Genome-wide analysis of *Phaseolus vulgaris* C2C2-YABBY transcription factors under salt stress conditions

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Abstract The aim of this study was to identify and characterize the C2C2-YABBY family of genes by a genome-wide scale in common bean. Various in silico approaches were used for the study and the results were confirmed through common molecular biology techniques. Quantitative real-time PCR (qPCR) analysis was performed for identified putative *PvulYABBY* genes in leaf and root tissues of two common bean cultivars, namely Yakutiye and Zulbiye under salt stress condition. Eight candidate *PvulYABBY* proteins were discovered and the length of these proteins ranged from 173 to 256 amino acids. The isoelectric points (pIs) of YABBY proteins were between 5.18 and 9.34 and ranged from acidic to alkaline, and the molecular weight of *PvulYABBY*s were between 18978.4 and 28916.8 Da. Three segmentally duplicated gene couples among the identified eight *PvulYABBY* genes were detected. These segmentally duplicated gene couples were *PvulYABBY-1/PvulYABBY-3*, *PvulYABBY-5/PvulYABBY-7* and *PvulYABBY-6/PvulYABBY-8*. The predicted number of exons among the *PvulYABBY* genes varied from 6 to 8 exons.

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Additionally, all genes found included introns within ORFs. *PvulYABBY-2*, -4, -5 and -7 genes were targeted by miRNAs of five plant species and a total of five miRNA families (miR5660, miR1157, miR5769, miR5286 and miR8120) were detected. According to RNA-seq analysis, all genes were up- or down-regulated except for *PvulYABBY-1* and *PvulYABBY-6* after salt stress treatment in leaf and root tissues of common bean. According to the qPCR analysis, six out of eight genes were expressed in the leaves but only four out of eight genes were expressed in the roots and these genes exhibited tissue- and cultivar-specific expression patterns.

Keywords C2C2-YABBY · Transcription factors · RNA-seq · In silico analysis · qPCR

Introduction

Transcription factors (TFs) play an important role in the growth and development of plants as well as all organisms in nature. To date, approximately 30 TF families have been identified and classified according to the conserved motifs that code for the DNA-binding domains and approximately half of them are considered as plant-specific TFs such as AP2/ERF, WRKY, NAC, B3, SBP and DOF families (Yamasaki et al. 2013).

The YABBY gene family is one of the plant transcription factors and is known to be specific to seed plants (Yang et al. 2016). These genes encode proteins which include two conserved domains which are N-terminal Cys2 Cys2 zinc-finger motif and C-terminal YABBY domain (Golz et al. 2004; Mackay and Crossley 1998). Previous studies have shown that some of the zinc fingers are observed as DNA-binding motifs, while many of them play roles in protein–protein interactions without binding DNA (Golz

et al. 2004). The main function of *YABBY* genes is to specify abaxial cell fates in lateral organs in *Arabidopsis* (Villanueva et al. 1999). In monocots, evolution has shown that *YABBY* genes have taken on different functions including other processes of plant growth and development such as controlling the carpel number of tomato flower (Cong et al. 2008). Notably, WRKY TFs, regulated by *YABBY*, play important roles in the regulation of plant stress response both as activators and repressors (Schluthofer and Yuan 2015).

The *YABBY* comprises a small gene family, which has only six members (*FIL*, *CRC*, *INO*, *YAB2*, *YAB3* and *YAB5*) in *Arabidopsis*, eight members in *Orzya sativa* and nine members in *Lycopersicum esculentum* (Huang et al. 2013). However, the molecular basis of their action has not been well understood yet (Sawa et al. 1999; Siegfried et al. 1999; Villanueva et al. 1999). In addition, *YABBY* is affected by Auxin, GA and other various hormones, it is estimated to be important for the regulation of the cold stress (Peng et al. 2015). The aim of this study was to identify and characterize *C2C2-YABBY* genes at genome-wide scale in common bean. Various in silico approaches were used and the results were confirmed through molecular biology techniques. In addition, the expression levels of eight putative *PvulYABBY* genes were analyzed using qPCR in leaf and root tissues of two common bean cultivars, namely Yakutiye and Zulbiye under salt stress conditions.

Materials and methods

In silico identification of *YABBY* proteins in *Phaseolus vulgaris*

Sequences of the *YABBY* gene family of *Phaseolus vulgaris* were obtained from Phytozome database v11 (www.phytozome.net) using key searching with Pfam Accession Number (PF04690), downloaded from Pfam Database (<http://pfam.xfam.org/>). To identify all the putative *YABBY* proteins in *P. vulgaris*, both blastp at Phytozome database v11 (www.phytozome.net) and hidden Markov model (HMM), (<http://www.ebi.ac.uk>) searches were performed against the *P. vulgaris* genome (Goodstein et al. 2012). Putative *P. vulgaris* *YABBY* proteins were used for query in blastp (NCBI) for characterization of hypothetical proteins. Redundant sequences were removed using the decrease redundancy tool (http://web.expasy.org/decrease_redundancy/) and sequences were checked for *YABBY* domains using HMMER (<http://www.ebi.ac.uk>) and Pfam databases. The physicochemical properties of *YABBY* proteins were calculated using ProtParam Tool (<http://web.expasy.org/protparam>).

Structure and physical locations of *PvulYABBY* genes, identification of gene duplication events and conserved motifs

The gene structure display server v2.0 (GSDS, <http://gsds.cbi.pku.edu.cn/>) was used (Guo et al. 2007) to obtain information on the exon–intron of *PvulYABBY* proteins. Both genome sequences and the coding sequences were utilized for predicting the positional information of the *PvulYABBY* genes using Phytozome database v11, chromosomal locations. The sizes (bp) and intron numbers of *PvulYABBY* genes were identified. The *PvulYABBY* genes were plotted on all *P. vulgaris* chromosomes and pictured with MapChart (Voorrips 2002). Gene duplication events were detected through the alignment of the coding nucleotide and sequences covered 70% of the longest genes and the amino acid identity between the sequences was >70% (Yang et al. 2008). To identify additional conserved motifs of *PvulYABBY* proteins, we used the Multiple EM for Motif Elicitation tool (MEME v4.11.1; <http://meme-suite.org/>) (Bailey et al. 2006).

Phylogenetic analysis and sequence alignment

The multiple sequence alignment of *PvulYABBY* proteins was carried out using the ClustalW (Tamura et al. 2011). The neighbor-joining (NJ) method with bootstrap value of 1000 replicates (MEGA6) was used for constructing phylogenetic trees and the tree was designed using Interactive tree of life (iTOL; <http://itol.embl.de/index.shtml>) (Letunic and Bork 2011).

Subcellular localization and promoter analysis of the *PvulYABBY* family

The 5' upstream regions (2 kb DNA sequence of each gene of the *PvulYABBY* family) were obtained from Phytozome database v11 (Supplementary Table S1) and analyzed using the plantCARE database (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>) for a cis-element scan. Subcellular localization of the *PvulYABBY* proteins was determined using the WoLF PSORT (http://www.genscript.com/psort/wolf_psort.html) (Horton et al. 2007) and TargetP 1.1 (<http://www.cbs.dtu.dk/services/TargetP/>) (Emanuelsson et al. 2007).

GO annotation

The functional annotation of *PvulYABBY* protein sequences were defined with Blast2GO (<http://www.blast2go.com>) (Conesa et al. 2005).

In silico prediction of miRNA targets in *PvuYABBY* genes

All known plant miRNA sequences were obtained from miRBase v21.0 (<http://www.mirbase.org>). psRNA target server (<http://plantgrn.noble.org/psRNATarget>) with default parameters was used for prediction of miRNAs accordingly (Zhang 2005). In silico predicted miRNA targets were identified by BLASTX with $\leq 1e-10$ against common bean Expressed Sequenced Tags (ESTs) at NCBI database.

Comparative physical mapping of YABBY proteins between common bean and other species

To obtain a orthologous relationship among the chromosomes of common bean, *Arabidopsis thaliana* and *Medicago truncatula* species, amino acid sequences of common bean YABBYs were searched against amino acid sequences of its corresponding *A. thaliana*, and *M. truncatula* YABBYs (www.phytozome.net) using NCBI-BLASTP. The comparative orthologous relationships of YABBY genes among common bean, *A. thaliana* and *M. truncatula*, chromosomes were drawn using MapChart.

Prediction of synonymous and non-synonymous substitution rates in *PvuYABBY* genes

CLUSTALW software was used for the prediction of amino acid sequences of tandemly and segmentally duplicated *PvuYABBY* genes. The CODEML program in PAML (PAL2NAL) (<http://www.bork.embl.de/pal2nal>) was used to estimate the synonymous (Ks) and non-synonymous (Ka) substitution rates (Suyama et al. 2006). Time (million years ago, Mya) of duplication and divergence of each YABBY genes were determined using the following formula: $T = Ks/2\lambda$ ($\lambda = 6.56E-9$) (Lynch and Conery 2003; Yang and Nielsen 2000).

Expression levels of *PvuYABBY* genes in transcriptome data

Illumina RNA-seq data were obtained from sequence read archive (SRA) to measure the expression levels of *PvuYABBY* genes. The accession numbers SRR957667 (control leaf), SRR958472 (salt-treated root), SRR958469 (control root), and SRR957668 (salt-treated leaf) were used for this purpose (Hiz et al. 2014). The analysis of transcriptomic data was performed as described by Buyuk et al. (2016). Finally, the heat maps of hierarchical clustering were constructed using the PermutMatrix (Caraux and Pinloche 2005).

Plant materials, growth conditions, and stress treatments

The seeds of drought-tolerant bean cv. 'Yakutiye' and drought-sensitive bean cv. 'Zulbiye' were supplied from 'Transitional Zone Agricultural Research Institute, Eskişehir, Turkey' (Guler et al. 2012). A preliminary experiment was performed to determine the salt tolerance capacity of both common bean cultivars under severe salt stress conditions (250 and 400 mM NaCl for 9 days) using malondialdehyde (MDA) analysis as an indicator test for stress. According to the preliminary data, drought-tolerant cv. 'Yakutiye' seemed to be more resistant to salt stress than cv. 'Zulbiye' exhibited (unpublished results).

For gene expression analysis, seeds of both cultivars were germinated, following the surface sterilization in a solution containing 5% (v/v) hypochlorite for 5 min, and were grown hydroponically in pots containing 0.2L of 1/10 Hoagland's solution (Buyuk et al. 2016). Common bean seedlings were incubated in a controlled environmental growth chamber in the light with $250 \text{ mmol m}^{-2} \text{ s}^{-1}$ photosynthetic photon flux at 25 °C, 70% relative humidity. Salt stress was applied with Hoagland solution including 150 mM of NaCl (for moderate salinity stress) for 9 days after common bean seedlings reached the first trifoliate stage in growth chamber. Following the ninth day of stress application, root and leaf tissues of two different common bean cultivars were harvested to be used in qPCR analysis.

RNA isolation, cDNA synthesis and quantitative qPCR analysis

Total RNAs of tissues (leaf and root) of the bean cultivars were extracted by NucleoSpin® RNA Kit (Macherey–Nagel, Germany) as described in the manufacturer's protocol. Nucleic acid measurements were achieved using the NanoDrop Lite UV–VIS spectrophotometer and RNAs were also confirmed by 1.5% agarose gel electrophoresis (NanoDrop Technologies, Wilmington, DE, USA). cDNAs were synthesized from 2 µg of common bean RNAs using high fidelity cDNA synthesis kit (Roche Applied Science, USA) according to the manufacturer's recommendations. The qPCR assay was conducted using a Light Cycler® Nano System (Roche Applied Science, USA). The primers were designed using Primer3 program and the actin was used as a housekeeping gene in the qPCR analysis (Supplementary Table S2). Three biological replicates consisting of three technical replicates each were performed in all qPCR reactions. The qPCR quantifications of cDNAs were carried out with the SYBR Green PCR Master Mix (Roche Applied Science, USA) according to the manufacturer's recommendations. The $2^{-\Delta\Delta CT}$ method was used to

analyze data from qPCR and one-way ANOVA was used for calculating statistics (Livak and Schmittgen 2001).

Results and discussion

Identification of *YABBY* gene family in common bean

We key-searched *P. vulgaris* genome, acquired from the Phytozome database, using the *YABBY* gene family obtained from Pfam database and found eight genes with *YABBY* protein homology. Subsequently, *YABBY* domains were searched using the HMMER and Pfam databases in putative *PvulYABBY* proteins and redundant sequences were removed after validation. We discovered eight candidate *PvulYABBY* genes in the common bean genome and listed in Table 1, which shows the number of isoelectric point (pI), amino acids (length), molecular weight and NCBI annotation. All non-redundant *PvulYABBY* genes were distributed on chromosomes 2, 3, 5, 10, and 11 of common bean and the largest number of *PvulYABBY*s was on chromosome 3 (four *PvulYABBY* genes) (Fig. 1). The length of *PvulYABBY* proteins ranged from 173 (*PvulYABBY-2*) to 256 (*PvulYABBY-1*) amino acids (aa). PIs of *PvulYABBY* proteins were between 5.18 (*PvulYABBY-1*) and 9.34 (*PvulYABBY-2*) ranging from acidic to alkaline, and the molecular weight of *PvulYABBY*s were between 18978.4 Da (*PvulYABBY-2*) and 28916.8 Da (*PvulYABBY-1*).

According to the previous studies and HMMER search, the highest number of *YABBY* proteins was observed in

Glycine max with 17 members and *Arabidopsis lyrata* was found to have the lowest number of *YABBY* proteins with 6 among the eudicotyledons (Han et al. 2015). *Musa acuminata* had the highest number of *YABBY* proteins with 25 and *Aegilops tauschii* had the lowest number with 5 among the *Liliopsida* members. In previous studies, it was shown that seedless plants do not have *YABBY* genes (Han et al. 2015). It was also found that the *Arabidopsis* genome has six *YABBY* genes. Four of these genes (*FIL*, *YAB2*, *YAB3* and *YAB5*) have a high expression level in vegetative tissues, whereas expression of other two (*CRC* and *INO*) genes is restricted to floral organs (Eckardt 2010).

The gene duplication analysis showed that three segmentally duplicated gene couples, among the eight identified *PvulYABBY* genes, were detected and segmentally duplicated gene couples were *PvulYABBY-1/PvulYABBY-3*, *PvulYABBY-5/PvulYABBY-7* and *PvulYABBY-6/PvulYABBY-8* (Supplementary Table S6). Ks/Ka distances and ratios were also estimated. The Ks of the segmental duplication of *PvulYABBY-1* and *PvulYABBY-3* was 0.598, which dated the duplication event at 4.6 Mya; *PvulYABBY-5* and *PvulYABBY-7* was 1.8122, dated the duplication event at 13.94 Mya and *PvulYABBY-6* and *PvulYABBY-8* was 0.4205, dated the duplication event at 3.23 Mya (Supplementary Table S6). The mean date of segmental duplication events showed that *PvulYABBY-1/PvulYABBY-3* (4.6 Mya) and *PvulYABBY-6/PvulYABBY-8* (3.23 Mya) genes were segmentally duplicated after the divergence of monocot–dicot split, which were observed at 170–235 Mya (Gupta et al. 2015). *PvulYABBY-5* and *PvulYABBY-7* (13.94 Mya) genes were segmentally duplicated before the divergence of the

Table 1 The information of eight *PvulYABBY* proteins

ID	Phytozome identifier	Chromosome location	Protein length	Molecular weight (Da)	pI	Stable or unstable	Instability index
<i>PvulYABBY-1</i>	Phvul.002G069700.1	9554540..9556683	256	28916.8	5.18	46.39	Unstable
<i>PvulYABBY-2</i>	Phvul.003G039800.1	4217179..4219619	173	18978.4	9.34	39.51	Unstable
<i>PvulYABBY-3</i>	Phvul.003G061800.1	8393693..8395131	237	26412.2	7.94	52.06	Unstable
<i>PvulYABBY-4</i>	Phvul.003G166100.1	37492965..37496762	186	20894.8	8.4	41.12	Unstable
<i>PvulYABBY-5</i>	Phvul.003G217700.1	43407696..43410807	215	23982.3	7.13	54.76	Unstable
<i>PvulYABBY-6</i>	Phvul.005G117600.1	33854923..33864003	185	20704.5	8.95	41.51	Unstable
<i>PvulYABBY-7</i>	Phvul.010G079200.1	29466002..29468643	215	23915.2	8.58	48.23	Unstable
<i>PvulYABBY-8</i>	Phvul.011G100300.1	10846106..10852521	183	20458.2	8.22	48.66	Unstable

Fig. 1 Distribution of *PvulYABBY* genes on common bean chromosomes

monocot–dicot split according to the K_s/K_a distances and ratios.

Phylogenetic analysis, conserved motifs, gene structure and subcellular localization of *PvulYABBYs*

To investigate the relationships among *PvulYABBY* proteins, a phylogenetic tree of *YABBY* proteins in common bean and *Arabidopsis* was constructed using amino acid sequences with well-supported bootstrap values (1000 replicates) (Fig. 2) through the neighbor-joining method. *PvulYABBY* proteins were classified into three groups (I, II and III) and the third group could be further classified into two subgroups (IIIa and IIIb) (Fig. 2).

The orthology analysis showed that *Arabidopsis* had six ortholog relationship in the common bean (*ATIG08465* and *YABBY 6-8*; *AT2G26580* and *YABBY 4*; *AT2G45190* and *YABBY 5-7*; *AT4G00180* and *YABBY 5-7*; *AT1G23420* and *YABBY 1-3*; *AT1G69180* and *YABBY 2*) and *Medicago truncatula* had seven ortholog relationship in common bean (*MEDTR2G087740* and *YABBY 8-6*; *MEDTR4G025900* and *YABBY 7-5*; *MEDTR4G050300* and *YABBY 8-6*; *MEDTR4G101660* and *YABBY 7-5*; *MEDTR4G114730* and *YABBY 4-6*; *MEDTR5G034030* and

YABBY 1-3; *MEDTR5G046230* and *YABBY 2*) (Supplementary Fig. S2).

To discover the conserved motifs in *PvulYABBY* proteins, MEME (v4.11.1) was used and a total of 15 conserved motifs were identified. The lengths of discovered motifs ranged from 10 to 50 amino acids. All *PvulYABBY* proteins included Motif 1 and Motif 2 (Supplementary Fig. S1, Table S3).

We investigated the gene structure of eight common bean *YABBY* genes. The predicted number of exons among the eight *PvulYABBY* genes varied from 6 to 8. In addition, all *PvulYABBY* genes included introns within ORFs (Fig. 3).

The upstream promoter region of the *PvulYABBY* family contained a total of 75 different *cis*-acting elements, which are categorized as light-responsive elements (30), development-related elements (12), environmental stress-related elements (6), hormone responsive elements (6), promoter-related elements (3), site-binding-related elements (3) and other elements (15) (Supplementary Table S4). The average number of *cis*-acting elements per *PvulYABBY* gene was 29.875 and the highest number (38) of *cis*-elements was found on *PvulYABBY-8*, while the least (23) was observed on *PvulYABBY-7*. GT-1 and TGACG motifs were related to salt stress in maize promoter (Hou et al. 2016).

Fig. 2 A phylogenetic tree of common bean YABBY proteins

Fig. 3 Gene structure of *PvulYABBY* genes

These motifs were found in *PvulYABBY-4* and *-7* out of eight *PvulYABBY* genes.

Detection of miRNAs targeting *PvulYABBY* genes

According to the results of psRNATarget server, the maximum expectation and accessibility of messenger RNA (mRNA) target site to miRNA ranged from 2.5 to 3.0 and 12.927 to 22.041, respectively (Supplementary Table S5). A total of four *PvulYABBY* genes (*PvulYABBY-2*, *-4*, *-5* and *-7*) were targeted by miRNAs of five plant species. A total of five miRNA families (miR5660, miR1157, miR5769, miR5286 and miR8120) were detected and the *PvulYABBY-2* gene was targeted by two different plant miRNAs (Supplementary Table S5).

In previous studies, several miRNAs were found against various abiotic stresses (Eldem et al. 2012; Kavas et al. 2016). A number of salt-responsive miRNAs were defined from the leaves and roots of wheat (Eren et al. 2015). Several salt stress-responsive miRNAs have been defined in diverse plant species. E.g., miR156, miR159, miR162, miR171 and miR319 were determined to be salt-responsive miRNAs in *Arabidopsis*, *Populus*, barley and rice (Eldem et al. 2013).

YABBY proteins have a zinc finger and a helix-loop-helix domain (YABBY gene family) and they are known to have crucial influence on transcriptional regulators (Juarez et al. 2004). In relation to that, miRNA-targeted zinc-finger proteins have been found as salt stress-responsive factors in plants (Fang et al. 2006). In a recent study, miR393 was found to target the helix-loop-helix domain in common bean (Kavas et al. 2016).

The miRNA-target relationship in the biological system may be more complex than was previously known (Barbato et al. 2009; Pasquinelli 2012). Specifically, miRNAs directly target the YABBY genes, however, certain miRNAs can indirectly affect the YABBY genes through a different gene. Our work presented herein, extensively covers the role YABBY genes at the genome level, shows a correlation between YABBY-related miRNAs and salt stress response. The results shown are considered to be very important for the definition of YABBY functions, which were previously unknown.

Genome-wide expression pattern of *PvulYABBY* genes

The expression profile of *PvulYABBY* genes, based on RNA-seq, was developed using the root and leaf tissues of common bean. Based on the RNA-seq analysis results, eight expressed *PvulYABBY* genes were identified through the Phytozome identifier (Table 1). According to normalized RPKM values, all *PvulYABBY* genes were up- or

Fig. 4 Heat map of differentially expressed *PvulYABBY* genes under normal and salt stress conditions

downregulated, except for *PvulYABBY-1* and *PvulYABBY-6*, after salt stress treatment in the leaf and root tissues of common bean (Fig. 4).

Figure 4 was derived from Illumina RNA-seq data, which was reported by Hiz et al. (2014) and downloaded from Sequence Read Archive Accession numbers; SRR957667 (control leaf), SRR958472 (salt-treated root), SRR958469 (control root), and SRR957668 (salt-treated leaf) (Hiz et al. 2014). RT: Root treated, RC: Root control, LT: Leaf treated, LC: Leaf control.

Salt stress responses of *PvulYABBY* genes

Expression levels of all putative *PvulYABBY* genes were analyzed using qPCR in leaf and root tissues of Yakutiye and Zulbiye cultivars under salt stress conditions. Six out of eight genes had significant levels of expression in the leaves and these genes exhibited tissue- and cultivar-specific expression patterns. The relative expression levels of *PvulYABBY-1*, *-4*, *-5*, *-6*, *-7* and *-8* genes were found to be at least 1.8 times higher in leaves of salt-tolerant cv. ‘Yakutiye’ under salt stress compared to the untreated control sample (Fig. 5). The most transcribed gene in the leaves of cv. ‘Yakutiye’ was *PvulYABBY-7* with approximately 1600-fold higher expression value than the control sample. On the other hand, except for *PvulYABBY-4* and *-6*, relative expression levels of all other genes were found to be lower in the leaves of salt-sensitive cv. ‘Zulbiye’ under salt stress when compared to the control sample (Fig. 5).

However, only four out of eight genes were found to be transcribed in the roots of cv. ‘Yakutiye’ and ‘Zulbiye’ in a tissue- and cultivar-specific manner. All of these genes (*PvulYABBY-1*, *-5*, *-7* and *-8*) were found to be downregulated in the roots of cv. ‘Yakutiye’ and the most downregulated gene was *PvulYABBY-5* with 0.02-fold lower expression value than the control sample (Fig. 5). In the roots of cv. ‘Zulbiye’, *PvulYABBY-1*, *-7* and *-8* genes were

Fig. 5 qPCR data indicating the relative expression levels (Log2 values) of *PvulYABBY* genes in leaves and roots of Zulbiye and Yakutiye common bean cultivars under salt (150 mM NaCl) stress

found to be upregulated, while *PvulYABBY-5* gene was downregulated compared to the untreated control sample. The downregulation of *PvulYABBY-5* gene was not statistically significant according to the statistical analysis. It is known that the *YABBY* is a quite complex gene family which consists of several members. These genes are usually found to be related with the leaf, flower, and fruit development (Dai et al. 2007). Recently, their role in formation of fruit shape has also been found in tomato (Han et al. 2015). In addition to these previous findings, this study clearly shows that *YABBY* genes show dynamic gene expression profile under salt stress conditions and this clue might support the idea that *YABBY* genes can be considered to play a role in salt stress response in common bean.

compared to their respective controls (unstressed tissue). Value of control sample (not shown in the histogram) is equivalent to 1

In conclusion, our identified 8 *PvulYABBY* genes in *Phaseolus vulgaris* genome were distributed on 11 different chromosomes. Gene expression analysis was carried out using all *PvulYABBY* genes and defined a significant variation between Yakutiye and Zulbiye variants under salt stress. The gene expression level in leaf of Yakutiye was found to be higher than those of Zulbiye. Alternatively, the expression level in root of Zulbiye was mostly higher compared to Yakutiye. The results of this study can be used for common bean breeding studies in the future.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest in the publication.

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