Table 1 Suppl. Gene specific primers along with respective references. * - stress inducible genes, ID – identification, Tm - melting temperature.

| Genes and their abbreviations | Primer sequences (5'-3') | Gene ID | Product length [bp] | Tm [°C] | Primer efficiency [%] | Regression coefficient ($R^2$) | Reference |
|---|---|---|---|---|---|---|---|
| Ubiquitin 2 (*UBQ2*) | F:ATGCAAATCTTTGTGAAGACCCTCAC<br>R:GTGATAGTCTTGCCAGTCAAGGTCTTG | HQ340170 | 269 | 61 | 81.38 | 0.989 | Brulle *et al*. (2014) |
| Histone 3 (*H3*) | F:GAAATTGCACAGGACTTCAAGACTGATC<br>R:AACCACTACTAACACTACGAACACATGCTTC | AF109910 | 250 | 59 | 106.47 | 0.965 | Li *et al*. (2016) |
| Alpha tubulin (*α-Tub*) | F:GTAGAACCATACAACAGTGTCCTCTCCAC<br>R:TGGAACTCAGTGACATCCACATTGATAG | MK123512 | 223 | 59 | 79.93 | 0.962 | Moraes *et al*. (2015); Reddy *et al*. (2016) |
| Beta tubulin (*β-Tub*) | F:GAACCTTACAATGCCACACTATCTGTCC<br>R:CGACCATGAAGAAATGGAGAAG | MK123513 | 268 | 59 | 93.07 | 0.995 | Moraes *et al*. (2015); Reddy *et al*. (2016) |
| Glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) | :CTTCTCTTCGGTGAGAAGGAGGTCAC<br>R:CTCCTTCTCATTGACACCAACAACAAAC | MK123514 | 213 | 59 | 80.47 | 0.998 | Pabuayon *et al*. (2016) |
| Eukaryotic initiation factor-4-alpha (*eIF4-α*) | F:CAGCAACTTGACTATGGATTGGTGGA<br>R:CATCCAGCACAAACATCTTAATGTGGTC | MK123515 | 270 | 63 | 104.44 | 0.969 | Gimeno *et al.* (2014) |
| Cyclophilin (*CYP*) | F:CTGAGAGGATCACATTTGAGCTGTTTG<br>R:CACCAGGTTGGTCATGCTTTAACTTG | MK123516 | 267 | 59 | 81.02 | 0.991 | Pabuayon *et al.* (2016) |
| Actin (*ACT*) | F:CTACCATGTTTCCTGGAATTGCTGATCG<br>R:TCAGAAGCACTTCATATGGACAATGCCAG | MK123517 | 249 | 59 | 105.35 | 0.989 | Pabuayon *et al*. (2016) |
| Alcohol dehydrogenase (*ADH*)* | F:GCATTCTGAGCTGTGGTATCTCTACTGG<br>R:TTACGAAGTCAGTGCAGCCAAACTTC | EU371995 | 216 | | - | - | Garg *et al*. (2013) |
| Dehydration-responsive element-binding protein 2A (*DREB2A*)* | F:TTCTGGTTTTGCTCCTTCCACC<br>R:ATGCTGTTTCGATTTGTGTCTTGC | KM349308.1 | 214 | | - | - | Sakuma *et al*. (2006) |

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Table 2 Suppl. Sequence information of PCR amplified genes from *Oryza coarctata* cDNA. For abbreviations of genes see Table 1 Suppl.

*>UBQ2*
CACCATTCGACAACGTCAAGGCCAAGATCCAGGACAAGGAGGGCATCCCCCCCGGACCAGCAGCGTCTCATCTTCGCTGGCAAGCAGCTT
GAGGATGGCCGCACCCTGGCTGACTACACATCCAGAAGGAGTCCACCCTCCACCTTGTGCTCAGGCTCAGGGGAGGCATGCAAATCTTCG
TCAAGACCTTGACTGGAAGAACTATCACA
*>H3*
CTCCAGGAAGCTTGCGGAGGCATACCTTGTTGGTCTCTTCGAGGACACCAACCTGTGCGCCATTCACGCCAAGCGCGTGACCATCATGCC
TAAGGACATTCAGCTGGCCAGGAGGATTCGTGGTGAGAGGGCTTAAGTTCCCCTCGATGATTCCTTTGACAAATGAAGCATGTGTTCGTA
GTGTTAGTAGTGGTTAA
*> α-Tub*
CAGTTCTCCTAGACAATCGAGGCTATCTATGACATATGCCGGAGATCCCTTGACATCGAGAGGCCAACCTACACCAACTTGAACAGGCTC
ATCTCACAGATCATATCTTCACTCACCACCTCCCTGAGGTTTGATGGCGCTATCAATGTGGATGTCACTGAGTTCCAA
*> β-Tub*
CTTGACAATGAAGCTCTATATGACATCTGCTTCCGCACTCTGAAGCTTGCGACACCCACCTTTGGTGATCTGAACCATCTTATTTCTGCAA
CCATGAGTGGCGTTACCTGCTGCCTGCGCTTCCCGGGACAGCTGAATTCTGACCTCCGCAAGCTTGCAGTCAACTTGATTCCCTTCCCTCG
TCTCCTTCTTTCCTGGTCGA
*>GAPDH*
GACTCCACTCATGGTCCGTTTAAGGTTCCATTAAGGTTGTTGGATGATTCAATCCCTGGAGATCAATGGAAAGAAAGTCACAATCACTAG
CAAAAGAGATCCTGCAGATATTCCTTGGGGTAACTTTGGAGCTGAGTATGTTGTTGAATCTTCAGGTGTA
*> eIF4-α*
AGCTTGCCCAGCAAATTGAAAAGGTCATGCGTGCTCTTGGGGACTACTTAGGTGTCAAGGTGCATGCCTGTGTTGGTGGAACATCTGTTC
GTGAGGACCAAAGGATTCTTGCTAGTGGCGTGCATGTTGTTGTTGGCACACCTGGACGTGTGTTTGATATGCTTCGCCGTCTATCTCTCCT
CCCATACTACATTAAATCTTTGTGCTGGATGACTCCCCCCCTCCCTATTCTTTT
*> CYP*
TTCCGGGCTCTCTGCACCGGTGAGAGAGGCCTCGGAGTATCCACACAAAAGTCACTTCATTATAAGCGAACAAACATGCATCGCATTTTG
AAAGGTTTTATGGCTCAGGGTGGTGATTTTTCAAGAGGAGATGGACGTGGTGGAGAGAGCATATATGGTGCAAAATTTGAAGATGAAAA
CTTCAAGTTAAAGCATGCCCAACCTGGTGA
*> ACT*
AGCAGTATGAAGGTTAAAGTGATTGCACCACCAGAAAGAAAATACAGTGTCTGGATTGGTGGTTCTATTTTGGCTTCTCTGAGCACTTTC
CAGCAGATGTGGATCTCCAAGGGCGAGTATGATGAATCTGGTCCTGGCATTGTCCATATAGTGCTTCTGAA
*> Adh*
AAAAGGCCAAGACAGTGGCTATTTTTCCGGTTTGGAAGCTGTTGGCCTTGCTGCTATGGAAGGTGCCAGGCTGTCTGGAGCATCAGAAGG
GAATCATTGGTGTGGACCTGAACCCTGCAAATTCGAACAAGCTAAGAAGTTTGGCTGCCTGACTTCGTAAAAGCATT
*> DREB2A*
ATGCTGTTTCGATTTGTGTCTTGCAATGTTCAGCTTTGTGGAATTATTGAGTTACCTCATTGGGTCAGGA
AGAAGAGGACGCGAAGGAAAAGCGATGGCCCTGATTCAATCACTGAAACCATCAAGTGGTGGAAGGAGCA
AAACCAGAA

Table 3 Suppl. Sequence validation of an amplified PCR product from *Oryza. coarctata* with *O. sativa*. For abbreviations of genes see Table 1 Suppl.

| Serial number | Genes | *BLASTN* identity [%] | E-value |
|---|---|---|---|
| 1 | *UBQ2* | 99 | 4.3e-91 |
| 2 | *H3* | 98 | 3.1e-92 |
| 3 | *α-Tub* | 99 | 9.6e-77 |
| 4 | *β-Tub* | 99 | 4.3e-76 |
| 5 | *GAPDH* | 99 | 1.0e-65 |
| 6 | *eIF4-α* | 90 | 5.0e-86 |
| 7 | *CYP* | 99 | 1.2e-86 |
| 8 | *ACT* | 99 | 1.2e-70 |
| 9 | *Adh* | 96 | 1.3e-55 |
| 10 | *DREB2A* | 100 | 7.0e-76 |

Table 4 Suppl. Rank orders of eight selected reference genes from *Oryza coarctata* based upon their expression stability value determined by the *delta Ct* method. For abbreviations of genes see Table 1 Suppl.

| Gene order | Cold | | Heat | | Drought | | Salinity | | Submergence | | ABA treatment | | Dual stress | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Gene | SD | gene | SD | gene | SD | Gene | SD | gene | SD | gene | SD | gene | SD |
| 1 | *H3* | 1.18 | *ACT* | 1.56 | *β-Tub* | 1.16 | *ACT* | 1.64 | *β-Tub* | 1.34 | *H3* | 1.65 | *β-Tub* | 1.08 |
| 2 | *α-Tub* | 1.18 | *CYP* | 1.70 | *eIF4-α* | 1.17 | *eIF4-α* | 1.65 | *ACT* | 1.53 | *ACT* | 1.73 | *eIF4-α* | 1.21 |
| 3 | *β-Tub* | 1.22 | *eIF4-α* | 1.73 | *CYP* | 1.19 | *UBQ2* | 2.03 | *H3* | 1.58 | *CYP* | 1.81 | *α-Tub* | 1.30 |
| 4 | *ACT* | 1.27 | *UBQ2* | 1.85 | *ACT* | 1.29 | *β-Tub* | 2.16 | *CYP* | 1.60 | *β-Tub* | 1.87 | *H3* | 1.50 |
| 5 | *eIF4-α* | 1.35 | *GAPDH* | 1.85 | *H3* | 1.36 | *H3* | 2.20 | *α-Tub* | 1.69 | *GAPDH* | 1.95 | *ACT* | 1.53 |
| 6 | *GAPDH* | 1.51 | *α-Tub* | 1.97 | *α-Tub* | 1.37 | *GAPDH* | 2.30 | *GAPDH* | 1.70 | *eIF4-α* | 2.14 | *GAPDH* | 1.66 |
| 7 | *CYP* | 1.60 | *β-Tub* | 1.99 | *UBQ2* | 1.86 | *α-Tub* | 2.47 | *eIF4-α* | 1.77 | *UBQ2* | 2.46 | *UBQ2* | 1.69 |
| 8 | *UBQ2* | 1.65 | *H3* | 2.27 | *GAPDH* | 1.89 | *CYP* | 2.70 | *UBQ2* | 2.07 | *α-Tub* | 2.49 | *CYP* | 1.73 |

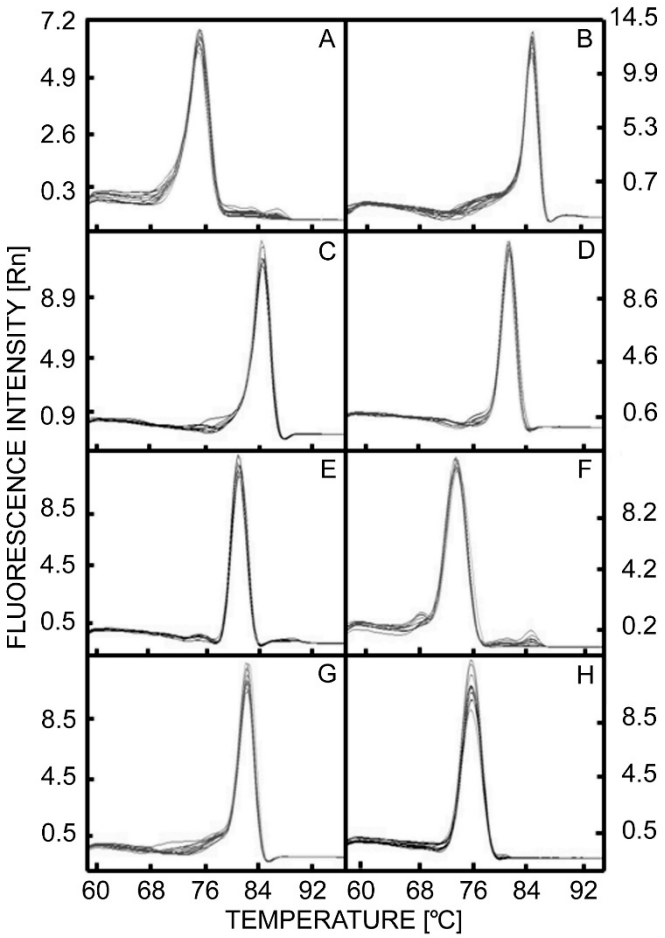


Fig. 1 Suppl. Melting curve analysis in real time quantitative PCR. Dissociation curves showing single peaks for each primer pair: *UBQ2* (*A*), *H3* (*B*), *α-Tub* (*C*), *β-Tub* (*D*), *GAPDH* (*E*), *eIF4-α* (*F*), *CYP* (*G*), and *ACT* (*H*). For abbreviations of genes see Table 1 Suppl.