

Table 1. Range analysis of the  $L_9(3)^4$  test results for the plant height.

Variable	Temperature	Photoperiod	GA <sub>3</sub>	BA
K <sub>1</sub>	<b>26.92</b>	<b>27.31</b>	20.43	26.23
K <sub>2</sub>	25.02	26.27	28.27	25.48
K <sub>3</sub>	26.71	25.08	<b>29.96</b>	<b>26.94</b>
R	1.90	2.23	<b>9.53</b>	1.47
Optimal level	23/17°C	8 h	100 mg·L <sup>-1</sup>	100 mg·L <sup>-1</sup>

Table 2. Range analysis of the  $L_9(3)^4$  test results for the petiole length.

Variable	Temperature	Photoperiod	GA <sub>3</sub>	BA
K <sub>1</sub>	<b>17.94</b>	<b>18.49</b>	12.96	17.36
K <sub>2</sub>	15.98	17.08	18.65	14.48
K <sub>3</sub>	17.32	15.68	<b>19.63</b>	<b>17.41</b>
R	1.96	2.81	<b>6.67</b>	2.93
Optimal level	23/17°C	8 h	100 mg·L <sup>-1</sup>	100 mg·L <sup>-1</sup>

Table 3. Range analysis of the  $L_9(3)^4$  test results for the leaf length.

Variable	Temperature	Photoperiod	GA <sub>3</sub>	BA
K <sub>1</sub>	8.98	8.69	7.42	8.91
K <sub>2</sub>	8.94	9.19	9.54	8.94
K <sub>3</sub>	<b>9.29</b>	<b>9.34</b>	<b>10.26</b>	<b>9.37</b>
R	0.35	0.65	<b>2.84</b>	0.46
Optimal level	23/17°C	8 h	100 mg·L <sup>-1</sup>	100 mg·L <sup>-1</sup>

Table 4. Range analysis of the  $L_9(3)^4$  test results for the leaf width.

Variable	Temperature	Photoperiod	GA <sub>3</sub>	BA
K <sub>1</sub>	<b>7.07</b>	6.27	6.07	6.55
K <sub>2</sub>	6.62	6.86	6.79	6.63
K <sub>3</sub>	6.58	<b>7.15</b>	<b>7.41</b>	<b>7.09</b>
R	0.49	0.88	<b>1.34</b>	0.54
Optimal level	23/17°C	16 h	100 mg·L <sup>-1</sup>	100 mg·L <sup>-1</sup>

Table 5. Range analysis of the  $L_9(3)^4$  test results for the runner length.

Variable	Temperature	Photoperiod	GA <sub>3</sub>	BA
K <sub>1</sub>	<b>27.89</b>	19.01	11.27	12.11
K <sub>2</sub>	20.04	20.92	19.79	26.23
K <sub>3</sub>	21.67	<b>29.68</b>	<b>38.55</b>	<b>31.26</b>

R	7.84	10.67	<b>27.29</b>	19.16
Optimal level	23/17°C	12 h	100 mg·L <sup>-1</sup>	100 mg·L <sup>-1</sup>

Table 6. Range analysis of the L<sub>9</sub>(3)<sup>4</sup> test results for the chlorophyll content.

Variable	Temperature	Photoperiod	GA <sub>3</sub>	BA
K <sub>1</sub>	35.43	36.54	<b>43.42</b>	37.38
K <sub>2</sub>	37.04	38.64	32.99	<b>38.44</b>
K <sub>3</sub>	<b>41.68</b>	<b>38.97</b>	37.74	38.33
R	6.26	2.43	<b>11.42</b>	1.06
Optimal level	23/17°C	8 h	100 mg·L <sup>-1</sup>	100 mg·L <sup>-1</sup>

Table 7. Range analysis of the L<sub>9</sub>(3)<sup>4</sup> test results for the soluble sugar content.

Variable	Temperature	Photoperiod	GA <sub>3</sub>	BA
K <sub>1</sub>	5.19	4.09	<b>7.45</b>	4.76
K <sub>2</sub>	<b>5.37</b>	<b>6.16</b>	4.28	<b>5.91</b>
K <sub>3</sub>	5.22	5.53	4.05	5.11
R	0.18	2.07	<b>3.40</b>	1.16
Optimal level	25/15°C	12 h	0 mg·L <sup>-1</sup>	50 mg·L <sup>-1</sup>

Table 8. Range analysis of the L<sub>9</sub>(3)<sup>4</sup> test results for the starch content.

Variable	Temperature	Photoperiod	GA <sub>3</sub>	BA
K <sub>1</sub>	1.74	1.63	<b>2.08</b>	1.60
K <sub>2</sub>	1.73	<b>1.85</b>	1.64	<b>1.95</b>
K <sub>3</sub>	<b>1.84</b>	1.83	1.59	1.76
R	0.12	0.23	<b>0.49</b>	0.35
Optimal level	27/13°C	12 h	0 mg·L <sup>-1</sup>	50 mg·L <sup>-1</sup>

The greatest values for K and R are expressed in bold. The equation used was  $R = \max\{K_i^X\} - \min\{K_i^X\}$ , where  $K_i^X$  is the average of the following variables: photoperiod, temperature, GA<sub>3</sub> and 6-BA, at the 1, 2, and 3 levels;  $X$  represents the photoperiod, temperature, GA<sub>3</sub>, or 6-BA; and  $i$  is 1, 2, or 3.

Table 9. GO classification of the DEPs identified in this study.

Spot no.	protein name	GO annotation		
		Biological Process	Molecular Function	Cellular Component
1	Catalase-like	Hydrogen peroxide catabolic process; oxidation-reduction process	Metal ion binding; oxidation-reduction process	Peroxisome
2	Annexin D1-like	acetyl-CoA metabolic process; polysaccharide transport; brassinosteroid biosynthetic process;	Calcium ion binding; calcium-dependent phospholipid binding;	Cytosol; thylakoid; cell surface; apoplast
3	Malate dehydrogenase, cytoplasmic-like	Response to cold	L-malate dehydrogenase activity	Mitochondrion; vacuolar membrane; chloroplast stroma; chloroplast envelope; apoplast
4	Chaperone protein ClpB1-like	Protein folding; response to high light intensity; heat acclimation; response to endoplasmic reticulum stress; response to hydrogen peroxide; protein unfolding; positive regulation of translation	Protein binding; ATP binding; ATPase activity	Chloroplast stroma; chloroplast envelope
5	Transcription factor bHLH135-like		Protein dimerization activity	—
6	Probable protein disulfide-isomerase A6-like	Oxidation-reduction process	Naringenin 3-dioxygenase activity	—
7	Probable mitochondrial-processing peptidase subunit beta-like	Proteolysis	Metalloendopeptidase activity; metal ion binding	—
8	Glucose-6-phosphate 1-Dehydrogenase, cytoplasmic isoform 2-like	Pentose-phosphate shunt, oxidative branch	Glucose-6-phosphate dehydrogenase activity	Cytosol
9	Sucrose synthase 2-like	Cytokinesis by cell plate formation; response to hypoxia; starch metabolic process; sucrose biosynthetic process; N-terminal protein myristoylation; cell-cell signaling; meristem initiation; vegetative phase change; meristem maintenance;	Sucrose synthase activity	Nucleus; cytosol; chloroplast
10	Coenzyme Q-binding protein COQ10 homolog, mitochondrial-like	Aromatic amino acid family metabolic process; oxidation-reduction process	4-hydroxyphenylpyruvate dioxygenase activity	—

11	Monodehydroascorbate reductase-like	Glucosinolate biosynthetic process; hydrogen peroxide catabolic process; response to cadmium ion	Monodehydroascorbate reductase (NADH) activity	Peroxisomal membrane; chloroplast envelope;
12	Fumarylacetoacetase-like	Tyrosine catabolic process; cell death; chlorophyll catabolic process; homogentisate catabolic process	Fumarylacetoacetase activity	Cytosol
13	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	Photorespiration; oxidation-reduction process	Magnesium ion binding; monooxygenase activity; ribulose-bisphosphate carboxylase activity	Chloroplast
14	(3S,6E)-nerolidol synthase 2, chloroplastic/mitochondrial OS	Terpenoid biosynthetic process	Magnesium ion binding; terpene synthase activity;	Mitochondrion; chloroplast
16	Probable calcium-binding protein CML45- like	—	—	—
17	Flavanone 3-hydroxylase	Oxidation-reduction process	Naringenin 3-dioxygenase activity	—
19	Chaperone protein ClpC, Chloroplastic- like	Proteolysis	ATP binding; peptidase activity; nucleoside- triphosphatase activity	Chloroplast
20	Glucan endo-1,3-beta-glucosidase	Carbohydrate metabolic process	Hydrolase activity, hydrolyzing O-glycosyl compounds	—
23	26S protease regulatory subunit 6B homolog	—	—	—
24	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	Carbon fixation; photosynthesis;	Magnesium ion binding; ribulose-bisphosphate carboxylase activity	Chloroplast
25	Putative lactoylglutathione lyase-like isoform 2	Gluconeogenesis; glycolytic process; response to salt stress	Lactoylglutathione lyase activity; calmodulin binding; metal ion binding	Cytosol
28	Chaperonin CPN60-2, mitochondrial-like	Response to stress; protein refolding	ATP binding	Mitochondrion
29	Chalcone-flavonone isomerase-like	Response to sucrose; response to UV-B; response to karrikin	—	Chloroplast
31	Major allergen Pru ar 1-like	Defense response; response to biotic stimulus	—	—
32	Pathogenesis-related protein 1C-like	—	—	Extracellular region

Table 10. KEGG classification of the DEPs identified in this study.

#Pathway	ko ID	Unigene	gene	Unigene all	Spot no.
Ascorbate and aldarate metabolism	ko00053	1	1	10	11
Carbon fixation in photosynthetic organisms	ko00710	3	3	10	13;24;3
Carbon metabolism	ko01200	4	4	10	13;24;3;8
Citrate cycle (TCA cycle)	ko00020	1	1	10	3
Phosphatidylinositol signaling system	ko04070	1	1	10	16
Glutathione metabolism	ko00480	1	1	10	8
Tyrosine metabolism	ko00350	1	1	10	12
Starch and sucrose metabolism	ko00500	1	1	10	9
Glyoxylate and dicarboxylate metabolism	ko00630	3	3	10	13;24;3
RNA degradation	ko03018	1	1	10	28
Protein processing in endoplasmic reticulum	ko04141	1	1	10	6
Plant-pathogen interaction	ko04626	1	1	10	16
Pentose phosphate pathway	ko00030	1	1	10	8
Pyruvate metabolism	ko00620	1	1	10	3
Cysteine and methionine metabolism	ko00270	1	1	10	3

Table 11. COG classification of DEPs identified in this study.

#Gene name	Protein ID in COG	E value	Identity	Score	COG id	COG class definition	Function code	Functional categories	Function class definition
1	gi 449088034 ref YP_007420475.1	3.00E-171	504	504	COG0753	Catalase	[P]	Metabolism	Inorganic ion transport and metabolism
3	gi 121997621 ref YP_001002408.1	5.00E-116	352	352	COG0039	Malate/lactate dehydrogenase	[C]	Metabolism	Energy production and conversion

4	gi 269926323 ref YP_003322946.1	0	870	870	COG0542	ATP-dependent Clp protease ATP-binding subunit ClpA	[O]	Cellular processes and signaling	Posttranslational modification, protein turnover, chaperones
6	gi 20807685 ref NP_622856.1	2.00E-26	112	112	COG3118	Negative regulator of GroEL	[O]	Cellular processes and signaling	Posttranslational modification, protein turnover, chaperones
7	gi 392382816 ref YP_005032013.1	3.00E-94	305	305	COG0612	Predicted Zn-dependent peptidase	[R]	Poorly characterized	General function prediction only
8	gi 383452925 ref YP_005366914.1	3.00E-123	384	384	COG0364	Glucose-6-phosphate 1-dehydrogenase Glycosyltransferase involved in cell wall bisynthesis	[G]	Metabolism	Carbohydrate transport and metabolism
9	gi 292493898 ref YP_003529337.1	0	880	880	COG0438	Ribosome association toxin PasT (RatA) of the RatAB toxin-antitoxin module	[M]	Cellular processes and signaling	Cell wall/membrane/envelope biogenesis
10	gi 414343662 ref YP_006985183.1	2.00E-25	107	107	COG2867	NADPH-dependent 2	[J]	Information storage and processing	Translation, ribosomal structure and biogenesis
11	gi 116622785 ref YP_824941.1	9.00E-63	219	219	COG0446	Ribulose 1	[I]	Metabolism	Lipid transport and metabolism
13	gi 434391829 ref YP_007126776.1	0	812	812	COG1850	Isopenicillin N synthase and related dioxygenases	[G]	Metabolism	Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
17	gi 470176812 ref YP_007562856.1	8.00E-14	77.8	77.8	COG3491	ATP-dependent Clp protease ATP-binding subunit ClpA	[Q]	Metabolism	Posttranslational modification, protein turnover, chaperones
19	gi 158335106 ref YP_001516278.1	0	1189	1189	COG0542		[O]	Cellular processes and signaling	

23	gi 11499558 ref NP_070800.1	7.00E-122	374	374	COG1222	ATP-dependent 26S proteasome regulatory subunit	[O]	Cellular processes and signaling	Posttranslational modification, protein turnover, chaperones
24	gi 434391829 ref YP_007126776.1	0	798	798	COG1850	Ribulose 1	[G]	Metabolism	Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
25	gi 17545239 ref NP_518641.1	1.00E-49	171	171	COG0346	Catechol 2	[Q]	Metabolism	Carbohydrate transport and metabolism Secondary metabolites biosynthesis, transport and catabolism
28	gi 389877554 ref YP_006371119.1	0	690	690	COG0459	Chaperonin GroEL (HSP60 family)	[O]	Cellular processes and signaling	Posttranslational modification, protein turnover, chaperones
32	gi 427726216 ref YP_007073493.1	5.00E-31	123	123	COG2340	Uncharacterized conserved protein YkwD	[S]	Poorly characterized	Function unknown