Arabidopsis CK2 family gene CKB3 involved in abscisic acid signaling

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Abstract

CKB3 is a regulatory (beta) subunit of CK2. In this study Arabidopsis thaliana homozygous T-DNA mutant ckb3 was studied to understand the role of CKB3 in abscisic acid (ABA) signaling. The results shown: CKB3 was expressed in all organs and the highest expression in the seeds, followed by the root. During seed germination and root growth the ckb3 mutant showed reduced sensitivity to ABA. The ckb3 mutant had more stomatal opening and increased proline accumulation and leaf water loss. The expression levels of number of genes in the ABA regulatory network had changed. This study demonstrates that CKB3 is an ABA signaling-related gene and may play a positive role in ABA signaling.

Keywords: proline, T-DNA mutant, ABA signaling, expression.

1. Introduction

Plants are protected by the expression of various stress-related genes to synthesize hormones and regulatory plant growth and development as well as mediators of environmental stress responses (Sreenivasulu et al., 2012; Gnutt et al., 2017). Among various phytohormones abscisic acid (ABA) is the major hormone which is the central regulator of abiotic stress resistance in plants and coordinates an array of functions (Finkelstein, 2013; Wani and Kumar, 2015), enabling plants to cope with different stresses. A previous study shown that ABA acts as a stress signal in plants and plays an important role in modulating plant response to various biotic and abiotic stresses including cold drought salinity stress and so on (Ma et al., 2019; Wang et al., 2019). Genetic and chemical studies exemplifying ABA in regulating seed maturation and dormancy are important as they have showed that a reduction this hormone level is associated to decreasing seed dormancy (Li et al., 2012; Lee et al., 2015).

Casein kinase 2 (CK2) is an essential and evolutionary conserved Ser/Thr protein kinase and is a heterotetramer composed of two catalytic (CK2α) and two regulatory subunits (CK2β) (Litchfield, 2003). Specifically, CK2 contains four α-subunits and four β-subunits, αA/CKA1, αB/CKA2, αC/CKA3 and αp and β1/CKB1, β2/CKB2, β3/CKB3 and β4/CKB4 in the Arabidopsis genome (Salinas et al., 2006). Molecular genetics studies have further showed that CK2 is a critical component of the circadian clock systems of various organisms including the long-day plant Arabidopsis (Arabidopsis thaliana) (Allada and Meng, 2005; Portolés and Más, 2007; Ogiso et al., 2010). According to reports CK2 is involved in various stress responses including heat, UV, drought, hormone...
responses, and so on (Wang et al., 2014; Olesen et al., 2015; Zhang et al., 2020; Nagatoshi et al., 2018).

CKB3 is a regulatory (beta) subunit of CK2 involved in regulation of the circadian clock in Arabidopsis (Sugano et al., 1999). Plant hormone and stress-response elements were found through gene chip analysis, including ABRE (ABA-responsive element), AuxRE (auxin-responsive element), CGTCA-motif (MeJA-responsive element) and HSE (Heat-responsive element). Thus the expression of CKB3 gene was also regulated by hormones and stresses and that it might play an important role in hormone and stress-response pathways.

In this study to understand the role of CKB3 in abiotic stress signaling *Arabidopsis thaliana* homozygous T-DNA mutant ckb3 was used. The physiological and biochemical indicators were measured, such as the germination, root growth, hypocotyl elongation, stomatal apertures, water-loss rate and so on, then combined the expression of CKB3 gene in response to various stresses of T-DNA mutant ckb3 and Col-0 analysis the role of CKB3 in abiotic stress. The results provide a basis for further study of CKB3 involved in various stress responses.

2. Material and Methods

2.1. Identification of homozygous T-DNA insertion mutants

The *Arabidopsis thaliana* Columbia wild-type (Col-0) was used as an Arabidopsis wild-type. From the *Arabidopsis Biological Resources Center* (ABRC) purchased the T-DNA insertion mutants ckb3 (Salk_093548 with Col-0 as background). Using tri-primer-PCR method to identify homozygous T-DNA insertion mutants, and the primers information were listed in Table 1. The primers were provided by ATIDB (the *Arabidopsis thaliana* Integrated Database).

2.2. Germination assays and root growth

To surface-sterilize the seeds for germination assay, using 75% ethanol to wash the seeds for 30 s followed by 20% NaClO for 10 min, then washed the seeds six to ten times with sterile distilled water and then placed in 4 °C for vernalization. The seeds were planted on Murashige and Skoog (MS) medium that contained 3% sucrose and 8% agar (PH = 5.8-6.0) with different concentrations of ABA (0 μM, 0.3 μM, 0.6 μM, 1 μM) after 4 days and then transferred to a growth chamber at 22 °C with about 8% agar (PH = 5.8-6.0) with different concentrations of ABA to the solution to the final concentration was 1 M. After the detached leaves were treated for 2 h, the stomatal apertures were measured as described previously (Sun et al., 2012).

2.3. Stomatal aperture measurement

Using rosette leaves of 4-week-old plants to measure the stomatal aperture. To incubate the detached leaves in solution containing 10 mM MES, 50 mM KCl and 10 mM CaCl₂ (pH 6.15) for 2 h under light. Then add ABA to the solution. The results provide a basis for further study of CKB3 involved in various stress responses.

2.4. Determination of the water-loss rate

To detect plant water-loss rate used the method was described by Shan et al. (2012). Getting the rosette leaves from an approximately 3-week-old T-DNA insertion mutants and Col-0 plants to detect the water-loss rate. Put the detached rosette leaves in clean filter paper, and then placed into a growth chamber with 25 °C and humidity of 60%. To recorded the fresh weight every 30 min. Each experiment was repeated three times.

2.5. Proline content measurement

To incubate the 14-day-old seedlings of Col-0 and T-DNA insertion mutants in MS solution containing 3% sucrose and 8% agar (PH = 5.8-6.0) with different concentrations of ABA (0 or 100 μmol). The 14-day-old seedling plants were collected and using the sulfosalicylic acid method to extract proline (Qin et al., 2014). The experiment was performed in triplicates.

2.6. RNA extraction and quantitative real-time polymerase chain reaction (qRT-PCR)

Total RNA was extracted from the 14-day-old Col-0 and mutant with TriZol (Takara) which was incubated in an ABA solution. To synthesize the first strand cDNA using the Maxima® First cDNA Synthesis Kit (Fermentas). Using a SYBR® Green I kit (TOYOBO, Japan) to perform quantitative PCR (qRT-PCR) in an Mx3000P thermal cycler (Stratagene USA). The procedure of the PCR reactions was started with a denaturing step for 10 min at 95 °C followed by 50 cycles of 15 s at 95 °C and a primer extension reaction at 55 °C for 1 min. The ACTIN2 gene was used as an internal control. All qRT-PCR tests were run in duplicates each with three biological replicates. The primers information was listed in Table 2. Analyze the data using MxPro (Stratagene) software.

3. Results

3.1. CKB3 T-DNA insertion mutants homozygous identification

Through PCR and qRT-PCR technology to identify the CKB3 T-DNA insertion mutants homozygous plants. The flanking region sequences of the T-DNA insertion mutant ckb3 showed that the insertion was located 80 bp...
downstream of the ATG start codon and inverted insertion. In the end we got three individuals homozygous of T-DNA insertion mutant ckb3 (Figure 1B). Through qRT-PCR technology to analyze the expression of homozygous of T-DNA insertion mutant ckb3. The result showed that the expression of CKB3 gene in T-DNA insertion mutant plant was zero indicating that the T-DNA insertion severely impaired the CKB3 gene expression.

3.2. Expression of the CKB3 gene in different organs and in response to various stresses

The expressions of CKB3 gene were analyzed in roots, stems, rosette, cauline leaves, flowers, silique and seeds of *Arabidopsis* (Figure 1D). CKB3 was expressed in all organs and the highest expression in the seeds, followed by the root. To analyze the expression of CKB3 gene under different stresses, the seedlings of 14 days old were

| Primer | Primer sequence 5'-3' |
|--------|----------------------|
| ABI3 (AT3G24650) F | ATGAAAGCCTTGCATGTGGC |
| ABI3 (AT3G24650) R | TCAATTACAGTTTGAGAAGT TGG |
| OST1 (AT4G33950) F | GGATCAACCCGGGCAAAG |
| OST1 (AT4G33950) R | TGAGTGCCTGCAGGAGGA |
| ABF2 (AT1G45249) F | TACAGCCAAAGCATCAGGA |
| ABF2 (AT1G45249) R | CACGGAAAACAAACAACCAAG |
| RAB18 (AT5G66400) F | AGCTCTAGCTCGGAGGAAG |
| RAB18 (AT5G66400) R | CATGATGACCTGCAACTTC |
| ABI5 (AT2G36270) F | TGAGGAGGAGGTGTTGTTG |
| ABI5 (AT2G36270) R | CCGGAAATAGAAGATCACC |
| EM1 (AT3G51810) F | CTGTGAGAGAGGGCAGCA |
| EM1 (AT3G51810) R | CTCAATCCCTTCTGTAAG |
| ACTIN2 (AT3G18780) F | TGGCGTCAAAGCAACTGC |
| ACTIN2 (AT3G18780) R | CACAAACGAGGCTGGAACAAG |

**Figure 1.** The identifications of the T-DNA insertion homozygous mutants and CKB3 transgenic plants of *Arabidopsis thaliana*. (A) A schematic structure of the ckb3 gene and the T-DNA locations in the ckb3 mutants; (B) Homozygotes for the T-DNA insertions identified by three primers. M is the marker, and 1, 2, 3 are homozygous mutants; (C) real-time fluorescence quantitative PCR analysis of the CKB3 gene expression in the T-DNA insertion mutants with actin-2 used as control; (D) Q-PCR analysis of the CKB3 gene expression in different organs of Arabidopsis with actin-2 used as control.
treated with ABA, GA, IAA and NaCl for different lengths of time (Figure 2). The expression of CKB3 peaked when treated by ABA for 6 h, IAA stress for 1 h. The expression decreased at first and then increased with time when treated by GA and NaCl. The results indicated that CKB3 may participate in the ABA stress signaling pathway.

3.3. CKB3 is involved in the ABA-mediated inhibition of seed germination and root elongation

CKB3 gene has the higher expression in seeds and roots than the other organ, to certain the effect CKB3 on seed germination and root growth. The seeds of T-DNA insertion mutant ckb3 and Col-0 were sown in a MS medium added with different concentrations of ABA after surface disinfection. The seed germination data was checked from 1 day to 7 day. The T-DNA mutant ckb3 displayed a higher germination rate than the wild-type Col-0 (Figure 3) in the presence of 0.3 μmol/L, 0.6 μmol/L and 1 μmol/L ABA. The ckb3 was less sensitive to ABA than the wild type. When treated with 10 μM ABA or 40 mM NaCl, the ckb3 had apparently higher root growth than Col-0 (Figure 4A). These results were match to the seed germination assay.

3.4. CKB3 gene affects stoma aperture, water loss and proline contents under ABA-mediated

Based on previous research results, in order to survive harsh conditions the plants can produce ABA to change stomatal openness, water loss and proline content (Schroeder et al., 2001; Verslues and Bray, 2006; Seiler et al., 2014; Eisenach et al., 2017). The results showed that the stomatal apertures of ckb3 were larger than those of the wild type with ABA treatment (10 μmol/L ABA) (Figure 4B). These results indicated that CKB3 might play a negative role under the influence of ABA in ABA-regulated stomatal closure. In this study shown the leaves of T-DNA insertion mutant ckb3 lost water at a slower rate than the Col-0 leaves (Figure 4C). To certain whether CKB3 affects proline accumulation in plants in response to ABA, the proline contents of the wild type ckb3 plants in response to ABA was determined. As shown in Figure 4D, the T-DNA insertion mutant ckb3 had significantly higher accumulated proline than Col-0. Thus, under the influence of ABA, CKB3 aslo plays a negative role.

3.5. CKB3 regulates the expression of ABA and stress responsive genes

In order to confirm whether CKB3 is involved in the ABA signaling pathway, expression levels of ABA signaling pathway related genes ABI3, ABI5, ABF2, OST1, RAB18 and EM1 (Yoshida et al., 2015; Skubacz et al., 2016; Gao et al., 2016; Wang et al., 2018). As shown in Figure 5, the expression level of ABI3 in T-DNA mutant plant was much lower than this in Col-0, but the expression levels were equal in ckb3 T-DNA mutant and Col-0 with ABA treatment displayed. The expression levels of ABI5, OST1, ABF2 and EM1 in the ckb3 plants were lower. These results showed that (Figure 5) CKB3 gene can regulate the expression level of ABA and stress-related genes, indicating that CKB3 may positively affect the ABA signaling.

4. Discussion

A previous have shown that several CK family genes are involved in the ABA signaling pathway, such as that three nuclear-located CK2 α-subunits (CKA1-3) in Arabidopsis have a synergistic role in ABA-induced blockage (Mulekar et al., 2012). CKA4 gene is an enhancing factor in abiotic stress signalling through modulating the expression of some molecular players in retrograde signaling (Wang et al., 2014). CKB1 is involved in abscisic

Figure 2. Real-time fluorescence quantitative PCR analysis of the expression of Arabidopsis thaliana CKB3 gene in response to exogenous ABA, NaCl, IAA and GA. Actin-2 was used as control.
acid to regulate stress responses in Arabidopsis thaliana (Yuan et al., 2017). Previous studies have shown that CKB3 gene is a key component of the plant circadian clock system, including the long-day plant Arabidopsis, there is no reports on the involvement of this gene in stress response. Through gene chip analysis we found certain plant hormone and stress-response elements, such as ABRE (ABA-responsive element), AuxRE (auxin-responsive element), CGTCA-motif (MeJA-responsive element) and HSE (Heat-responsive element). In this study to understand the role of CKB3 in abiotic stress signaling Arabidopsis thaliana homozygous T-DNA mutant ckb3 was used. The germination, root growth, hypocotyl elongation, stomatal apertures, water-loss rate, proline content and the expression of CKB3 in response to ABA of T-DNA mutant ckb3 and Col-0 were measured. These results can determine whether CKB3 gene is involved in the ABA signaling pathway. Although expression of CKB3 in all organs, its expression increased in roots and seeds and this result agrees with the expression of CKB1 gene (Yuan et al., 2017). The ckb3 mutant showed reduced sensitivity to ABA during seed germination and seedling growth more stomatal opening and increased proline accumulation, these results indicate CKB3 may be play a negative role in regulating seed germination, seedling growth, stomatal opening and proline accumulation under the influence of ABA. ABI3 (ABA Insensitive 3) plays a negative feedback regulatory role in seed germination (Reyes and Chua, 2007). ABI5 (ABA Insensitive 5) is a basic leucine zipper transcription factor that plays a pivotal role in the regulation of early seedling growth and seed germination in the abiotic stresses and ABA (Skubacz et al., 2016). Without ABA treatment the expression analysis of stress-responsive genes showed that the expressions of ABI3 and ABI5 were lower in CKB3 T-DNA mutants plants than in Col-0 plants, the expression ABI3 was equal in T-DNA mutants ckb3 and Col-0 and ABI5 was lower in CKB3 T-DNA mutants plants than in Col-0 plants when treatment with ABA.

These results shown CKB3 plays a role in regulating seed germination under the influence of ABA. OST1 is well characterized at molecular and physiological levels.

Figure 3. Effects of exogenous ABA on germination inhibition of seeds from Col-0, Arabidopsis thaliana homozygous T-DNA mutant ckb3. *indicate that the value of Two-way ANOVA was P<0.05, this value indicate significant differences between the Col-0 and mutant.

Figure 4. The analysis of root length, water-loss rate, stomatal aperture and proline accumulation in wild type and mutants of Arabidopsis thaliana. (A) The analysis of root length with ABA treatments; (B) Stomatal aperture of the wild type, and ckb3 in response to ABA treatments; (C), Assessment of the water-loss rate. (D) Proline accumulation of Col-0, and ckb3 in response to ABA. Data are expressed as the ratio of the traverse to the longitudinal diameter diameter (T/L) of stomata. *indicate that the value of Two-way ANOVA was P<0.05, this value indicates significant differences between the Col-0 and mutant.
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...to control stomata closure in response to water-deficit stress (Xuanyuan et al., 2017). After ABA processing the OST1 expression was lower in the T-DNA mutant ckb3 than in the Col-0 plants. The expression of ABF2 (ABRE binding factor 2) and EM1 was similar to the level of OST1. The expression of ABF2 has been reported to be strongly induced by salt, drought and ABA (Zandkarimi et al., 2015; Zhou et al., 2016). EM1 (Early Methionine-Labeled) was ABA-related gene the expression can be induced by ABI5 (Skubacz et al., 2016). These results indicate that CKB3 is an ABA signaling related gene and future is to explore whether this gene is involved in the plant stress response.

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References

ALLADA, R. and MEISSNER, R.A., 2005. Casein kinase 2 circadian clocks and the flight from mutagenic light. Molecular and Cellular Biochemistry, vol. 274, no. 1-2, pp. 141-149. http://dx.doi.org/10.1007/s11010-005-2943-1. PMid:16335534.

EISENACH, C., BAETZ, U., HUCK, N.V., ZHANG, J., ANGELI, A., BECKERS, G.J.M. and MARTINOIA, E., 2017. ABA-Induced stomatal closure involves ALMT4 a phosphorylation-dependent vacuolar anion channel of Arabidopsis. The Plant Cell, vol. 29, no. 10, pp. 2552-2569. http://dx.doi.org/10.1105/tpc.17.00452. PMid:28874508.

FINKELSTEIN, R., 2013. Abscisic acid synthesis and response. The Arabidopsis Book, vol. 11, pp. e0166. http://dx.doi.org/10.1199/tab.0166. PMid:24273463.

GAO, S., GAO, J., ZHU, X., SONG, Y., LI, Z., REN, G., ZHOU, X. and KUAI, B., 2016. ABF2, ABF3 and ABF4 promote ABA-mediated chlorophyll degradation and leaf senescence by transcriptional activation of chlorophyll catabolic genes and senescence-associated genes in Arabidopsis. Molecular Plant, vol. 9, no. 9, pp. 1272-1285. http://dx.doi.org/10.1016/j.molp.2016.06.006. PMid:27373216.
GNUTT, D., BRYLSKI, O., EDENGEISER, E., HAVENITH, M. and EBBINGHAUS, S., 2017. Imperfect crowding adaptation of mammalian cells towards osmotic stress and its modulation by osmolytes. *Molecular BioSystems*, vol. 13, no. 11, pp. 2218-2221. http://dx.doi.org/10.1039/C7MB00432J. PMID:28929156.

LEE, H.G., LEE, K. and SEO, P.J., 2015. The Arabidopsis MYB96 transcription factor plays a role in seed dormancy. *Plant Biochemistry*, vol. 87, no. 4-5, pp. 371-381. http://dx.doi.org/10.1007/s11103-015-0283-4. PMID:25561734.

LI, C., LIU, Z., ZHANG, Q., WANG, R., XIAO, L., MA, H., CHONG, K. and XU, Y., 2012. SKP1 is involved in abscisic acid signaling to regulate seed germination stomatal opening and root growth in *Arabidopsis thaliana*. *Plant, Cell & Environment*, vol. 35, no. 5, pp. 952-965. http://dx.doi.org/10.1111/j.1365-3040.2011.02464.x. PMID:22074111.

LITCHFIELD, D.W., 2003. Protein kinase CK2: structure regulation and role in cellular decisions of life and death. *The Biochemical Journal*, vol. 369, no. Pt 1, pp. 1-15. http://dx.doi.org/10.1042/bj20021469. PMID:12996231.

MA, Q., ZHOU, Q., CHEN, C., CUI, Q., ZHAO, Y., WANG, K., ARKORFUL, E., CHEN, X., SUN, K. and LI, X., 2019. Isolation and expression analysis of CsCML genes in response to abiotic stresses in the tea plant (*Camellia sinensis*). *Scientific Reports*, vol. 9, no. 1, pp. 8221. http://dx.doi.org/10.1038/s41598-019-44681-7. PMID:31160625.

MULEKAR, J.J., BU, Q., CHEN, F. and HUQ, E., 2012. Casein kinase II α subunits affect multiple developmental and stress-responsive pathways in Arabidopsis. *The Plant Journal*, vol. 69, no. 2, pp. 343-354. http://dx.doi.org/10.1111/j.1365-313X.2011.04794.x. PMID:21905772.

NAGATOSHI, Y., FUJITA, M. and FUJITA, Y., 2018. Casein kinase 2 α and β subunits inversely modulate ABA signal output in Arabidopsis protoplasts. *Planta*, vol. 248, no. 3, pp. 571-578. http://dx.doi.org/10.1007/s00425-018-2919-5. PMID:29799081.

OGISO, E., TAKAHASHI, Y., SASAKI, T., YANO, M. and IZAWA, T., 2010. The role of casein kinase II β in flowering time regulation has diversified during evolution. *Plant Physiology*, vol. 152, no. 2, pp. 808-820. http://dx.doi.org/10.1104/pp.110.149808. PMID:20007447.

OLESEN, S.H., INGLES, D.J., ZHU, J.Y., MARTIN, M.P., BETZI, S., GEORG, G.I., TASH, J.S. and SCHÖNBRUNN, E., 2015. Stability of the human Hsp90-p50Cdc37 chaperone complex in Arabidopsis protoplasts. *Planta*, vol. 20, no. 1, pp. 1643-1660. http://dx.doi.org/10.1007/molecules20011643. PMID:25680845.

PORTOLES, S. and MÁS, P., 2017. Altered oscillation function affects clock resonance and is responsible for the reduced day-length sensitivity of CKB4 overexpressing plants. *The Plant Journal*, vol. 51, no. 6, pp. 966-977. http://dx.doi.org/10.1111/j.1365-313X.2007.03186.x. PMID:17662034.

QIN, L.X., LI, L., LI, D.D., XU, W.L., ZHENG, Y. and LI, X.B., 2014. Arabidopsis drought-induced protein Di19-3 participates in plant response to drought and high salinity stresses. *Plant Molecular Biology*, vol. 86, no. 6, pp. 609-625. http://dx.doi.org/10.1007/s11103-014-0251-4. PMID:25218132.

REYES, J.L. and CHUA, N.H., 2007. ABA induction of miR159 controls transcript levels of two MYB factors during Arabidopsis seed germination. *The Plant Journal*, vol. 49, no. 4, pp. 592-606. http://dx.doi.org/10.1111/j.1365-313X.2006.02980.x. PMID:17217461.
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in Plant Science, vol. 10, pp. 630. http://dx.doi.org/10.3389/fpls.2019.00630. PMid:31156685.

WANG, Y., CHANG, H., SU, S., LU, X., YUAN, C., ZHANG, C., WANG, P., XIAO, W., XIAO, L., XUE, G.P. and GUO, X., 2014. Plastid casein kinase 2 knockout reduces abscisic acid (ABA) sensitivity and expression of ABA- and heat-stress-responsive nuclear genes. Journal of Experimental Botany, vol. 65, no. 15, pp. 4159-4175. http://dx.doi.org/10.1093/jxb/eru190. PMid:24803505.

WANI, S.H. and KUMAR, V., 2015. Plant stress tolerance: engineering ABA: a potent phytohormone. Transcriptomics, vol. 3, no. 2, pp. 1000113. http://dx.doi.org/10.4172/2329-8936.1000113.

XUANYUAN, G., LU, C., ZHANG, R. and JIANG, J., 2017. Overexpression of StNt-YB31 reduces photosynthetic capacity and tuber production and promotes ABA-mediated stomatal closure in potato (Solanum tuberosum L.). Plant Science, vol. 261, pp. 50-59. http://dx.doi.org/10.1016/j.plantsci.2017.04.015. PMid:28554693.

YOSHIDA, T., FUJITA, Y., MARUYAMA, K., MOGAMI, J., TODAKA, D., SHINOZAKI, K. and YAMAGUCHI-SHINOZAKI, K., 2015. Four Arabidopsis AREB/ABF transcription factors function predominantly in gene expression downstream of SnRK2 kinases in abscisic acid signalling in response to osmotic stress. Plant, Cell & Environment, vol. 38, no. 1, pp. 35-49. http://dx.doi.org/10.1111/pce.12351. PMid:24738645.

YUAN, C., AL, J., CHANG, H., XIAO, W., LIU, L., ZHANG, C., HE, Z., HUANG, J., LI, J. and GUO, X., 2017. CKB1 is involved in abscisic acid and gibberellic acid signaling to regulate stress responses in Arabidopsis thaliana. Journal of Plant Research, vol. 130, no. 3, pp. 587-598. http://dx.doi.org/10.1007/s10265-017-0924-6. PMid:28342111.

ZANDKARIMI, H., EBADI, A., SALAMI, S.A., ALIZADE, H. and BAISAKH, N., 2015. Analyzing the expression profile of AREB/ABF and DREB/CBF genes under drought and salinity stresses in grape (Vitis vinifera L.). PLoS One, vol. 10, no. 7, pp. e0134288. http://dx.doi.org/10.1371/journal.pone.0134288. PMid:26230273.

ZHANG, C., LI, H., YUAN, C., LIU, S., LI, M., ZHU, J., LIN, X., LU, Y. and GUO, X., 2020. CKB1 regulates expression of ribosomal protein L10 family gene and plays a role in UV-B response. Plant Biology, vol. 22, suppl. 1, pp. 143-152. http://dx.doi.org/10.1111/plb.12954. PMid:30597713.

ZHOU, Y., SUN, X., YANG, Y., LI, X., CHENG, Y. and YANG, Y., 2016. Expression of Stipa purpurea SpCIPK26 in Arabidopsis thaliana enhances salt and drought tolerance and regulates abscisic acid signaling. International Journal of Molecular Sciences, vol. 17, no. 6, pp. 966. http://dx.doi.org/10.3390/ijms17060966. PMid:27338368.