Identification of a Pale Green Mutant *pgm3* in Chinese Cabbage (*Brassica rapa* L. ssp. *pekinensis*)

Yonghui Zhao [1], Ruonan Li [1], Zixian Song [1], Ruitong Zhang [1], Yuxuan Bai [1], Wei Fu [1] and Hui Feng [2,*]

[1] College of Life Science, Shenyang Normal University, Shenyang 110034, China; zhaoyonghui2020@163.com (Y.Z.); ruonan324@163.com (R.L.); songzixian2026@126.com (Z.S.); zhangru1t@163.com (R.Z.); yuxuan_bai1213@163.com (Y.B.); fu260242@126.com (W.F.)
[2] College of Horticulture, Shenyang Agricultural University, Shenyang 110866, China
* Correspondence: fenghuiaaa@syau.edu.cn



Figure S1. Phenotypic characterization of *pgm3* and FT in Chinese cabbage.

(a) Seedling stage of wide-type FT. (b) Seedling stage of *pgm3*. (c) Heading stage of wide-type FT. (d) Heading stage of *pgm3* (right). (e) Bolting stage of wide-type FT (left) and *pgm3* (right).

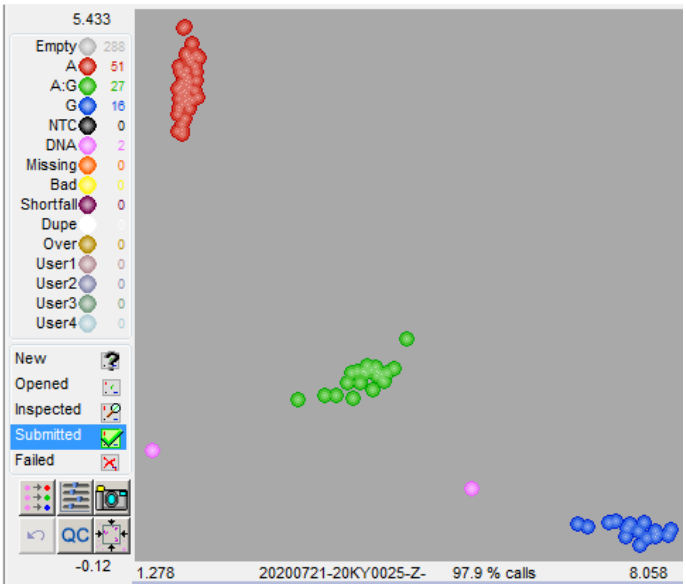


Figure S2. F_2 individuals genotype detecting by KASP (Part of results)

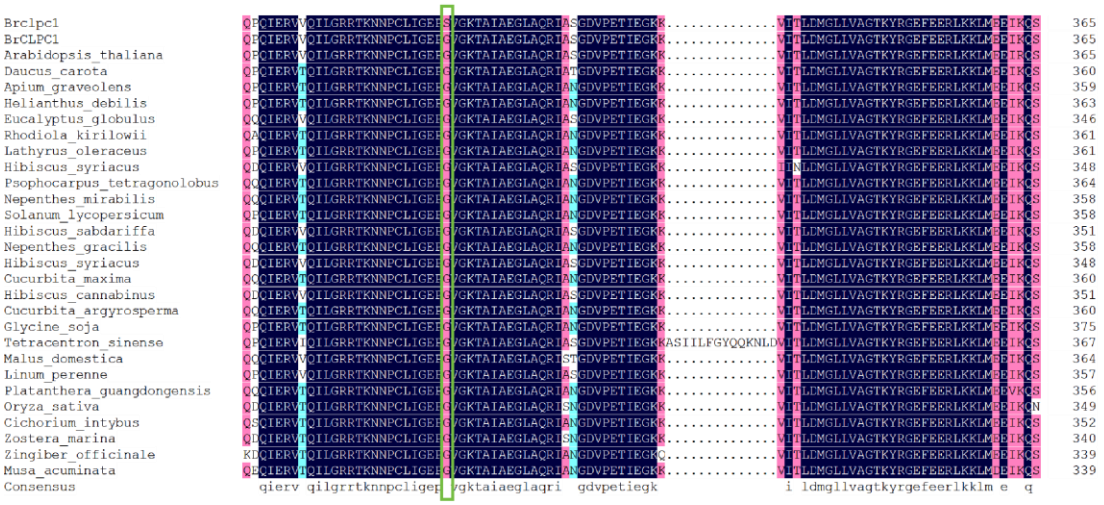


Figure S3. Sequence alignment of ClpC1 homologs in 28 species and the protein mutation site of Brclpc1.

The species name and accession numbers of the 28 ClpC1 homologs were as follows: Arabidopsis thaliana (NP_568746.1:1-929); Daucus carota (KAL1814551.1:895-1810); Apium graveolens (KAL8117524.1:537-1452); Helianthus debilis (KAM0018808.1:199-1117); Eucalyptus globulus (KAL3716243.1:973-1868); Rhodiola kirilowii (CAM8912608.1:3-913); Lathyrus oleraceus (NP_001413787.1:3-913); Hibiscus syriacus (KAE8663359.1:13-913); Psophocarpus tetragonolobus (KAK7410991.1:170-1092); Nepenthes mirabilis (CAM9034212.1:109-1022); Solanum lycopersicum (NP_001332862.1:6-914); Hibiscus sabdariffa (KAK9045732.1:237-1146); Nepenthes gracilis (GMH26129.1:274-1187); Hibiscus syriacus (KAE8710628.1:13-920); Cucurbita maxima (XP_022987153.1:833-1751); Hibiscus cannabinus (KAL4280681.1:218-1127); Cucurbita argyrosperma (KAG6589342.1:582-1500); Glycine soja (KAL5192233.1:3-936); Tetracentron sinense (KAF8408479.1:24-939); Malus domestica (KAM1209418.1:1-914); Linum perenne (CAN1790541.1:75-987); Platanthera guangdongensis (KAK8937784.1:8-913); Oryza sativa Japonica Group (NP_001406239.1:11-909); Cichorium intybus (KAI3766082.1:463-1364); Zostera marina (KMZ65741.1:23-916); Zingiber officinale (XP_042419867.1:25-922); Musa acuminata (XP_009404743.2:24-917).

Table S1. Primer sequence for KASP

Marker	Allele primer -F1	Allele primer -F2	Common primer
Kasp-1	GAAGGTCGGAGTCAACG	GAAGGTGACCAAGTTCATG	TGTCCTTACCT
	GATTAACCCATGTCTTATT	CTCCCATGTCTTATTGGAGA	TCTTCCCTTCA
	GGAGAACCTA	ACCTG	ATA

Table S2. Primer sequence for gene clone

Marker	Forward sequence (5′-3′)	Reverse sequence (5′-3′)
BrClpC1-CDS	ATGGCTATGGCCACAAGGGTG	ATGGCTATGGCCACAAGGGTG
BrClpC1-FL-1	CCACAAGGGTGATGTCTCAATAT	ATCGTTTCATCCACAGTAGGCTC
BrClpC1-FL-2	GGAGCGACAACATTAGACGAAT	TCAAGCAACGGGGAGAGAAT

Table S3. Primer sequence for qRT-PCR

Marker	Forward sequence (5′-3′)	Reverse sequence (5′-3′)
Actin	ATCTACGAGGGTTATGCT	CCACTGAGGACGATGTTT
BrClpC1-qRT	CTGGTCCTACCGGTGTCGG	CTGTGTAAGGGCGGCGTCT

Table S4. Chloroplast features of FT and *pgm3* in Chinese cabbage

Feature	FT	*pgm3*
Length of chloroplast	70.74 ± 3.68 *	54.42 ± 6.67
Width of chloroplast	9.97 ± 0.59	10.63 ± 1.57
Number of starch granules	3.6 ± 1.62	5.8 ± 2.93
Area of starch granules	7.37 ± 2.39 *	1.24 ± 0.44

Note: The '*' represents significant differences at 5% levels at t-test.

Table S5. KASP Sequencing results of A03: 7194530

Number	Sample ID	Phenotype	Genotype-SNP A03: 7194530
1	FT	Wild-type	G:G
2	FT	Wild-type	G:G
3	*Pgm3*	Mutated	A:A
4	*Pgm3*	Mutated	A:A
5	F_1	Wild-type	G:A
6	F_1	Wild-type	G:A
7	F_2-w1	Wild-type	G:A
8	F_2-w2	Wild-type	G:G
9	F_2-w3	Wild-type	G:A
10	F_2-w4	Wild-type	G:G
11	F_2-w5	Wild-type	G:A
12	F_2-w6	Wild-type	G:A
13	F_2-w7	Wild-type	G:G
14	F_2-w8	Wild-type	G:A
15	F_2-w9	Wild-type	G:A
16	F_2-w10	Wild-type	G:A
17	F_2-w11	Wild-type	G:A
18	F_2-w12	Wild-type	G:G
19	F_2-w13	Wild-type	G:A
20	F_2-w14	Wild-type	G:G
21	F_2-w15	Wild-type	G:G
22	F_2-w16	Wild-type	G:A
23	F_2-w17	Wild-type	G:A
24	F_2-w18	Wild-type	G:G
25	F_2-w19	Wild-type	G:A
26	F_2-w20	Wild-type	G:A
27	F_2-w21	Wild-type	G:A
28	F_2-w22	Wild-type	G:A
29	F_2-w23	Wild-type	G:G
30	F_2-w24	Wild-type	G:A
31	F_2-w25	Wild-type	G:A
32	F_2-w26	Wild-type	G:G
33	F_2-w27	Wild-type	G:A
34	F_2-w28	Wild-type	G:A
35	F_2-w29	Wild-type	G:G
36	F_2-w30	Wild-type	G:A
37	F_2-w31	Wild-type	G:G
38	F_2-w32	Wild-type	G:G
39	F_2-w33	Wild-type	G:G
40	F_2-w34	Wild-type	G:A
41	F_2-w35	Wild-type	G:G
42	F_2-w36	Wild-type	G:A

43	F_2-w37	Wild-type	G:G
44	F_2-w38	Wild-type	G:A
45	F_2-w39	Wild-type	G:A
46	F_2-w40	Wild-type	G:A
47	F_2-w41	Wild-type	G:A
49	F_2-1	Mutated	A:A
50	F_2-2	Mutated	A:A
51	F_2-3	Mutated	A:A
52	F_2-4	Mutated	A:A
53	F_2-5	Mutated	A:A
54	F_2-6	Mutated	A:A
55	F_2-7	Mutated	A:A
56	F_2-8	Mutated	A:A
57	F_2-9	Mutated	A:A
58	F_2-10	Mutated	A:A
59	F_2-11	Mutated	A:A
60	F_2-12	Mutated	A:A
61	F_2-13	Mutated	A:A
62	F_2-14	Mutated	A:A
63	F_2-15	Mutated	A:A
64	F_2-16	Mutated	A:A
65	F_2-17	Mutated	A:A
66	F_2-18	Mutated	A:A
67	F_2-19	Mutated	A:A
68	F_2-20	Mutated	A:A
69	F_2-21	Mutated	A:A
70	F_2-22	Mutated	A:A
71	F_2-23	Mutated	A:A
72	F_2-24	Mutated	A:A
73	F_2-252	Mutated	A:A
74	F_2-6	Mutated	A:A
75	F_2-27	Mutated	A:A
76	F_2-28	Mutated	A:A
77	F_2-29	Mutated	A:A
78	F_2-30	Mutated	A:A
79	F_2-31	Mutated	A:A
80	F_2-32	Mutated	A:A
81	F_2-33	Mutated	A:A
82	F_2-34	Mutated	A:A
83	F_2-35	Mutated	A:A
84	F_2-36	Mutated	A:A
85	F_2-37	Mutated	A:A
86	F_2-38	Mutated	A:A
87	F_2-39	Mutated	A:A

88	F_2-40	Mutated	A:A
89	F_2-41	Mutated	A:A
90	F_2-42	Mutated	A:A
91	F_2-43	Mutated	A:A
92	F_2-44	Mutated	A:A
93	F_2-45	Mutated	A:A
94	F_2-46	Mutated	A:A
95	F_2-47	Mutated	A:A
96	F_2-48	Mutated	A:A
97	F_2-49	Mutated	A:A
98	F_2-50	Mutated	A:A
99	F_2-51	Mutated	A:A
100	F_2-52	Mutated	A:A
101	F_2-53	Mutated	A:A
102	F_2-54	Mutated	A:A
103	F_2-55	Mutated	A:A
104	F_2-56	Mutated	A:A
105	F_2-57	Mutated	A:A
106	F_2-58	Mutated	A:A
107	F_2-59	Mutated	A:A
108	F_2-60	Mutated	A:A
109	F_2-61	Mutated	A:A
110	F_2-62	Mutated	A:A
111	F_2-63	Mutated	A:A
112	F_2-64	Mutated	A:A
113	F_2-65	Mutated	A:A
114	F_2-66	Mutated	A:A
115	F_2-67	Mutated	A:A
116	F_2-68	Mutated	A:A
117	F_2-69	Mutated	A:A
118	F_2-70	Mutated	A:A
119	F_2-71	Mutated	A:A
120	F_2-72	Mutated	A:A
121	F_2-73	Mutated	A:A
122	F_2-74	Mutated	A:A
123	F_2-75	Mutated	A:A
124	F_2-76	Mutated	A:A
125	F_2-77	Mutated	A:A
126	F_2-78	Mutated	A:A
127	F_2-79	Mutated	A:A
128	F_2-80	Mutated	A:A
129	F_2-81	Mutated	A:A
130	F_2-82	Mutated	A:A
130	F_2-83	Mutated	A:A

131	F_2-84	Mutated	A:A
132	F_2-85	Mutated	A:A
133	F_2-86	Mutated	A:A
134	F_2-87	Mutated	A:A
135	F_2-88	Mutated	A:A
136	F_2-89	Mutated	A:A
137	F_2-90	Mutated	A:A
138	F_2-91	Mutated	A:A
139	F_2-92	Mutated	A:A
140	F_2-93	Mutated	A:A
141	F_2-94	Mutated	A:A
142	F_2-95	Mutated	A:A
143	F_2-96	Mutated	A:A
144	F_2-97	Mutated	A:A
145	F_2-98	Mutated	A:A
146	F_2-99	Mutated	A:A
147	F_2-100	Mutated	A:A
148	F_2-101	Mutated	A:A
149	F_2-102	Mutated	A:A
150	F_2-103	Mutated	A:A
151	F_2-104	Mutated	A:A
152	F_2-105	Mutated	A:A
153	F_2-106	Mutated	A:A
154	F_2-107	Mutated	A:A
155	F_2-108	Mutated	A:A
156	F_2-109	Mutated	A:A
157	F_2-110	Mutated	A:A
158	F_2-111	Mutated	A:A
159	F_2-112	Mutated	A:A
160	F_2-113	Mutated	A:A
161	F_2-114	Mutated	A:A
162	F_2-115	Mutated	A:A
163	F_2-116	Mutated	A:A
164	F_2-117	Mutated	A:A
165	F_2-118	Mutated	A:A
166	F_2-119	Mutated	A:A
167	F_2-120	Mutated	A:A
168	F_2-121	Mutated	A:A
169	F_2-122	Mutated	A:A
170	F_2-123	Mutated	A:A
171	F_2-124	Mutated	A:A
172	F_2-125	Mutated	A:A
173	F_2-126	Mutated	A:A
174	F_2-127	Mutated	A:A

175	F_2-128	Mutated	A:A
176	F_2-129	Mutated	A:A
177	F_2-130	Mutated	A:A
178	F_2-131	Mutated	A:A
179	F_2-132	Mutated	A:A
180	F_2-133	Mutated	A:A
181	F_2-134	Mutated	A:A
182	F_2-135	Mutated	A:A
183	F_2-136	Mutated	A:A
184	F_2-137	Mutated	A:A
185	F_2-138	Mutated	A:A
186	F_2-139	Mutated	A:A
187	F_2-140	Mutated	A:A
188	F_2-141	Mutated	A:A
189	F_2-142	Mutated	A:A
190	F_2-143	Mutated	A:A