vulgaris*, *Arabidopsis thaliana*, *Hordeum vulgare*, *Oryza sativa*, and *Volvox carteri* were identified.

Changes in the expression levels of ADK genes in *P. vulgaris* under drought and salt stress were investigated, and the roles of ADK genes were predicted based on bioinformatics analysis results. This study serves as an important preliminary investigation to understand the response of ADK genes in bean plants to abiotic stresses and highlights the potential effects of these genes on stress tolerance.

Materials And Methods

Identification of ADK Genes in *Phaseolus*

***vulgaris* Genomes:** Pfam access number (PF00406) was used to identify members of the ADK gene family in the genomes of *P. vulgaris* (Schmutz et al., 2014), *A. thaliana* (Lamesch et al., 2012), *Hordeum vulgare* (Beier et al., 2017), *Oryza sativa* (Ouyang et al., 2007), and *Volvox carteri* (Prochnik et al., 2010). Using this access number, ADK protein sequences were retrieved from the Phytozome v13 database (<https://phytozome-next.jgi.doe.gov/>). The BLASTP tool and Hidden Markov Model (HMM) scanning method (<http://www.ebi.ac.uk>) were used on Phytozome v13 to identify ADK proteins. The ADK domains were then validated using the HMMER database (<http://hmmer.org/>). Additionally, the amino acid count, stability status, instability index, theoretical isoelectric point (pI), and molecular weights of the ADK proteins found in beans were analyzed using the ProtParam tool (<https://web.expasy.org/protparam/>).

Structure of *Phvul*-ADK Genes, Chromosomal Location, and Determination of Gene Duplications:

The TBtools program was used to identify the coding and non-coding regions of *Phvul*-ADK genes (Chen et al., 2023). In this analysis, bean genome files (gff3) were downloaded from the Phytozome v13 database (<https://phytozome-next.jgi.doe.gov/>) and visualized in the TBtools program. The chromosomal locations and sizes of *Phvul*-ADK genes were identified through the Phytozome v13 database.

The positions of *Phvul*-ADK genes on chromosomes were visualized using the TBtools program (Chen et al., 2023), and the same software was used to identify gene duplications. Additionally, the non-synonymous (Ka) and synonymous (Ks) ratios between gene pairs, as well as the evolutionary selection ratios (Ka/Ks), were calculated using the TBtools program (Chen et al., 2023).

Conserved Motif, Sequence Logo and Phylogenetic Analyses:

The “Multiple EM for Motif Elicitation (MEME)” tool was used to identify conserved motifs in *Phvul*-ADK amino acid sequences. The identified motifs were analyzed using the InterProScan database (Quevillon et al., 2005). They were visualized using the TBtools program (Chen et al., 2023).

Phylogenetic analyses were performed using the Neighbor-Joining (NJ) method with 1000 bootstrap replicates. ADK protein sequences from *P. vulgaris*, *A. thaliana*, *H. vulgare*, *O. sativa*, and *V. carteri* were aligned using MEGA v11 software (Tamura et al., 2011). The phylogenetic tree constructed based on these alignment data was visualized using the iTOL (Interactive Tree Of Life) platform (Letunic and Bork, 2011).

Homology Modeling of *Phvul*-ADK Proteins and Protein-Protein Interactions:

The three-dimensional structures of ADK proteins were generated using the Phyre2 tool with the protein

homology modeling method (Kelley et al., 2015). The reliability rates of protein models were compared and the most suitable three-dimensional structures were selected. Representative images were generated using Chimera (Pettersen et al., 2004). The STRING database was used to identify protein-protein interactions (Szkarczyk et al., 2021).

Synteny Analysis: Genome and transcript sequences of *P. vulgaris* and *A. thaliana* were compared using the One Step MCScanX tool. The synthesis map of ADK genes was drawn using the TBtools tool (Chen et al., 2023).

Intracellular Localization and Promoter Analyses:

Cis-acting element analysis was performed on the 5' upstream region of each member of the bean ADK gene family, containing approximately 2 kb DNA fragments, using the PlantCARE database (Lescot et al., 2002). The phenogram was drawn using the TBtools tool (Chen et al., 2023). The WoLF PSORT database was used to predict the intracellular localization of members of the bean ADK gene family (Horton et al., 2007).

In Silico Gene Expression Analysis:

Illumina RNA-seq data were obtained from the NCBI Sequence Read Archive (SRA) database for the purpose of examining *Phvul*-ADK genes. The relevant RNA-seq data are SRR957668 (salt stress), SRR958469 (salt control) (Hiz et al., 2014), SRR8284480 (drought control), and SRR8284481 (drought stress). Transcriptome data for *Phvul*-ADK genes in different tissues of the bean (green mature pods, young pods, stems, roots, nodules, leaves, flowers, and flower buds) were obtained from the Phytozome v13 database in million base pairs per million mapped reads (FPKM) units. Expression profiles were calculated using RPKM (Reads per kilobase per million mapped reads) (Mortazavi et al., 2008) and the log2 transformation of FPKM values, and a heatmap was created using the Tbttools tool (Chen et al., 2023).

Results and Discussion

Identification and Characterization of ADK Genes in *Phaseolus vulgaris*: Seven genes with ADK protein homology were identified. The presence of Phvul-ADK domains was verified using the HMMER database and redundant sequences were subsequently removed. Additionally, the isoelectric points (pI), chromosome location, amino acid count, and molecular weight (kDa) of the identified ADK proteins are listed in Table 1. The length of the ADK proteins ranges from 239 to 597 amino acids, and their molecular weights range from 26,903.88 to 66,903.70 kDa. Among these, the protein with the longest amino acid sequence was identified as Phvul-ADK-6 with 597 amino acids.

The shortest protein was identified as Phvul-ADK-7, with a sequence of 239 amino acids.

The chromosomal locations of *Phvul-ADK* genes have been determined as Chr01, Chr03, Chr07, Chr09, and Chr11 in the bean genome (Figure 1). These genes are distributed across five different chromosomes in the bean genome, with the highest number of genes located on chromosomes Chr01 and Chr11. To examine the evolutionary status of *Phvul-ADK* genes, duplication events in the *P. vulgaris* genome were analyzed in detail. These analyses revealed a segmentally duplicated gene pair within the *Phvul-ADK* gene family. Specifically, the *Phvul-ADK-2* and *Phvul-ADK-5* genes were identified as genes resulting from segmental duplication (Figure 1).

Table 1. Information table about ADK proteins identified in the *P. vulgaris* genome

Gene Name	Phytozome Id	Chr Loc	Start	End	Strand	Aa	MW(Da)	Pi	Instability Index	
<i>Phvul-ADK-1</i>	<i>Phvul.001G095650.1</i>	Chr01	179813 22	17983 826	forward	266	29834,96	6,76	56,22	unstable
<i>Phvul-ADK-2</i>	<i>Phvul.001G173800.1</i>	Chr01	43043 129	43045 557	reverse	265	29207,73	6,46	54,36	unstable
<i>Phvul-ADK-3</i>	<i>Phvul.003G209400.1</i>	Chr03	43531 093	43534 773	reverse	242	26609,86	6,97	34,39	stable
<i>Phvul-ADK-4</i>	<i>Phvul.007G162600.1</i>	Chr07	27444 957	27448 334	reverse	286	31418,32	8,7	47,50	unstable
<i>Phvul-ADK-5</i>	<i>Phvul.009G208900.1</i>	Chr09	31640 233	31652 582	reverse	597	66903,70	8,85	40,58	unstable
<i>Phvul-ADK-6</i>	<i>Phvul.011G003000.1</i>	Chr11	22785 4	23029 7	forward	282	31354,75	8,36	38,75	stable
<i>Phvul-ADK-7</i>	<i>Phvul.011G004800.1</i>	Chr11	35993 6	36380 7	forward	239	26903,88	6,36	50,35	unstable

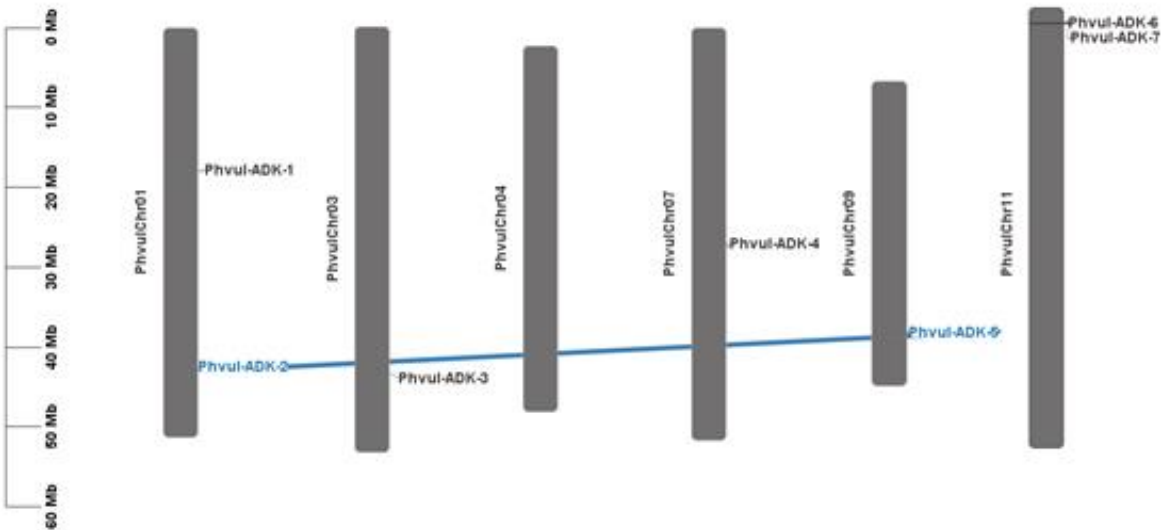


Figure 1. Distribution of ADK gene chromosomal locations in *P. vulgaris** *Genes shown in blue indicate segmental duplication.

In addition, to examine the evolutionary processes of duplicated genes in greater detail, non-synonymous divergence (Ka), synonymous divergence (Ks), and their ratio (Ka/Ks) were calculated to analyze the segmental duplications and evolutionary processes of ADK genes (Table 2).

Table 2. Ka/Ks ratios for *Phvul*-ADK genes

Gene 1	Gene 2	Ka	Ks	Ka/Ks
<i>Phvul</i> -ADK-2	<i>Phvul</i> -ADK-5	0,1353	0,4315	0,3134

The Ka/Ks ratio calculated for beans was determined to be 0.3134. In general, $Ka/Ks > 1$ indicates positive selection, $Ka/Ks < 1$ indicates purifying selection, and $Ka/Ks = 1$ indicates neutral selection (Li et al., 2009; Khan et al., 2020). As a

result of these analyses, it was determined that ADK genes evolved under purifying selection.

The exon-intron structure of *Phvul*-ADK genes has been analyzed in detail. The results show that all *Phvul*-ADK genes contain between 4 and 19 exons (Figure 2).

Conserved Motif and Domain Analysis of ADK Proteins in Bean: Conserved motifs were analyzed to investigate the structural properties of ADK proteins using the MEME program. A total of 10 different conserved motifs were identified (Figure 3). It contains a conserved motif in all *Phvul*-ADK proteins. *Phvul*-ADK-5 (9) had the highest number of motifs, while *Phvul*-ADK-7 (4) had the lowest number of motifs.

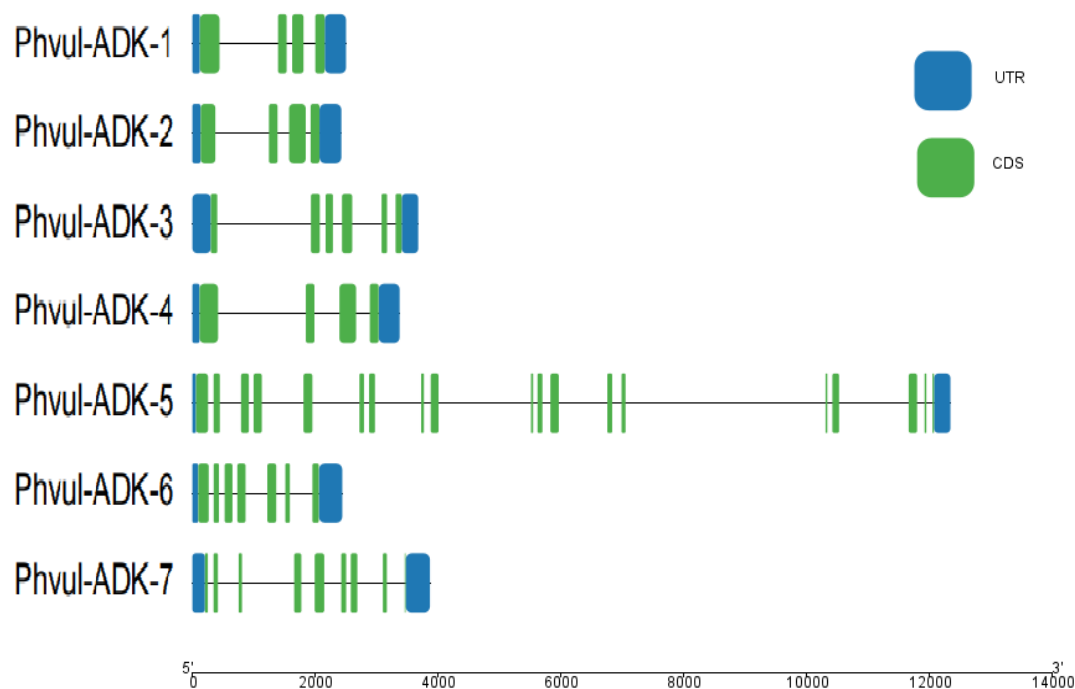


Figure 2. Number, length, and position of exons and introns in *Phvul*-ADK genes* *Blue boxes indicate 5'-UTR and 3'-UTR, green boxes indicate exons, and the black line indicates intron regions.

In addition, Table 3 shows the best possible match sequences corresponding to the motifs. Motifs 2 and 3 contain the adenylate kinase domain, while Motif 5 contains the mitochondrial ADK insert

"zinc finger" domain. Furthermore, all *Phvu1*-ADK proteins contain Motif 1, Motif 2, Motif 3, and Motif 4, and these proteins have been confirmed to belong to the adenylate kinase/UMP-CMP kinase family.

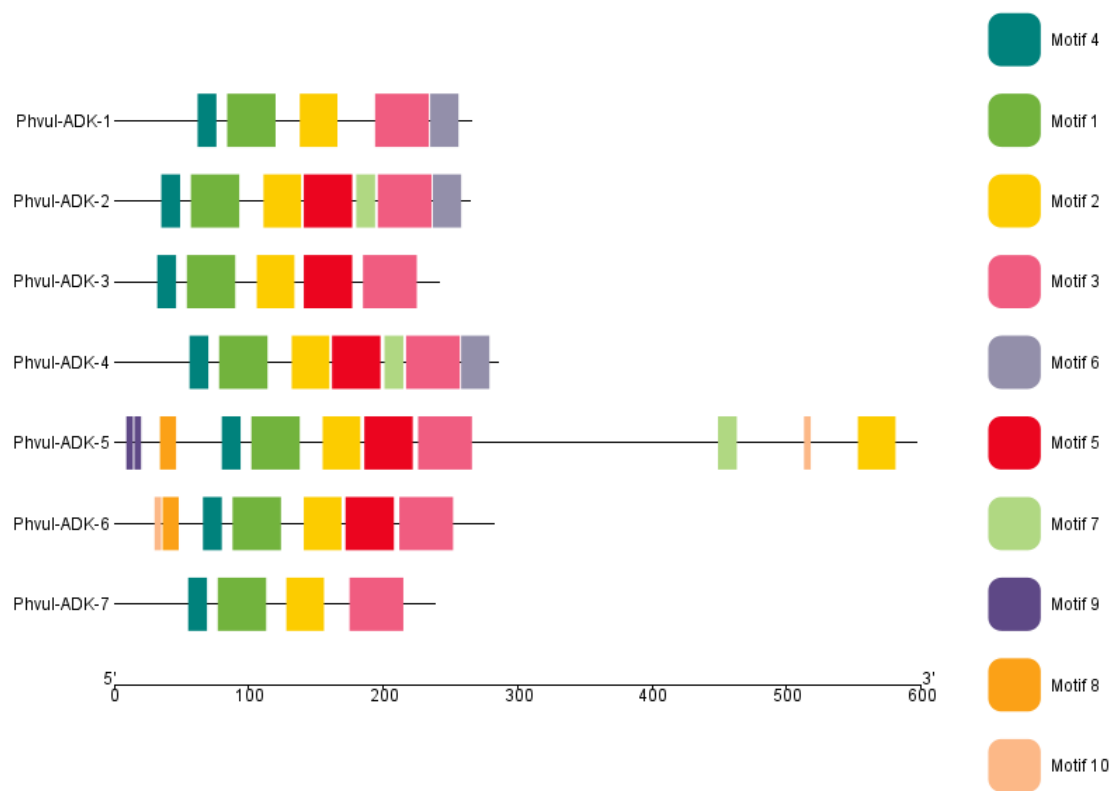


Figure 3. Predicted motif distribution in *Phvul-ADK* genes

Table 3. Sequence information for potential motifs in *Phvul-ADK* genes

Motif No	WIDTH	BEST POSSIBLE MATCH	Domain
MOTIF-1	37	GLPHIATGDLLRAELASGSPLGSQAKEIMEQGKLV D	Adenylate kinase/UMP-CMP kinase family
MOTIF-2	29	KEKGFJLDGFPRTLKQAZILEGITDKDLV	Adenylate kinase domain
MOTIF-3	41	RLITRSDDTTEEVVKERLRIYHZNTZPVIDYYSNKGKL LEFN	Adenylate kinase/UMP-CMP kinase family /N Adenylate kinase domain
MOTIF-4	15	VVILGAPGSGKGTQC	NA
MOTIF-5	37	NLKIEEEVLJERCVGRRIDPVTGKNYHVKFPPKAE N	Mitochondrial ADK, insert "zinc finger" domain
MOTIF-6	22	LPGGIPESWPKLLQALBLDDYE	NA
MOTIF-7	15	PGIVMDPLLPPANC	NA
MOTIF-8	13	RHRCHHHCRFSFC	NA
MOTIF-9	6	FHRTTT	NA
MOTIF-10	6	FCYFFR	NA

Phylogenetic Tree and Synteny Analysis:
The phylogenetic relationships of the ADK proteins in the *A. thaliana*, *H. vulgare*, *O. sativa*, and *V. carteri* genomes were examined by multiple sequence alignment of the full-length amino acid

sequences, and the ADK family was clustered into three groups (A, B, and C). All groups were further divided into two subgroups (Figure 4). Group C has a total of 37 members, and the most numerous is group C.

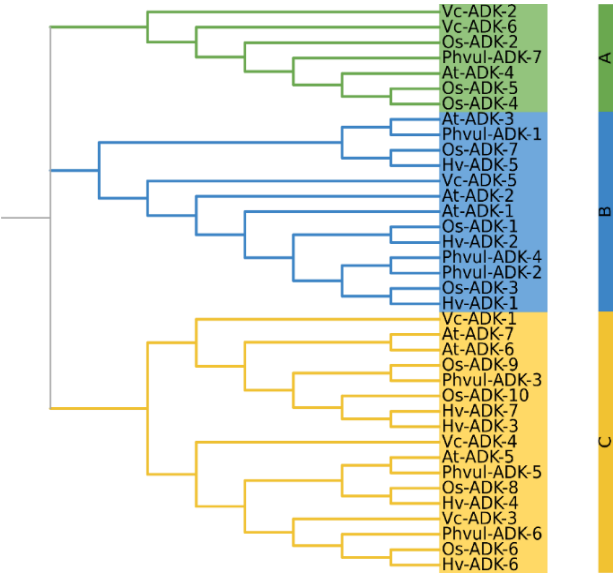


Figure 4. Phylogenetic tree drawn with ADK proteins from *P. vulgaris*, *A. thaliana*, *H. vulgare*, *O. sativa*, and *V. carteri* plants

To date, ADK genes have been identified in numerous plant species. It is known that various homologous differentiations have occurred in these species over time and that their genomes have undergone countless duplication events. This situation indicates that structural and functional changes have emerged in the gene family as the evolutionary process has progressed (Huang et al., 2024). In this study, a synteny analysis with *A. thaliana* was performed to evaluate the evolutionary process of ADK genes more comprehensively. As a result of the analysis, a synteny relationship was detected between *P. vulgaris* and *A. thaliana* plants. Synteny relationships were detected between *Phvul-ADK-8* and *AT5G35170.1*, *Phvul-ADK-7* and *AT5G60340.1*, *Phvul-ADK-4* and *AT5G63400.1*, *Phvul-ADK-3* and *AT5G50370.1*, *Phvul-ADK-1* and *AT3G01820.1*, *Phvul-ADK-2* and *AT2G39270.1*, *Phvul-ADK-5* and *Phvul-ADK-6* and *AT2G37250.1* genes (Figure 5).

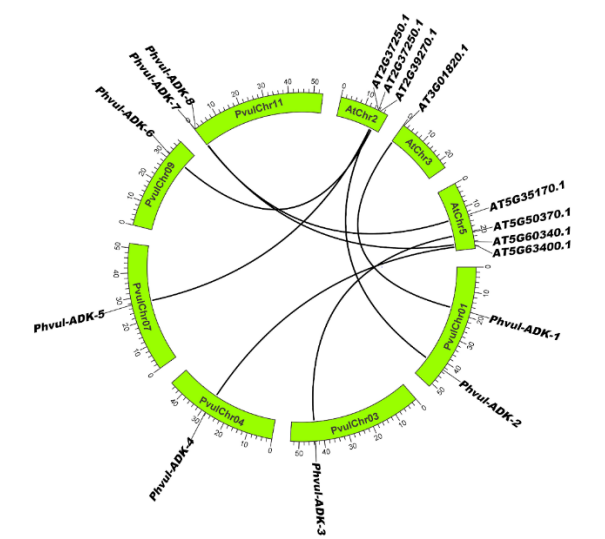


Figure 5. Genome-wide synthesis analysis of *Phvul-ADK* genes. Comparative map between *P. vulgaris* and *A. thaliana*.

Cellular Localization and Cis-acting Element Analysis: The WoLF PSORT tool was used to predict the cellular localization of *P. vulgaris* ADK proteins. The results are presented in Table 4.

Table 4. Cellular localization of *Phvul-ADK* proteins

Name	Cellular Location
Phvul-ADK-1	mito: 10, nucl: 2, cyto: 2
Phvul-ADK-2	chlo: 12, mito: 1.5, cyto_mito: 1.5
Phvul-ADK-3	cyto: 8, hlo: 3, cysk: 2, mito: 1
Phvul-ADK-4	nucl: 3, mito: 3, chlo: 2, extr: 2, pero: 2, cyto: 1, plas: 1
Phvul-ADK-5	mito: 10.5, cyto_mito: 6, chlo: 3
Phvul-ADK-6	mito: 8, chlo: 6
Phvul-ADK-7	chlo: 11, cyto: 2, mito: 1

Analyses of promoter regions revealed the presence of 32 different cis-acting elements involved in gene transcription. Cis-acting elements associated with abiotic stress were particularly considered (Figure 6).

Homology Modeling of *Phvul-ADK* Proteins and Protein-Protein Interactions: Bean ADK protein sequences obtained from databases were uploaded to the Phyre2 database tool, and high-probability 3D modeling of the proteins was

performed. The 3D predicted structures of the *P. vulgaris* ADK proteins are shown in Figure 7.

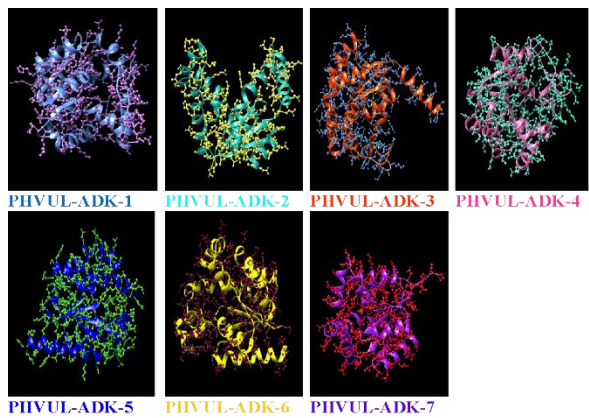


Figure 7. 3D homology modeling of *P. vulgaris* ADK genes

In the 3D modelling analysis, while the confidence level of all Phvul-ADK proteins was nearly 100%, differences were observed in their coverage rates. The highest coverage rate was observed in PhvulADK-3, while the lowest rate was observed in Phvul-ADK-5. The interactions between the Phvul-ADK proteins are shown in Figure 8. Data were obtained and visualized using the STRING database (Szklarczyk et al., 2021). Analysis showed that the Phvul-ADK-7 protein interacted most with

all ADK proteins. Additionally, Phvul-ADK-1 and Phvul-ADK-6 proteins were found to interact more strongly with each other.

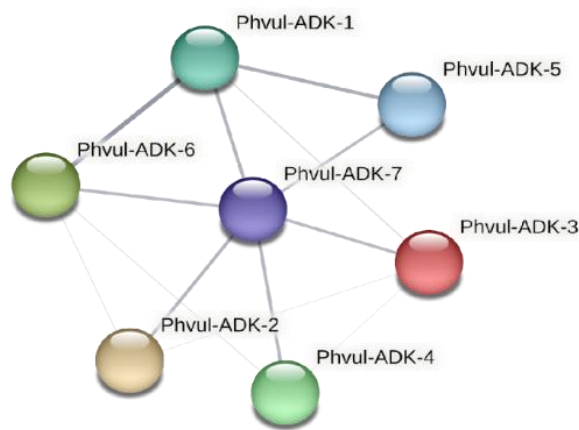


Figure 8. Phvul-ADK protein-protein interactions

Genome-wide expression of *Phvul*-ADK genes:

Gene expression profiles of ADK genes in *P. vulgaris* were evaluated to determine their potential functions in response to drought and salt stress. Analysis using TBtools revealed that *Phvul*-ADK genes exhibited different expression levels under drought and salt stress. Compared to drought stress, an increase in the *Phvul*-ADK-3 gene was observed under salt stress (Figure 9).

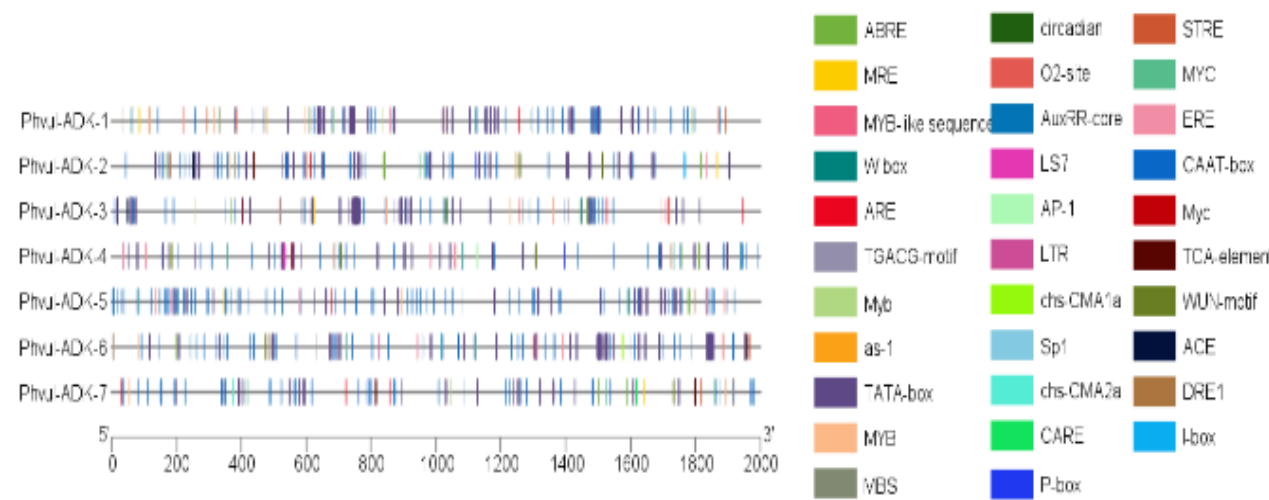


Figure 6. Cis-element prediction for *Phvul*-ADK genes

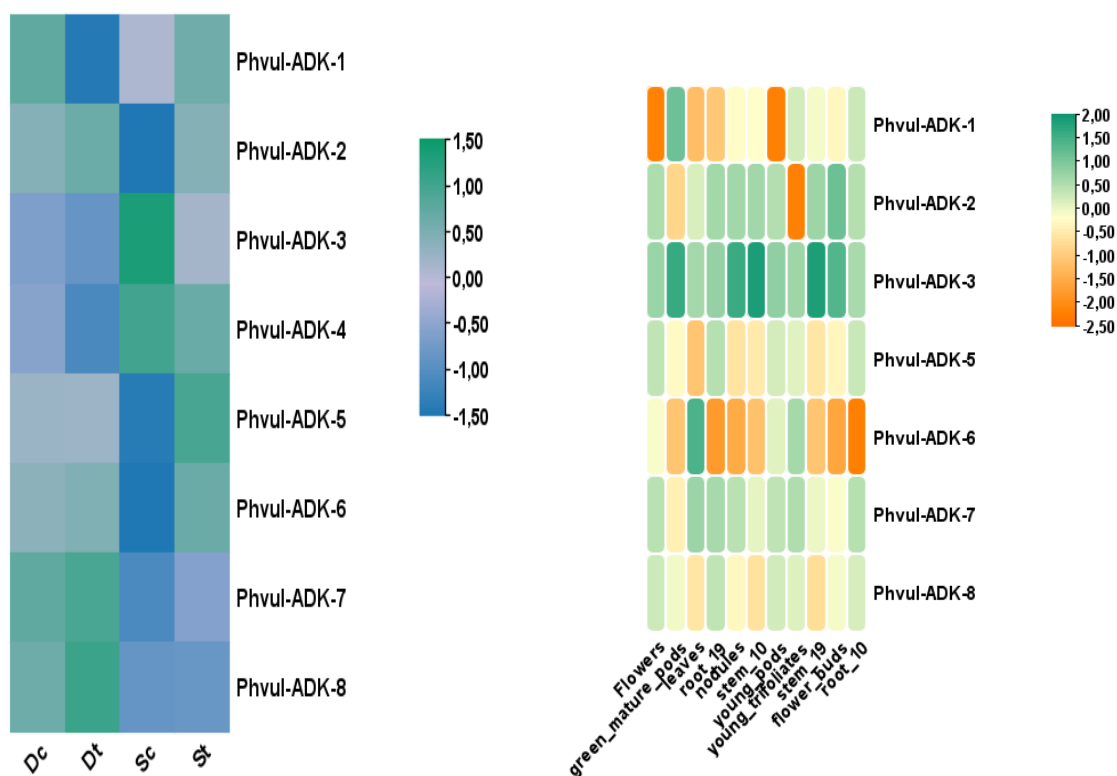


Figure 9. Expression analysis of members of the *ADK* gene family in *P. vulgaris* under abiotic stress conditions and in different tissues (Heatmap)

The expression profiles of *ADK* genes were examined in *P. vulgaris* flowers, green mature pods, leaves, nodules, young trifoliate leaves, stems, young pods, flower buds, and root tissues (Figure 9). The highest gene expression was observed for the *Phvul-ADK-3* gene in green mature pods, nodules, and roots. The most highly expressed gene in leaf tissues was *Phvul-ADK-6*. *Phvul-ADK-2* has the lowest expression profile.

Discussion

Adenosine monophosphate (AMP) is one of the fundamental components of cellular energy balance and nucleotide metabolism (Dzheia et al., 1986; Huang et al., 2024). The adenylate kinase enzyme associated with AMP regulates the conversions between ATP, ADP, and AMP, ensuring the continuity of energy metabolism and playing a critical role in plant growth, development, and adaptation to stress conditions (Lange et al., 2008; Huang et al., 2024). The location and structural differences of adenylate

kinase genes within plant genomes also provide noteworthy findings. Also it has been determined that the *Phvul-ADK-6* and *Phvul-ADK-7* genes are located at the ends of chromosomes, unlike the distribution of other genes on other chromosomes. Similarly, 11 *SLADK* genes in the tomato genome are distributed across nine different chromosomes. It has been reported that these 11 *ADK* genes in the tomato genome share similar protein homology when compared to beans and other plants (Yang et al., 2021). Furthermore, all *Phvul-ADK* proteins showed similar homology and all contained alpha helices and beta sheets (Figure 7).

The expansion and evolutionary development of gene families are closely related to gene duplication events (Holland et al., 1994; Xu et al., 2012; Buttanri et al., 2024). In this regard, the *Phvul-ADK-1* and *Phvul-ADK-2* genes have similar structural exon lengths, with *Phvul-ADK-5* containing the most exons. When examining the exon/intron structures of *ADK* genes found in

tomatoes and cotton, it was determined that these genes contain between 4 and 19 exons. This similarities that all of these proteins may have similar functions (Yang et al., 2021; Huang et al., 2024). Analyses conducted to examine the collinearity of the *ADK* gene family identified seven collinearity pairs between potato and *A. thaliana* and twelve collinearity pairs between cotton and *A. thaliana*. These findings reveal that the *ADK* gene family is highly related to this species in the evolutionary process and that it shares distinct similarities with other plant species in terms of the number of gene family members, genetic structure, and other characteristics (Li et al., 2023; Huang et al., 2024).

The phylogenetic analysis of the *ADK* gene family provides important clues about diversification and evolutionary relationships in different plant species. In this context, only *Phvul-ADK-7* is classified in group 'A' based on the distance matrix. Groups 'B and C' contain the segmentally duplicated *Phvul-ADK-2* and *Phvul-ADK-5*. Additionally, *H. vulgare* is not included in group A. Similarly, tomato *ADK* genes are classified into four groups, while potato *ADK* genes are classified into six groups. Furthermore, phylogenetic analyses conducted on four different cotton species in cotton have shown that all *ADK* proteins cluster into six groups (Yang et al., 2021; Li et al., 2023; Huang et al., 2024). This phylogenetic diversity suggests that *ADK* proteins may exhibit not only evolutionary but also cellular functional differences. Analyses have revealed that bean *ADK* proteins are predominantly localized in chloroplasts and mitochondria. It has been determined that a large portion of *StADK* proteins are found in mitochondria, affecting the metabolic balance of magnesium ions in the cytoplasm and adenylate pool. It has been shown that *ADK* proteins are generally localized in mitochondria and chloroplasts in various plant species (Hampp et al., 1982; Stitt et al., 1982; Li et al., 2023).

To understand the potential functions and regulatory mechanisms of the *Phvul-ADK* gene family during abiotic stress responses and hormone applications, cis-acting element analysis was performed. These elements were classified as light-responsive, environmental stress-related, plant development-related, promoter region-related, and plant hormone-responsive elements. The presence of elements such as MBS, LTR, TGA element, TGACG motif, and DRE, which are associated with drought and salt stress, was detected (Yamniuk and Vogel, 2004; Saeediazar et al., 2014; Yuan et al., 2021). Furthermore, CAAT-box and TATA-box elements were found to be prevalent in the promoters of *Phvul-ADK* genes. The MBS element was particularly observed in *Phvul-ADK-1* and *Phvul-ADK-2*. Furthermore, the DRE1 element was detected only in *Phvul-ADK-1*. In addition, elements associated with light response and elements regulated by stress hormones, such as MYC, ARE, ERE, and P-box, have also been identified in the promoters of some *ADK* genes. Previous studies have reported 17 different cis-acting elements responding to stress and hormone signals on *SlADK11* genes in tomatoes and 30 different cis-acting elements on *GhADK* genes in cotton. Among these elements, regulatory regions such as G-box, TGACG motif, MYB, MYC, and LTR have been noted (Yang et al., 2021; Huang et al., 2024).

Abiotic stresses such as drought, high salinity, extreme heat, and flooding are among the main causes of crop losses worldwide and reduce the yield of many important agricultural crops by more than 50% (Bray, 2000). Previous studies have shown that *ADK* genes play important roles in plant growth and development as well as in abiotic stress responses (Peterson et al., 1987; Zhou et al., 2007; Gong et al., 2010; Raveneau et al., 2017). Under drought stress, *Phvul-ADK-7* and *Phvul-ADK-8* showed high expression levels compared to other genes. In contrast, the lowest expression level

was determined for *Phvul-ADK-4*. The *Phvul-ADK-1* gene was found to be completely absent under drought stress. In response to salt stress, the *Phvul-ADK-5* gene showed the highest expression levels, but a decrease in the expression level of *Phvul-ADK-3* was observed with salt stress. It has been reported that *SLADK* genes are highly expressed in tomatoes in response to abiotic stresses and particularly confer resistance to salt and drought stress (Yang et al., 2021). Similarly, it is known that *ADK* genes are actively expressed in response to abiotic stresses in plants such as rice, potato, and maize. For example, it has been noted that *ADK* gene expression in maize roots and stems exhibits significant changes at different $\text{Ca}^{2+}/\text{Na}^{+}$ ratios (Peterson et al., 1987). The results obtained reveal that *ADK* genes exhibit different expression profiles under abiotic stress conditions and that these genes may play important roles in stress response and adaptation. These findings suggest that *ADK* genes could be utilized to develop plant varieties that are resistant to abiotic stresses.

Conclusion

In this study, a detailed genome-wide analysis of the *ADK* gene family in beans was performed, and a total of 7 *ADK* genes were identified. These genes are located on 6 different chromosomes. The study is unique in that it characterizes *ADK* genes in beans for the first time and determines their expression profiles in plant leaves exposed to salt and drought stress. This study has the potential to be a valuable resource for future genetic breeding studies on bean plants and can guide research on similar topics.

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Author Contributions:

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