Table 1 Suppl. List of RT-qPCR primers used in this study. Protein ID according to the *Phytozome* database or Genbank accession number (*).

| Gene name | Protein ID | Sequence | |
|---|---|---|---|
| *S*-adenosylmethionine synthetase family | Glyma15g21890.1 | forward | 5'-GTGCTTCTGGAAGTTAAAATGG-3' |
| | | reverse | 5'-TGATCTCTCCGAAAACCATC-3' |
| *S*-adenosylmethionine synthetase 1 | Glyma03g38190.3 | forward | 5'-GACTGGCAGTATATCCAGTTACAG-3' |
| | | reverse | 5'- GATGCAAAAGAAGGGTGAT-3' |
| *S*-adenosylmethionine synthetase 2 | Glyma19g40810.1 | forward | 5'-CTGCTTCTTCAGCTTGAGAAATG-3' |
| | | reverse | 5'-CAAAGACCATGACCATGTTGG-3' |
| ACC synthase | Glyma18g47280.1 | forward | 5'-CCTTAGACTCAGCTTCTCCAAC-3' |
| | | reverse | 5'-TCCTGTATATGTGGACCGCA-3' |
| ACC oxidase | Glyma05g36310.1 | forward | 5'-GGAAATTCGGTTGACCATT-3' |
| | | reverse | 5'-CAAAGATGGAGATCCCTGTGATA-3' |
| 18S rRNA | X02623.1* | forward | 5'-TGATTAACAGGGACAGTCGG-3' |
| | | reverse | 5'-ACG GTA TCT GAT CGT CTT CG-3' |

Table 2 Suppl. List of 3 proteins commonly identified in 2-d-flooded soybean and 2-d-drought stressed soybean compared to control 2-d-old soybean. Protein ID, according to the *Phytozome* database; M.P. - number of matched peptide; Ratio - relative abundance of protein; 4(2) F - 4-d-old soybean treated with flooding for 2 d; 4(2) D - 4-day-old soybean treated with drought for 2 d. These proteins were identified by Oh and Komatsu (2015).

| Protein ID | Description | M.P. | Ratio 4(2) F | *P*-value 4(2) F | Ratio 4(2) D | *P*-value 4(2) D |
|---|---|---|---|---|---|---|
| Glyma15g21890.1 | *S*-adenosylmethionine synthetase family | 4 | 0.4175 | 0.0127 | 9.0403 | 0.0383 |
| Glyma03g38190.3 | *S*-adenosylmethionine synthetase 1 | 3 | 0.4185 | 0.0213 | 10.6780 | 0.0101 |
| Glyma19g40810.1 | *S*-adenosylmethionine synthetase 2 | 3 | 0.4185 | 0.0213 | 10.6780 | 0.0101 |

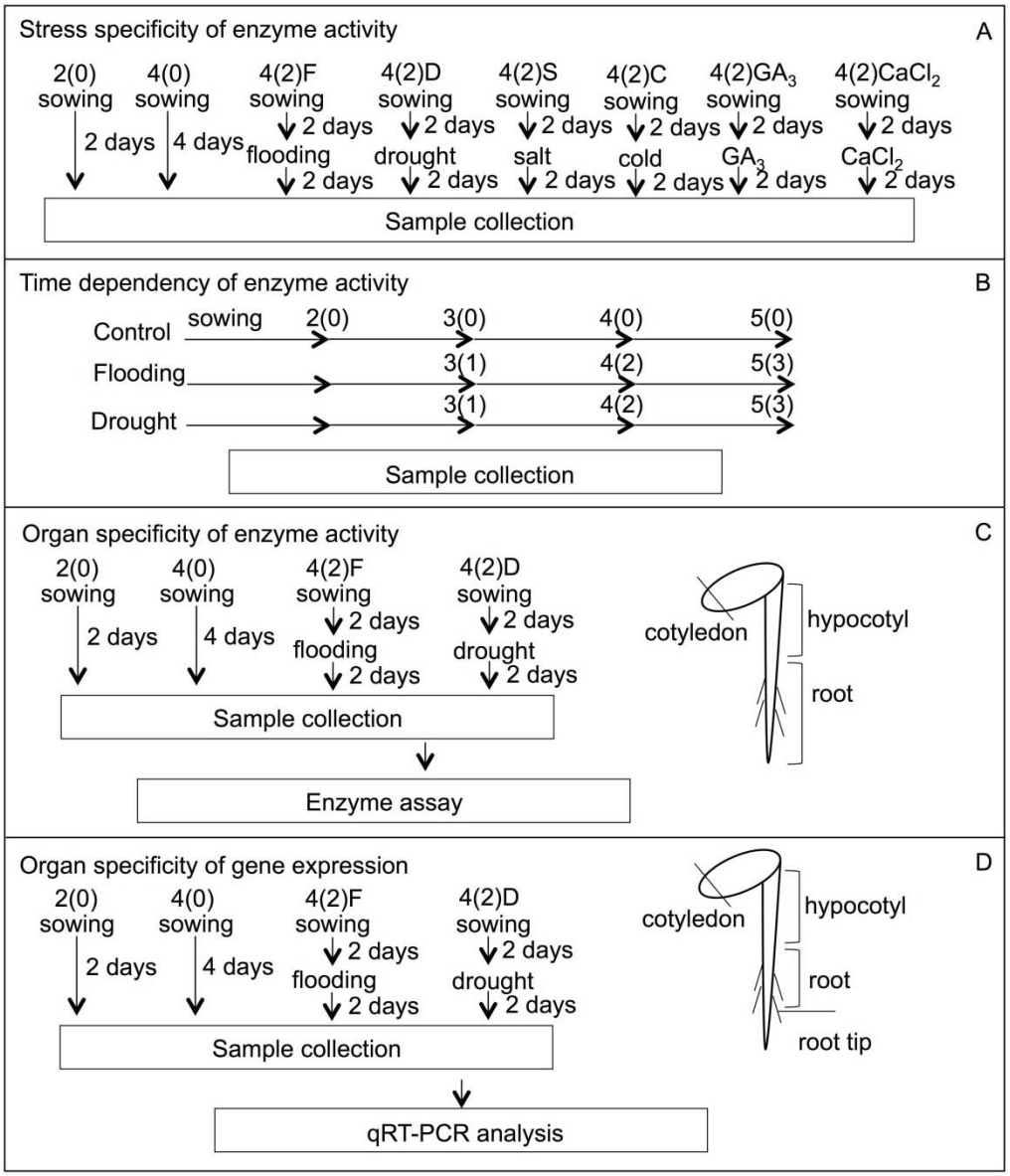


Fig. 1 Suppl. Experimental workflow of this study. To examine stress-specific enzyme activity, 2-d-old soybeans were treated with flooding, drought, salt, cold, $GA_3$, or $CaCl_2$ for 2 d, and then root was collected (*A*). To investigate temporal changes in enzyme activity, 2-d-old soybeans were treated with flooding or drought for 1, 2, and 3 d, and then root was collected (*B*). To examine organ specificity of enzyme activity, 2-d-old soybeans were treated with flooding or drought for 2 d, and then root, hypocotyl, and cotyledon were collected (*C*). To examine organ specificity of gene expression, 2-d-old soybeans were treated with flooding or drought for 2 d, and root tip, root, hypocotyl, and cotyledon were collected (*D*). Three independent experiments were performed as biological replicates.

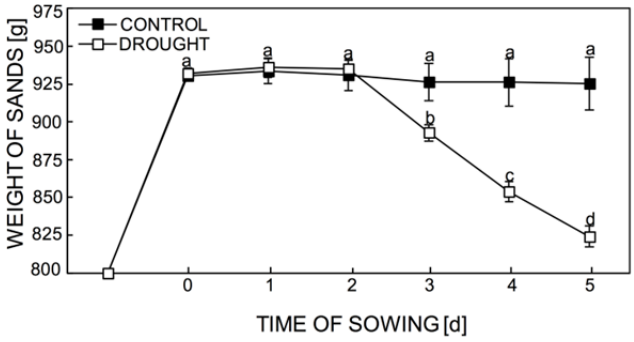


Fig. 2 Suppl. Reduction of the sand mass under drought stress. In this study, silica sands (800 g) was used in a plastic case (180 × 140 × 45 mm) and 150 $cm^3$ of water was added (0 day). Additional 50 $cm^3$ of water was supplied to maintain the normal condition for soybean for next 2 d. For control, 50 $cm^3$ water was supplied on days 3, 4 and 5; for drought, water was withheld for 3 d. All the plastic cases were kept in growth chamber under irradiamce of 160 μmol $m^{-2}$ $s^{-1}$, 16-h photoperiod, and a temperature of 25 °C. Data are shown as means ± SD from 3 independent biological replicates. Means with different letters indicate significant changes according to Duncan's multiple comparison test ($P < 0.05$).

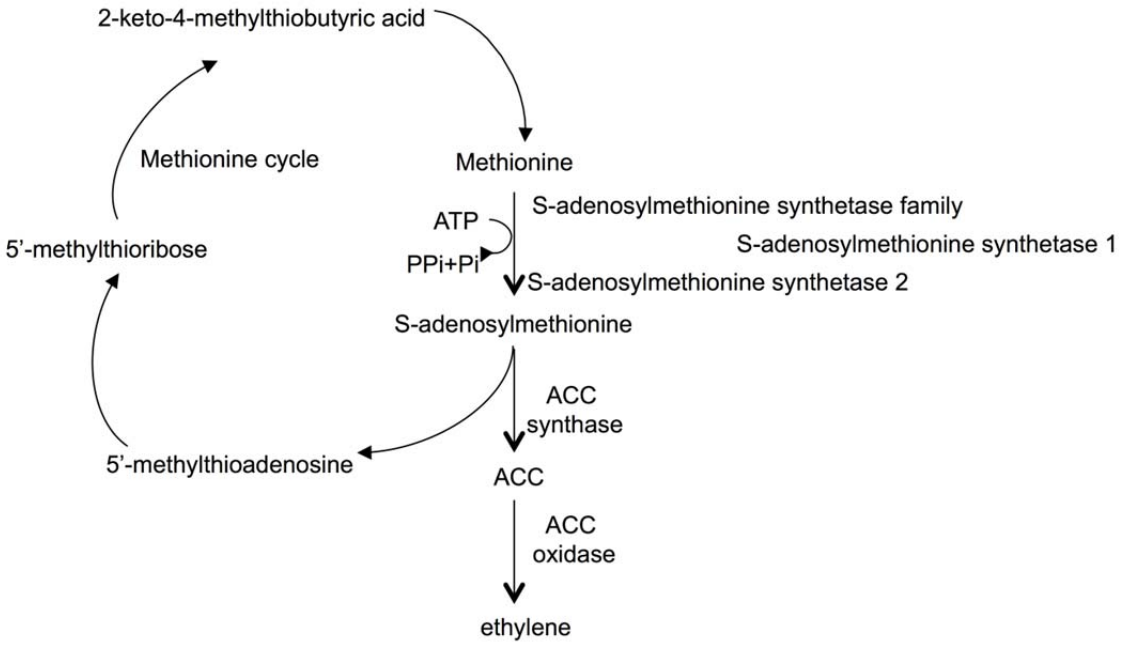


Fig. 3 Suppl. Pathway of ethylene biosynthesis. *S*-adenosylmethionine synthetase converts methionine to *S*-adenosylmethionine which is further converted into ACC by ACC synthase. Ethylene is converted from ACC by ACC oxidase (Wang *et al*. 2002).

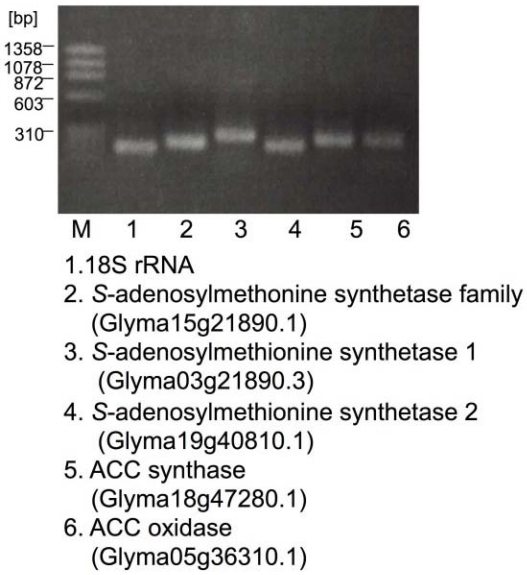


Fig. 4 Suppl. Agarose gel electrophoresis of RT-qPCR products obtained with the primers listed in Table 1 Suppl. They were visualized in agarose gel stained by ethidium bromide. M indicates marker.