Barley Genetics Newsletter

Volume 46 - 2016

Editorial Committee
P. Bregitzer - U. Lundqvist - V. Blake

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<<Information about the Barley Genetics Newsletter>>

The Barley Genetics Newsletter is published electronically at
https://wheat.pw.usda.gov/ggpages/bgn

The Barley Genetics Newsletter (BGN) was first published in 1971, and in the years since then has served to disseminate to the barley community announcements, memoria, informal research reports, and detailed descriptions of barley genetic stocks.

In recent years, new forms of rapid communication of ideas and data, principally on-line, have reduced the demand for many aspects of BGN. At the 12th International Barley Genetics Symposium, held in Minneapolis, Minnesota, USA June 26-30, 2016, discussion of the fate of BGN resulted in the consensus that a forum for informal communication, memoria, documentation of resources, and any other topic of interest to the community was beneficial.

Thanks to resources provided by GrainGenes, past issues of BGN will be preserved and available in electronic format. GrainGenes will serve also as a mechanism for publishing new submissions from the barley community.

Contributions to the Barley Genetics Newsletter can be sent to Phil Bregitzer, phil.bregitzer@ars.usda.gov. Dr. Bregitzer can be reached also at 208-397-4162 ext. 116.

Acknowledgements

BGN has been made possible by the contributors of research reports, the diligence of the many coordinators, and by the special efforts of leaders in the barley genetics community. Of special note, the compilation of the detailed and extensive new and updated barley genetic stock descriptions published in the last several issues of BGN has been made possible by the time and expertise of Jerry Franckowiak and Udda Lundqvist. Special thanks to the USDA-ARS GrainGenes team.

Barley Genetics Newsletter (2016) 46:1-3.

Descriptions of Barley Genetic Stocks for 2016

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In this volume of the Barley Genetics Newsletter, fifty revised and new Barley Genetic Stock (BGS) descriptions are published (Table 1). The current lists of new and revised BGS descriptions, including those in Table 1, are presented by BGS number order (Table 2) and by locus symbol in alphabetic order (Table 3) in another section of this issue. Information on the description location, recommended locus name, chromosomal location, previous gene symbols, and the primary genetic stock (GSHO number and/or NGB number) are included in these lists. The GSHO stocks are held in the USDA-ARS Barley Genetic Stocks collection at the National Small Grains Collection (U.S. Department of Agriculture – Agricultural Research Service, National Small Grains Germplasm Research Facility, 1691 S 2700 W) Aberdeen, ID 83210, USA. The NGB stocks are held in the Nordic Genetic Resource Center (NordGen), Smedjevägen 3, SE-230 53 Alnarp, Sweden. This information is available through the Internet at the following addresses:

(1) www.ars.usda.gov.PacWest/Aberdeen

(2) www.ars-grin.gov:7000/npgs/descriptors/barley-genetics (GRIN)

(3) http://wheat.pw.usda.gov/ggpages/bgn/

(4) http:/www.nordgen.org/sesto

(5) http://www.nordgen.org/bgs

Table 1. A listing of new and revised Barley Genetic Stock (BGS) descriptions published in volume 46 of the Barley Genetics Newsletter, giving recommended locus symbols and names, chromosomal locations, and stock source information.

BGS no.	Locus symbol*		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
30	ert-m	ert-m	7HS	Erectoides-m	46: 47	487
33	ant1	rs, rub-a	7HS	Anthocyanin-less 1	46: 49	1620
45	sdw4		7HL	Semidwarf 4	46: 51	
76	Pre2	Re2, P	2HL	Red lemma and Pericarp 2	46: 53	234
80	ant2	pr, rub	2HL	Anthocyanin-less 2	46: 55	1632
98	Eam6	Ea6, Ea	2HS	Early maturity 6	46: 57	
106	abo6	a_c	3HS	Albino seedling 6	46: 60	30
108	alm1	al, ebu-a	3HS	Albino lemma 1	46: 61	270
117	fch2	f2, lg5	3HL	Chlorina seedling 2	46: 63	107
202	trd1	t, bra-c	1HL	Third outer glume 1	46: 65	227
203	Blp1	B	1HL	Black lemma and pericarp 1	46: 67	988
214	eam8	$ea_{k,}$ mat-a	1HL	Early maturity 8	46: 69	765
221	wst5	wst5	1HL	White streak 5	46: 73	591
235	lel1	lel	2H	Leafy lemma 1	46: 74	1780
239	sci-b	sci-4	1H/6H	Scirpoides-b	46: 76	
240	sdw6	sdw.f	1H/7H	Semidwarf 6	46: 77	2449
254	rob1	o, rob-o	6HS	Orange lemma 1	46: 78	707
262	cur1	cu1	3HL	Curly 1	46: 81	1705
304	wst2	wst2	5HL	White streak 2	46: 83	766
312	raw1	r	5HL	Smooth awn 1	46: 84	27
321	srh1	s, l	5HL	Short rachilla hair	46: 86	27
323	nld1	nld	5HL	Narrow leafed dwarf 1	46: 88	769
326	blf1	bb	5HL	Broad leaf 1	46: 90	1393
340	raw2	r2	5HL	Smooth awn 2	46: 92	27
351	gsh1	gs1, cer-q	2HS	Glossy sheath 1	46: 94	735
352	gsh2	gs2, cer-b	3HL	Glossy sheath 2	46: 98	736
356	gsh6	gs6, cer-c	2HS	Glossy sheath 6	46:101	740
413	gsh8	cer-u, gs8	2HS	Glossy sheath 8	46:105	442
439	cer-zv	cer-zv	4HL	Eceriferum-zv	46:109	1529
441	cer-zx	cer-zx	3H	Eceriferum-zx	46:111	1531
453	fer1	fer1		Few roots 1	46:112	2538
474	lax-a	lax-a	5HL	Laxatum-a	46:113	1775
525	cer-yl	cer-yl	4HL	Eceriferum-yl	46:116	1545
526	cer-ym	cer-ym	4HL	Eceriferum-ym	46:118	1546

Table 1 continued

BGS no.	Locus symbol*		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
557	ari-p	ari-p		Breviaristatum-p	46:120	1664
562	ert-k	ert-k	6H	Erectoides-k	46:121	485
578	mat-b	mat-b	7HL	Praematurum-b	46:123	1788
579	mat-c	mat-c	2H	Praematurum-c	46:125	1789
599	ant17	ant17	3HS	Anthocyanin-free 17	46:128	1628
608	ant28	ant28	3HL	Anthocyanin-free 28	46:131	
617	cul4	uc-5, uc-3	3HL	Uniculme 4	46:132	2495
663	sdw3	gai	2HS	Semidwarf 3	46:134	
716	ibl1	ibl1	5HL	Intense blue aleurone 1	46:136	
730	lab1	lab1	5HL	Labile 1	46:137	
731	rpr2	γ08-118; R43-22#1	6H	Required for *Puccinia graminis resistance* 2	46:139	3693
732	rpr3	γ08-118; R43-22#3		Required for *Puccinia graminis resistance* 3	46:141	3696
733	rpr4	γ08-114; R36-37#1		Required for *Puccinia graminis resistance* 4	46:142	3697
734	rpr5	γ08-117; R42-33#5		Required for *Puccinia graminis resistance* 5	46:143	3699
735	rpr6	γ08-119; R47-23#1		Required for *Puccinia graminis resistance* 6	46:144	3700
736	rpr7	γ08-115; R3-18#3		Required for *Puccinia graminis resistance* 7	46:145	3701

* Recommended locus symbols are based on utilization of a three letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996.

[†] Chromosome numbers and arm designations are based on a resolution passed at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

[‡] The seed stock associated with each BGS number is held as a GSHO stock number in the Barley Genetics Stock Collection at the USDA-ARS National Grains Germplasm Research Facility, Aberdeen, Idaho, USA.

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Descriptions of Barley Genetic Stocks
Tables 2 and 3 (2016).

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In this section of the Barley Genetics Newsletter, you will find two updated tables with new and revised barley locus descriptions. The descriptions are listed by BGS numbers (Table 2) and by alphabetic order using the existing and recommended locus symbols (Table 3). As research in barley is proceeding rapidly, it is necessary to update the latest research and findings about specific barley genes.

Table 2. A listing of Barley Genetic Stock (BGS) descriptions in recent issues of the Barley Genetics Newsletter with recommended locus symbols, recommended locus names, chromosome location information, description citation, and stock location information.

Table 3. An alphabetic listing of recently published Barley Genetic Stock (BGS) descriptions for loci in barley (*Hordeum vulgare*), including information on recommended locus names, recommended locus symbols, chromosomal locations, description citation, and original cultivars.

Table 2. A listing of Barley Genetic Stock (BGS) descriptions in recent issues of the Barley Genetics Newsletter with recommended locus symbols, recommended locus names, chromosome location information, description citation, and stock location information.

BGS no.	Locus symbol[*]		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
1	brh1	br, ari-i	7HS	Brachytic 1	43: 48	25
2	fch12	f_c, clo-fc	7HS	Chlorina seedling 12	41: 60	36
3	yvs2	y_c	7HS	Virescent seedling 2	26: 46	41
4	abo8	a_{c2}, alb-m	7HS	Albino seedling 8	26: 47	61
5	fch8	f8	7HS	Chlorina seedling 8	41: 62	40
6	vrs1	v, Int-d	2HL	Six-rowed spike 1	37:192	196
7	nud1	n, h	7HL	Naked caryopsis 1	44: 51	115
9	dsp1	l	7HS	Dense spike 1	43: 50	1232
10	lks2	lk2, lk4	7HL	Short awn 2	45: 80	566
11	ubs4	lks2, ari-d	7HL	Unbranched style 4	45: 84	567
12	des1	lc	7H	Desynapsis 1	42: 58	592
13	des4	des4	7H	Desynapsis 4	44: 54	595
14	des5	des5	7HL	Desynapsis 5	44: 56	596
15	blx1	bl	4HL	Non-blue aleurone xenia 1	26: 60	185
16	wax1	wx, glx	7HS	Waxy endosperm 1	42: 65	908
17	fch4	f4, yv	7HL	Chlorina seedling 4	43: 54	1214
18	fch5	f5, yv2	7HS	Chlorina seedling 5	43: 56	1215
19	blx2	bl2	7HS	Non-blue aleurone xenia 2	26: 65	209
20	Rym2	Ym2	7HL	Reaction to BaYMV 2	26: 66	984
21	Run1	Un	7HS	Reaction to *Ustilago nuda* 1	26: 67	1324
22	Rsg1	Grb	7H	Reaction to *Schizaphis graminum* 1	37:199	1317
23	wnd1	wnd	4HL	Winding dwarf 1	42: 74	2499
24	fst3	fs3	7HS	Fragile stem 3	41: 74	1746
25	Xnt1	X_a	7HL	Xantha seedling 1	26: 71	1606
26	snb1	sb	7HS	Subnodal bract 1	26: 72	1217
27	lbi3	lb3	7HL	Long basal rachis internode 3	42: 79	536
28	ert-a	ert-a	7HS	Erectoides-a	41: 76	468
29	ert-d	ert-d	7HS	Erectoides-d	42: 82	475
30	ert-m	ert-m	7HS	Erectoides-m	46: 47	487
31	sex6	ssIIa	7HS	Shrunken endosperm xenia 6	45: 86	2476
32	Rph9	Pa9, Pa12	5HL	Reaction to *Puccinia hordei* 9	37:201	1601
33	ant1	rs, rub-a	7HS	Anthocyanin-less 1	46: 49	1620

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
34	msg50	msg,,hm	7HL	Male sterile genetic 50	45: 88	2404
35	rsm1	sm	7HS	Reaction to BSMV 1	26: 84	2492
36	xnt4	x_{c2}	7HL	Xantha seedling 4	26: 85	42
37	xnt9	xan,,i	7HL	Xantha seedling 9	26: 86	584
38	smn1	smn	3H/5H	Seminudoides 1	43: 58	1602
39	mss2	mss2	7HS	Midseason stripe 2	44: 59	2409
40	prm1	prm	7HS	Premature ripe 1	44: 60	2429
41	brh7	brh.w	7H	Brachytic 7	42: 98	1687
42	Pyr1	Pyr.g,Pyr.i	3HL	Pyramidatum 1	41: 78	1581
43	mov1	mo5	7HL	Multiovary 1	43: 59	3641
44	brh16	brh.v,ari-o	7HL	Brachytic 16	45: 89	1686
45	sdw4		7HL	Semidwarf 4	46: 51	
48	Rpt4	QRpt7	7HL	Reaction to *Pyrenophora teres* 4	43: 61	
49	sld8	sld.i	7HS/4HL	Slender dwarf 8	43: 63	2484
51	rtt1	rt	2HS	Rattail spike 1	26: 87	216
52	fch15	or	2HS	Chlorina seedling 15	40: 48	49
53	abo2	a2	2HS	Albino seedling 2	26: 89	70
55	fch1	f, lg	2HS	Chlorina seedling 1	40: 49	112
56	wst4	wst4	2HL	White streak 4	44: 61	568
57	eog1	e, lep-e	2HL	Elongated outer glume 1	43: 64	29
58	vrs1	lr, v^{lr}	2HL	Six-rowed spike 1	26: 94	153
59	gpa1	gp, gp2	2HL	Grandpa 1	45: 91	1379
60	lig1	li, aur-a	2HL	Liguleless 1	45: 93	6
61	trp1	tr	4HL	Triple awned lemma 1	41: 82	210
62	sbk1	sk, cal-a	2HS	Subjacent hood 1	40: 51	267
63	yvs1	y_x, alb-c.7	2HS	Virescent seedling 1	26: 99	68
64	des7	des7	3H	Desynapsis 7	43: 67	598
65	Eam1	Ppd-H1, Ea	2HS	Early maturity 1	44: 64	1316
66	vrs1	V^d	2HL	Two-rowed spike 1	26:103	346
67	vrs1	V^t	2HL	Deficiens 1	26:104	684
68	Pvc 1	P_c	2HL	Purple veined lemma 1	44: 67	132
69	Gth 1	G	2HL	Toothed lemma 1	44: 68	309
70	Rph1	Pa	2H	Reaction to *Puccinia hordei* 1	26:107	1313
71	com2	bir2	2HS	Compositum 2	45: 95	1700

Table 2. (continued)

BGS no.	Locus symbol[*]		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
74	flo-c	flo-a	6HL	Extra floret-c	45: 97	1743
75	Lks1	Lk	2HL	Awnless 1	41: 84	44
76	Pre2	Re2, P	2HL	Red lemma and pericarp 2	46: 53	234
77	hcm1	h	2HL	Short culm 1	26:113	2492
78	mtt4	mtt,,e, mt	2HL	Mottled leaf 4	41: 86	1231
79	wst7	rb	2HL	White streak 7	41: 87	247
80	ant2	pr, rub	2HL	Anthocyanin-less 2	46: 55	1632
81	gsh7	gs7	1H/2H /5H	Glossy sheath 7	40: 55	1759
82	Zeo1	Knd, Ert-r	2HL	Zeocriton 1	41: 89	1613
83	sld2	sld2	2HS	Slender dwarf 2	44: 74	2491
84	mss1	mss	5H	Midseason stripe 1	44: 75	1404
85	yst4	yst4	2HL	Yellow streak 4	44: 76	2502
86	fch13	f13	5HL	Chlorina seedling 13	44: 77	16
87	fch14	f14	2HL	Chlorina seedling 14	44: 78	1739
88	Rph2	Pa2, A	5HS	Reaction to *Puccinia hordei* 2	37:212	1593
89	ari-g	ari-g, lk10	2H	Breviaristatum-g	44: 79	1655
90	ert-j	ert-j	2H	Erectoides-j	43: 70	484
91	ert-q	ert-q	6H	Erectoides-q	43: 71	1562
92	ert-u	br5, ari-o	7HL	Erectoides-u	45:100	496
93	ert-zd	br7, ari-o	7HL	Erectoides-zd	45:102	504
94	abo4	a4	2H	Albino seedling 4	26:133	167
95	abo13	alb,,p	2HL	Albino seedling 13	26:134	585
96	Rph15	Rph16	2HS	Reaction to *Puccinia hordei* 15	37:214	1586
97	acr1	acr	2HL	Accordion rachis 1	40: 56	1617
98	Eam6	Ea6, Ea	2HS	Early maturity 6	46: 57	
99	lin1	s, rin	2HL	Lesser internode number 1	41: 92	2492
100	sld4	sld.d	2HS	Slender dwarf 4	43: 72	2479
101	als1	als	3HL	Absent lower laterals 1	43: 74	1065
102	uzu1	u, *HvBRI1*	3HL	Uzu 1 or semi brachytic 1	45:104	1300
104	yst1	yst, ys	3HS	Yellow streak 1	42:178	1140
105	xnt3	x_c, vir-l	3HS	Xantha seedling 3	26:139	66
106	abo6	a_c	3HS	Albino seedling 6	46: 60	30
107	wst1	wst, wst3	3HL	White streak 1	41: 97	159
108	alm1	al, ebu-a	3HS	Albino lemma 1	46: 61	270
109	yst2	yst2	3HS	Yellow streak 2	44: 81	570

Table 2. (continued)

BGS no.	Locus symbol[*]		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
111	dsp10	l_c	3HL	Dense spike 10	41: 99	71
112	abo9	a_n	3HS	Albino seedling 9	26:146	348
113	xnt6	x_s	3HS	Xantha seedling 6	26:147	117
114	cur2	cu2	3HL	Curly 2	44: 82	274
115	btr1	bt1	3HS	Non-brittle rachis 1	43: 78	1233
116	btr2	bt2	3HS	Non-brittle rachis 2	43: 80	842
117	fch2	f2, lg5	3HL	Chlorina seedling 2	46: 63	107
118	lnt1	rnt, int-l	3HL	Low number of tillers 1	43: 82	833
119	des2	ds	3H	Desynapsis 2	43: 84	593
120	zeb1	zb	3HL	Zebra stripe 1	43: 86	1279
121	Rph3	Pa3	7HL	Reaction to *Puccinia hordei* 3	26:156	1316
122	Rph5	Pa5, Pa6	3HS	Reaction to *Puccinia hordei* 5	37:224	1597
123	Ryd2	Yd2	3HL	Reaction to BYDV 2	26:158	1315
124	vrs4	mul, int-e	3HL	Six-rowed spike 4	41:101	775
125	lzd1	dw4	3H	Lazy dwarf 1	43: 87	1787
126	sld1	dw1	3HL	Slender dwarf 1	41:103	2488
127	Pub1	Pub	3HL	Pubescent leaf blade 1	44: 84	1576
128	sca1	sca	3HS	Short crooked awn 1	44: 85	2439
129	wst6	wst,,j	3HL	White streak 6	41:105	2500
130	eam10	ea_{sp}	3HL	Early maturity 10	44: 86	2504
131	gra-a	gran-a	7H	Granum-a	44: 88	1757
132	ari-a	ari-a, lk7	3HS	Breviaristatum-a	41:106	1648
133	sdw2	sdw-b	3HL	Semidwarf 2	45:108	2466
134	ert-c	ert-c	3HL	Erectoides-c	41:108	471
135	ert-ii	uzu1	3HL	Erectoides-ii	45:104	483
136	Rph7	Pa7, Pa5	3HS	Reaction to *Puccinia hordei* 7	37:228	1318
137	Rph10	Rph10	3HL	Reaction to *Puccinia hordei* 10	26:174	1588
138	nec4	nec4	3H	Necrotic leaf spot 4	43: 88	
139	nec5	nec5	3H	Necrotic leaf spot 5	43: 89	
140	xnt8	xan,,h	3HS	Xantha seedling 8	26:177	582
141	rym5	Ym	3HL	Reaction to barley yellow mosaic virus 5	32: 90	
142	brh8	brh.ad	3HL	Brachytic 8	42:232	1671
143	sex8	sex.j	3HS	Shrunken endosperm xenia 8	43: 90	2471
144	sld5	sld5	3HS	Slender dwarf 5	44: 90	2483
146	cal-d	cal-d	3H	Calcaroides-d	40: 58	1698

Table 2. (continued)

BGS no.	Locus symbol[*]		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
147	mov2	mo	3HS	Multiovary 2	43: 91	3642
148	brh14	brh.q,ari-o	7HL	Brachytic 14	45:111	1682
149	Rpc1		3H	Reaction to *Puccinia coronata* var. *hordei* 1	37:232	1601
150	scl-b	scl-5	3H/6H	Scirpoides leaf-b	40: 60	
151	fch9	f9	4HS	Chlorina seedling 9	44: 92	571
152	Kap1	K	4HS	Hooded lemma 1	26:179	985
155	glf1	gl, cer-zh	4HL	Glossy leaf 1	40: 61	98
156	lbi2	lb2, ert-i	4HS	Long basal rachis internode 2	44: 93	572
157	brh2	br2, ari-l	4HL	Brachytic 2	44: 95	573
158	yhd1	yh	4HL	Yellow head 1	42:250	574
160	min2	en-min		Enhancer of minute 1	26:186	266
161	min1	min	4HL	Semi-minute dwarf 1	44: 97	987
163	sgh1	sh1	4HL	Spring growth habit 1	26:188	575
164	Hln1	Hn	4HL	Hairs on lemma nerves 1	44: 99	576
165	glf3	gl3, cer-j	4HL	Glossy leaf 3	43: 92	577
166	msg25	msg,,r	4HL	Male sterile genetic 25	45:113	744
167	rym1	Ym	4HL	Reaction to barley yellow mosaic virus 1	32: 96	
168	glo-a	glo-a	4H	Globosum-a	45:115	1328
169	lgn2	lg2	4HS	Light green 2	42:264	171
170	lgn3	lg3, lg7	1HL	Light green 3	44:103	171
171	lgn4	lg4, lg1	4HL	Light green 4	44:105	681
172	lks5	lk5, ari-c	4HL	Short awn 5	41:110	1297
173	blx3	bl3	4HL	Non-blue aleurone xenia 3	26:198	2506
174	blx4	bl4	4HL	Non-blue (pink) aleurone xenia 4	26:199	2507
176	ovl1	ovl	4H	Ovaryless 1	35:191	
177	fch10		4H	Chlorina seedling 10	43: 95	1737
178	int-c	i, v5	4HS	Intermedium spike-c	37:237	776
179	Hsh1	Hs	4HL	Hairy leaf sheath 1	44:107	986
180	sid1	nls	4HL	Single internode dwarf 1	43: 97	2477
181	eam9	ea,,c	4HL	Early maturity 9	26:204	1732
182	flo-a	flo-a	6HL	Extra floret-a	45:116	1741
183	Ynd1	Yn	4HS	Yellow node 1	44:109	1607
184	Zeo3	Zeo.h	4HL	Zeocriton 3	32: 99	1611
185	brh5	brh.m	4HS	Brachytic 5	44:110	1678

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
186	sld3	ant17.567	4HS	Slender dwarf 3	40: 63	2480
187	brh9	brh.k	4HL	Brachytic 9	43: 99	1676
189	Acr2	Acr, lax	4HL	Accordion rachis 2	40: 65	1071
190	tfm1		1HL	Thick filament 1	40: 67	
191	fch17	vy	1H/3H	Chlorina seedling 17	40: 68	1079
193	viv-b	viv-6	4HS	Viviparoides-b	43:100	
194	sld7	sld.f	4HL	Slender dwarf 7	43:101	2481
195	sex9	sex.l	4HL	Shrunken endosperm xenia 9	43:102	2473
196	sdw7	sdw.u	4HL	Semidwarf 7	43:103	2462
197	nec34	nec.k	4HS	Necroticans 34	43:104	
198	Rpt8	QRpts4	4HS	Reaction to *Pyrenophora teres* 8	43:105	
201	fch7	f7, clo-f7	1HL	Chlorina seedling 7	41:113	4
202	trd1	t, bra-c	1HL	Third outer glume 1	46: 65	227
203	Blp1	B	1HL	Black lemma and pericarp 1	46: 67	988
207	abo1	a_t	1HL	Albino seedling 1	26:210	51
208	fst2	fs2	1HL	Fragile stem 2	41:114	578
213	Sgh3	Sh3	1HL	Spring growth habit 3	26:212	764
214	eam8	ea_k, mat-a	1HL	Early maturity 8	46: 69	765
215	des6	des6	1HL/ 5HL	Desynapsis 6	43:106	597
218	Rph4	Pa4	1HS	Reaction to *Puccinia hordei* 4	42:302	1314
220	fch3	f3	1HS	Chlorina seedling 3	40: 71	851
221	wst5	wst5	1HL	White streak 5	46: 73	591
222	nec1	sp,,b	1HL	Necrotic leaf spot 1	43:108	989
223	zeb3	zb3, zb_c	1HL	Zebra stripe 3	40: 72	1451
224	ert-b	ert-b	1HL	Erectoides-b	40: 74	470
225	clh1	clh	7H/5H	Curled leaf dwarf 1	40: 76	1212
226	rvl1	rvl	1HL	leaf 1	40: 77	608
227	sls1	sls	1HL	Small lateral spikelet 1	40: 78	2492
228	Sil1	Sil	1H	Subcrown internode length 1	40: 79	1604
229	cud2	cud2	1HL	Curly dwarf 2	44:111	1712
230	glo-e	glo-e	3HL	Globosum-e	45:117	1755
231	cur5	cu5	2HS	Curly 5	41:120	1710
232	Lys4	sex5	1HS	High lysine 4	40: 80	2475
233	xnt7	xan,,g	1HL	Xantha seedling 7	26:231	581
234	mov3	mo-a	1H	Multiovary 3	32:102	

Table 2. (continued)

BGS no.	Locus symbol[*]		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
235	lel1	lel	2H	Leafy lemma 1	46:74	1780
237	Rpt2	Rpt2c	1HS	Reaction to *Pyrenophora teres* 2	43:110	
238	ari-t	ari-25	1H	Breviaristatum-t	40: 82	
239	sci-b	sci-4	1H/6H	Scirpoides-b	46: 76	
240	sdw6	sdw.f	1H/7H	Semidwarf 6	46:77	2449
241	Acr3	acr	1HL	Accordionrachis 3	40: 85	1071
242	sld6	sld.g	1H	Slender dwarf 6	40: 87	2482
244	dsp11	dsp.am, dsp.ao	1HL	Dense spike 11	41:121	1722 1723
251	mul2	mul2	6HL	Multiflorus 2	26:232	1394
252	eam7	HvCO7	6HS	Early maturity 7	45:118	579
253	cul2	uc2	6HL	Uniculm 2	43:112	531
254	rob1	o, rob-o	6HS	Orange lemma 1	46: 78	707
255	xnt5	x_n	6HL	Xantha seedling 5	26:237	43
257	raw5	r,,e	6HL	Smooth awn 5	44:112	785
258	dsp9	l9, ert-e	6HL	Dense spike 9	43:114	1774
260	fch11	f11	6HL	Chlorina seedling 11	45:120	1738
261	nec2	nec2	6HS	Necrotic leaf spot 2	26:241	1224
262	cur1	cu1	3HL	Curly 1	46: 81	1705
263	cur3	cu3	6HL	Curly 3	41:125	1707
264	mtt5	mt,,f	6HL	Mottled leaf 5	41:126	2410
265	nec3	nec3	6HS	Necrotic leaf spot 3	43:116	1330
266	ert-e	ert-e, dsp9	6HL	Erectoides-e	43:118	477
267	Rph11	Rph11	6HL	Reaction to *Puccinia hordei* 11	26:247	1589
268	lax-b	lax-b	6HL	Laxatum-b	44:113	1776
269	lys6	lys6	6H	High lysine 6	44:114	1786
270	abo14	alb,,q	6HL	Albino seedling 14	26:250	586
271	abo15	alb,,t	6HS	Albino seedling 15	26:251	
272	Rpt5	Pt_a	6HL	Reaction to *Pyrenophora teres* 5	43:120	
274	ari-x	ari-22	6H	Breviaristatum-x	43:124	
301	fst1	fs	5HL	Fragile stem 1	26:252	629
302	mtt2	mt2	5HL	Mottled leaf 2	41:127	1398
303	var3	va3	5HL	Variegated 3	44:115	1277
304	wst2	wst2	5HL	White streak 2	46: 83	766
305	crm1	cm	5HL	Cream seedling 1	26:256	20
306	var1	va	5HL	Variegated 1	37:259	1278

Table 2. (continued)

BGS no.	Locus symbol[*] Rec.	Prev.	Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
308	lbi1	lb, rac-a	5HL	Long basal rachis internode 1	43:125	580
309	Sgh2	Sh2	5HL	Spring growth habit 2	26:259	770
311	dex1	sex2	5HS	Defective endosperm xenia 1	26:260	
312	raw1	r	5HL	Smooth awn 1	46: 84	27
313	fch6	f6, yv	5HL	Chlorina seedling 6	44:116	1390
314	vrs2	v2	5HL	Six-rowed spike 2	26:263	773
315	vrs3	v3, int-a	1HL	Six-rowed spike 3	40: 90	774
317	ddt1	ddt	5HS	Reaction to DDT 1	26:266	331
319	rpg4	rpg4	5HL	Reaction to *Puccinia graminis* 4	26:267	2438
320	int-b	int-b	5HL	Intermedium spike-b	44:118	1764
321	srh1	s, l	5HL	Short rachilla hair 1	46: 86	27
322	dsk1	dsk	5HL	Dusky 1	41:128	1714
323	nld1	nld	5HL	Narrow leafed dwarf 1	46: 88	769
324	cud1	cud	5HL	Curly dwarf 1	26:272	1711
325	crl1	crl, cl	6H	Curly lateral 1	41:129	1211
326	blf1	bb	5HL	Broad leaf 1	46: 90	1393
327	flo-b	flo-a	6HL	Extra floret-b	45:121	1742
328	ari-e	ari-e, lk9	5HL	Breviaristatum-e	41:131	1653
329	ari-h	ari-h	5HL	Breviaristatum-h	26:277	1656
330	ert-g	ert-g, br3	1HL	Erectoides-g	41:133	479
331	ert-n	ert-n	5HL	Erectoides-n	44:120	488
332	Ert-r	Ert-r	2HL	Erectoides-r	41:135	492
333	Rph12	Pa12, Pa9	5HL	Reaction to *Puccinia hordei* 12	26:281	1590
334	raw6	r6	5HL	Smooth awn 6	26:282	2437
335	msg49	msg,,jw	5HL	Male sterile genetic 49	45:122	2402
336	glo-b	glo-b	5HL	Globosum-b	26:284	1326
337	blf2	bb2, nlh	5HL	Broad leaf 2	41:137	1667
338	lys1	lys	5HL	High lysine 1	26:286	1784
339	lys3	sex3	5HL	High lysine 3	43:127	1785
340	raw2	r2	5HL	Smooth awn 2	46: 92	27
341	abo12	alb,,o	5HS	Albino seedling 12	26:290	583
342	glo-f	glo-e	5HL	Globosum-f	26:291	
343	Lfb1	Lfb	5HL	Leafy bract 1	41:140	1577
344	var2	va2	5HL	Variegated 2	32:104	2496
345	rym3	ym3	5HS	Reaction to barley yellow mosaic virus 3	32:105	

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
346	yst5	yst5	7HS	Yellow streak 5	43:130	2501
347	mnd4	m4	5HL	Many noded dwarf 4	44:122	1798
348	Eam5	HvPhyC-e	5HL	Early maturity 5	45:123	
349	brh4	brh.j	2HL	Brachytic 4	42:407	1675
350	brh6	brh.s	5HS	Brachytic 6	42:408	1683
351	gsh1	gs1, cer-q	2HS	Glossy sheath 1	46: 94	735
352	gsh2	gs2, cer-b	3HL	Glossy sheath 2	46: 98	736
353	gsh3	gs3, cer-a	7HS	Glossy sheath 3	41:143	737
354	gsh4	gs4, cer-x	6HL	Glossy sheath 4	41:146	738
355	gsh5	gs5, cer-s	2HL	Glossy sheath 5	44:126	739
356	gsh6	gs6, cer-c	2HS	Glossy sheath 6	46:101	740
357	msg1	ms1	1HL	Male sterile genetic 1	45:126	1810
358	msg2	ms2	2HL	Male sterile genetic 2	45:128	2371
359	msg3	ms3	2HS	Male sterile genetic 3	45:130	1130
360	msg4	ms4	1H	Male sterile genetic 4	45:132	2392
361	msg5	ms5	3HS	Male sterile genetic 5	45:133	2403
362	msg6	ms6	6HS	Male sterile genetic 6	45:135	2405
363	msg7	ms7	5HL	Male sterile genetic 7	45:137	2406
364	msg8	ms8	5HL	Male sterile genetic 8	45:139	2407
365	msg9	ms9	2HS	Male sterile genetic 9	45:141	2408
366	msg10	ms10	7HS	Male sterile genetic 10	45:142	1811
367	msg11	ms11	5HS	Male sterile genetic 11	45:144	1812
368	msg13	ms13	3HL	Male sterile genetic 13	45:146	1813
369	msg14	ms14	7HS	Male sterile genetic 14	45:147	1814
370	msg15	ms15		Male sterile genetic 15	45:149	1815
371	msg16	ms16	5HS	Male sterile genetic 16	45:150	1816
372	msg17	ms17	5HL	Male sterile genetic 17	45:152	1817
373	msg18	ms18	5HL	Male sterile genetic 18	45:153	1818
374	msg19	ms19	5HS	Male sterile genetic 19	45:155	1819
375	msg20	Msg,,ad	4H	Male sterile genetic 20	45:156	2372
376	msg21	ms21	1HL	Male sterile genetic 21	45:157	2373
377	seg1	se1	7HL	Shrunken endosperm genetic 1	45:158	750
378	seg2	se2	7HS	Shrunken endosperm genetic 2	26:326	751
379	seg3	se3, ant17	3H	Shrunken endosperm genetic 3	45:160	752
380	seg4	se4	7HL	Shrunken endosperm genetic 4	37:267	753
381	seg5	se5	7HS	Shrunken endosperm genetic 5	26:329	754

Table 2. (continued)

BGS no.	Locus symbol[*] Rec.	Prev.	Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
382	sex1	lys5	6HL	Shrunken endosperm xenia 1	26:330	755
383	msg22	ms22	7H	Male sterile genetic 22	45:162	741, 2374
384	msg23	ms23	7HL	Male sterile genetic 23	45:163	2375
385	msg24	ms24	4HL	Male sterile genetic 24	45:164	2376
386	des3	des3	2H/ 5HL	Desynapsis 3	43:140	594
387	des8	des8	3H	Desynapsis 8	41:151	599
388	des9	des9	7HL	Desynapsis 9	44:131	600
389	des10	des,,p	5HL	Desynapsis 10	41:152	601
390	des11	des11	3HL	Desynapsis 11	44:132	602
391	des12	des12	3H	Desynapsis 12	44:133	603
392	des13	des13	3H	Desynapsis 13	44:134	604
393	des14	des14	7H	Desynapsis 14	44:135	605
394	des15	des15	3HL	Desynapsis 15	44:136	606
395	msg26	msg,,u	7HS	Male sterile genetic 26	45:166	745
396	seg6	se6	3HL	Shrunken endosperm genetic 6	44:138	2467
397	seg7	se7		Shrunken endosperm genetic 7	37:269	2468
399	cer-d	cer-d	5HL	Eceriferum-d	41:153	425
400	cer-e	cer-e	1HL	Eceriferum-e	40:102	1518
401	cer-f	cer-f	1H	Eceriferum-f	40:104	427
402	cer-g	cer-g	2HL	Eceriferum-g	44:140	428
403	cer-h	cer-h	4HS	Eceriferum-h	41:157	429
404	cer-i	cer-i	5HL	Eceriferum-i	41:158	430
405	cer-k	cer-k	4HL	Eceriferum-k	41:160	432
406	cer-l	cer-l	3HL	Eceriferum-l	44:142	433
407	cer-m	cer-m	1HL/ 3HL	Eceriferum-m	41:161	434
408	cer-n	gs9	2HL	Eceriferum-n	44:143	435
409	cer-o	cer-o	1HL	Eceriferum-o	40:106	436
410	cer-p	cer-p	7HL	Eceriferum-p	41:162	437
411	cer-r	cer-r	3HL	Eceriferum-r	45:168	439
413	gsh8	cer-u, gs8	2HS	Glossy sheath 8	46:105	442
414	cer-v	cer-v	2HS	Eceriferum-v	44:147	443
415	cer-w	cer-w	5HL	Eceriferum-w	41:166	1519
417	cer-y	cer-y	1HS	Eceriferum-y	44:149	446

Table 2. (continued)

BGS no.	Locus symbol[*] Rec.	Prev.	Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
418	cer-z	cer-z	7HS	Eceriferum-z	44:150	447
419	cer-za	cer-za	5HL	Eceriferum-za	43:144	1521
420	cer-zb	cer-zb	5HS	Eceriferum-zb	42:508	1522
421	cer-zc	cer-zc	4HL/ 2HS	Eceriferum-zc	42:510	450
422	cer-zd	cer-zd	3HL	Eceriferum-zd	40:110	451
423	cer-ze	gl5	7HS	Eceriferum-ze	44:152	452
424	cer-zf	cer-zf	3H/ 7HS	Eceriferum-zf	42:516	453
425	cer-zg	cer-zg	4HL	Eceriferum-zg	26:377	454
427	cer-zi	cer-zi	1HL	Eceriferum-zi	41:168	456
428	cer-zj	cer-zj	5HL	Eceriferum-zj	42:520	457
429	cer-zk	cer-zk	2H	Eceriferum-zk	43:146	458
430	cer-zl	cer-zl		Eceriferum-zl	26:382	459
431	cer-zn	cer-zn	1H	Eceriferum-zn	40:112	1523
432	cer-zo	cer-zo	3HS	Eceriferum-zo	44:154	462
433	cer-zp	cer-zp	5HL	Eceriferum-zp	26:385	463
434	cer-zq	cer-zq		Eceriferum-zq	26:386	1524
435	cer-zr	cer-zr	5HL	Eceriferum-zr	44:155	1525
436	cer-zs	cer-zs		Eceriferum-zs	44:156	1526
437	cer-zt	cer-zt	2HS	Eceriferum-zt	44:157	1527
438	cer-zu	cer-zu	1HS	Eceriferum-zu	41:170	1528
439	cer-zv	cer-zv	4HL	Eceriferum-zv	46:109	1529
440	cer-zw	cer-zw		Eceriferum-zw	26:392	1530
441	cer-zx	cer-zx	3H	Eceriferum-zx	46:109	1531
442	cer-zy	cer-zy	1HS	Eceriferum-zy	40:116	1532
443	cer-zz	cer-zz	3HL	Eceriferum-zz	44:159	1533
444	cer-ya	cer-ya	3HS	Eceriferum-ya	26:396	1534
445	cer-yb	cer-yb	2HL	Eceriferum-yb	41:171	1535
446	cer-yc	cer-yc	6H/ 7HS	Eceriferum-yc	41:172	1536
447	cer-yd	cer-yd	3HS	Eceriferum-yd	26:399	1537
448	cer-ye	cer-ye	4H	Eceriferum-ye	43:149	1538
449	cer-yf	cer-yf	7H	Eceriferum-yf	44:160	1539
450	cer-yg	cer-yg	7HS	Eceriferum-yg	44:161	1540
451	cer-yh	cer-yh	3HS	Eceriferum-yh	26:403	1541

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
453	fer1			Few roots 1	46:112	2538
454	blx5	bl5	7HL	Non-blue aleurone xenia 5	26:404	2509
455	seg8	seg8	7H	Shrunken endosperm genetic 8	45:170	2469
460	cur4	cu4, glo-d	2HL	Curly 4	45:172	1708
461	zeb2	zb2, fch10	4HS	Zebra stripe 2	43:152	93
462	yst3	yst,,c	3HS	Yellow streak 3	44:163	48
463	gig1	gig, sf	2HL	Gigas 1	44:164	1650
464	msg27	msg,,ae	2HS	Male sterile genetic 27	45:174	2379
465	msg28	msg,,as	2HS	Male sterile genetic 28	45:175	2380
466	msg29	msg,,a	5HL	Male sterile genetic 29	45:176	2381
467	msg30	msg,,c	7HL	Male sterile genetic 30	45:177	2382
468	msg31	msg,,d	1HL	Male sterile genetic 31	45:178	2383
469	msg32	msg,,w	7H	Male sterile genetic 32	45:179	2384
470	msg33	msg,,x	2HS	Male sterile genetic 33	45:180	2385
471	msg34	msg,,av	6HS/ 7HS	Male sterile genetic 34	45:181	2386
472	abr1	abr	2HL	Accordion basal rachis internode 1	26:419	1563
473	com1	bir1	5HL	Compositum 1	40:118	1702
474	lax-a	lax-a	5HL	Laxatum-a	46:113	1775
475	lax-c	lax-c	6HL	Laxatum-c	41:174	1777
498	msg35	msg,,dr	2HL	Male sterile genetic 35	45:183	2387
499	msg36	msg,,bk	6HS	Male sterile genetic 36	45:184	2388
500	msg37	msg,,hl	3HL	Male sterile genetic 37	45:186	2389
501	msg38	msg,,jl	3H	Male sterile genetic 38	45:187	2390
502	msg39	msg,,dm	3H	Male sterile genetic 39	45:188	2391
503	msg40	msg,,ac	6HL	Male sterile genetic 40	45:190	2393
504	msg41	msg,,aj	6HS	Male sterile genetic 41	45:191	2394
505	msg42	msg,,db	3H	Male sterile genetic 42	45:193	2395
506	msg43	msg,,br	2HL	Male sterile genetic 43	45:194	2396
507	msg44	msg,,cx	5HL	Male sterile genetic 44	45:195	2397
508	msg45	msg,,dp	5HL/ 7HS	Male sterile genetic 45	45:196	2398
509	msg46	msg,,ec	2H/6H	Male sterile genetic 46	45:197	2399

Table 2. (continued)

BGS no.	Locus symbol[*]		Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
	Rec.	Prev.				
510	msg47	msg,,ep	3HS/ 7HS	Male sterile genetic 47	45:198	2400
511	Rpg1	T	7HS	Reaction to *Puccinia graminis* 1	26:437	701
512	Rpg2	T2		Reaction to *Puccinia graminis* 2	26:439	187
513	xnt2	x_b		Xantha seedling 2	26:440	2
515	Rsp1	Sep		Reaction to *Septoria passerinii* 1	26:441	2510
516	Rsp2	Sep2		Reaction to *Septoria passerinii* 2	37:275	2511
517	Rsp3	Sep3		Reaction to *Septoria passerinii* 3	37:276	2512
518	sdw1	denso	3HL	Semidwarf 1	41:176	2513
519	mnd1	m	2H	Many-noded dwarf 1	43:154	253
520	msg48	msg,,jt	1H	Male sterile genetic 48	45:199	2401
521	mtt1	mt. mt3	1HL	Mottled leaf 1	41:179	622
522	cer-yi	cer-yi	2H	Eceriferum-yi	41:180	1542
523	cer-yj	cer-yj	1HS	Eceriferum-yj	40:124	1543
524	cer-yk	cer-yk	7HL	Eceriferum-yk	44:167	1544
525	cer-yl	cer-yl	4HL	Eceriferum-yl	46:116	1545
526	cer-ym	cer-ym	4HL	Eceriferum-ym	46:118	1546
527	cer-yn	cer-yn	1H	Eceriferum-yn	40:125	1547
528	cer-yo	cer-yo	4HS	Eceriferum-yo	44:168	1548
529	cer-yp	cer-yp	5HS	Eceriferum-yp	44:169	1549
530	cer-yq	cer-yq	5H	Eceriferum-yq	44:170	1550
531	cer-yr	cer-yr	5HL	Eceriferum-yr	44:171	1551
532	cer-ys	cer-ys	2HL	Eceriferum-ys	44:172	1552
533	cer-yt	cer-yt	1H/5H	Eceriferum-yt	40:126	1553
534	cer-yu	cer-yu	1H	Eceriferum-yu	40:127	1554
535	cer-yx	cer-yx	1H/3H/5H	Eceriferum-yx	40:128	1555
536	Cer-yy	Gle1	1HS	Eceriferum-yy	40:129	1556
537	cer-yz	cer-yz	1H/5H	Eceriferum-yz	44:173	1557
538	cer-xa	cer-xa	2HL/4H/5HL	Eceriferum-xa	44:174	1558
539	cer-xb	cer-xb	4H	Eceriferum-xb	44:175	1559
540	cer-xc	cer-xc	1H	Eceriferum-xc	44:176	1560
541	cer-xd	cer-xd	4H/5HL	Eceriferum-xd	44:177	1561
542	Dwf2	Dwf2		Dominant dwarf 2	24:170	

Table 2. (continued)

BGS no.	Locus symbol[*] Rec.	Prev.	Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	GSHO no.[‡]
544	int-h	int-h	5H	Intermedium spike-h	44:179	1768
545	int-i	int-i	2HS	Intermedium spike-i	41:181	1769
546	int-k	int-k	7H	Intermedium spike-k	44:180	1770
547	int-m	int-m	5HL	Intermedium spike-m	44:181	1772
548	Fol-b	Ang	1HS	Angustifolium-b	40:131	17
549	Lga1	Log	7HS	Long glume awn 1	44:183	835
550	ari-b	ari-b		Breviaristatum-b	44:185	1649
551	ari-f	ari-f	7H	Breviaristatum-f	41:182	1654
552	ari-j	ari-j		Breviaristatum-j	44:186	1658
553	ari-k	ari-k	3H	Breviaristatum-k	44:187	1659
554	ari-m	ari-m	7HS	Breviaristatum-m	41:184	1661
555	ari-n	ari-n	7H	Breviaristatum-n	41:185	1662
556	ari-o	ari-o	7HL	Breviaristatum-o	45:200	1663
557	ari-p	ari-p		Breviaristatum-p	46:120	1664
558	ari-q	ari-q	4H	Breviaristatum-q	44:188	1665
559	ari-r	ari-r	5H	Breviaristatum-r	41:187	1666
560	ert-f	ert-f	1H	Erectoides-f	40:133	478
561	ert-h	ert-h	5HL	Erectoides-h	44:189	481
562	ert-k	ert-k	6H	Erectoides-k	46:121	485
563	ert-l	ert-l		Erectoides-l	26:489	486
564	ert-p	ert-p		Erectoides-p	26:490	490
565	ert-s	ert-s		Erectoides-s	26:491	493
566	ert-t	brh3	2HS	Erectoides-t	45:203	494
567	ert-v	ert-v	6H	Erectoides-v	41:188	497
568	ert-x	ert-x	1H/7H	Erectoides-x	40:136	498
569	ert-y	ert-y		Erectoides-y	26:495	499
570	ert-z	ert-z		Erectoides-z	26:496	500
571	ert-za	ert-za	5H	Erectoides-za	44:190	501
572	ert-zb	ert-zb	7HL	Erectoides-zb	45:205	502
573	ert-zc	ert-zc	7HS	Erectoides-zc	45:206	503
574	ert-ze	ert-ze	5HS	Erectoides-ze	45:207	505
575	Rph6	Pa6		Reaction to *Puccinia hordei* 6	26:501	1598
576	Rph8	Pa8		Reaction to *Puccinia hordei* 8	26:502	1600
577	Rsg2	Rsg2		Reaction to *Schizaphis graminum* 2	37:283	2513
578	mat-b	mat-b	7HL	Praematurum-b	46:123	1788

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
579	mat-c	Eam6	2H	Praematurum-c	46:125	1789
580	mat-d	mat-d	4Hl/ 6HL	Praematurum-d	45:208	1790
581	mat-e	mat-e		Praematurum-e	26:508	1791
582	mat-f	mat-f	1H	Praematurum-f	45:210	1792
583	mat-g	mat-g		Praematurum-g	26:510	1793
584	mat-h	mat-h	4HL	Praematurum-h	45:212	1794
585	mat-i	mat-i	7HL	Praematurum-i	45:214	1795
586	bra-d	bra-d	1HL	Bracteatum-d	40:139	1696
587	abo3	a2, alb-za		Albino seedling 3	26:514	165
588	abo10	a_{t2}		Albino seedling 10	26:515	57
589	abo11	a_{t3}, alb^{t}		Albino seedling 11	26:516	233
590	Rph13	Rph13		Reaction to *Puccinia hordei* 13	28: 31	1591
591	Rph14	Rph14		Reaction to *Puccinia hordei* 14	28: 32	1592
592	yhd2	yh2		Yellow head 2	45:215	757
593	adp1	adp	3HL	Awned palea 1	43:158	1618
594	ant3	rub		Anthocyanin-deficient 3	29: 82	1641
595	ant4	ant4	4H	Anthocyanin-deficient 4	45:216	1642
596	ant5	rs2		Anthocyanin-deficient 5	29: 84	1643
597	ant6	ant6		Anthocyanin-deficient 6	29: 85	1644
598	ant13	ant13	6HL	Proanthocyanin-free 13	29: 86	1624
599	ant17	ant17	3HS	Proanthocyanin-free 17	46:128	1628
600	ant18	ant18		Proanthocyanin-free 18	45:221	1630
601	ant19	ant19		Proanthocyanin-free 19	29: 92	1631
602	ant20	ant20		Anthocyanin-rich 20	29: 93	1633
603	ant21	ant21	6H	Proanthocyanin-free 21	29: 94	1634
604	ant22	ant22	2HL	Proanthocyanin-free 22	41:191	1635
605	ant25	ant25		Proanthocyanin-free 25	29: 96	1638
606	ant26	ant26		Proanthocyanin-free 26	29: 97	1639
607	ant27	ant27		Proanthocyanin-free 27	29: 98	1640
608	ant28	ant28	3HL	Proanthocyanin-free 28	46:131	
609	ant29	ant29		Proanthocyanin-free 29	29:100	
610	ant30	ant30		Proanthocyanin-free 30	29:101	
611	Nec6	Sp	7HS	Necrotic leaf spot 6	43:159	977
612	gig2	gig2	4HL	Gigas 2	44:191	1750

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
613	brc1	brc-5, com2	2HS	Branched 1	45:224	
614	Zeo2	Mo1, Zeo3	2HL	Zeocriton 2	41:193	637
615	wxs1	wxs1	7H/ 2HL	Waxy spike 1	43:160	3649
616	cul3	cul3	3HL	Uniculme 3	43:161	2494
617	cul4	uc-5, uc-3	3HL	Uniculme 4	46:132	2495
618	mnd3	mn3, m3	4HS	Many noded dwarf 3	44:194	1797
619	bra-a	bra-a	7H	Bracteatum-a	44:196	1693
620	cal-b	cal-b	5HL	Calcaroides-b	44:197	1697
621	Cal-c	Cal-c	5HL	Calcaroides-c	41:195	1567
622	cal-e	cal-23	5HS	Calcaroides-e	32:123	
623	eli-a	lig-a		Eligulum-a	44:199	3647
624	ops1	op-3	7HS	Opposite spikelets 1	45:226	2427
625	sci-a	sci-3	5H	Scirpoides 1	44:200	
626	scl-a	scl-6	1HL	Scirpoides leaf-a	44:201	
627	viv-a	viv-5	2H	Viviparoides-a	45:227	2498
628	sex7	sex.i	5HL	Shrunken endosperm 7	32:129	2470
629	mtt6	mtt6	7HS	Mottled leaf 6	45:228	2411
630	Ari-s	ari-265	5H/7H	Breviaristatum-s	41:197	
631	brh3	brh.g, ert-t	2HS	Brachytic 3	45:229	1672
632	mnd5	mnd5	7HL	Many noded dwarf 5	44:202	
633	mnd6	den-6	5HL	Many noded dwarf 6	44:203	1713
634	pmr2	nec-50		Premature ripe 2	32:135	2421
635	nec7	nec-45	1H/6H/7H	Necroticans 7	43:166	2420
636	tst2		4HL	Tip sterile 2	43:167	1781
637	nar1	nar1	6HS	NADH nitrate reductase-deficient 1	35:194	2431
638	nar2	nar2	5HL	NADH nitrate reductase-deficient 2	35:195	2415
639	nar3	nar3	7HS	NADH nitrate reductase-deficient 3	35:196	2416
640	nar4	nar4	2Hl	NADH nitrate reductase-deficient 4	35:197	

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
641	nar5	nar5	5HL	NADH nitrate reductase-deficient 5	35:198	2417
642	nar6	nar6	2HL	NADH nitrate reductase-deficient 6	35:199	
643	nar7	nar7	6HL	NADH nitrate reductase-deficient 7	35:200	2418
644	nar8	nar8	6HS	NADH nitrate reductase-deficient 8	35:201	
645	bsp1			Bushy spike 1	43:168	3652
646	ovl2	ovl2		Ovaryless 2	43:169	3655
647	tst1	tst1	6HL	Tip sterile 1	43:170	3644
648	mov4	mo8		Multiovary 4	43:171	3643
649	asp1	asp1		Aborted spike 1	43:172	3654
650	sun1	sun1		Sensitivity to *Ustilago nuda* 1	43:173	3650
651	lam1	lam1		Late maturity 1	43:174	3653
652	ylf1	ylf1	7HS	Yellow leaf 1	43:175	
653	brh10	brh.l	2HS	Brachytic 10	45:231	1677
654	brh11	brh.n	5HS	Brachytic 11	45:232	1679
655	brh12	brh.o	5HS	Brachytic 12	45:233	1680
656	brh13	brh.p	5HS	Brachytic 13	45:234	1681
657	brh15	brh.u	2HL	Brachytic 15	44:205	1685
658	brh17	brh.ab	5HS	Brachytic 17	45:236	1669
659	brh18	brh13	5HS	Brachytic 18	45:237	1670
660	nld2		5H/6H/7H	Narrow leafed dwarf 2	43:176	3645
661	dub1		5HL	Double seed 1	37:301	
663	sdw3	gai	2HS	Semidwarf 3	46:134	
667	Rpt1	Pt	3HL	Reaction to *Pyrenophora teres* 1	43:177	
671	nec8	nec.w	5HL	Necrotic leaf spot 8	43:179	3600
672	nec9		3HL	Necrotic leaf spot 9	43:181	3599
673	cst1	cs	5HL	Corn stalk	41:199	
674	mtt8	Mut 1661		Mottled leaf 8	43:182	3597
675	mtt9	Mut 2721		Mottled leaf 9	44:207	3598
676	fch16	clo.117	2HS	Chlorina seedling 16	40:144	
677	mtt7	mtt.h	2HS	Mottled leaf 7	42:753	

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
678	ari-u	ari-245	2HS	Breviaristatum-u	45:239	
679	acr4	acr-3	2H/ 6HL	Accordion rachis 4	41:201	
680	ari-v	ari-137	5HS	Breviaristatum-v	41:202	
681	nec10	necS 1-1	3H	Necroticans 10	43:184	3607
682	nec11		1H	Necroticans 11	43:185	3610
683	nec12			Necroticans 12	43:186	3613
684	nec13			Necroticans 13	43:187	3616
685	nec14			Necroticans 14	43:188	3619
686	nec15			Necroticans 15	43:189	3620
687	nec16			Necroticans 16	43:190	3621
688	nec17			Necroticans 17	43:191	3622
689	nec18			Necroticans 18	43:192	3623
690	nec19			Necroticans 19	43:193	3624
691	nec20			Necroticans 20	43:194	3625
692	nec21			Necroticans 21	43:195	3626
693	Nec22			Necroticans 22	43:196	3627
694	nec23			Necroticans 23	43:197	3628
695	Nec24			Necroticans 24	43:198	3629
696	nec25			Necroticans 25	43:199	3630
697	Nec26			Necroticans 26	43:200	3631
698	nec27			Necroticans 27	43:201	3633
699	nec28			Necroticans 28	43:202	3635
700	nec29			Necroticans 29	43:203	3636
701	nec30			Necroticans 30	43:204	3637
702	nec31			Necroticans 31	43:205	3638
703	nec32			Necroticans 32	43:206	3639
704	nec33			Necroticans 33	43:207	3640
707	Rpr1		4H	Required for *Puccinia graminis* resistance 1	42:757	
711	Rpt3	QRptts2	2HS	Reaction to *Pyrenophora teres* 3	43:208	
713	Rpt6		5HL	Reaction to *Pyrenophora teres* 6	43:210	
714	Rpt7	Qrpts4	4HL	Reaction to *Pyrenophora teres* 7	43:211	
716	ibl1	ibl1	5HL	Intense blue aleurone 1	46:136	
718	ops2	op-2	5HL	Opposite spikelets 2	43:213	2426

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	BGS no.
719	ops3	op-1	5HS	Opposite spikelets 3	43:214	2425
720	viv-c	viv-1	5H	Viviparoides-c	43:215	2497
721	ari-w	ari-153	7H	Breviaristatum-w	43:216	
722	ari-y	ari-9	5H	Breviaristatum-y	43:217	
723	mov5	mov.o		Multiovary 5	43:218	3671
724	lks6	lks.q	1H/5H /6H	Short awn 6	43:219	3674
725	ovl3			Ovaryless 3	43:220	3687
726	mnd7			Many noded dwarf 7	43:221	3686
727	ubs5			Unbranched style 5	43:222	3675
728	fxp1			Fenoxaprop-p-ethyl reaction 1	43:223	3684
729	dsk2	msg,,df	7HL	Dusky 2	44:208	
730	lab1		5HL	Labile 1	46:137	
731	rpr2	γ08-118; R43-22#1	6H	Required for *Puccinia graminis* resistance 2	46:139	3693
732	rpr3	γ08-112; R12-31#3		Required for *Puccinia graminis* resistance 3	46:141	3696
733	rpr4	γ08-114; R36-37#1		Required for *Puccinia graminis* resistance 4	46:142	3697
734	rpr5	γ08-117; R42-33#5		Required for *Puccinia graminis* resistance 5	46:143	3699
735	rpr6	γ08-119; R47-23#1		Required for *Puccinia graminis* resistance 6	46:144	3700
736	rpr7	γ08-115; R3-18#3		Required for *Puccinia graminis* resistance 7	46:145	3701
737	rcr1	γ08-122; (R4-29)		Required for resistance to *Cochliobolus sativus* 1	45:249	3703
738	rcr2	γ08-123; (R4-40)		Required for resistance to *Cochliobolus sativus* 2	45:250	3704
739	rcr3	γ08-124		Required for resistance to *Cochliobolus sativus* 3	45:251	3705

* Recommended locus symbols are based on utilization of a three-letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 5 1996.

† Chromosome numbers and arm designations are based on a resolution passed at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on August 05 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

‡ The seed stock associated with each BGS number is held as a GSHO stock number in the Barley Genetics Stock Collection at the USDA-ARS National Small Grains Germplasm Research Facility, Aberdeen, ID 83210, USA.

Table 3. An alphabetic listing of recently published Barley Genetic Stock (BGS) descriptions for loci in barley (*Hordeum vulgare*), including information on recommended locus names, recommended locus symbols, chromosomal locations, description citation, and original cultivars.

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
abo1	a_t	207	1HL	Albino seedling 1	26:210	Trebi
abo2	a2	53	2HS	Albino seedling 2	26: 89	Nilsson-Ehle No 2
abo3	alb-za	587		Albino seedling 3	26:514	Unknown cultivar
abo4	a4	94	2H	Albino seedling 4	26:133	Unknown cultivar
abo6	a_c	106	3HS	Albino seedling 6	46: 60	Colsess
abo8	a_{c2}	4	7HS	Albino seedling 8	26: 47	Coast
abo9	a_n	112	3HS	Albino seedling 9	26:146	Nigrinudum
abo10	a_{t2}	588		Albino seedling 10	26:515	Canadian Thorpe
abo11	a_{t3}	589		Albino seedling 11	26:516	Trebi
abo12	alb,,o	341	5HS	Albino seedling 12	26:290	Titan
abo13	alb,,p	95	2HL	Albino seedling 13	26:134	Titan
abo14	alb,,q	270	6HL	Albino seedling 14	26:250	Shabet
abo15	alb,,t	271	6HS	Albino seedling 15	26:251	Betzes
abr1	abr	472	2HL	Accordion basal rachis internode 1	26:419	Bonus
acr1	acr	97	2HL	Accordion rachis 1	40: 56	ACBV89B229
Acr2	Acr,lax	189	4HL	Accordion rachis 2	40: 65	CIho 6164
Acr3	acr	241	1HL	Accordion rachis 3	40: 85	Burma Girl
acr4	acr-3	679	2H/ 6HL	Accordion rachis 4	41:201	Bonus
adp1	adp	593	3HL	Awned palea 1	43:158	Unknown line
alm1	al	108	3HS	Albino lemma 1	46: 61	Russia 82
als1	als	101	3HL	Absent lower laterals 1	43: 74	Montcalm
ant1	rs	33	7HS	Anthocyanin-less 1	46: 49	Bonus
ant2	pr	80	2HL	Anthocyanin-less 2	46: 55	Foma
ant3		594		Anthocyanin-deficient 3	29: 82	Bonus
ant4	ant4	595	4H	Anthocyanin-deficient 4	45:216	Foma
ant5		596		Anthocyanin-deficient 5	29: 84	Bonus
ant6		597		Anthocyanin-deficient 6	29: 85	Foma
ant13		598	6HL	Proanthocyanidin-free 13	29: 86	Foma
ant17		599	3HS	Proanthocyanidin-free 17	46:128	Nordal
ant18		600	3H	Proanthocyanidin-free 18	45:221	Nordal
ant19		601		Proanthocyanidin-free 19	29: 92	Alf

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
ant20		602		Anthocyanidin-rich 20	29: 93	Foma
ant21		603	6H	Proanthocyanidin-free 21	29: 94	Georgie
ant22		604	2HL	Proanthocyanidin-free 22	41:191	Hege 802
ant25		605		Proanthocyanidin-free 25	29: 96	Secobra 18193
ant26		606		Proanthocyanidin-free 26	29: 97	Grit
ant27		607		Proanthocyanidin-free 27	29: 98	Zebit
ant28		608	3HL	Proanthocyanidin-free 28	46:131	Grit
ant29		609		Proanthocyanidin-free 29	29:100	Ca 708912
ant30		610		Proanthocyanidin-free 30	29:101	Gunhild
ari-a		132	3HS	Breviaristatum-a	41:106	Bonus
ari-b		550		Breviaristatum-b	44:185	Bonus
ari-e		328	5HL	Breviaristatum-e	41:131	Bonus
ari-f		551	7H	Breviaristatum-f	41:182	Bonus
ari-g		89	2H	Breviaristatum-g	44: 79	Bonus
ari-h		329	5HL	Breviaristatum-h	26:277	Foma
ari-j		552		Breviaristatum-j	44:186	Bonus
ari-k		553	3H	Breviaristatum-k	44:187	Bonus
ari-m		554	7HS	Breviaristatum-m	41:184	Bonus
ari-n		555	7H	Breviaristatum-n	41:185	Bonus
ari-o		556	7HL	Breviaristatum-o	45:200	Bonus
ari-p		557		Breviaristatum-p	46:120	Foma
ari-q		558	4H	Breviaristatum-q	44:188	Kristina
ari-r		559	5H	Breviaristatum-r	41:187	Bonus
Ari-s	ari-265	630	5H/7H	Breviaristatum-s	41:197	Kristina
Ari-t	ari-25	238	1H	Breviaristatum-t	40: 82	Bonus
ari-u	ert-t	678	2HS	Breviaristatum-u	45:100	Foma
ari-v	ari-137	680	5HS	Breviaristatum-v	41:202	Foma
ari-w	ari-153	721	7H	Breviaristatum-w	43:216	Foma
ari-x	ari-22	274	6H	Breviaristatum-x	43:124	Bonus
ari-y	ari-9	722	5H	Breviaristatum-y	43:217	Bonus
asp1		649		Aborted spike 1	43:172	Steptoe
blf1	bb	326	5HL	Broad leaf 1	46: 90	Bonus
blf2	bb2	337	5HL	Broad leaf 2	41:137	Hannchen
Blp1	B	203	1HL	Black lemma and pericarp 1	46: 67	Nigrinudum
blx1	bl	15	4HL	Non-blue aleurone xenia 1	26: 60	Goldfoil

Table 3. (continued)

Locus symbol*		BGS no.	Chr. Loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
blx2	bl2	19	7HS	Non-blue aleurone xenia 2	26: 65	Nepal
blx3	bl3	173	4HL	Non-blue aleurone xenia 3	26:198	Blx
blx4	bl4	174	4HL	Non-blue (pink) aleurone xenia 4	26:199	Ab 6
blx5	bl5	454	7HL	Non-blue aleurone xenia 5	26:404	BGM 122
bra-a		619	7H	Bracteatum-a	44:196	Bonus
bra-d		586	1HL	Bracteatum-d	40:139	Foma
brc1	brc-5, com2	613	2HS	Branched 1	45:224	BGRC 13145
brh1	br	1	7HS	Brachytic 1	43: 48	Himalaya
brh2	br2	157	4HL	Brachytic 2	44: 95	Svanhals
brh3	brh.g, ert-t	631	2HS	Brachytic 3	45:229	Birgitta
brh4	brh.j	349	2HL	Brachytic 4	42:407	Birgitta
brh5	brh.m	185	4HS	Brachytic 5	44:110	Birgitta
brh6	brh.s	350	5HL	Brachytic 6	42:408	Akashinriki
brh7	brh.w	41	7H	Brachytic 7	42: 98	Volla
brh8	brh.ad	142	3HL	Brachytic 8	42:232	Birgitta
brh9	brh.k	187	4HL	Brachytic 9	43: 99	Birgitta
brh10	brh.l	653	2HS	Brachytic 10	45:231	Birgitta
brh11	brh.n	654	5HS	Brachytic 11	45:232	Birgitta
brh12	brh.o	655	5HS	Brachytic 12	45:233	Birgitta
brh13	brh.p	656	5HS	Brachytic 13	45:234	Birgitta
brh14	ari-o	148	7HL	Brachytic 14	45:111	Akashinriki
brh15	brh.u	657	2HL	Brachytic 15	44:205	Julia
brh16	brh.v	44	7HL	Brachytic 16	45: 89	Korál
brh17	brh.ab	658	5HS	Brachytic 17	45:236	Morex
brh18	brh13	659	5HS	Brachytic 18	45:237	Triumph
bsp1		645		Bushy spike 1	43:168	Morex
btr1	bt1	115	3HS	Non-brittle rachis 1	43: 78	A 222
btr2	bt2	116	3HS	Non-brittle rachis 2	43: 80	Sakigoke
cal-b		620	5HL	Calcaroides-b	44:197	Bonus
Cal-c		621	5HL	Calcaroides-c	41:195	Bonus
cal-d		146	3H	Calcaroides-d	40: 58	Foma
cal-e		622	5HS	Calcaroides-e	32:123	Semira
cer-d		399	5HL	Eceriferum-d + ++ ++	41:153	Bonus

Table 3. (continued)

Locus symbol*		BGS no.	Chr. Loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
cer-e		400	1HL	Eceriferum-e -/+ ++ ++	40:102	Bonus
cer-f		401	1H	Eceriferum-f + + ++	40:104	Bonus
cer-g		402	2HL	Eceriferum-g + + ++	44:140	Bonus
cer-h		403	4HS	Eceriferum-h - ++ ++	41:157	Bonus
cer-i		404	5HL	Eceriferum-i - ++ ++	41:158	Bonus
cer-k		405	4HL	Eceriferum-k + ++ ++	41:160	Bonus
cer-l		406	3HL	Eceriferum-l + ++ ++	44:142	Bonus
cer-m		407	1H/3H	Eceriferum-m +/++ + ++	41:161	Bonus
cer-n	gs9	408	2HL	Eceriferum-n - - ++ & - +/- ++	44:143	Bonus
cer-o		409	1HL	Eceriferum-o -/+ ++ ++	40:106	Bonus
cer-p		410	7HL	Eceriferum-p ++ ++ +	41:162	Bonus
cer-r		411	3HL	Eceriferum-r +/- + ++	45:168	Bonus
cer-t		412	5HL	Eceriferum-t +/- ++ ++	41;164	Bonus
cer-v		414	2HS	Eceriferum-v +/- ++ ++	44:147	Bonus
cer-w		415	5HL	Eceriferum-w +/- ++ ++	41:166	Bonus
cer-xa		538	2HL/4H/5HL	Eceriferum-xa ++ ++ -	44:174	Foma
cer-xb		539	4H	Eceriferum-xb - ++ ++	44:175	Bonus
cer-xc		540	1H	Eceriferum-xc + + ++	44:176	Bonus
cer-xd		541	4H/5HL	Eceriferum-xd + + ++	44:177	Bonus
cer-y		417	1HS	Eceriferum-y + +/++ ++	44:149	Bonus
cer-ya		444	3HS	Eceriferum-ya ++ ++ -	26:396	Bonus
cer-yb		445	2HL	Eceriferum-yb ++ ++ -	41:171	Bonus
cer-yc		446	6H/7HS	Eceriferum-yc - ++ ++	41:172	Bonus
cer-yd		447	3HS	Eceriferum-yd - ++ ++	26:399	Bonus
cer-ye		448	4H	Eceriferum-ye ++ ++ -	43:149	Foma
cer-yf		449	7H	Eceriferum-yf ++ ++ +	44:160	Bonus
cer-yg		450	7HS	Eceriferum-yg - - -	44:161	Carlsberg II
cer-yh		451	3HS	Eceriferum-yh - ++ ++	26:403	Bonus
cer-yi		522	2H	Eceriferum-yi ++ ++ -	41:180	Foma
cer-yj		523	1HS	Eceriferum-yj ++ ++ -	40:124	Bonus
cer-yk		524	7HL	Eceriferum-yk + + ++	44:167	Bonus
cer-yl		525	4HL	Eceriferum-yl - - ++	46:116	Bonus

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
cer-ym		526	4HL	Eceriferum-ym - - -	46:118	Bonus
cer-yn		527	1H	Eceriferum-yn + + ++	40:125	Kristina
cer-yo		528	4HS	Eceriferum-yo ++ ++ +	44:168	Bonus
cer-yp		529	5HS	Eceriferum-yp ++ ++ +	44:169	Bonus
cer-yq		530	5H	Eceriferum-yq ++ ++ -	44:170	Kristina
cer-yr		531	5HL	Eceriferum-yr -/+ + ++	44:171	Foma
cer-ys		532	2HL	Eceriferum-ys ++ ++ -	44:172	Bonus
cer-yt		533	1H/5H	Eceriferum-yt - ++ ++	40:126	Bonus
cer-yu		534	1H	Eceriferum-yu ++ ++ -	40:127	Bonus
cer-yx		535	1H/3H/5H	Eceriferum-yx + + ++	40:128	Foma
Cer-yy	Gle1	536	1HS	Eceriferum-yy - ++ ++	40:129	Bonus
cer-yz		537	1H/5H	Eceriferum-yz + + ++	44:173	Bonus
cer-z		418	7HS	Eceriferum-z - - ++	44:150	Bonus
cer-za		419	5HL	Eceriferum-za ++ ++ -	43:144	Foma
cer-zb		420	5HS	Eceriferum-zb - ++ ++	42:508	Bonus
cer-zc		421	4HL/2HS	Eceriferum-zc +/- ++ ++	42:510	Bonus
cer-zd		422	3HL	Eceriferum-zd ++ ++ -	40:110	Bonus
cer-ze	gl5	423	7HS	Eceriferum-ze ++ ++ -	44:152	Bonus
cer-zf		424	3H/7HS	Eceriferum-zf ++ ++ +	42:516	Bonus
cer-zg		425	4HL	Eceriferum-zg ++ ++ +	26:377	Foma
cer-zi		427	1HL	Eceriferum-zi + + ++	41:168	Bonus
cer-zj		428	5HL	Eceriferum-zj ++ ++ -	42:520	Bonus
cer-zk		429	2H	Eceriferum-zk + + +/-	26:381	Bonus
cer-zl		430		Eceriferum-zl - - ++	26:382	Bonus
cer-zn		431	1H	Eceriferum-zn +/- ++ ++	40:112	Foma
cer-zo		432	3HS	Eceriferum-zo - ++ ++	44:154	Foma
cer-zp		433	5HL	Eceriferum-zp ++ ++ -	26:385	Bonus
cer-zq		434		Eceriferum-zq ++ ++ -	26:386	Foma
cer-zr		435	5HL	Eceriferum-zr +/- ++ ++	44:155	Foma
cer-zs		436		Eceriferum-zs + ++ ++	44:156	Foma
cer-zt		437	2HS	Eceriferum-zt + ++ ++	44:157	Foma
cer-zu		438	1HS	Eceriferum-zu - + ++	41:170	Foma

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
cer-zv		439	4HL	Eceriferum-zv - - -	46:109	Foma
cer-zw		440		Eceriferum-zw + + ++	26:392	Foma
cer-zx		441	3H	Eceriferum-zx + + ++	46:111	Bonus
cer-zy		442	1HS	Eceriferum-zy ++ ++ +	40:116	Bonus
cer-zz		443		Eceriferum-zz ++ ++ -	44:159	Bonus
clh1	clh	225	7H/5H	Curled leaf dwarf 1	40: 76	Hannchen
com1	bir1	473	5HL	Compositum 1	40:118	Foma
com2	bir2	71	2HS	Compositum 2	45: 95	CIMMYT freak
crl1	cl	325	6H	Curly lateral 1	41:129	Montcalm
crm1	cm	305	5HL	Cream seedling 1	26:256	Black Hulless
cst1	cs	673	5HL	Corn stalk	41:199	Husky
cud1	cud	324	5HL	Curly dwarf 1	26:272	Akashinriki
cud2		229	1HL	Curly dwarf 2	44:111	Akashinriki
cul2	uc2	253	6HL	Uniculm 2	43:112	Kindred
cul3	cul3	616	3HL	Uniculme 3	43:161	Donaria
cul4	uc-5	617	3HL	Uniculme 4	46:132	Bonus
cur1	cu1	262	3HL	Curly 1	46: 81	48-cr cr-17
cur2	cu2	114	3HL	Curly 2	44: 82	Choshiro
cur3	cu3	263	6HL	Curly 3	41:125	Akashinriki
cur4	glo-d	460	2HL	Curly 4	45:172	Asahi 5
cur5	cu5	231	2HS	Curly 5	41:120	Glenn
ddt1	ddt	317	5HS	Reaction to DDT 1	26:266	Spartan
des1	lc	12	7H	Desynapsis 1	42: 58	Mars
des2	ds	119	3H	Desynapsis 2	43: 84	Husky
des3		386	2H/ 5HL	Desynapsis 3	43:140	Betzes
des4		13	7H	Desynapsis 4	44: 54	Betzes
des5		14	7HL	Desynapsis 5	44: 56	Betzes
des6		215	1HL	Desynapsis 6	43:106	Betzes
des7		64	3H	Desynapsis 7	43: 67	Betzes
des8		387	3H	Desynapsis 8	41:151	Betzes
des9		388	7HL	Desynapsis 9	44:131	Betzes
des10		389	3HL	Desynapsis 10	41:152	Betzes
des11		390	3HL	Desynapsis 11	44:132	Betzes
des12		391	3H	Desynapsis 12	44:133	Betzes

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
des13		392	3H	Desynapsis 13	44:134	Betzes
des14		393	7H	Desynapsis 14	44:135	Betzes
des15		394	3HL	Desynapsis 15	44:136	Ingrid
dex1	sex2	311	5HS	Defective endosperm xenia 1	26:260	BTT 63-j-18-17
dsk1	dsk	322	5HL	Dusky 1	41:128	Chikurin-Ibaraki 1
dsk2		729	7HL	Dusky 2	44:208	Betzes
dsp1	l	9	7HS	Dense spike 1	43: 50	Honen 6
dsp9	l9, ert-e	258	6HL	Dense spike 9	43:114	Akashinriki
dsp10	l_c	111	3HS	Dense spike 10	41: 99	Club Mariout
dsp11	dsp	244	1HL	Dense spike 11	41:121	Akashinriki
dub1		661	6HL	Double seed 1	37:301	Bonus
Dwf2		542		Dominant dwarf 2	24:170	Klages / Mata
Eam1	Ppd-H1, Ea	65	2HS	Early maturity 1	44: 64	Estate
Eam5	HvPhyC-e	348	5HL	Early maturity 5	45:123	Higuerilla*2/ Gobernadora
eam6	Ea6, Ea	98	2HS	Early maturity 6	46: 57	Morex
eam7	HvCO7	252	6HS	Early maturity 7	45:118	California Mariout
eam8	ea_k,mat-a	214	1HL	Early maturity 8	46: 69	Kinai 5
eam9	ea,,c	181	4HL	Early maturity 9	26:204	Tayeh 8
eam10	ea_{sp}	130	3HL	Early maturity 10	44: 86	Super Precoz
eli-a	lig-a	623		Eligulum-a	44:199	Foma
eog 1	e	57	2HL	Elongated outer glume 1	43: 64	Triple Bearded Club Mariout
ert-a	ert-6	28	7HS	Erectoides-a	41: 76	Gull
ert-b	ert-2	224	1HL	Erectoides-b	40: 74	Gull
ert-c	ert-1	134	3HL	Erectoides-c	41:108	Gull
ert-d	ert-7	29	7HS	Erectoides-d	42: 82	Gull
ert-e	dsp9	266	6HL	Erectoides-e	43:118	Bonus
ert-f	ert-18	560	1H	Erectoides-f	40:133	Bonus
ert-g	ert-g	330	1HL	Erectoides-g	41:133	Bonus
ert-h	ert-25	561	5HL	Erectoides-h	44:189	Bonus
ert-ii	uzu1	135	3HL	Erectoides-ii	45:109	Bonus
ert-j	ert-31	90	2H	Erectoides-j	43: 70	Bonus

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
ert-k	ert-32	562	6H	Erectoides-k	46:121	Bonus
ert-l	ert-12	563		Erectoides-l	26:489	Maja
ert-m	ert-34	30	7HS	Erectoides-m	46: 47	Bonus
ert-n	ert-51	331	5HL	Erectoides-n	44:120	Bonus
ert-p	ert-44	564		Erectoides-p	26:490	Bonus
ert-q	ert-101	91	6H	Erectoides-q	43: 71	Bonus
Ert-r	Ert-52	332	2HL	Erectoides-r	41:135	Bonus
ert-s	ert-50	565		Erectoides-s	26:491	Bonus
ert-t	brh3	566	2HS	Erectoides-t	45:203	Bonus
ert-u	ari-o	92	7HL	Erectoides-u	45:100	Bonus
ert-v	ert-57	567	6H	Erectoides-v	41:188	Bonus
ert-x	ert-58	568	1H/7H	Erectoides-x	40:136	Bonus
ert-y	ert-69	569		Erectoides-y	26:495	Bonus
ert-z	ert-71	570		Erectoides-z	26:496	Bonus
ert-za	ert-102	571	5H	Erectoides-za	44:189	Bonus
ert-zb	ert-132	572	7HL	Erectoides-zb	45:205	Bonus
ert-zc	ert-149	573	7HS	Erectoides-zc	45:206	Bonus
ert-zd	ari-o	93	7HL	Erectoides-zd	45:102	Bonus
ert-ze	ert-105	574	5HS	Erectoides-ze	45:207	Bonus
fch1	f, lg	55	2HS	Chlorina seedling 1	40: 49	Minn 84-7
fch2	f2, lg5	117	3HL	Chlorina seedling 2	46: 63	28-3398
fch3	f3	220	1HS	Chlorina seedling 3	40: 71	Minn 89-4
fch4	f4	17	7HL	Chlorina seedling 4	43: 54	Montcalm
fch5	f5	18	7HS	Chlorina seedling 5	43: 56	Gateway
fch6	f6	313	5HL	Chlorina seedling 6	44:116	Himalaya
fch7	f7	201	1HL	Chlorina seedling 7	41:113	Smyrna
fch8	f8	5	7HS	Chlorina seedling 8	41: 62	Comfort
fch9	f9	151	4HS	Chlorina seedling 9	44: 92	Ko A
fch10		177	4H	Chlorina seedling 10	43: 95	Unknown cultivar
fch11	f11	260	6HL	Chlorina seedling 11	45:207	Himalaya
fch12	f_c	2	7HS	Chlorina seedling 12	41:60	Colsess
fch13	f13	86	5HL	Chlorina seedling 13	44: 77	Nigrinudum
fch14	f14	87	2HL	Chlorina seedling 14	44: 78	Shyri
fch15	or	52	2HS	Chlorina seedling 15	40: 48	Trebi IV

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
fch16	clo.117	676	2HS	Chlorina seedling 16	40:144	Bonus
fch17	vy	191	1H/3H	Chlorina seedling 17	40: 68	Himalaya / Ingrescens
fer1		453		Few roots 1	46:112	Bomi Abed
flo-a		182	6HL	Extra floret-a	45:116	Foma
flo-b	flo-a	327	6HL	Extra floret-b	45:121	Foma
flo-c	flo-a	74	6HL	Extra floret-c	45: 97	Foma
fol-a		73	2HL	Angustifolium-a	43: 69	Proctor
Fol-b	Ang	548	1HS	Angustifolium-b	40:131	Unknown
fst1	fs	301	5HL	Fragile stem 1	26:252	Kamairazu
fst2	fs2	208	1HL	Fragile stem 2	41:114	Oshichi
fst3	fs3	24	7HS	Fragile stem 3	41: 74	Kobinkatagi 4
fxp1		728		Fenoxaprop-p-ethyl reaction 1	43:223	Morex
gig1	gig	463	2H	Gigas 1	44:164	Tochigi Golden Melon
gig2		612	4HL	Gigas 2	44:191	ND12463
glf1	gl,cer-zh	155	4HL	Glossy leaf 1 ++ ++ -	40: 61	Himalaya
glf3	gl3,cer-j	165	4HL	Glossy leaf 3 ++ ++ -	43: 92	Goseshikoku
glo-a		168	4H	Globosum-a	45:115	Proctor
glo-b		336	5HL	Globosum-b	26:284	Villa
glo-c	glo-c	72	2H	Globosum-c	43: 68	Villa
glo-e		230	1HL	Globosum-e	45:117	Foma
glo-f		342	5HL	Globosum-f	26:291	Damazy
gpa1	gp	59	2HL	Grandpa 1	45: 91	Lyallpur
gra-a	gran-a	131	7H	Granum-a	44: 88	Donaria
gsh1	gs1, cer-q	351	2HS	Glossy sheath 1 - - ++	46: 94	PI 195285
gsh2	gs2	352	3HL	Glossy sheath 2 - - ++	46: 98	Atlas
gsh3	gs3	353	7HS	Glossy sheath 3 - - ++	41:143	Mars
gsh4	gs4	354	6HL	Glossy sheath 4 - - ++	41:146	Gateway
gsh5	gs5	355	2HL	Glossy sheath 5 + - ++	44:126	Jotun
gsh6	cer-c, gs6	356	2HS	Glossy sheath 6 - - ++	46:101	Betzes
gsh7	gs7	81	1H/2H/5H	Glossy sheath 7 - - ++	40: 55	Akashinriki

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p	Parental cultivar
Rec.	Prev.					
gsh8	cer-u, gs8	413	2HS	Glossy sheath 8 + + ++	46:105	Akashinriki
Gth1	G	69	2HL	Toothed lemma 1	44: 68	Machine (Wexelsen)
hcm1	h	77	2HL	Short culm 1	26:115	Morex
Hln1	Hn	164	4HL	Hairs on lemma nerves 1	44: 99	Kogane-mugi
Hsh1	Hs	179	4HL	Hairy leaf sheath 1	44:107	Kimugi
ibl1	ibl1	716	5HL	Intense blue aleurone 1	46:136	Ethiopian 637
int-b		320	5HL	Intermedium spike-b	44:118	Bonus
int-c	i	178	4HS	Intermedium spike-c	37:237	Gamma 4
int-f		543	2HS/ 3HL	Intermedium spike-f	44:178	Foma
int-h		544	5H	Intermedium spike-h	44:179	Kristina
int-i		545	2HS	Intermedium spike-i	41:181	Kristina
int-k		546	7H	Intermedium spike-k	44:180	Kristina
int-m		547	5HL	Intermedium spike-m	44:181	Bonus
Kap1	K	152	4HS	Hooded lemma 1	26:179	Colsess
lab1		730	5HL	Labile 1	46:137	
lam1		651		Late maturity 1	43:174	Steptoe
lax-a		474	5HL	Laxatum-a	46:113	Bonus
lax-b		268	6HL	Laxatum-b	44:113	Bonus
lax-c		475	6HL	Laxatum-c	41:174	Bonus
lbi1	lb	308	5HL	Long basal rachis internode 1	43:125	Wisconsin Pedigree 38
lbi2	lb2	156	4HS	Long basal rachis internode 2	44: 92	Montcalm
lbi3	lb3	27	7HL	Long basal rachis internode 3	42: 79	Montcalm
lel1	lel	235	2H	Leafy lemma 1	46: 74	G7118
Lfb1	Lfb	343	5HL	Leafy bract 1	41:140	Montcalm
Lga1	Log	549	7HS	Long glume awn 1	44:183	Guy Mayle
lgn2	lg2	169	4HS	Light green 2	42:264	Minn 75
lgn3	lg3	170	1HL	Light green 3	44:103	No 154
lgn4	lg4	171	4HL	Light green 4	44:105	Himalaya / Ingrescens
lig1	li, aur-a	60	2HL	Liguleless 1	45: 93	Muyoji
lin1	s, rin	99	2HS	Lesser internode number 1	41: 92	Natural occurrence

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
lgn3	lg3, lg7	170	1HL	Light green 3	44:103	No 154
lgn4	lg4, lg1	171	4HL	Light green 4	44:105	Himalaya / Ingrescens
lig1	li, aur-a	60	2HL	Liguleless 1	45: 93	Muyoji
lin1	s, rin	99	2HS	Lesser internode number 1	41: 92	Natural occurrence
Lks1	Lk	75	2HL	Awnless 1	41: 84	*Hordeum inerme*
lks2	lk2	10	7HL	Short awn 2	45: 80	Honen 6
lks5	lk5	172	4HL	Short awn 5	41:110	CIho 5641
lks6	lks.q	724	1H/5H/ 6H	Short awn 6	43:219	Morex
lnt1	rnt	118	3HL	Low number of tillers 1	43: 82	Mitake
lys1	lys	338	5HL	High lysine 1	26:286	Hiproly
lys3	sex3	339	5HL	High lysine 3	43:127	Bomi Abed
Lys4	sex5	232	1HS	High lysine 4	26:230	Bomi Abed
lys6		269	6H	High lysine 6	44:114	Bomi Abed
lzd1	dw4	125	3H	Lazy dwarf 1	43: 87	Akashinriki
mat-b		578	7HL	Praematurum-b	46:123	Bonus
mat-c	Eam6	579	2H	Praematurum-c	46:125	Bonus
mat-d		580	4HL/ 6HL	Praematurum-d	45:208	Bonus
mat-e		581		Praematurum-e	26:508	Bonus
mat-f		582	1H	Praematurum-f	45:210	Bonus
mat-g		583		Praematurum-g	26:510	Bonus
mat-h		584	4HL	Praematurum-h	45:212	Bonus
mat-i		585	7HL	Praematurum-i	45:214	Bonus
min1	min	161	4HL	Semi-minute dwarf 1	44: 97	Taisho-mugi
min2	en-min	160		Enhancer of minute 1	26:186	Kaiyo Bozu
mnd1	m	519	2H	Many noded dwarf 1	43:154	Mesa
mnd3	m3	618	4HS	Many noded dwarf 3	44:194	Montcalm
mnd4	m4	347	5HL	Many noded dwarf 4	44:122	Akashinriki
mnd5		632	7HL	Many noded dwarf 5	44:202	C2-95-199
mnd6	den-6	633	5HL	Many noded dwarf 6	44:203	Bonus
mnd7		726		Many noded dwarf 7	43:221	Steptoe
mov1	mo5	43	7HL	Multiovary 1	43: 59	Steptoe
mov2	mo	147	3HS	Multiovary 2	43: 91	Steptoe
mov3	mo-a	234	1H	Multiovary 3	32:102	Akashinriki

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
mov4	mo8	648		Multiovary 4	43:171	Steptoe
mov5	mov.o	723		Multiovary 5	43:218	Morex
msg1	ms, ms1	357	1HL	Male sterile genetic 1	45:126	CIho 5368
msg2	ms2	358	2HL	Male sterile genetic 2	45:128	Manchuria
msg3	ms3	359	1HL	Male sterile genetic 3	45:130	Gateway
msg4	ms4	360	1H	Male sterile genetic 4	45:132	Freja
msg5	ms5	361	3HS	Male sterile genetic 5	45:133	Carlsberg II
msg6	ms6	362	6HS	Male sterile genetic 6	45:135	Hanna
msg7	ms7	363	5HL	Male sterile genetic 7	45:137	Dekap
msg8	ms8	364	5HL	Male sterile genetic 8	45:139	Betzes
msg9	ms9	365	2HS	Male sterile genetic 9	45:141	Vantage
msg10	ms10	366	7HS	Male sterile genetic 10	45:142	Compana
msg11	ms11	367	5HS	Male sterile genetic 11	45:144	Gateway
msg13	ms13	368	3HL	Male sterile genetic 13	45:146	Haisa II
msg14	ms14	369	7HS	Male sterile genetic 14	45:147	Unitan
msg15	ms15	370		Male sterile genetic 15	45:149	Atlas/2*Kindred
msg16	ms16	371	5HS	Male sterile genetic 16	45:150	Betzes
msg17	ms17	372	5HL	Male sterile genetic 17	45:152	Compana
msg18	ms18	373	5HL	Male sterile genetic 18	45:153	Compana
msg19	ms19	374	5HS	Male sterile genetic 19	45:155	CIho 14393
msg20	msg,,ad	375	4H	Male sterile genetic 20	45:156	Hannchen
msg21	ms21	376	1HL	Male sterile genetic 21	45:157	Midwest Bulk
msg22	ms22	383	7H	Male sterile genetic 22	45:162	Glacier / Compana
msg23	ms23	384	5H	Male sterile genetic 23	45:163	Betzes
msg24	ms24	385	4HL	Male sterile genetic 24	45:164	Betzes
msg25	msg,,r	166	2HS	Male sterile genetic 25	45:113	Betzes
msg26	msg,,u	395	7HS	Male sterile genetic 26	45:166	Unitan
msg27	msg,,ae	464	2HS	Male sterile genetic 27	45:174	Firlbecks III
msg28	msg,,as	465	2HS	Male sterile genetic 28	45:175	York
msg29	msg,,a	466	5HL	Male sterile genetic 29	45:176	Ackermans MGZ
msg30	msg,,c	467	7HL	Male sterile genetic 30	45:177	Compana
msg31	msg,,d	468	1HL	Male sterile genetic 31	45:178	51Ab4834
msg32	msg,,w	469	7H	Male sterile genetic 32	45:179	Betzes
msg33	msg,,x	470	2HS	Male sterile genetic 33	45:180	Betzes

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
msg34	msg,,av	471	6HS/ 7HS	Male sterile genetic 34	45:181	Paragon
msg35	msg,,dr	498	2HL	Male sterile genetic 35	45:183	Karl
msg36	msg,,bk	499	6HS	Male sterile genetic 36	45:184	Betzes
msg37	msg,,hl	500	3HL	Male sterile genetic 37	45:186	Clermont
msg38	msg,,jl	501	3H	Male sterile genetic 38	45:187	Ingrid
msg39	msg,,dm	502	3H	Male sterile genetic 39	45:188	P11
msg40	msg,,ac	503	6HL	Male sterile genetic 40	45:190	Conquest
msg41	msg,,aj	504	6HS	Male sterile genetic 41	45:191	Betzes
msg42	msg,,db	505	3H	Male sterile genetic 42	45:193	Betzes
msg43	msg,,br	506	2HL	Male sterile genetic 43	45:194	Betzes
msg44	msg,,cx	507	5HL	Male sterile genetic 44	45:195	HA6-33-02
msg45	msg,,dp	508	5HL/ 7HS	Male sterile genetic 45	45:196	RPB439-71
msg46	msg,,ec	509	2H/6H	Male sterile genetic 46	45:197	Hector
msg47	msg,,ep	510	3HS/ 7HS	Male sterile genetic 47	45:198	Sel12384CO
msg48	msg,,jt	520	1H	Male sterile genetic 48	45:199	Simba
msg49	msg,,jw	335	5HL	Male sterile genetic 49	45:122	ND7369
msg50	msg,,hm	34	7HL	Male sterile genetic 50	45: 88	Berac
mss1	mss	84	5H	Midseason stripe 1	44: 75	Montcalm
mss2		39	7HS	Midseason stripe 2	44: 59	ND11258
mtt1	mt	521	1HS	Mottled leaf 1	41:179	Montcalm
mtt2	mt2	302	5HL	Mottled leaf 2	41:127	Montcalm
mtt4	mt,,e	78	2HL	Mottled leaf 4	41: 86	Victorie
mtt5	mt,,f	264	6HL	Mottled leaf 5	41:126	Akashinriki
mtt6		629	7HS	Mottled leaf 6	45:228	ND6809
mtt7	mtt.h	677	2HS	Mottled leaf 7	42:753	Morex
mtt8	Mut 1661	674		Mottled leaf 8	43:182	Bowman Rph3.c
mtt9	Mut 2721	675		Mottled leaf 9	44:207	Bowman Rph3.c
mul2		251	6HL	Multiflorus 2	26:232	Montcalm
nar1		637	6HS	NADH nitrate reductase-deficient 1	35:194	Steptoe
nar2		638	5HL	NADH nitrate reductase-deficient 2	35:196	Steptoe

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
nar3		639	7HS	NADH nitrate reductase-deficient 3	35:197	Winer
nar4		640	2HL	NADH nitrate reductase-deficient 4	35:198	Steptoe
nar5		641	5HL	NADH nitrate reductase-deficient 5	35:199	Steptoe
nar6		642	2HL	NADH nitrate reductase-deficient 6	35:200	Steptoe
nar7		643	6HL	NADH nitrate reductase-deficient 7	35:201	Steptoe
nar8		644	6HS	NADH nitrate reductase-deficient 8	35:202	Steptoe
nec1	sp,,b	222	1HL	Necrotic leaf spot 1	43:108	Carlsberg II
nec2	nec2	261	6HS	Necrotic leaf spot 2	26:241	Carlsberg II
nec3	nec3	265	6HS	Necrotic leaf spot 3	43:116	Proctor
nec4	nec4	138	3H	Necrotic leaf spot 4	43: 88	Proctor
nec5	nec5	139	3H	Necrotic leaf spot 5	43: 89	Diamant
Nec6	Sp	611	7HS	Necrotic leaf spot 6	43:159	Awnless Atlas
nec7	nec-45	635	1H/6H/7H	Necroticans 7	43:166	Kristina
nec8	nec.w	671	5HL	Necrotic leaf spot 8	43:179	Bowman Rph3.c
nec9	Mut 3091	672	3HL	Necrotic leaf spot 9	43:181	Bowman Rph3.c
nec10	necS 1-1	681	3H	Necroticans 10	43:184	Steptoe
nec11		682	1H	Necroticans 11	43:185	Steptoe
nec12		683		Necroticans 12	43:186	Steptoe
nec13		684		Necroticans 13	43:187	Steptoe
nec14		685		Necroticans 14	43:188	Steptoe
nec15		686		Necroticans 15	43:189	Steptoe
nec16t		687		Necroticans 16	43:190	Steptoe
nec17		688		Necroticans 17	43:191	Steptoe
nec18		689		Necroticans 18	43:192	Steptoe
nec19		690		Necroticans 19	43:193	Steptoe
nec20		691		Necroticans 20	43:194	Steptoe
nec21		692		Necroticans 21	43:195	Steptoe
Nec22		693		Necroticans 22	43:196	Steptoe
nec23		694		Necroticans 23	43:197	Steptoe

Nec24		695		Necroticans 24	43:198	Steptoe

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
nec25		696		Necroticans 25	43:199	Steptoe
Nec26		697		Necroticans 26	43:200	Steptoe
nec27		698		Necroticans 27	43:201	Steptoe
nec28		699		Necroticans 28	43:202	Morex
nec29		700		Necroticans 29	43:203	Morex
nec30		701		Necroticans 30	43:204	Morex
nec31		702		Necroticans 31	43:205	Morex
nec32		703		Necroticans 32	43:206	Morex
nec33		704		Necroticans 33	43:207	CIho 4196
nec34	nec.k	197	4HS	Necroticans 34	43:104	ND13917
nld1	nld	323	5HL	Narrow leafed dwarf 1	46: 88	Nagaoka
nld2		660	5H/6H/7H	Narrow leafed dwarf 2	43:176	Steptoe
nud1	n, nud	7	7HL	Naked caryopsis 1	44: 51	Himalaya
ops1	op-3	624	7HS	Opposite spikelets 1	45:226	Bonus
ops2	op-2	718	5HL	Opposite spikelets 2	43:213	Foma
ops3	op-1	719	5HS	Opposite spikelets 3	43:214	Bonus
ovl1		176	4H	Ovaryless 1	35:191	Kanto Bansei Gold
ovl2	ovl2	646		Ovaryless 2	43:169	Harrington
ovl3		725		Ovaryless 3	43:220	Harrington
pmr1	pmr	40	7HS	Premature ripe 1	44: 60	Glenn
pmr2	nec-50	634		Premature ripe 2	32:135	Bonus
Pre2	Re2	76	2HL	Red lemma and pericarp 2	46: 53	Buckley 3277
Pub1	Pub	127	3HL	Pubescent leaf blade 1	44: 84	Multiple Dominant
Pvc1	P_c	68	2HL	Purple veined lemma 1	44: 67	Buckley 2223-6
Pyr1	Pyr.g	42	3HL	Pyramidatum 1	41: 78	Pokko/Hja80001
raw1	r	312	5HL	Smooth awn 1	46: 84	Lion
raw2	r2	340	5HL	Smooth awn 2	46: 92	Lion
raw5	r,,e	257	6HL	Smooth awn 5	44:112	Akashinriki
raw6	r6	334	5HL	Smooth awn 6	26:282	Glenn
rcr1	γ08-122	737		Required for resistance to *Cochliobolus sativus* 1	45:249	Morex
rcr2	γ08-123	738		Required for resistance to *Cochliobolus sativus* 2	45:250	Morex

rcr3	γ08-124	739		Required for resistance to *Cochliobolus sativus* 3	45:251	Morex

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
rob1	o	254	6HS	Orange lemma 1	46: 78	CIho 5649
Rpc1		149	3H	Reaction to *Puccinia coronata* var. *hordei* 1	37:232	Hor 2596
Rpg1	T	511	7HS	Reaction to *Puccinia graminis* 1	26:437	Chevron
Rpg2	T2	512		Reaction to *Puccinia graminis* 2	26:439	Hietpas 5
rpg4		319	5HL	Reaction to *Puccinia graminis* 4	26:267	Q21861
Rph1	Pa	70	2H	Reaction to *Puccinia hordei* 1	26:107	Oderbrucker
Rph2	Pa2	88	5HS	Reaction to *Puccinia hordei* 2	37:212	Peruvian
Rph3	Pa3	121	7HL	Reaction to *Puccinia hordei* 3	26:156	Estate
Rph4	Pa4	218	1HS	Reaction to *Puccinia hordei* 4	42:302	Gull
Rph5	Pa5	122	3HS	Reaction to *Puccinia hordei* 5	37:224	Magnif 102
Rph6	Pa6	575	3HS	Reaction to *Puccinia hordei* 6	26:501	Bolivia
Rph7	Pa7	136	3HS	Reaction to *Puccinia hordei* 7	37:228	Cebada Capa
Rph9	Pa9, Pa12	32	5HL	Reaction to *Puccinia hordei* 9	37:201	HOR 2596
Rph10		137	3HL	Reaction to *Puccinia hordei* 10	26:174	Clipper C8
Rph11		267	6HL	Reaction to *Puccinia hordei* 11	26:247	Clipper C67
Rph12	Pa12, Pa9	333	5HL	Reaction to *Puccinia hordei* 12	26:281	Triumph
Rph13		590		Reaction to *Puccinia hordei* 13	28: 31	PI 531849
Rph14		591		Reaction to *Puccinia hordei* 14	28: 32	PI 584760
Rph15	Rph16	96	2HL	Reaction to *Puccinia hordei* 15	37:214	PI 355447

rpr1		707	4H	Required for *Puccinia graminis* resistance 1	42:757	Morex

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
rpr2	γ08-118	731	6H	Required for *Puccinia graminis* resistance 2	46:139	Morex
rpr3	γ08-112	732		Required for *Puccinia graminis* resistance 3	46:141	Morex
rpr4	γ08-114	733		Required for *Puccinia graminis* resistance 4	46:142	Morex
rpr5	γ08-117	734		Required for *Puccinia graminis* resistance 5	46:143	Morex
rpr6	γ08-119	735		Required for *Puccinia graminis* resistance 6	46:144	Morex
rpr7	γ08-115	736		Required for *Puccinia graminis* resistance 7	46:145	Morex
Rpt1	Pt	667	3HL	Reaction to *Pyrenophora teres* 1	43:177	Tifang
Rpt2	Rpt2c	237	1HS	Reaction to *Pyrenophora teres* 2	43:110	CIho 9819
Rpt3	QRptts2	711	2HS	Reaction to *Pyrenophora teres* 3	43:208	Tennessee Awnless D22-5
Rpt4	QRpt7	48	7HL	Reaction to *Pyrenophora teres* 4	43: 61	Galleon
Rpt5	Rpt_a	272	6HL	Reaction to *Pyrenophora teres* 5	43:120	CIho 5791, CIho 9819
Rpt6		713	5HL	Reaction to *Pyrenophora teres* 6	43:210	CIho 9819
Rpt7	Qrpts4	714	4HL	Reaction to *Pyrenophora teres* 7	43:211	Halcyon
Rpt8	QRpts4	198	4HS	Reaction to *Pyrenophora teres* 8	43:105	Q21861
Rsg1	Grb	22	7H	Reaction to *Schizaphis graminum* 1	37:199	Omugi
Rsg2		577		Reaction to *Schizaphis graminum* 2	37:283	PI 426756
rsm1	sm	35	7HS	Reaction to BSMV 1	26: 84	Modjo 1
Rsp1	Sep	515		Reaction to *Septoria passerinii* 1	26:441	CIho 14300
Rsp2	Sep2	516		Reaction to *Septoria passerinii* 2	37:275	PI 70837

Rsp3	Sep3	517		Reaction to *Septoria passerinii* 3	37:276	CIho 10644
rtt1	rt	51	2HS	Rattail spike 1	26: 87	Goldfoil

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
Run1	Un	21	7HS	Reaction to *Ustilago nuda* 1	26: 67	Trebi
rvl1	rvl	226	1HL	Revoluted leaf 1	40: 77	Hakata 2
Ryd2	Yd2	123	3HL	Reaction to BYDV 2	26:158	CIho 2376
Rym1	Ym	167	4HL	Reaction to BaYMV 1	32: 96	Mokusekko 3
Rym2	Ym2	20	7HL	Reaction to BaYMV 2	26: 66	Mihori Hadaka 3
rym3	ym3	345	5HS	Reaction to BaYMV 3	32:105	Chikurin Ibaraki
rym5	Ym	141	3HL	Reaction to BaYMV 5	32: 90	Mokusekko 3
sbk1	sk, cal-a	62	2HS	Subjacent hood 1	40: 51	Tayeh 13
sca1	sca	128	3HS	Short crooked awn 1	44: 85	Akashinriki
sci-a	sci-3	625	5H	Scirpoides-a	44:200	Bonus
sci-b	sci-4	239	1H/6H	Scirpoides-b	46: 76	Bonus
scl-a	scl-6	626	1HL	Scirpoides leaf-a	44:201	Foma
scl-b	scl-5	150	3H/6H	Scirpoides leaf-b	40: 60	Bonus
sdw1	sdw	518	3HL	Semidwarf 1	41:176	M21
sdw2	sdw-b	133	3HL	Semidwarf 2	45:108	Mg2170
sdw3	gai	663	2HS	Semidwarf 3	46:134	Hv287
sdw4		45	7HL	Semidwarf 4	46: 51	
sdw6	sdw.f	240	1H/7H	Semidwarf 6	46: 77	Vada
sdw7	sdw.u	196	4HL	Semidwarf 7	43:103	Glenn
seg1	se1	377	7HL	Shrunken endosperm genetic 1	45:158	Betzes
seg2	se2	378	7HS	Shrunken endosperm genetic 2	26:326	Betzes
seg3	se3	379	3H	Shrunken endosperm genetic 3	45:160	Compana
seg4	se4	380	7HL	Shrunken endosperm genetic 4	37:267	Compana
seg5	se5	381	7HS	Shrunken endosperm genetic 5	26:329	Sermo / 7*Glacier
seg6	se6	396	3HL	Shrunken endosperm genetic 6	44:138	Ingrid
seg7	se7	397		Shrunken endosperm genetic 7	37:269	Ingrid

sex7	sex.i	628	5HL	Shrunken endosperm xenia 7	32:129	I90-374
sex8	sex.j	143	3HS	Shrunken endosperm xenia 8	43: 90	I89-633-1

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p	Parental cultivar
Rec.	Prev.					
sex9	sex.1	195	4HL	Shrunken endosperm xenia 9	43:102	Alf
sgh1	sh1	163	4HL	Spring growth habit 1	26:188	Iwate Mensury C
Sgh2	Sh2	309	5HL	Spring growth habit 2	26:259	Indian Barley
Sgh3	Sh3	213	1HL	Spring growth habit 3	26:212	Tammi / Hayakiso 2
sid1	nls	180	4HL	Single internode dwarf 1	43: 97	Akashinriki
Sil1	Sil	228	1H	Subcrown internode length 1	40: 79	NE 62203
sld1	dw-1	126	3HL	Slender dwarf 1	41:103	Akashinriki
sld2		83	2HS	Slender dwarf 2	44: 74	Akashinriki
sld3	ant-567	186	4HS	Slender dwarf 3	40: 63	Manker
sld4	sld.d	100	2HS	Slender dwarf 4	43: 72	Glacier
sld5		144	3HS	Slender dwarf 5	44: 90	Indian Dwarf
sld6	sld.gs	242	1H	Slender dwarf 6	40: 87	Glenn
sld7	sld.f	194	4HL	Slender dwarf 7	43:101	Glenn
sld8	sld.i	49	7HS/ 4HL	Slender dwarf 8	43: 63	Wisconsin Pedigree 38
sls1	sls	227	1HS	Small lateral spikelet 1	40: 78	Morex
smn1	smn	38	3H/5H	Seminudoides 1	43: 58	Haisa
snb1	sb	26	7HS	Subnodal bract 1	26: 72	L50-200
srh1	S, l	321	5HL	Short rachilla hair 1	46: 86	Lion
sun1	sun1	650		Sensitivity to *Ustilago nuda* 1	43:173	Steptoe
tfm1		190	1HL	Thick filament 1	40: 67	Volla
trd1	t, bra-c	202	1HL	Third outer glume 1	46: 65	Valki
trp1	tr	61	4HL	Triple awned lemma 1	41: 82	CIho 6630
tst1	tst1	647	6HL	Tip sterile 1	43:170	Steptoe
tst2		636	4HL	Tip sterile 2	43:167	Donaria
ubs4	lks2, ari-d	11	7HL	Unbranched style 4	45: 84	Ao-Hadaka
ubs5		727		Unbranched style 5	43:222	Harrington
uzu1	uz	102	2HL	Uzu 1 or semi brachytic 1	45:104	Baitori

var1	va	306	5HL	Variegated 1	37:259	Montcalm
var2	va2	344	5HL	Variegated 2	32:104	Montcalm
var3	va3	303	5HL	Variegated 3	44:115	Montcalm
viv-a	viv-5	627	2H	Viviparoides-a	45:227	Foma

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.[†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
viv-b	viv-6	193	4HS	Viviparoides-b	43:100	Foma
viv-c	viv-1	720	5H	Viviparoides-c	43:215	Foma
vrs1	v	6	2HL	Six-rowed spike 1	37:192	Trebi
vrs1	lr	58	2HL	Six-rowed spike 1	26: 94	Nudihaxtoni
vrs1	V^d	66	2HL	Two-rowed spike 1	26:103	Svanhals
vrs1	V^t	67	2HL	Deficiens 1	26:104	White Deficiens
vrs2	v2	314	5HL	Six-rowed spike 2	26:263	Svanhals
vrs3	v3	315	1HL	Six-rowed spike 3	40: 90	Hadata 2
vrs4	v4	124	3HL	Six-rowed spike 4	41:101	MFB 104
wax1	wx	16	7HS	Waxy endosperm 1	42: 65	Oderbrucker
wnd1	wnd	23	4Hl	Winding dwarf 1	42: 74	Kogen-mugi
wst1	wst	107	3HL	White streak 1	41: 97	CIho 11767
wst2	wst2	304	5HL	White streak 2	46: 83	Manabe
wst4		56	2HL	White streak 4	44: 51	Kanyo 7
wst5	wst5	221	1HL	White streak 5	46: 73	Carlsberg II
wst6	wst,,j	129	3HL	White streak 6	41:105	Akashinriki
wst7	rb	79	2HL	White streak 7	41: 87	GS397
wxs1	wxs	615	7H/ 2HL	Waxy spike 1	43:160	Steptoe
Xnt1	X_a	25	7HL	Xantha seedling 1	26: 71	Akashinriki
xnt2	x_b	513		Xantha seedling 2	26:440	Black Hulless
xnt3	x_c	105	3HS	Xantha seedling 3	26:139	Colsess
xnt4	x_{c2}	36	7HL	Xantha seedling 4	26: 85	Coast
xnt5	x_n	255	6HL	Xantha seedling 5	26:237	Nepal
xnt6	x_s	113	3HS	Xantha seedling 6	26:147	Smyrna
xnt7	xan,,g	233	1HL	Xantha seedling 7	26:231	Erbet
xnt8	xan,,h	140	3HS	Xantha seedling 8	26:177	Carlsberg II
xnt9	xan,,i	37	7HL	Xantha seedling 9	26: 86	Erbet
yhd1	yh	158	4HL	Yellow head 1	42:250	Kimugi
yhd2	yh2	592		Yellow head 2	45:215	Compana
ylf1	ylf1	652	7HS	Yellow leaf 1	43:175	Villa

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
Ynd1	Yn	183	4HS	Yellow node 1	44:109	Morex
yst1	yst	104	3HS	Yellow streak 1	42:178	Gateway
yst2		109	3HS	Yellow streak 2	44: 81	Kuromugi 148 / Mensury C
yst3	yst,,c	462	3HS	Yellow streak 3	44:163	Lion
yst4		85	2HL	Yellow streak 4	44: 76	Glenn
yst5	yst5	346	7HS	Yellow streak 5	43:130	Bowman / ant10.30
yvs1	y_x	63	2HS	Virescent seedling 1	26: 99	Minn 71-8
yvs2	y_c	3	7HS	Virescent seedling 2	26: 46	Coast
zeb1	zb	120	3HL	Zebra stripe 1	43: 86	Mars
zeb2	zb2, fch10	461	4HL	Zebra stripe 2	43:152	Unknown cultivar
zeb3	zb3, zb	223	1HL	Zebra stripe 3	40: 72	Utah 41
Zeo1	Knd	82	2HL	Zeocriton 1	41: 89	Donaria
Zeo2	Mo1	614	2HL	Zeocriton 2	41:193	36Ab51
Zeo3	Mo1	184	4HL	Zeocriton 3	32: 99	Morex

* Recommended locus symbols are based on utilization of a three-letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996.

† Chromosome numbers and arm designations are based on the Triticeae system. Utilization of this system for naming of barley chromosomes was at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

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BGS 30, Erectoides-m, *ert-m*

Stock number: BGS 30
Locus name: Erectoides-m
Locus symbol: *ert-m*

Previous nomenclature and gene symbolization:

Erectoides-34 = *ert-34* (3, 4).

Inheritance:

Monofactorial recessive (3, 4, 10).

Located in chromosome 7HS (6, 7, 8, 10); *ert-m.34* is about 14.7 cM distal from the *cer-f* (eceriferum-f) locus (11, 12, 13); *ert-m.34* is near the *ant1* (anthocyanin-less 1) locus (10); *ert-m.34* is associated with SNP markers 2_1326 to 2_1270 (positions 65.26 to 93.97 cM) in 7H bins 05 to 06 of the Bowman backcross-derived line BW316 (1); *ert-m.34* mapped to a 4.7 cM interval flanked by SNP markers 3_0576 and 1_0721 (15).

Description:

Spiikes have a compact appearance caused by a reduction in rachis internode length, with rachis internode length values from 2.0 to 2.8 mm. However, the rachis internodes within each spike are often variable in length, and the spike appears irregular similar to those of opposite spikelet mutants. Plants with an allele at the *ert-m* locus are often 10 to 15 cm shorter than parental cultivars, and some tillers of most plants have one or more extremely shortened upper culm internodes (10). Some tillers of most plants have one or more extremely shortened and twisted upper culm internodes (5, 10, 15). Leaf blades show a scirpoid-like phenotype (5, 15). Alleles at the *ert-m* locus respond positively to GA_3 treatments designed to increase rachis internode length (14). Some alleles at the *ert-m* locus lack normal anthocyanin pigmentation. The anthocyanin deficiency can not be separated from the *ert-m* allele and is apparently an allele at the *ant1* locus (9, 10). Plants of the Bowman backcross-derived line for *ert-m.34,* BW316, were slightly shorter than Bowman with an average rachis internode length of 3.8 vs. 4.5 mm. Kernels of BW316 varied in size from equal to 20% larger than those of Bowman, but test weight was 10% lower. Grain yields of BW316 averaged about 2/3 those of Bowman (2). The *ert-m* mutants have a spike that varies from irregular two-rowed with non-twisted rachis internodes to regular cross-rowed with twisted alternating rachis internodes. Because elongation of the upper culm internodes is often variable, the emerging spike is frequently trapped in the leaf sheath, which often results in a twisted culm and peduncle (15). Sequencing of HvERECTA in barley *ert-m* mutants identified severe DNA changes in 15 mutants, including full gene deletions *in ert-m.40* and *ert-m.64*. Both deletions additionally cause anthocyanin deficiency associated with the closely linked anthocyanin-less 1 (*ant1*) locus (15).

Origin of mutant:

A thermal neutron induced mutant in Bonus (NGB 14657, PI 189763) (4, 10).

Mutational events:

ert-m.34 (NGB 112635, GSHO 487)*, -m.35* (NGB 112636)*, -m.40* (NGB 112640) with an *ant1* mutant*, -m.41* (NGB 112641)*, -m.42* (NGB 112642)*, -m.54* (NGB 112653)*, -m.64* (NGB 112663) with an *ant1* mutant in Bonus (NGB 14657, PI 189763) (4); *ert-m.87* (NGB 112686) with an *ant1* mutant*, -m.107* (NGB 112706)*, -m.115* (NGB 112714)*, -m.130* (NGB 112729)*, -m.144* (NGB 112743)*, -m.168* (NGB 112768)*, -m.169* (NGB 112769) in Bonus, *-m.314* (NGB 112829) in Foma (NGB 14659, CIho 11333) (10); *ert-m.328* (NGB 112843) in Foma (5); *ert-m.330* (NGB 112845)*, -m.363* (NGB 112879)*, -*

m.384 (NGB 112899), *-m.426* (NGB 112942) in Foma (10). Mutants *ert-m.41* (NGB 112641), *ert-m.314* (NGB 112829), *ert-m.328* (NGB 112843), and *ert-m.384* (NGB 112899) were demonstrated to be non-allelic to *ert-m.40* (NGB 112640) (15).

Mutant used for description and seed stocks:

ert-m.34 (NGB 112635, GSHO 487) in Bonus; *ert-m.34* in Bowman (PI 483237)*8 (GSHO 1843, BW316, NGB 22111).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:78-79.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:57-58.
U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:47-48.

BGS 33, Anthocyanin-less 1, *ant1*

Stock number:	BGS 33
Locus name:	Anthocyanin-less 1
Locus symbol:	*ant1*

Previous nomenclature and gene symbolization:

Green stem = *rs* (1).

Exrubrum-a = *rub-a* (5).

Inheritance:

Monofactorial recessive (1, 8).

Located in chromosome 7HS (1); *ant1.b* is near the centromere (3); near the *ert-m* (erectoides-m) locus (9); *ant1.b* is about 15.0 cM distal from the *nud1* (naked caryopsis 1) locus (1); *Rst1.a* is associated with SNP markers 2_0074 to 2_0113 (positions 71.81 to 75.21 cM) in 7H bin 05 of the Bowman backcross-derived line BW762 (2); *ant1.1* is associated with SNP markers 1_0838 to 2_0103 (positions 49.53 to 139.86 cM) in 7H bins 04 to 08 of the Bowman backcross-derived line BW013 (2), in 7H bin 05. The closely linked *ert-m.34* (erectoides-m) mutant mapped to a 4.7 cM interval flanked by SNP markers 3_0576 and 1_0721 (12).

Description:

When grown under favorable light conditions, red pigmentation of the stem does not occur (1). Anthocyanin pigments are not observed in the stem, auricles, awns, or lemma veins of induced *ant1* mutants (4). However, moderate to strong pigmentation of these plant parts is observed in plants homozygous for the normal allele *Rst1.a* at this locus. The *ant1.b* allele, which occurs frequently in cultivars of Manchurian origin and is present in Bowman (PI 483237), reduces considerably the red pigmentation of stem, auricles, awns, and lemma veins. Expression of alleles at the *ant1* locus is easier to observe at the stem base of seedlings (4, 12). Sequencing of HvERECTA in barley *ert-m* (erectoides-m) mutants identified full gene deletions in both *ert-m.40* and *ert-m.64*, which additionally caused anthocyanin deficiency. Analyses of *ert-m* and *ant1* single and double deletion mutants suggested that *Ant1* encodes a R2R3 myeloblastosis (MYB) transcription factor (7, 11, 12).The *ant1.b* variant is a leaky mutant that can synthesize small amounts of anthocyanin (12). The relative anthocyanin content of the leaf sheath extracts from Bowman (*ant1.b*) as measured by OD_{530} (anthocyanin content measured spectrophotometrically at 530 nm) was less than half that of Bowman backcross-derived lines with the normal allele, *Ant1.a* (*HvMpc1*) (11).

Origin of mutant:

Natural occurrence in some cultivars, frequently in those of Oriental origin (4); an alpha ray induced mutant in Bonus (NGB 14657, PI 189763) (8).

Mutational events:

ant1.b (*rst1.b*) in Manchurian introductions (4); *ant1.1* (NGB 114552), *ant1.2* (NGB 114553), *ant1.4* (NGB 114555) in Bonus (NGB 14657, PI 189763) (8); *ant1.56* in Bonus (8); *ert-m.40* (NGB 112640) and *ert -m.64* (NGB 112663) with *ant1* mutant in Bonus (NGB 14657, PI 189763) (6, 10, 11).

Mutant used for description and seed stocks:

ant1.1 (NGB 114552, GSHO 1620) in Bonus; *ant1.1* from Bonus in Bowman (PI 483237)*3 (BW013, NGB 20421); *Ant1.a* (*Rst1.a*) in Goldfoil (PI 5975, GSHO 185) (1, 3); *ant1.b* from six-rowed Manchurian type cultivars is in Bowman (4); *Ant1.a* from Mut. 4128 of Haisa (PI 197617) in Bowman*6 (GSHO 1834); *Ant1.a* from Mut. 4128 in

Bowman*7 (BW762, NGB 22230).

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Prepared:

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Revised:

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J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:49-50.

Barley Genetics newsletter (2016) 46:47-145.

BGS 045, Semidwarf 4, *sdw4*

Stock number:	BGS 045
Locus name:	Semidwarf 4
Locus symbol:	*sdw4*

Previous nomenclature and gene symbolization:

Culm length QTL on 7H = qCUL.ak-7H (4).

Inheritance:

Monofactorial recessive (3, 7, 8).

Location in chromosome 7HL (4); *sdw4.ba* is about 1.2 cM from codominant STS marker ABG608 in bin 11 (3, 4); *sdw4.ba* is near DArT marker bPb-2328 in 7HL (6); *sdw4.ba* is associated with SNP markers 1_1243 to 2_1363 (positions 167.56 to 198.70 cM) in 7H bins 10 to 12 of the Bowman backcross-derived line BW831 (1); likely in 7H bin 11.

Description:

Semidwarf 4 (*sdw4*) is a monofactorial recessive that reduces culm length by about 20 to 30% (3, 4, 6) by affecting the length of the 3rd and 4th culm internodes proportional more than the upper internodes (3, 4). The *sdw4* gene was associated with reduced lodging (4). Combining *sdw4* with *uzu1* (uzu 1) further reduced plant height to less than half normal (3). In the Bowman backcross-derived line for *sdw4.ba* (BW831), plants were shorter, but the culms were slightly more robust and the flag leaves were larger than those of Bowman. Delayed heading was observed in plants with the *sdw4.ba* gene in some genetic backgrounds (2). The *sdw4.ba* mutation in China was reported to have originated as dwarf mutant (68-142) induced in the late 1960s by gamma-rays in the Chinese landrace Zhenongguangmangerleng (7). The first cultivar containing this mutant was Zhepi 1, released in 1978 by the Zhejiang Academy of Agricultural Science (7). Most cultivars now grown in the lower valley of Yangtze River were selected from crosses to Zhepi 1 (7).

Origin of mutant:

A gamma-ray induced mutant in the Chinese landrace Zhenongguangmangerleng (7); a spontaneous variant in the Japanese cultivar Kanto Nakate Gold (OUJ 518) released in 1953 (4), both parents of Kanto Nakate Gold, Shikoku (OUJ 546) and Golden Melon (OUJ808. PI 263410) are tall cultivars (4, 5).

Mutational events:

sdw4.ba (68-142) in Zhenongguangmangerleng (7), *sdw4.ba* in the Japanese cultivar Kanto Nakate Gold (OUJ 518, PI383933) (4). Based on morphological traits and chromosomal location of mutant, both mutational events are very similar (2).

Mutant used for description and seed stocks:

sdw4.ba in Zhepi 1 and Zhenongda 7; *sdw4.ba* in Kanto Nakate Gold (OUJ 518; PI 383933), *sdw4.ba* from Zhenongda 7 in Bowman*2 (BW831, NGB 22268).

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Prepared:

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Revised:

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:51-52.

Barley Genetics newsletter (2016) 46:47-145.

BGS 76, Red lemma and pericarp 2, *Pre2*

Stock number:	BGS 76
Locus name:	Red lemma and pericarp 2
Locus symbol:	*Pre2*

Previous nomenclature and gene symbolization:

Purple chaff color = *P* (1, 7).
Purple chaff color = P_1 (11).
Purple pericarp = *P* (3, 12, 15).
Purple lemma = *P* (2).
Red pericarp = *R* (2).
Red pericarp 2 = *Re2* (13).

Inheritance:

Purple pericarp is controlled by one dominant gene (1, 3). Two dominant complementary genes (*Pre1* and *Pre2*) control purple or red pigmentation of the lemma, palea, and pericarp (2, 11, 16). The second gene controlling purple lemma and pericarp (now identified as *Pre1*) was loosely associated with chromosome 5H (2).

Located in chromosome 2HL (2); *Pre2.a* is about 17.1 cM distal from the *vrs1* (six-rowed spike 1) locus (2, 3, 11, 12, 16); *Pre2.a* is over 11.2 cM proximal from the *ant2* (anthocyanin-less 2) locus (4, 8, 9); *Pre2.a* is associated with SNP markers 1-0214 to 1_0876 (positions 150.96 to 161.08 cM) in 2H bins 10 to 11 of Bowman backcross-derived line BW648 (5); *Pre2.a* mapped in 2HL between the SSR markers Bmag0125 and GBMS244 and was about 5.1 cM distal from the *vrs1* locus *(10)*, in 2H bin 10.

Description:

Purple or red coloration of the hull (chaff) and pericarp develops during the soft dough stage of grain fill, and fades as the grain matures. Anthocyanin pigments in an acid cell solution produce the red to violet color observed in the pericarp and lemma (2). Bowman and the Bowman backcross-derived line for *Pre2.a*, BW648, were similar for all agronomic and morphological traits expect kernel color (6). The recessive allele at the *Pre2* locus has a 179 bp insertion in the promoter region and is not transcribed in Bowman, but *Pre2.b* is up-regulated in the purple-grained line (BW648, NGB 22213) with coordinately co-expressed flavonoid biosynthesis structural genes (*Chs*, *Chi*, *F3h*, *Dfr*, *Ans*) (15). The *Pre2* and *Ant2* loci are positioned near each other, but controlled by different genes, which modify kernel and plant pigmentation (10).

Origin of mutant:

Natural occurrence in a few cultivars and some *Hordeum vulgare* subsp *spontaneum* accessions (2, 16).

Mutational events:

Pre2.a in Buckley 3277 (NSL 32606, GSHO 234) (2).

Mutant used for description and seed stocks:

Pre2.a in Buckley 3277 (GSHO 234); *Pre2.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1565) in Bowman (PI 483237, NGB 22812)*9 (GSHO 1926, BW648, NGB 22213).

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Prepared:
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Revised:
J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:70-71.
J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:53-54.

BGS 80, Anthocyanin-less 2, *ant2*

Stock number:	BGS 80
Locus name:	Anthocyanin-less 2
Locus symbol:	*ant2*

Previous nomenclature and gene symbolization:

Non-purple straw = p_r or *pr* (10).

Anthocyanin-less = *ant-2* (3, 7).

Exrubrum = *rub* (5).

Colorless leaf tip 2 = clt_2 (6), c_2 (6).

Inheritance:

Monofactorial recessive (3, 10).

Located in chromosome 2HL (3, 10); *ant2* is about 15.1 cM distal from the *vrs1* (six-rowed spike 1) locus (10, 12, 13); *ant2.20* has no SNP markers in the Bowman backcross-derived line, BW019, that are deviant from those of Bowman (2); *ant2.h* is associated with SNP markers 1_0247 to 2_0182 (positions 150.96 to 185.53 cM) in 2H bins 10 to 12 in Bowman backcross-derived line BW020 (2); *ant2* from Saffron cosegregated with SNP markers 2_1007 and 2_1175 [position 98.82 cM (155.04 to 155.98 cM)] in 2H bin 10 (1).

Description:

Anthocyanin pigments are not observed in any vegetative plant parts, including the stem, auricles, lemma, and awn (3, 6, 7). The straw does not develop a purple pigmentation as it approaches maturity (10). The recommended symbol for the dominant allele is *Ant2.c* (formerly *Pr*). Besides anthocyanin pigmentation, no other morphological differences were observed between Bowman and the Bowman backcross-derived lines for *ant2.20* (BW019) and *ant2.h* (BW020) (4). Resequencing the putative anthocyanin pathway gene *ant2* (*HvbHLH1*) identified a 16-bp deletion resulting in a premature stop codon upstream of the basic helix-loop-helix domain (1). Since Shoeva et al. (11) did not study the *ant2* mutants, allelism between variants at the *Pre2* and *Ant2* loci could not be determined. The *Pre2* and *Ant2* loci are positioned near each other, but controlled by different genes, which modify kernel and plant pigmentation (9).

Origin of mutant:

Natural occurrence in few cultivars (8, 10), the first 3 or 4 alleles are likely natural occurrences the same locus.

Mutational events:

ant2.d (*pr1.b*) in Alva (NGB 1507, NSGC1866), *ant2.e* (*pr1.c*) in Balder (NGB 14668, PI 195481), *ant2.f* (*pr1.d*) in Cambrinus (PI 321779), *ant2.g* (*pr1.e*) in Sultan (PI 339814) (8); *ant2.15* (NGB 114564), *2.20* (NGB 114569, GSHO 1632), *2.23* (NGB 114572), *2.25* (NGB 114575), *2.26* (NGB 114576), *2.27* (NGB 114278) in Foma (NGB 14659, CIho 11333) (7); *ant2.41* (NGB 114596) in Mari (NGB 14656, PI 428407) (8); *ant2.46* (NGB 111505) in Foma, *2.47* (NGB 111823), *2.48* (NGB 111782), *2.49* (NGB 111808), *2.50* (NGB 111811), *2.51* (NGB 111817), *2.54* (NGB 111872), *2.55* (NGB 111787) in Bonus (NGB 14657, PI 189763) (8); *2.112, 2.113, 2.114, 2.115, 2.116, 2.117, 2.118, 2.120, 2.121, 2.122, 2.130* in Nordal (NGB 13680, NGB 4704) (8); *ant2.h (pr1.f*) in Shyri (GSHO 2430) (4).

Mutant used for description and seed stocks:

ant2.20 (NGB 114569, GSHO 1632) in Foma; *ant2.h* (GSHO 2430) in Shyri; *ant2.h* from Shyri in Bowman (PI 483237)*5 (GSHO 1919); *ant2.h* in Bowman*7 (BW020, NGB

20428); *ant2.20* (NGB 114569, GSHO 1632) from Foma in Bowman*2 (GSHO 1920); *ant2.20* in Bowman*6 (BW019, NGB 20427).

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Prepared:

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Revised:

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BGS 98, Early maturity 6, *Eam6*

Stock number:	BGS 98
Locus name:	Early maturity 6
Locus symbol:	*Eam6*

Revised locus symbol:

The *Eam6.h* variant was demonstrated to be an allele at the Praematurum-c (*mat-c*) locus (2). However, continued use of the *Eam6* nomenclature as locus and allele symbols is recommended because the large phenotypic differences occur between the *mat-c* mutants (see BGS 579) and the *Eam6.h* allele.

Previous nomenclature and gene symbolization:

Early heading = *Ea* (16).
Early maturity 6 = *Ea6* (13).
Earliness per se 2S = *eps2S* (8).
Early 16 = *ea-c16* (6).
Praematurum-c = *mat-c* (2, 14).
Hordeum vulgare CENTRORADIALIS = *HvCEN* (2).

Inheritance:

Monofactorial dominant (16).

Located in chromosome 2HS (16); *Eam6.h* is about 13.5 cM proximal from the *vrs1* (six-rowed spike 1) locus (16); *Eam6.h* is near the *gsh5* (glossy sheath 5) locus based on linkage drag (4, 5); *Eam6.h* is near molecular marker ABC167b in 2H bin 08 (11, 15); a maturity QTL mapped near SNP marker bPb-3677 at 57.5 cM in the progeny of a Nure/Tramois cross (2); the praematurum-c (*mat-c*) mutants were determined to allelic and the structural gene *HvCEN* (*Hordeum vulgare* CENTRORADIALIS) and mapped at 57.5 cM (2); the *mat-c.19* deletion is in a 0.27 cM segment of 2H near SNP markers 2_887, 2_0537, and 2_0390 (10), in 2H bin 07.

Description:

Alleles at the *Eam6* locus alter the timing of floral initiation when barley is grown under long-day conditions. In temperate climates, the *Eam6.h* gene induces spring barley to head two to five days earlier than plants with the recessive allele (4, 11). A much stronger response to long photoperiods is associated with the Early maturity 1 (*Eam1*, *Ppd-H1*) gene. Tohno-oka et al. (15) reported that *Eam6* gene from Morex (CIho 15773) is effective when the photoperiod is 13 hours or longer and that the *Eam1* gene from Steptoe (CIho 15229) induced early heading when the photoperiod is 14 hours or longer. In North Dakota, plants with both the *Eam1* and *Eam6* genes head one to two days earlier than those with only the *Eam1* gene (4). The maturity factors, *Eam1* and *Eam6*, were studied by Yasuda and named “A” and “B”, respectively (17). A QTL for response to long photoperiods in North American two- and six-rowed barleys was reported in the *Eam6* region of 2H (7, 12). *Eam6* may interact with other maturity genes because a QTL for early heading was detected in 2HS under both short- and long-day environments in the Harrington/Morex mapping population (8). In the dihaploid progeny from Nure (winter) barley crossed to Tramois (spring) barley, the earliness allele from Nure was associated with fewer days to head and higher kernel weights and yields over 13 Mediterranean sites (2). These are short-day environments in which the *Eam1* gene is not expressed. A QTL for earliness was present at the *Eam6* position in a genome-wide association study (GWAS) in collections of Mediterranean spring and winter barleys (3) and a worldwide core collection of spring barleys (1). The *mat-c.19* deletion and several other *mat-c* mutants affect the barley ortholog of *Antirrhinum majus CENTRORADIALIS* (*AmCEN*) gene (2) and *Arabidopsis thaliana TERMINAL FLOWER 1* (*AtTFL1*) gene (10).

Origin of mutant:

Natural occurrence in many spring, six-rowed barley, represented by the cultivar Morex (CIho 15773) (15). The early variant (haplotype II) at the (*Hordeum vulgare* CENTRORADIALIS (*HvCEN*) locus occurs in both wild and cultivated barleys (2).

Mutational events:

Eam6.h in an unknown cultivar (15), possibly introduced into Midwest six-rowed spring barleys via Trebi (CIho 936) (4); *Eam6.h* in Morex (CIho 15773) (8, 11, 15). The early variant (haplotype II) at the *Eam6* locus is present in many winter barley cultivars (2).

Mutant used for description and seed stocks:

Eam6.h in Morex (CIho 15773, GSHO 2492); *Eam6.h* (haplotype I) from Nordic (CIho 15216) is present in Bowman (PI 483237) (2, 4).

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Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:216-217.

J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:57-59.

BGS 106, Albino seedling 6, *abo6*

Stock number:	BGS 106
Locus name:	Albino seedling 6
Locus symbol:	*abo6*

Previous nomenclature and gene symbolization:

White seedling c = a_c (2).

Albino seedling c = a_c (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HS (4); *abo6.f* is about 10.7 cM distal from the *uzu1* (uzu 1) locus (4); *abo6.f* is about 2.4 cM from the *msg5* (male sterile genetic 5) locus (1).

Description:

Seedlings are white in color, devoid of normal pigments, and die about 10 days after emergence (2). Plants with this phenotype are classified as albino mutants (3). The *abo6.f* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Colsess (CIho 2792) (2).

Mutational events:

abo6.f (Colsess III, GSHO 63) in Colsess (CIho 2792) (2); Colsess I (GSHO 30) and Colsess II in Colsess (2).

Mutant used for description and seed stocks:

abo6.f (GSHO 30, Colsess I) in Colsess (CIho 2792).

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Prepared:

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Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:140.

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:60.

BGS 108, Albino lemma 1, *alm1*

Stock number:	BGS 108
Locus name:	Albino lemma 1
Locus symbol:	*alm1*

Previous nomenclature and gene symbolization:

Albino lemma = *al* (13).
Eburatum = *ebu-a* (5).
White husk = *wh* (7).

Inheritance:

Monofactorial recessive (13).

Located in chromosome 3HS (13); *alm1.a* is about 16.5 cM distal from the *uzu1* (uzu 1) locus (3, 9, 11, 12, 13); *alm1.a* is about 4.8 cM proximal from RFLP marker MWG844B in 3H bin 04 (1); *alm1.a* is associated with SNP markers 2_1402 to 1_0628 (positions 78.82 to 135.80 cM) in 3H bins 05 to 08 of the Bowman backcross-derived line BW011 (2); the *alm1.f* (*wh*) mutant was mapped 0.27 proximal from *Bmag508A* and 0.34 cM distal from *Bmac67* (7), in 3H bin 05.

Description:

The lemma and palea are white in color and mostly devoid of chlorophyll, but they terminate into green tips with green awns. The basal part of lower leaf sheaths and stem nodes are devoid of chlorophyll. Ligules and joints between the leaf sheath and blade are white in color (13, 14). Plant vigor was reduced slightly and heading was delayed by 2 to 4 days in the Bowman backcross-derived line for *alm1.a*, BW011 (4). Kernels of BW011 were thin and weighted nearly 20% less, 4.6 vs. 5.6 mg, than those of Bowman. Grain yields of BW011 were 1/2 to 3/4 those of Bowman (4). Based on a transmission electron microscopy examination, the *alm1.f* (*wh*) mutant exhibited abnormal chloroplast development (7).

Origin of mutant:

Spontaneous occurrence in an unknown cultivar (Russia 82) (OUU086, NSL 43389) (13).

Mutational events:

alm1.a (GSHO 270) in Russia 82 (OUU086, NSL 43389) (13); *alm1.b* in Liberty (CIho 9549) (3); *alm1.c* (Mut 966/61) in Proctor (PI 280420) (6); *ebu-a.1* (NGB 115236), *-a.2* (NGB 115237), *-a.3* (NGB 115238) in Foma (NGB 14659, CIho 11333) (5, 14); *ebu-a.4* (NGB 115239), *-a.5* (NGB 115240) in Foma (10); *alm1.d* (γ06-03, GSHO 3682) and *alm1.e* (FN530, GSHO 3683) in Morex (CIho 15773) may be alleles based on phenotypic similarity (8); *alm1.f* (white husk = *wh,* and likely an *alm1* allele) was isolated in Supi 3 (Kinuyu Taka/Kanto Nijo 25//Hu 94-043) (7).

Mutant used for description and seed stocks:

alm1.a (GSHO 270) in Russia 82; *alm1.a* in Bowman (PI 483237)*8 (GSHO 1953, BW011, NGB 20419).

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Barley Genetics newsletter (2016) 46:47-145.

BGS 117, Chlorina seedling 2, *fch2*

Stock number: BGS 117
Locus name: Chlorina seedling 2
Locus symbol: *fch2*

Previous nomenclature and gene symbolization:

Chlorina seedling 2 = *f2* (12).
Light green 5 = *lg5* (11).
Chlorina seedling f2 = *clo-f2* (8).

Inheritance:

Monofactorial recessive (3, 4, 12).

Located in chromosome 3HL (10, 12, 13, 14); *fch2.c* is about 7.7 cM distal from the *cur2* (curly 2) locus (15); *fch2.c* is associated with SNP markers 1_0702 to 1_0694 (positions 239.73 to 248.51 cM) in 3H bin 15 in Bowman backcross-derived line BW358 (1).

Description:

The *fch2.c* seedlings have a pale yellow-green color, which persists until near maturity under greenhouse or field conditions. Development of homozygous plants is delayed, but the stunted plants survive to produce seed (3). A complete absence or greatly reduced levels of chlorophyll b were found in mutant plants (3, 4, 8). The respiratory and photosynthetic rates of detached leaves and intact plants are not significantly different from those of normal plants. However, the growth rate of mutant plants decreases after the endosperm is depleted (4). Plants of the Bowman backcross-derived line for *fch2.c*, BW358, showed a drastic response to environmental stress during the growing season. The heading date for BW358 plants was about 13 days later than Bowman. Plant height varied from near normal to a 20% reduction. Average kernel weights were reduced up to 40%. Grain yields of BW358 were 1/3 to 1/2 those of Bowman (2). An absence of chlorophyll b-binding proteins in the photosynthetic membranes is found in *fch2* mutants (5, 6). Alleles at the *fch2* locus were shown to have DNA sequence changes in the gene encoding chlorophyllide a oxygenase or interfere with regulators of enzyme production (7). The enzyme converts chlorophyllide a to chlorophyllide b and it is essential for Chl b biosynthesis (7).

Origin of mutant:

A spontaneous mutant in progeny from the cross Moister (CIho 2799) X California Coast (CIho 6115) (3).

Mutational events:

fch2.c (28-3398 Chlorina, GSHO 107) in Moister/California Coast (3, 10); *fch2.y* (*lg5*, GSHO 294) in CIho 6151 (11); *clo-f2.2800*, *-f2.2807*, *-f2.3613* in Donaria (PI 209784), -*f2.101, -f2.102, -f2.103, -f2.105, -f2.107, -f2.108, -f2.109* in Tron, *-f2.122, -f2.123, -f2.133* in Bonus (NGB 14657, PI 189763) (8, 9).

Mutant used for description and seed stocks:

fch2.c (28-3398, GSHO 107) in Moister/California Coast; *fch2.c* in Bowman (PI 483237)*7 (GSHO 1993, BW358, NGB 20597).

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Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:151-152.
J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:63-64.

BGS 202, Third outer glume 1, *trd1*

Stock number: BGS 202
Locus name: Third outer glume 1
Locus symbol: *trd1*

Previous nomenclature and gene symbolization:

Third glume = *t* (7).
Bracteate (10).
Bracteatum-c = *bra-c* (4, 14).

Inheritance:

Monofactorial recessive (7, 8, 10, 12).

Located in chromosome 1HL (7, 8, 11, 12); *trd1.a* is about 16.0 cM distal from the *Blp1* (Black lemma and pericarp 1) locus (7, 8, 12); *trd1.a* is about 11.4 cM proximal from the *eam8* (early maturity 8) locus (13); *trd1.a* is associated with SNP markers 2_0383 to 2_0840 (positions 192.78 to 202.26 cM) in 1H bins 13 to 14 of the Bowman backcross-derived line BW880 (2); *bra-c.1* is associated with SNP markers 1_0041 to 2_0772 (positions 199.04 to 206.07 cM) in 1H bin 14 of the Bowman backcross-derived line BW069 (2); *trd1.a* is between to SNP markers 1_1127 and 2_1105 in1H bin 14 (6).

Description:

The characteristic trait of this mutant is the presence of a bract, third outer glume, outside the two empty glumes of the central spikelet. The bract associated with the lowest spikelet is always the largest, embracing in some cases about one-half the spike, and the bracts become progressively smaller toward the tip of the spike (12). The *trd1.a* mutant is described as a transitional mutant in which suppression of leaf (sheath) development at nodes in the spike is poorly suppressed (1, 11). Basal rachis internodes may be elongated (3, 6). Although allelism tests were not conducted for the first three *trd* mutants, similar linkage values between the *trd1* and *Blp1* loci are reported (7, 8, 12). Takahashi et al. (12) assumed that they used the same material studied by Miyake and Imai (10). Compared to Bowman, plants of the Bowman backcross-derived lines for *trd1.a* and *bra-c.1*, BW880 and BW069, headed 2 to 4 days later and were slightly shorter. Spikes of BW880 and BW069 had 2 to 3 fewer fertile rachis nodes per spike; and their grain .yields were 1/2 to 2/3 that of Bowman (3). The *Trd1* locus was identified as the GATA transcription factor, an ortholog of rice *Nl1* and maize *Tsh1* genes (5).

Origin of mutant:

A spontaneous mutant found by Vavilov in a black six-rowed accession classified as *Hordeum vulgare* var. *afghanicum* (7).

Mutational events:

trd1.a in *Hordeum vulgare* var. *afghanicum* (7, 10); *trd1.b* (GSHO 227) in Valki (CIho 5478) (8); *trd1.c* in a Japanese cultivar (10, 12); *trd1.d* (Mut 1969/61) in Proctor (PI 280420) (5); *bra-c.1* (NGB 114303, GSHO 1695) in Bonus (NGB 14657, PI 189763) (4); *bra-c.2* (NGB 114304), *-c.3* (NGB 114305), *-c.4* (NGB 111306), *-c.5* (NGB 114307) in Bonus, *-c.6* (NGB 1140308) in Foma (NGB 14659¸ CIho 11333), *-c.8* (NGB 114312) in Kristina (NGB 14661, NGB 1500) (9).

Mutant used for description and seed stocks:

trd1.b (GSHO 227) in Valki; *bra-c.1* (NGB 114303, GSHO 1695) in Bonus; *trd1.b* from R.I. Wolfe's Chromosome 5 Marker Stock in Bowman (PI 483237)*7 (GSHO 2060); *trd1.b* in Bowman*8 (BW880, NGB 22314); *bra-c.1* in Bowman*4 (GSHO 2061); *bra-c.1* in Bowman*5 (BW069, NGB 20477).

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BGS 203, Black lemma and pericarp 1, *Blp1*

Stock number:	BGS 203
Locus name:	Black lemma and pericarp 1
Locus symbol:	*Blp1*

Previous nomenclature and gene symbolization:

Black lemma and caryopsis = *B* (9).
Black pericarp = *Bk* (1).
Black lemma and pericarp = *B* (10).

Inheritance:

Monofactorial dominant (1, 6, 9).

Located in chromosome 1HL (5, 7); *Blp1.b* is about 16.0 cM proximal from the *trd1* (third outer glume 1) locus (5); *Blp1.b* is in 1H bin 13 about 8.8 cM proximal from RFLP marker ABC261 (2); *Blp1.b* is associated with SNP markers 2_0959 to 2_0603 (positions 173.49 to 199.04 cM) in 1H bins 13 to 15 of the Bowman backcross-derived line BW062 (3); *Blp1.g* is associated with SNP marker 2_0940 (about position 179 cM) in 1H bin 13 of the Bowman backcross-derived line BW060 (3); *Blp1.b* in BW062 was located between microsatellites *Xgbms0012* and *Xgbms0184* (8), in 1H bin 13.

Description:

Black pigmentation of the lemma and pericarp develops slightly before maturation of the spike. Pigmented organs may include all parts of the spike, awns, the upper portion of the stem, and upper leaves. The intensity of pigmentation associated with each of the dominant alleles at the *Blp1* locus is characteristic of that allele, and is relatively stable over environments (10). Black seed is produced by melanin-like pigment in the pericarp (1). Woodward (10) reported that the dominance ranking of alleles at the *Blp1* locus is related to the intensity of black pigmentation they confer, with the *Blp1.b* (*B*) allele conferring extreme black pigmentation. The *Blp1.mb* (B^{mb}) allele is associated with medium black and a reduced distribution pattern; and the *Blp1.g* (B^{g}) allele is associated with light black or gray coloration (10, 11). In the Bowman backcross-derived lines for the *Blp1* locus, BW060 and BW062, the expression of other morphological traits appeared similar to those of Bowman (4). The flavonoid pigments are not involved in development of the black lemma and pericarp trait (8).

Origin of mutant:

Natural occurrence in several cultivars (9, 10).

Mutational events:

Blp1.b (*B*) in *Hordeum distichon* var. *nigrinudum* No 1 (NSL 3286, GSHO 988) (10); *Blp1.mb* (B^{mb}) in CIho 2970 (GSHO 226) (10); *Blp1.g* (B^{g}) in Blackhull (CIho 878, GSHO 199) and Black Smyrna (CIho 191, GSHO 222) (10).

Mutant used for description and seed stocks:

Blp1.b in *Hordeum distichon* var *nigrinudum* No 1 (GSHO 988); *Blp1.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 3450) in Bowman (PI 483237)*8 (GSHO 2054, BW062, NGB 20470); likely *Blp1.g* from a Composite Cross in Bowman*5 (BW060, NGB 20468).

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BGS 214, Early maturity 8, *eam8*

Stock number: BGS 214
Locus name: Early maturity 8
Locus symbol: *eam8*

Previous nomenclature and gene symbolization:

Early heading k = ea_k (31).
Early maturity-a = *ea-a* (12, 25).
Praematurum-a = *mat-a* (7, 12, 17, 18, 32).
Erectoides-o = *ert-o* (12, 22).
Hordeum vulgare Early Flowering3 = *HvELF3* (2, 6, 32).

Inheritance:

Monofactorial recessive (7, 11).

Located in chromosome 1HL (25), *eam8.k* is about 11.4 cM distal from the *trd1* (third outer glume 1) locus and 20.9 cM distal from the *Blp1* (Black lemma and pericarp 1) locus (25, 29); *eam8.w* is associated with SNP markers 2_0603 to 2_0138 (positions 199.04 to 202.26 cM) in 1H in bin 14 of the Bowman backcross-derived line BW290 (5); *eam8.k* is associated with SNP markers 1_0782 to 1_0443 (positions 193.83 to 206.12 cM) in 1H bin 14 of the Bowman backcross-derived line BW289 (5); *ert-o.16* is associated with SNP markers 1_0911 to 1_1509 (positions 177.51 to 199.04) in1H bins 13 to 14 of the Bowman backcross-derived line BW319 (5), in 1H bin 14.

Description:

Early heading of early maturity 8 (*eam8*) mutants is associated with decreased culm length, spike length, kernels per spike, and grain yield (20, 29, 31). Mutant plants are day-length neutral or photoperiod insensitive when grown in the fall at Kurashiki, Japan. They headed about 20 days earlier than the standard mid-season cultivar, Akashinriki (31). Day-length neutrality was observed in early heading mutants isolated from spring barley in Sweden (4, 13). Under controlled environmental conditions, number of days to heading did not change as photoperiod is altered (4, 14). All *mat-a* induced mutants were characterized by yellowish-green seedlings at an early stage of development under controlled environmental conditions (3). Other *eam8* mutants showed a similar response by becoming yellow green under specific growing conditions, 8 to 12 hours of illumination at low temperatures (below 10°C) plus high temperature (20°C or higher) during the dark period (9, 25, 29). The color change is caused by photothermal stress, which increases the zeaxanthin content at the expense of chlorophyll and other pigments (9, 23, 29). The mutant stock *mat-a.8* was released as the cultivar Mari (NGB 14656, NGB 1491, PI 428407) (13, 15). When grown under 12 h days, the levels of phytochrome B (*phyB)* decreased in light-grown BMDR-1 plants, containing a mutant allele at the eam8 locus, compared to normal plants (16). The instability in phyB content was reported to be responsible for photoperiod insensitivity of *eam8* mutants *(*16). Under continuous light and with far-red light treatment for seven days, most differences in heading date between BMDR-1 (*eam8.y)* and BMDR-8 (Shabet) were eliminated (23). The selection of independent *eam8* mutations facilitated short growth-season adaptation and expansion of the geographic range of barley (6). When the *eam8.k* gene was placed in a winter barley genetic background [controlled by the *sgh1.a* (spring growth habit 1 or Hv*Vrn2*) gene], the vernalization requirement *sgh1* (*Vrn2*) was expressed under all photoperiods and the early flowering phenotype was partially repressed in unvernalized plants (27). The *Mat-a* or *Eam8* (*HvELF3*) locus has been cloned and is a homolog of the *Arabidopsis thaliana* circadian clock regulator *EARLY FLOWERING3* (*ELF3*) (6, 32). Among 87 *mat-a* alleles identified more than 20 different *mat-a* alleles had mutations leading to the defective putative *ELF3* protein (32). The *eam8* mutants have increased expression of the floral activator *HvFT1* (*Sgh3*,, *Vrn3*). which is independent of allelic variation at *Eam1* (*Ppd-H1*) locus (6). Early flowering of the *mat-a* (*elf3)* mutants lail to block excess gibberellin (GA) synthesis and expression of *HvFT1* (2). Alvarez et al. reported that *EARLY FLOWERING3* (*ELF3*) is a candidate gene for the earliness *per se* locus *Eps-A*^{m}*1* in *Triticum monococcum* (1).

Origin of mutant:

An X-ray induced mutant in Maja Abed (NGB 8815, PI 184884) (10, 11, 14); natural occurrence in Kinai 5 (OUJ493) and Kagoshima Gold (OUJ219) (25, 30).

Mutational events:

ert-o.16 (NGB 112618, GSHO 489) in Maja Abed (NGB 8815, PI 184884) (10); *eam8.k* in Kagoshima Gold (OUJ 219), Kinai 5 (OUJ493, GSHO 765, CIho 11560), and Kindoku (OUU332) (25, 26, 30); *mat-a.8* (NGB 110008, NGB 14656, NGB 1491, NGB 4694), -*a.11* (NGB 110011), -*a.12* (NGB 110012) in Bonus (NGB 14657, PI 189763) (11, 18); *mat-a.27* (NGB 110027), -*a.45* (NGB 110045), -*a.46* (NGB 110046), -*a.48* (NGB 110048), -*a.62* (NGB 110062) in Bonus, -*a.110* (NGB 110110), -*a.130* (NGB 110130), -*a.153* (NGB 110153), -*a.221* (NGB 110221), -*a.238* (NGB 110238), -*a.255* (NGB 110255), -*a.272* (NGB 110272), -*a.274* (NGB 110274), -*a.287* (NGB 110287), -*a.289*(NGB 110289), -*a.294* (NGB 110294), -*a.325* (NGB 110325), -*a.338* (NGB 110338), -*a.370* (NGB 110370), -*a.384* (NGB 110384), -*a.390* (NGB 110390),-*a.404* (NGB 110404), -*a.406* (NGB 110406), -*a.407* (NGB 110407) in Foma (NGB 14659, CIho 11333), -*a.509* (NGB 110509), -*a.641* (NGB 110641), -*a.703* (NGB 110703), -*a.733* (NGB 110733),in Kristina (NGB 1500, NGB 14661), -*a.753* (NGB 110753), -*a.796* (NGB 110796), -*a.797* (NGB 110797), -*a.813* (NGB 110813), -*a.832* (NGB 110832), -*a.903* (NGB 116858), -*a.909* (NGB 117440), -*a.921* (NGB 117452) in Bonus, -*a.961* (NGB 117492), -*a.970* (NGB 117501), -*a.976* (NGB 117507), -*a.984* (NGB 117515), -*a.1011* (NGB 117542), in Sv 79353, -*a.1032* (NGB 117563), -*a.1033* (NGB 117564), -*a.1034* (NGB 117565), -*a.1035* (NGB 117566), -*a.1036* (NGB 117567), -*a.1037* (NGB 117568), -*a.1039* (NGB 117570), -*a.1040* (NGB 117571), -*a.1041* (NGB 117572), -*a.1042* (NGB 117573), -*a.1043* (NGB 117574), -*a.1044* (NGB 117575), -*a.1045* (NGB 117576), -*a.1046* (NGB 117577), -*a.1047* (NGB 117578), -*a.1048* (NGB 117579), -*a.1049* (NGB 117580) in Sv Vg74233 (17); *mat-a.1050* (NGB 117581), -*a.1051* (NGB 117582), -*a.1052* (NGB 117583), -*a.1053* (NGB 117584), -*a.1054* (NGB 117585), -*a.1055* (NGB 117586), -*a.1056* (NGB 117587), -*a.1057* (NGB 117588), -*a.1058* (NGB 117589), -*a.1059* (NGB 117590), -*a.1060* (NGB 117591), -*a.1061* (NGB 117592), -*a.1062* (NGB 117593), -*a.1063* (NGB 117594), -*a.1064* (NGB 117595), -*a.1065* (NGB 117596), -*a.1067* (NGB 117598), -*a.1069* (NGB 117600), -*a.1070* (NGB 117601), -*a.1071* (NGB 117602), -*a.1072* (NGB 117603), -*a.1073* (NGB 117604), -*a.1074* (NGB 117605) in Sv Vg74233 (19); *eam8.q* (Ea8), *eam8.r* (Ea9), *eam8.s* (Ea10), *eam8.t* (Ea16) in Chikurin Ibaraki 1 (OUJ069, CIho 7370, GSHO 783) (28); *eam8.u* (Mut 2571) in Donaria (PI 161974) (9, 21); *eam8.v* in Munsing (CIho 6009, GSHO 636) (8, 23, 24); *eam8.w* in Early Russian (CIho 13839) (8), BMDR-1 (*eam8.y)* from the original mutant in a dwarf line backcrossed to Shabet (CIho 13827) (23).

Mutant used for description and seed stocks:

eam8.k in Kinai 5 (OUJ493, GSHO 765, CIho 11560); *ert-o.16* in Maja Abed (NGB 112618, GSHO 489); *eam8.k* from Kinai 5 in Bonus*5 (30); *mat-a.8* from Bonus in Tochigi Golden*5 (28); *eam8.v* from Munsing in Titan (CIho 16526)*7 (23); *eam8.k* from

Kinai 5 in Bowman (PI 483237)*7 (GSHO 2063, BW289, NGB 20573); *eam8.w* from Early Russian in Bowman*7 (BW290, NGB 20574); *ert-o.16* from Maja Abed in Bowman*7 (GSHO 2064); *ert-o.16* in Bowman*8 (BW319, NGB 22114).

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BGS 221, White streak 5, *wst5*

Stock number:	BGS 221
Locus name:	White streak 5
Locus symbol:	*wst5*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 1HL (4); *wst5.e* is about 34.5 cM distal from the *nec1* (necrotic leaf spot 1) locus (2, 3, 4); *wst5.e* is about 21.7 cM proximal from the *Blp1* (Black lemma and pericarp 1) locus (2, 3, 5); *wst5.a* is associated in chromosome 1HL with SNP markers 2_0780 to 1_1509 (positions 154.89 to 199.04 cM) in 1H bins 12 to 14 of the Bowman backcross-derived line BW914 (1), likely in 1H bin 12.

Description:

White streaks with poorly defined margins may develop on the foliage, but expression is influenced by environment and possibly genetic background. Some environmental conditions cause the plants to be nearly albinotic from the seedling stage until heading when the plants turn green; while under other conditions the streaks seem absent (4).

Origin of mutant:

A mutant induced by combined treatment with gamma-rays and diethyl sulfate of Carlsberg II (NGB 5085, CIho 10114) (5).

Mutational events:

wst5.e (Mutant no 10, GSHO 591) in Carlsberg II (NGB 5085, CIho 10114) (3).

Mutant used for description and seed stocks:

wst5.e (GSHO 591) in Carlsberg II; *wst5.e* in Bowman (PI 483237) (GSHO 2053), *wst5.e* in Bowman*2 (BW914, NGB 22345),

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Prepared:

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Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:219.

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:73.

BGS 235, Leafy lemma 1, *lel1*

Stock number:	BGS 235
Locus name:	Leafy lemma 1
Locus symbol:	*lel1lks5.p*

Previous nomenclature and gene symbolization:

Leafy lemma = *lel* (1).

Inheritance:

Monofactorial recessive, but a second gene *lel2*, which should have been identified as *lks5.f* (2, 3, 4), is required for expression of leafy lemma phenotype (1, 5).
Located in chromosome 2H (2); *lel1.a* is associated with SNP markers 1_0876 to 2_0943 (positions 161.08 to 237.13 cM) in 2H bins 11 to 14 of Bowman backcross-derived line BW474 (2). The second gene required for leafy lemma expression is associated with SNP markers 2_1122 to 1_1019 (positions 47.8 to 183.54 cM) in 4H bins 05 to 13 of the Bowman backcross-derived line BW474 and with SNP markers 2_0422 to 2_0072 (positions 38.41 to 95.92 cM) in 4H bins 04 to 09 of the Bowman backcross-derived line BW475 (2). The *lel1.a* mutant was previously located in chromosome 1HL (5); about 6.1 cM distal from molecular marker MWG733 in 1H bin 12 (5).

Description:

The overall shape of the leafy lemma is similar to that of the typical, but miniature, grass leaf. The leafy lemma has a basal zone that is wider and more elongated to the transition zone, and a distal domain similar in shape to a leaf blade (1, 5). In all crosses analyzed, F_2 *lel1* plants always had awnless lemmas, the caryopsis was longer than normal and was partially naked, there was a tendency for the rachilla to bear more than one floret, and rachis internodes were elongated (5). The *lks2* gene was reported as required for full expression of the leafy lemma phenotype (5), but the short variant isolated from the leafy lemma stock was allelic at the *lks5* locus (3). The second mutant isolated from original stock was identified as *lel2.b* (2), but a review of Gerd Bossinger’s Thesis (4), allelism tests (3), and molecular marker data (2) indicated that the second gene is *lks5.f*. The kernels of BW474 were lighter, 4.6 vs 5.7 mg, test weights were 30 to 40% lower, and grain yield was about 50% lower (3).

Origin of mutant:

A spontaneous mutant isolated at the Istituto Sperimentale per la Cerealicoltura (Fiorenzuola, Italy) in a plot having a recessive mutant for short awn identified as the *lks5* (short awn 5) line from the Small Grains Germplasm Research Facility (USDA-ARS), Aberdeen, Idaho (1, 4, 5).

Mutational events:

lel1.a (G7118, GSHO 1780) in short awn 5 (*lks5.f*) of an introduction (1, 2, 3, 4, 5). Reexamination of the original Ph.D. Thesis confirmed that the original stock in which the leaf mutant phenotype was isolated was introduced as an *lks5* variant, likely *lks5.f* (GSHO 1297) from CIho 5641 (4).

Mutant used for description and seed stocks:

lel1.a (G7118, GSHO 1780) in an *lks5.f* stock (1, 4, 5); *lel1.a* in Bowman (PI 483237)*3 (GSHO 2279), *lel1.a* in Bowman*4 (BW474, NGB 20704). The second gene required of trait express, *lks5.p*, has been isolated from G7118 in Bowman*5 (BW475, NGB 20705) (2, 3, 4, 5).

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Prepared:

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Revised:

J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:74-75.

BGS 239, Scirpoides-b, *sci-b*

Stock number:	BGS 239
Locus name:	Scirpoides-b
Locus symbol:	*sci-b*

Previous nomenclature and gene symbolization:

Scirpoides-1 = *sci-4* (3).

Inheritance:

Monofactorial recessive (2).

The location is limited to chromosomes 1H or 6H based on SNP markers retained in the Bowman backcross-derived line BW771 (1); *sci-b.4* is between 1_0259 to 2_0780 (positions 70.78 to 154.89 cM) in 1H bins 07 to 11 or between 1_0061 and 2_0118 (positions 70.15 to 156.09 cM) in 6H bins 06 to 09 (1).

Description:

Plants expressing the *sci-b.4* gene have narrow leaves and lower leaf blades are folded inward (4). In the Bowman backcross-derived line for *sci-b.4*, BW771, rachis internodes were slightly elongated. BW771 plants were 2/3 to almost normal height; kernels were slightly smaller and lighter; and seed yields were about 3/4 of normal (2). Based on differences in morphology compared to the *sci-a* (scirpoides-a) mutants and different chromosomal segments retained in their Bowman backcross-derived lines (1), a new locus name is assigned.

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

sci-b.4 (NGB 117099) in Bonus (NGB 14657, PI 189763) (4).

Mutant used for description and seed stocks:

sci-b.4 (NGB 117099) in Bonus; *sci-b.4* in Bowman (PI 483237)*2 (BW771, NGB 22239).

References:

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Prepared:

J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl 40:83.

Revised:

J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl 46:76.

BGS 240, Semidwarf 6, *sdw6*

Stock number: BGS 240
Locus name: Semidwarf 6
Locus symbol: *sdw6*

Previous nomenclature and gene symbolization:

Semidwarf f = *sdw.f* (2).

Inheritance:

Monofactorial recessive (4).

The location is limited to chromosomes 1H or 7H based on SNP markers retained in the Bowman backcross-derived line BW806, between 1_0764 to 1_0075 (positions 61.55 to 82.35 cM) in 1H and between 2_1270 and 1_1219 (positions 93.97 to 107.44 cM) in 7H (1).

Description:

Plants with the *sdw6.f* gene are 10 to 20% shorter than normal sibs in the Bowman backcross-derived line BW806. Kernels were slightly shorter and were 10 to 20% lighter. The number of kernels per spike was slightly reduced. Grain yields were about 3/4 of normal and test weights were slightly lower. Based on the heterogeneous marker positions in line BW806, *sdw6.f* is not an allele at any of the previously named semidwarf loci (1, 2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Vada (PI 243182) isolated as Betina (PI 362200) by Institute de la Recherche Agronomique, Versailles, Yvelines, France; released as a cultivar in 1970 (3, 4).

Mutational events:

sdw6.f [GSHO 2449, Betina (PI 362200)] in Vada (PI 241382) (3).

Mutant used for description and seed stocks:

sdw6.f (GSHO 2449, PI 362200) in Vada; *sdw6.f* in Bowman (PI 483237)*4 (GSHO 2331), *sdw6.f* in Bowman*5 (BW806, NGB 20783).

References:

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Prepared:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:84.

Revised:

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:77.

BGS 254, Orange lemma 1, *rob1*

Stock number: BGS 254
Locus name: Orange lemma 1
Locus symbol: *rob1*

Previous nomenclature and gene symbolization:

Orange lemma = *pl* (18).
Orange lemma = *br* (1, 3).
Orange lemma = *o* (19).
Robiginosum-o = *rob-o* (9).

Inheritance:

Monofactorial recessive (1, 3, 18, 19).

Located in chromosome 6HS (6, 7, 21, 22); *rob1.a* is about 10.8 cM proximal from the *msg36* (Male sterile genetic 36) locus (7, 13); *rob1.a* is about 2.2 cM distal from the *cul2* (uniculm 2) locus (7, 10, 13); *rob1.a* is near RFLP marker HVM031 in 6H bin 06 (4); *rob1.a* is associated with SNP markers 1_0462 to 1_0185 (positions 73.90 to 134.55 cM) in 6H bins 06 to 08 of the Bowman backcross-derived line BW666 (5);. *rob1.a* and *cul2.b* (Uniculm 2) are associated with SNP markers 2_0600 to 1_0185 (positions 90.99 to 134.55 cM) in 6H bins 06 to 08 of the Bowman backcross-derived line BW206 (5); *rob1.a* and *gsh4.l* (Glossy sheath 4) are associated with SNP markers 1_0462 to 2_0118 (positions 73.90 to 156.09 cM) in 6H bins 06 to 09 of the Bowman backcross-derived line BW407 (5), likely in 6H bin 06.

Description:

The lemma, palea, and rachis have an orange pigmentation that is present in immature spikes, can be observed at heading, and is retained in mature grain and spikes (3, 19). The orange pigmentation is visible at the base of sheath of seedlings and in exposed nodes after jointing. Internodes have a layer of orange tissue, and stems have an orange color as the straw dries. The mutant stock for *rob1.f* (OUM189) has a lighter orange lemma color than that in other mutants at the *rob1* locus (14). The Bowman backcross-derived line with the *rob1.a* gene, BW666, had slightly lower acid-detergent lignin (ADL) content than Bowman (17), and it was also more susceptible to common root rot, caused by *Bipolaris sorokiniana* (15). Compared to Bowman, BW666 had slightly lower grain yields (8). The *rob1* mutants have a sequence change in the gene encoding cinnamyl alcohol dehydrogenase (CAD) (2, 23). Cattle have shown a grazing performance for orange lemma barley (8), as has been reported for low lignin mutants in other crops (12).

Origin of mutant:

A spontaneous mutant in CIho 5649 (15).

Mutational events:

rob1.a in CIho 5649 (GBC340, GSHO 707) (11, 19); *rob1.b* (OUM185), *rob1.c* (OUM186), *rob1.d* (OUM187), *rob1.e* (OUM188), *rob1.f* (OUM189) in Akashinriki (OUJ659, PI 467400) (14); *rob1.1* (NGB 115071)*, rob1.2* (NGB 115072) in Bonus (NGB 14657, PI 189763), *rob1.3* (NGB 115073), *rob1.4* (NGB 115074)*, rob1.5* (NGB 115075), *rob1.6* (NGB 115076) in Foma (NGB 14659, CIho 11333), *rob1.7* (NGB 115077) in Kristina (NGB 14661, NGB 1500) (16); *rob1.g* (200A12/8/2) from Emir (CIho 11790) isolated following a cross to *Hordeum bulbosum* (20).

Mutant used for description and seed stocks:

rob1.a (GSHO 707) in CIho 5649; *rob1.a* in Bowman (PI 483237)*8 (GSHO 2069, BW666, NGB 20752): *rob1.a* with *cul2.b* in Bowman*8 (GSHO 2075, BW206, NGB

22034); *rob1.a* with *gsh4.l* in Bowman*7 (GSHO 2072, BW407, NGB 20640).

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Prepared:

C.R. Burnham. 1971. Barley Genet. Newsl. 1:157.

Revised:

J.D. Franckowiak, T. Konishi, and U. Lundqvist. 1997. Barley Genet. Newsl. 26:235-236.
J.D. Franckowiak and U. Lundqvist. 2007. Barley Genet. Newsl. 37:255-256.
J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:78-80.

BGS 262, Curly 1, *cur1*

Stock number: BGS 262
Locus name: Curly 1
Locus symbol: *cur1*

Previous nomenclature and gene symbolization:

Curly 1 = *cu1* (5).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HL (1); *cur1.a* is associated with SNP markers 1_1436 to 2_0339 (positions 230.99 to 248.51 cM) in 3H bin 15 of the Bowman backcross-derived line BW219 (1). Previously, *cur1.a* was positioned over 31.5 cM distal from the *rob1* (orange lemma 1) locus in 6HL (5); *cur1.a* was reported not linked to *rob1* locus (3).

Description:

All plant parts appear curved or twisted. Lemmas and awns are extremely curly. The rachis is usually bent, and tillers and their internodes are curved or wavy (5). Roots are extensively coiled. Phenotypically, the *cur1.a*, *cur2.b*, and *cur2.g* mutants as isolated in Bowman backcross-derived stocks, BW219, BW220, and BW221, respectively, were very similar except the *cur2.b* line originally has hull-less kernels (2). The SNP molecular marker retained from donor parents in these three Bowman back-cross lines indicate that the mutants are of independent origin even though they are positioned in the same region of 3HL (1). Plants of the Bowman backcross-derived line for *cur1.a*, BW219, were short, 1/3 to 1/2 the height of Bowman and produced very little grain in many trials. Heading was delayed by 2 to 7 days and awns were about 1/3 normal length. Kernel of BW219 were shorter and thinner than those of Bowman and weighed about 1/2 as much (2).

Origin of mutant:

The origin is unknown.

Mutational events:

cur1.a (Alb Acc 23, G395, GSHO 1705) in 48-cr cr-17 (5).

Mutant used for description and seed stocks:

cur1.a (GSHO 1705) in 48-cr cr-17; *cur1.a* in Bowman (PI 483237)*4 (GSHO 2088); *cur1.a* in Bowman*4 (BW219, NGB 22046) [The *cur1.a* mutant stock in Bowman (BW219, NGB 22046) is likely an allele at the *cur2* locus (1, 2).]

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:242.

Revised:

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:81-82.

Barley Genetics newsletter (2016) 46:47-145.

BGS 304, White streak 2, *wst2*

Stock number:	BGS 304
Locus name:	White streak 2
Locus symbol:	*wst2*

Previous nomenclature and gene symbolization:

White streak 2 = *wst2* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5HL (3); *wst2.b* is about 3.6 cM proximal from the *srh1* (short rachilla hair 1) locus (3). Based on retained molecular markers, the *wst2.b* allele was not retained during backcrossing in the Bowman backcross-derived line BW911 (1).

Description:

When plants are grown at low temperatures, mutants exhibited wide and numerous white stripes on the developing leaves and plants become almost albinic or chlorotic. Exposure to 3°C for about two weeks immediately after sowing induced on the first and second leaf blades distinct streaks. As temperatures rise, subsequent leaf blades had only a few, narrow white stripes (3). Because of poor expression under warm environments, retention of the *wst2.b* mutant in the Bowman backcross-derived line, BW911, did not occur (2). However, the *vrs5.n* allele at the intermedium-spike-c (*int-c*) was likely retained in BW911, based on spike phenotype and the presence of donor parent DArT markers in the region from 2_1385 to 2_1397 (positions 31.82 to 47.80 cM) in 4HS bins 03 to 05 (1, 2).

Origin of mutant:

A spontaneous mutant in a Japanese naked "uzu" cultivar grown on Manabe Island (3).

Mutational events:

wst2.b in OUL067 (GSHO 766) (3).

Mutant used for description and seed stocks:

wst2.b in OUL067 (GSHO 766); *wst2.b* is unlikely to be in Bowman (PI 483237)*5 (GSHO 2102, BW911, NGB 22342).

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Prepared:

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Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:255.
J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:83.

BGS 312, Smooth awn 1, *raw1*

Stock number:	BGS 312
Locus name:	Smooth awn 1
Locus symbol:	*raw1*

Previous nomenclature and gene symbolization:

Smooth awn = *r* (3).
Smooth awn = *a* (4).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5HL (4, 7); *raw1.a* is about 35 cM from the *srh*1 (short rachilla hair 1) locus (4); *raw1.a* is about 26.8 cM distal from the *srh*1 (short rachilla hair 1) locus based on several reports (5, 6, 7); *raw1* is associated with SNP markers 1_1200 to 1_0095 (positions 180.02 to 310.59 cM) in 5H bins 10 to 11 of the Bowman backcross-derived line BW663 (1).

Description:

Barbs or teeth on the margins of the awn are absent and the size and number of barbs on the central vein are reduced (3). Plants homozygous for the *raw1.a* allele have a semi-smooth awn when other recessive genes reducing the number and/or size of the barbs are absent (8). The presence of these other genes may cause a complete absence of barbs on the awn. The number of stigma hairs is relatively small in plants homozygous for *raw1.a*, and reduced seed set may occur in some genotype-environment combinations (10). Plants of the Bowman backcross-derived line for *Raw1*, BW663, were morphologically similar to Bowman with slight, inconsistent advantages in kernel weight and grain yield (2).

Origin of mutant:

Natural occurrence in several cultivars, especially from Turkey and Southwest Asia (8, 9).

Mutational events:

raw1.a in Lion (CIho 923, PI 32767) (3), but this stock does not have smooth awns based on the USDA-GRIN data. A more correct source of Lion might be CIho 2338.

Mutant used for description and seed stocks:

raw1.a in Lion (GSHO 27, CIho 2338); *raw1.a* is present in Bowman (PI 483237), probably from Lion via Midwestern six-rowed cultivars; *Raw1* from ND4880 (Klages/3/H316/ND B137//Bonanza) in Bowman*8 (GSHO 2124, BW663, NGB 22228).

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Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:261.
J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:84-85.

Barley Genetics newsletter (2016) 46:47-145.

BGS 321, Short rachilla hair 1, *srh1*

Stock number: BGS 321
Locus name: Short rachilla hair 1
Locus symbol: *srh1*

Previous nomenclature and gene symbolization:

Short rachilla hairs = *l* (2, 7).
Short-haired rachilla = *s* (13).
Short glume hairs = *gh* (16).

Inheritance:

Monofactorial recessive (1, 5, 15).

Located in chromosome 5HL (12, 13, 14); *srh1.a* is about 35 cM from the *raw1* (smooth awn 1) locus (6); *srh1.a* is about 26.8 cM proximal from the *raw1* (smooth awn 1) locus (9, 11, 13, 14); *srh1.a* is closely linked to and proximal from SSR maker Bmag223 (3, 10); *srh1.a* is 4.0 cM from SSR marker Bmag223 (8); *srh1.a* is associated with SNP markers 2_1001 to 2_0850 (positions 116.66 to 157.13 cM) in 5H bins 07 to 09 of the Bowman backcross-derived line BW873 (4), likely in 5H bin 08.

Description:

Long rachilla hairs are unicellular, while short rachilla hairs are multicellar and branched (17). Short rachilla hair is associated with short pubescence on the glumes and rachis (2, 5, 7). Plants of the Bowman backcross-derived line for *srh1.a*, BW873, were similar to Bowman in maturity and grain yield (6).

Origin of mutant:

Natural occurrence in landraces of Middle Eastern origin (8); in the cultivar Lion (CIho 923, PI 32767) (7).

Mutational events:

srh1.a in Lion (GSHO 27, CIho 923, PI 32767) (2, 5); *srh1.a* in Plumage (CIho 2511) (5, 13). The stock maintained as Lion (PI 32767) does not have short rachilla hairs. The rachilla hair trait of GSHO 27 and CIho 2238 was not determined.

Mutant used for description and seed stocks:

srh1.a in Lion (GSHO 27); *srh1.a* via R.I. Wolfe's Multiple Recessive Stock (GSHO 3451) in Bowman (PI 483237)*7 (GSHO 2108, BW873, NGB 22307).

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Prepared:

T.E. Haus. 1978. Barley Genet. Newsl. 8:160 as BGS 312, Short-haired rachilla, *s*.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:269.
J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:86-87.

BGS 323, Narrow leafed dwarf 1, *nld1*

Stock number: BGS 323
Locus name: Narrow leafed dwarf 1
Locus symbol: *nld1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (6).

Located in chromosome 5HL (4, 6, 7); *nld1.a* is about 21.6 cM proximal from the *fst1* (fragile stem 1) locus (3, 6); *nld1.a* is associated with SNP markers 2_1260 to 2_1133 (positions 77.47 to 124.50 cM) in 5H bins 04 to 07 of the Bowman backcross-derived line BW635 (1).

Description:

Mutant plants have narrow, dark green leaves, which are erect with well-developed midribs. Auricles degenerate to tiny projections, but ligules are normal. Stem internodes are short, and the upper ones are curved. Spikelets are relatively narrow and small, and seed set may be low (5). Leaf blade widths were about 60% of those of wildtype plants and the lemma and palea only partially cover the caryopsis (8). The spike commonly emerges from the side of the sheath before anthesis. In the Bowman backcross-derived line for *nld1.a*, BW635, plants were short (1/3 to 2/3 normal height with plants short in heat stressed environments); peduncle were 1/3 to 1/2 normal length, and kernels were small and thin, about 1/2 normal weight. Grain yields of BW635 ranged from nil to about 20% of those recorded for Bowman (2). Map-based cloning revealed that *NLD1* encodes a WUSCHEL-RELATED HOMEOBOX 3 (WOX3), an ortholog of the maize *NARROW SHEATH* genes. *In situ* hybridization showed that *NLD1* transcripts were localized in the marginal edges of leaf primordia. *NLD1* plays pivotal role in the increase of organ width and in the development of marginal tissues in lateral organs in barley (8).

Origin of mutant:

A spontaneous mutant in the F_2 population of the cross Nagaoka (OUJ025) X Marumi 16 (OUJ007) isolated as "Nagaoka Dwarf" (5).

Mutational events:

nld1.a in Nagaoka dwarf (OUL054, GSHO 769) (5, 6, 7); *nld1.d* (*nld1.b*) in Kanto Nljo 29 (8).

Mutant used for description and seed stocks:

nld1.a in Nagaoka dwarf (GSHO 769, OUL054); *nld1.a* in Bowman (PI 483237)*7 (GSHO 2093, BW635, NGB 22201).

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Prepared:

T. Konishi and J.D. Franckowiak 1997. Barley Genet. Newsl. 26:271.

Revised:

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:88-89.

BGS 326, Broad leaf 1, *blf1*

Stock number:	BGS 326
Locus name:	Broad leaf 1
Locus symbol:	*blf1*

Previous nomenclature and gene symbolization:

Bredbladig = *bb* (7).
Latifolium (4).
Broad leaf = *bb* (6).
Broad leaf 1-1 = *blf1-1* (3).

Inheritance:

Monofactorial recessive (4, 7).

Located in chromosome 5HL (7); *blf1.a* is about 20.6 cM proximal from the *srh1* (short rachilla hair 1) locus (7); *blf1.a* (*blf1-1*) is positioned in 5HL at 65 cM (3). The *blf1.a* mutant is associated with SNP markers 1_0525 to 2_1078 (positions 65.03 to 118.78 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW058 (SNP associations on 3HL and 6HL are shorter) (1).

Description:

Plants are somewhat lighter green than normal. All leaf blades are very broad, about twice normal width, and markedly crinkled, especially at the margins (4). Leaf blades of flag minus 1 leaves of the Bowman backcross-derived line for *blf1.a*, BW058, are nearly twice as wide as those of Bowman. Heading of BW058 plants was delayed by 5 to 10 days compared to Bowman; plants were slightly shorter; and kernel weights and grain yields were slightly less (2). The comparison of the *blf1.a* (*blf1-1*) mutant plants with its parent, Bonus, demonstrated an increase cell number across the leaf blades and greater number of vascular bundles and stomata. Also, the width of the lemma, palea, and kernel were increased in the mutant (3). The *BLF1* gene encodes a presumed transcriptional regulator of the INDETERMINATE DOMAIN (IDD) family and shows a dynamic expression pattern in the shoot apical meristem and young leaf primordia (3). The normal *BLF1* gene regulates barley leaf size by restricting cell proliferation in the leaf-width direction (3).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (4, 7).

Mutational events:

blf1.a (Alb. Acc. 55, GSHO 1393) in Bonus (NGB 14657, PI 189763) (7), identified as *blf1-1* by Jöst et al. (3); *blf1-2*, *blf1-3, blf1-4, blf1-5* named as mutants in the *blf1* locus isolated from the Barke TILLING Population (3); *blf1.7* (*blf1-6*) (NGB 117240), *blf1.8* (*blf1-6*) (NGB 117241) in Bonus (3, 5); *blf1.3* (NGB 117237), *blf1.5* (NGB 117238) in Bonus having a complete deletion of the *blf1* locus (3, 5).

Mutant used for description and seed stocks:

blf1.a (GSHO 1393) in Bonus; *blf1.a* in Bowman (PI 483237)*1 (GSHO 2166), *blf1.a* in Bowman*3 (BW058, NGB 20466).

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U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:274.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. Barley Genet. Newsl. 41:130.

U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:90-91.

BGS 340, Smooth awn 2, *raw2*

Stock number: BGS 340
Locus name: Smooth awn 2
Locus symbol: *raw2*

Previous nomenclature and gene symbolization:

Intermediate-smooth awn = *S* (3, 8).
Smooth awn = $rr\ r'r'$ (5).
Smooth awn 2 = r_1 (3).

Inheritance:

Monofactorial recessive for semi-smooth verse smooth awns (1). The F2 ratio rough, semi-smooth, and smooth awn fit a 12:3:1 segregation ratio (3, 5). The F2 ratio for rough, intermediate-rough, intermediate-smooth, and smooth awns fit a 9:3:3:1 segregation ratio (8). F2 segregation ratios observed in progeny from crosses of rough vs smooth awned accessions fit neither a 3:1 nor 15:1 ratio (4). The segregation ratios are distorted because the *raw2* locus is linked to the *raw1* (smooth awn 1) locus (1). Located in chromosome 5HL (1); the *raw2* locus is about 26.0 cM (probably distal) from the *raw1* (smooth awn 1) locus (1).

Description:

The number of barbs present on the awn is reduced by the recessive allele at the *raw2* locus (1, 3, 4, 5, 8). When the recessive allele is present at only the *raw2* locus, awns are intermediate or semi-rough (2). When recessive alleles occur at both the *raw1* and *raw2* loci, awns are very smooth or devoid of barbs (see photos in [1]). The existence of two or more genes controlling barbing of awns is reported in several studies (3, 4, 5, 6, 7).

Origin of mutant:

Natural occurrence in Lion (CIho 923, PI 32767) and derivatives, but this specific stock does not have smooth awns based on the USDA-GRIN data. A more correct source of Lion might be CIho 2338. The *raw2.b* gene is likely present semi-rough spring two-rowed cultivars from Europe.

Mutational events:

raw2.b in Lion (GSHO 27, CIho 2338), but this stock does not have smooth awns based on the USDA-GRIN data. A more correct source of Lion might be CIho 2338. The *raw2.b* trait was observed in Mich 832-188 (1, 7).

Mutant used for description and seed stocks:

raw2.b in Lion (GSHO 27, CIho 2338). The *raw2.b* gene is likely a second gene for smooth awn in this original stock. The *raw2.b* is not present in Bowman based on its semi-smooth awn. The *raw1.a* and *raw2.b* genes are present in Conlon (PI 597789).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:289.

Revised:

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:92-93.

BGS 351, Glossy sheath 1, *gsh1*

Stock number: BGS 351
Locus name: Glossy sheath 1
Locus symbol: *gsh1*

Previous nomenclature and gene symbolization:

Glaucous sheath = *gs* (6).
Glossy sheath and spike = *gs* (30).
Glossy sheath 1 = *gs1* (18).
Eceriferum-q = *cer-q* (8).
A member of the gene cluster *Cer-cqu* (21, 27).

Inheritance:

Monofactorial recessive (6, 8), except *Cer-q.1440* (15).

Located in chromosome 2HS (23, 24); *gsh6.s* is in a sub-terminal position (22); *gsh1.c* is over 36.5 cM distal from the *Eam1* (early maturity 1) locus (1); *gsh1.a* is associated with SNP markers 2_0562 to 1_0943 (positions 22.43 to 34.31 cM) in 2HS bin 02 to 03 of the Bowman backcross-derived line BW404 (2); the *Cer-cqu* gene cluster is near SNP marker 1_0718 and 2.7 cM distal from 1_1059 (21), likely in 2H bins 01 or 02.

Description:

A bright, green glossy color is apparent on the spike, leaf sheath, and stem (wax code - - ++) (8, 18). The *gsh1* locus is the *cer-q* component of the complex locus named *cer-cqu* (3, 17), which controls formation of β-diketone lipids in epicuticular wax layer (25, 27, 29). The *cer-q* mutants affect the β-ketoacyl condensing enzyme (19, 27). Since two types of β-diketones and the alkan-2-ol containing esters are absent in the leaf blades (25) and awns (28), mutants in the *Cer-cqu* cluster of genes do not change the surface wax composition on these organs (25, 28). Morphological differences, except for surface waxes, were not observed between Bowman and its backcross-derived line BW404 (4). The *Gsh1* (*Cer-q*) locus is a member of the β-diketone synthase polyketide pathway for synthesis of β-diketone aliphatics, which are part of the complex of epicuticular or surface waxes present in Triticeae species (21). The *Cer-q* (*MLOC_13397*) gene is a lipase/carboxyl transferase, has a single exon, and is positioned distal to the C*er-c* (*Gsh6*) and *Cer-u* (*Gsh8*) loci (21). The β-diketone biosynthesis *Cer-cqu* locus of barley is similar to the wheat *W1* locus, which contains a metabolic gene cluster mediating β-diketone biosynthesis (5).

Origin of mutant:

A spontaneous mutant in PI 95285 (6), an iodine vapor induced mutant in Bonus (NGB 14657, PI 189763) (8). More information on the origins of *cer-q* mutants is presented in www.nordgen.org/bgs and in Schneider et al. (21).

Mutational events:

gsh1.a (GSHO 735) in PI 95285 (6, 18, 20); *gsh1.b* in Piroline (PI 539132) (18); *gsh1.c* in Velvon (CIho 6109) (18, 30); *gsh1.y* in Minn 549 (18, 20); *cer-q.35* (GSHO 438, NGB 110919) in Bonus (NGB 14657, PI 189763) (3, 8, 9); *cer-q.42* (NGB 110926), *-q.50* (NGB 110934), *-q.56* (NGB 110940), *-q.103* (NGB 110988) in Bonus (8, 9); *cer-q.82* (NGB 110966), *-q.83* (NGB 110967), *-q.84* (NGB 110968), *-cqu.124* (NGB 111009), *-q.128* (NGB 111013), *-q.131* (NGB 111016), *-q.132* (NGB 111017), *-q.133* (NGB 111018), *-q.141* (NGB 111027), *-q.151* (NGB 111037) in Bonus, *-q.213* (NGB 111100), *-q.217* (NGB 111104), *-q.218* (NGB 111105), *-q.239* (NGB 111126), *-q.241* (NGB 111128), *-q.245* (NGB 111132), *-q.246* (NGB 111133), *-q.261* (NGB 111148), *-q.262*

(NGB 111149), *-q.292* (NGB 111179), *-q.295* (NGB 111182), *-q.297* (NGB 111184), *-q.299* (NGB 111186), *-q.310* (NGB 111197), *-q.320* (NGB 111207), *-q.326* (NGB 111213), *-q.327* (NGB 111214), *-q.334* (NGB 111221), *-q.335* (NGB 111222), *-q.341* (NGB 111228), *-q.365* (NGB 111252), *-q.395* (NGB 111282), *-q.396* (NGB 111283), *-q.400* (NGB 111287), *-q.403* (NGB 111291), *-q.411* (NGB 111299), *-cqu.416* (NGB 111304), *-cqu.420* (NGB 111308), *-q.425* (NGB 111313), *-q.440* (NGB 111328), *-q.488* (NGB 111376), *-q.509* (NGB 111397), *-qu.510* (NGB 111398) in Foma (NGB 14659, CIho 11333) (9, 17); *cer-q.129* (NGB 111014), *-q.176* (NGB 111062) in Bonus, *-q.483* (NGB 111371), *-q.516* (NGB 111404), *-q.519* (NGB 111407), *-q.524* (NGB 111412), *-q.527* (NGB 111415), *-q.533* (NGB 111421), *-q.536* (NGB 111424), *-q.548* (NGB 111436), *-q.555* (NGB 111443), *-q.557* (NGB 111445), *-q.566* (NGB 111454), *-q.574* (NGB 111462), *-q.579* (NGB 111467), *-q.597* (NGB 111485) in Foma, *-q.675* (NGB 111563), *-q.683* (NGB 111571), *-q.688* (NGB 111576), *-cqu.724* (NGB 111612), *-cqu.733* (NGB 111621) in Bonus, *-q.1016* (NGB 111904), *-q.1018* (NGB 111906), *-q.1040* (NGB 111928), *-q.1061* (NGB 111949), *-q.1063* (NGB 111951), *-q.1064* (NGB 111952), *-q.1065* (NGB 111953), *-q.1068* (NGB 111956), *-q.1070* (NGB 111958), *-q.1073* (NGB 111961), *-q.1074* (NGB 111962), *-q.1083* (NGB 111971) in Carlsberg II (NGB 5085, CIho 10114) (9); *cer-q.153* (NGB 111039), *-q.754* (NGB 111642), *-q.755* (NGB 111643), *-q.756* (NGB 111644), *-q.757* (NGB 111645), *-q.759* (NGB 111647), *-q.772* (NGB 111660), *-qu.813* (NGB 111701), *-q.822* (NGB 111710), *-q.827* (NGB 111715), *-q.837* (NGB 111725), *-q.848* (NGB 111736), *-q.876* (NGB 111764) in Bonus, *-q.401* (NGB 111289) in Foma, *-q.1079* (NGB 111967) in Carlsberg II, *-q.1105* (NGB 111993), *-q.1128* (NGB 112016), *-q.1131* (NGB 112019), *-q.1141* (NGB 112029), *-q.1143* (NGB 112031) in Kristina (NGB 14661,NGB 1500) (10); *cer-q.629* (NGB 111517), *-q.634* (NGB 111522), *-q.636* (NGB 111524), *-cq.645* (NGB 111533), *-q.900* (NGB 111788), *-cqu.925* (NGB 111813), *-cqu.944* (NGB 111832) in Bonus, *-q.1158* (NGB 112046), *-q.1167* (NGB 112055) in Kristina (11); *cer-q.1011* (NGB 111899) in Carlsberg II, *-q.1121* (NGB 112009), *-q.1193* (NGB 112081), *-q.1209* (NGB 112097), *-q.1225* (NGB 112113), *-q.1234* (NGB 112122), *-q.1238* (NGB 112126), *-q.1242* (NGB 112130), *-q.1243* (NGB 112131) in Kristina (12); *cer-q.598* (NGB 111486) in Foma, *-q.1260* (NGB 112148), *-q.1281* (NGB 112169), *-q.1283* (NGB 112171), *-q.1285* (NGB 112173) in Kristina, *-q.1320* (NGB 112208), *-q.1330* (NGB 112218) in Bonus (13); *cer-q.1230* (NGB 112118) in Kristina, *-q.1345* (NGB 112233), *-q.1358* (NGB 112246, 116826, 117275), *-q.1362* (NGB 112250), *-q.1363* (NGB 112251), *-q.1368* (NGB 112256), *-q.1369* (NGB 112257), *-q.1375* (NGB 112263), *-q.1400* (NGB 112288), *-q.1406* (NGB 112294), *-q.1412* (NGB 112300), *-q.1430* (NGB 112318), *-q.1459* (NGB 112347), *-q.1464* (NGB 112352) in Bonus, *-q.1504* (NGB 112392), *-q.1512* (NGB 112400), *-q.1514* (NGB 112402) in Nordal (14); *Cer-q.1440* (NGB 112328), *cer-q.1490* (NGB 112378), *-q.1499* (NGB 112387), *-q.1706* (NGB 112519), *-q.1708* (NGB 112521), *-q.1742* (NGB 112555), *-q.1748* (NGB 112562), *-q.1753* (NGB 112567) in Bonus (15); *-q.1517* (NGB 112405), *-q.1521* (NGB 112409), *-q.1522* (NGB 112410), *-q.1527* (NGB 112415), *-q.1528* (NGB 112416), *-q.1533* (NGB 112421), *-q.1534* (NGB 112422), *-q.1537* (NGB 112425), *-q.1538* (NGB 112426), *-q.1539* (NGB 112427), *-q.1542* (NGB 112430), *-q.1551* (NGB 112439), *-q.1556* (NGB 112444), *-q.1572* (NGB 112460) in Nordal (NGB 13680, NGB 4704) (15); *cer-q.571* (NGB 111459) in Foma (16); *gsh1.aa* (OUM018), *gsh1.ad* (OUM021), *gsh1.ak* (OUM028) in Akashinriki (PI 467400, OUJ659), *gsh1.an* (T119, OUL045) in a tester line, *gsh1.ap* (PI 95285, OUE093), *gsh1.ar* (PI 151791, OUE121), *gsh1.as* (PI 151815, OUE128), *gsh1.at* (PI 194916, OUE168), *gsh1.au* (CIho 14093, OUE330), *gsh1.av* (CIho 14139, OUE370), *gsh1.ax* (CIho 14094, OUE630), *gsh1.ay* (CIho 14140, OUE670), *gsh1.az* (CIho 4361, OUE676) in Ethiopian introductions, *gsh1.ba* in Bozu Omugi 1 (OUJ655) (7).

Mutant used for description and seed stocks:

gsh1.a (GSHO 735) in PI 95285; *cer-q.35* (GSHO 438, NGB 110919) in Bonus (NGB 14657, PI 189763); *cer-q-42* (NGB 110926) in Bonus is used for wax chemistry and wax structure studies (25, 27); *gsh1.a* in Bowman (PI 483237)*7 (GSHO 1868, BW404, NGB 20637).

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BGS 352, Glossy sheath 2, *gsh2*

Stock number:	BGS 352
Locus name:	Glossy sheath 2
Locus symbol:	*gsh2*

Previous nomenclature and gene symbolization:

Glossy sheath 2 = *gs2* (20, 22).

Eceriferum-b = *cer-b* (8, 22).

Inheritance:

Monofactorial recessive (8, 19).

Located in chromosome 3HL (2, 4, 21); the *gsh2* or *cer-b* locus is about 5.1 cM proximal from the *als1* (absent lower laterals 1) locus (5, 6); it is over 32.5 cM distal from the *uzu1* (uzu 1) locus (2, 5, 6); *gsh2.f* is associated with SNP markers 2_1161 to 1_0584 (positions 169.94 to 178.12 cM) in 3H bin 11 of the Bowman backcross-derived line BW405; *cer-b.2* is associated with SNP markers 22_1513 to 1_1172 (positions 190.97 cM) in 3H bins 11 and 12 of the Bowman backcross-derived line BW107 (1); *gsh2* variants mapped at position 96.6 cM in 3H (18) in the POPSEQ map (16), in 3H bin 11.

Description:

Surface wax coating appears absent on the spike, leaf sheath, and stem (wax code - - ++) (8, 19). The nodes of mutant plants appear to lack surface wax (3). The Bowman backcross-derived lines for the *gsh2* mutants, BW107 with *cer-b.2* and BW405 with *gsh2.f*, had agronomic traits similar to those of Bowman, but grain yields were slightly lower (3).

Origin of mutant:

Spontaneous occurrence in Vantage (CIho 7324) (17); an X-ray induced mutant in Maja Abed (NGB 8815, PI 184884,) (8).

Mutational events:

gsh2.d in Vantage (CIho 7324), *gsh2.e* in Ymer (NGB 14860. CIho 7275), *gsh2.f* (GSHO 736), *gsh2.g* in Atlas (CIho 4118), *gsh2.h* in Klargrin (16); *cer-b.2* (NGB 110886, GSHO 434; GSHO 1081) in Maja Abed (NGB 8815, PI 184884) (7, 8, 9, 22); *cer-b.4* (NGB 110888), *-b.64* (NGB 110948), *-b.66* (NGB 110950), *-b.109* (NGB 110994 in Bonus (NGB 14657, PI 189763) (8, 9); *cer-b.79* (NGB 110963), *-b.94* (NGB 110978), *-b.96* (NGB 110980) in Bonus, *-b.209* (NGB 111096), *-b.222* (NGB 111109), *-b.319* (NGB 111206), *-b.336* (NGB 111223), *-b.337* (NGB 111224), *-b.377* (NGB 111264), *-b.418* (NGB 111306), *-b.424* (NGB 111312), *-b.427* (NGB 111315) in Foma (NGB 14659, CIho 11333) (9, 15); *cer-b.169* (NGB 111055), *-b.193* (NGB 111079) in Bonus, *-b.412* (NGB 111300), *-b.531* (NGB 111419), *-b.549* (NGB 111437) in Foma, *-b.1037* (NGB111925), *-b.1059* (NGB 111947) in Carlsberg II (NGB 5085, CIho 10114) (9); *cer-b.751* (NGB 111639), *-b.769* (NGB 111657), *-b.791* (NGB 111679), *-b.799* (NGB 111687), *-b.800* (NGB 111688) in Bonus, *-b.1129* (NGB 112017) in Kristina (NGB 14661, NGB 1500) (10); *cer-b.910* (NGB 111798) in Bonus (11); *cer-b.932* (NGB 111820) in Bonus (12); *cer-b.147* (NGB 111033), *-b.182* (NGB 111068), *-b.623* (NGB 111511) in Bonus, *-b.1099* (NGB 111987), *-b.1267* (NGB 112155), *-b.1269* (NGB 112157) in Kristina (13); *cer-b.1699* (NGB 119343) in Bonus (14); *gsh2.ab* (OUM019), *gsh2.ah* (OUM025) in Akashinriki (OUJ659, PI 467400) (4, 6); *gsh2.bb* in the cross NDB112/Fr926-77 (3); *gsh2.bd* in Ms13551 and *gsh2.be* in PI 282610 both in *Hordeum vulgare* subsp. *spontaneum* (1, 3); *gsh2* variants in *H. vulgare* ssp. *spontaneum* accessions WBDC032, WBDC035, and WBDC348 (17).

Mutant used for description and seed stocks:

gsh2.f (GSHO 736) in Atlas; *cer-b.2* (NGB 110886, GSHO 434; GSHO 1081) in Maja Abed (NGB 8815, PI 184884); *gsh2.f* in Bowman (PI 483237)*7 (GSHO 1988); *gsh2.f* in Bowman*8 (BW405, NGB 20678); *cer-b.2* in Bowman*6 (GSHO 1989); *cer-b.2* in Bowman*7 (BW107, NGB 20513): *gsh2.bd* from Ms13551in Bowman*4 (BW402, NGB 22150); *gsh2.be* from PI 282610 in Bowman*7 (BW403, NGB 22151).

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BGS 356, Glossy sheath 6, *gsh6*

Stock number: BGS 356
Locus name: Glossy sheath 6
Locus symbol: *gsh6*

Previous nomenclature and gene symbolization:

Glossy sheath 6 = *gs6* (17).
Eceriferum-c = *cer-c* (6).
Eceriferum-cqu = *cer-cqu* (15, 25).
A member of the gene cluster *Cer-cqu* (18, 25).

Inheritance:

Monofactorial recessive (6, 17, 20).

Located in chromosome 2HS (20, 21, 22); *gsh6.s* is in a subterminal position (19); *gsh6.s* is associated with SNP markers 1_0326 to 2_0563 (positions 16.91 to 21.19 cM) in 2HS bin 02 of the Bowman backcross-derived line BW409 (1); the *Cer-cqu* gene cluster is near SNP marker 1_0718 and 2.7 cM distal from 1_1059 (19), likely in 2H bins 01 or 02.

Description:

A bright, glossy green color is apparent on the spike, leaf sheath, and stem (17). The *gsh6* locus is the *cer-c* component of the complex locus *cer-cqu* (2), which controls formation of β-diketone lipids in epicuticular wax layer (23, 25, 27). Most alleles have the wax code - - ++, but a few alleles show delayed development of surface waxes on the sheath (wax code - +/- ++) (6, 16). Since two types of β-diketones and the alkan-2-ol containing esters are absent in the leaf blades (24) and awns (26), mutants in the *Cer-cqu* cluster of genes do not change the surface wax composition on these organs (24, 26). The only observed morphological difference between Bowman and the backcross-derived line BW409 was an increase in kernel length (3). The *Gsh6* (*Cer-c*) locus is a member of the β-diketone synthase polyketide pathway for synthesis of β-diketone aliphatics, which are part of the complex of epicuticular or surface waxes present in Triticeae species (18). The *Cer-c* (*MLOC_59804*) gene is a chalcone synthase-like polyketide synthase, designated diketone synthase (DKS) with two exons and is positioned proximal from the *Cer-q* (*Gsh1*) and *Cer-u* (*Gsh8*) loci (18). The β-diketone biosynthesis *Cer-cqu* locus of barley is similar to the wheat *W1* locus, which contains a metabolic gene cluster mediating β-diketone biosynthesis (4).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (6), a radiation induced mutant in Domen (NGB 2104, CIho 9562) (17). More information on the origins of *cer-c* mutants is presented in www:nordgen.org/bgs and in Schneider et al. (18).

Mutational events:

cer-c.3 (NGB 110887, GSHO 212. GSHO 424, GSHO 959) in Bonus (NGB 14657, PI 189763) (2, 6); *cer-c.7* (NGB 110891), *-c.29* (NGB 110913), *-c.36* (NGB 110920), *-c.44* (NGB 110928), *-c.61* (NGB 110945), *-c.63* (NGB 110947) in Bonus (6, 7); *cer-c.73* (NGB 110957), *-c.89* (NGB 110973), *-c.95* (NGB 110979), *-cu.108* (NGB 110993), *-c.115* (NGB 111000), *-c.123* (NGB 111008), *-cqu.124* (NGB 111009) in Bonus, *-c.201* (NGB 111088), *-c.206* (NGB 111093), *-c.220* (NGB 111107), *-c.223* (NGB 111110), *-c.234* (NGB 111121), *-c.238* (NGB111125), *-c.240* (NGB 111127), *-c.250* (NGB 111137), *-c.270* (NGB 111157), *-c.282* (NGB 111169), *-c.283* (NGB 111170), *-c.284* (NGB 111171), *-c.290* (NGB 111177), *-c.291* (NGB 111178), *-c.293* (NGB 111180). *-c.306*

(NGB 111193), *-c.315* (111202), *-c.332* (NGB 111219), *-c.343* (NGB 111230), *-c.354* (NGB 111241), *-c.361* (NGB 111248), *-c.364* (NGB 111251), *-c.367* (NGB 111254), *-c.368* (NGB 111255), *-c.374* (NGB 111261), *-c.379* (NGB 111266), *-c.398h* (NGB 111285), *-c.398l* (NGB 111288), *-c.405* (NGB 111293), *-c.406* (NGB 111294), *-c.413* (NGB 111301), *-cqu.416* (NGB 111304), *-cqu.420* (NGB 111308), *-c.431* (NGB 111319), *-c.445* (NGB 111333), *-c.455* (NGB 111343), *-c.469* (NGB 111357), *-c.471* (NGB 111359), *-c.502* (NGB 111390) in Foma (NGB 14659, CIho 11333) (7, 15); *cer-c.143* (NGB 111029), *-c.171* (NGB 111057), *-c.175* (NGB 111061) in Bonus, *-c.345* (NGB 111232), *-c.451* (NGB 111339), *-c.459* (NGB 111347), *-c.508* (NGB 111396), *-c.513* (NGB 111401), *-c.514* (NGB 111402), *-c.520* (NGB 111408), *-c.526* (NGB 111414), *-c.544* (NGB 111432), *-c.550* (NGB 111438), *-c.563* (NGB 111451), *-c.596* (NGB 111484), *-c.601* (NGB 111489), *-c.661* (NGB 111549) in Foma, *-c.669* (NGB 111557), *-c.673* (NGB 111561), *-c.690* (NGB 111578), *-c.693* (NGB 111581), *-c.698* (NGB 111586), *-c.703* (NGB 111591), *-c.711* (NGB 111499), *-cqu.724* (NGB 111612), *-cqu.733* (NGB 111621) in Bonus, *-c.1001* (NGB 111889), *-c.1004* (NGB 111892), *-c.1008* (NGB 111896), *-c.1010* (NGB 111898), *-c.1015* (NGB 111903), *-c.1022* (NGB 111910), *-c.1029* (NGB 111917), *-c.1034* (NGB 111922), *-c.1035* (NGB 111923), *-c.1039* (NGB 111927), *-c.1062* (NGB 111950), *-c.1067* (NGB 111955), *-c.1082* (NGB 111970) in Carlsberg II (NGB 5085, CIho 10114) (7); *cer-c.589* (NGB 111477) in Foma, *-c.748* (NGB 111636), *-c.760* (NGB 111648), *-c.764* (NGB 111652), *-c.767* (NGB 111655), *-c.770* (NGB 111658), *-c.774* (NGB 111662), *-c.786* (NGB 111674), *-c.793* (NGB 111681), *-c.794* (NGB 111682), *-c.841* (NGB 111729), *-c.845* (NGB 111733) -, *c.847* (NGB 111735), *-c.851* (NGB 111739), *-c.860* (NGB 111748), *-c.870* (NGB 111758), *-c.881* (NGB 111769), *-c.883* (NGB 111771) in Bonus, *-c.1032* (NGB 111920) in Carlsberg II, *-c.1098* (NGB 111986), *-c.1100* (NGB 111988), *-c.1109* (NGB 111997), *-c.1117* (NGB 112005), *-c.1123* (NGB 112011), *-c.1125* (NGB 112013), *-c.1135* (NGB 112023), *-c.1136* (NGB 112024), *-c.1140* (NGB 112028), *-c.1147* (NGB 112035) in Kristina (NGB 14661, NGB 1500) (8); *cer-c.499* (NGB 111387), *-c.609* (NGB 111497) in Foma, *-c.630* (NGB 111518), *-c.635* (NGB 111523), *-c.640* (NGB 111528), *-cu.644* (NGB 111532), *-cq.645* (NGB 111533), *-c.648* (NGB 111536), *-c.890* (NGB 111778), *-c.897* (NGB 111785), *-c.902* (NGB 111790), *-c.903* (NGB 111791), *-c.904* (NGB 111792), *-c.907* (NGB 111795), *-c.912* (NGB 111800), *-c.915* (NGB 111803), *-cqu.925* (NGB 111813), *-c.942* (NGB 111830), *-cqu.944* (NGB 111832), *-c.945* (NGB 111833), *-c.980* (NGB 111868) in Bonus, *-c.1156* (NGB 112044), *-c.1187* (NGB 112075) in Kristina (9); *cer-c.144* (NGB 111030), *-cu.947* (NGB 111835), *-c.987* (NGB 111875) in Bonus, *-c.1110* (NGB 111998), *-c.1212* (NGB 112100), *-c.1229* (NGB 112117), *-c.1248* (NGB 112136), *-c.1258* (NGB 112146), *-c.1264* (NGB 112152), *-c.1276* (NGB 112164) in Kristina (10); *cer-c.511* (NGB 111399) in Foma, *-c.1200* (NGB 112088), *-c.1254* (NGB 112271, 1168212), *-c.1278* (NGB 116824, 117273), *-c.1287* (NGB 112175), *-c.1291* (NGB 112179) in Kristina, *-c.1319* (NGB 112207), *-c.1325* (NGB 112213), *-c.1329* (NGB 112217), *-c.1334* (NGB 112222), *-c.1338* (NGB 112226) in Bonus (11); *cer-c.993* (NGB 111881), *-c.994* (NGB 111882), *-c.995* (NGB 111883), *-c.999* (NGB 111887), *-c.1348* (NGB 112236), *-c.1355* (NGB 112243), *-c.1359* (NGB 112247), *-c.1365* (NGB 112253), *-c.1376* (NGB 112264), *-c.1381* (NGB 112269), *-c.1382* (NGB 112270), *-c.1385* (NGB 112273), *-c.1386* (NGB 112274), *-c.1389* (NGB 112277), *-c.1416* (NGB 112304), *-c.1421* (NGB 112309), *-c.1439* (NGB 112327), *-c.1448* (NGB 112336), *-c.1460* (NGB 112348), *-c.1462* (NGB 112350), *-c.1466* (NGB 112354), *-c.1467* (NGB 112355) in Bonus, *-c.1501* (NGB 112389), *-c.1502* (NGB 112390), *-c.1503* (NGB 112391), *-c.1505* (NGB 112393), *-c.1506* (NGB 112394), *-c.1511* (NGB 112399), -

c.1515 (NGB 112403) in Nordal (NGB 13680, NGB 4704) (12); *cer-c.1491* (112379), -*c.1701* (NGB 112514), -*c.1702* (NGB 112515), -*c.1703* (NGB 112516), -*c.1705* (NGB 112518), -*c.1707* (NGB 112520), -*c.1714* (NGB 112527), -*c.1737* (NGB 112550, 117329), -*c.1739* (NGB 112552), -*c.1749* (NGB 112563), -*c.1755* (NGB 112569), -*c.1757* (NGB 112572) in Bonus, -*c.1516* (NGB 112404), -*c.1520* (NGB 112408), -*c.1525* (NGB 112413), -*c.1526* (NGB 112414), -*c.1532* (NGB 112420), -*c.1553* (NGB 112441), -*c.1555* (NGB 112443), -*c.1560* (NGB 112448) in Nordal (13); *cer-c.602a* (NGB 119348) in Foma (14); *gsh6.o* in Domen (NGB2104, CIho 9562), *gsh6.p* in PI 184877, *gsh6.q* in Kogane Mugi (OUL010, PI 225020), *gsh6.r* in Barbless (CIho 5105), *gsh6.s* (GSHO 740) in Betzes (PI 129430), *gsh6.t* in Heines Hanna (PI 539131), *gsh6.u, gsh6.v, gsh6.w*, and *gsh6.x* in Compana (PI 539111) (15); *gsh6.z* (OUM017), *gsh6.ac* (OUM020), *gsh6.ai* (OUM026) in Akashinriki (PI 467400, OUJ659) (5); *gsh6.aq* in an Ethiopian introduction (PI 151787, OUE120) (5).

Mutant used for description and seed stocks:

cer-c.3 (NGB 110887, GSHO 212, GSHO 424, GSHO 959) in Bonus, *cer-c.36* (NGB 110920 is used for wax chemistry and wax structure studies (23, 25); *gsh6.s* (GSHO 740) in Betzes, *gsh6.s* via R.I. Wolfe's Multiple Marker Stock for chromosome 2 in Bowman (PI 483237)*7 (GSHO 1869, BW409, NGB 20642).

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BGS 413, Glossy sheath 8, *gsh8*

Stock number: BGS 413
Locus name: Glossy sheath 8
Locus symbol: *gsh8*

Previous nomenclature and gene symbolization:

Eceriferum-u = *cer-u* (7).
Glossy sheath 8 = *gs8* (5).
Eceriferum-cqu = *cer-cqu* (16, 23).
A member of the gene cluster *Cer-cqu* (17, 23).

Inheritance:

Monofactorial recessive (5, 7).

Located in chromosome 2HS (19, 20); *gsh8* is located in 2HS based on close association with the *gsh6* (glossy sheath 6) locus (2, 6, 19, 20); *gsh6.s* is in a subterminal position (18); *gsh8.ag* is associated with SNP markers 2_1377 to 1_0919 (positions 20.11 to 66.78 cM) in 2H bins 02 to 03 of the Bowman backcross-derived line BW411 (1); the *Cer-cqu* gene cluster is near SNP marker 1_0718 and 2.7 cM distal from 1_1059 (17), likely in 2H bins 01 or 02.

Description:

The wax coating on the spike, stem and leaf sheath appears reduced (wax code + + ++) (7). The *gsh8* locus is the *cer-u* component of the complex locus *cer-cqu* which controls epicuticular wax layer formation on the surface of the spike, leaf sheath, and stem (21, 23, 25). Deposition of β-diketone lipids is reduced or eliminated by mutants in the *cer-cqu* locus (23), specifically the *cer-u* mutants have impaired hydroxyl group insertion (21). Since two types of β-diketones and the alkan-2-ol containing esters are absent in the leaf blades (22) and awns (24), mutants in the *Cer-cqu* cluster of genes do not change the surface wax composition on these organs (22, 24). The original *cer-u.21* stock exhibited reduced seed set (7). Morphological differences, except for surface waxes, were not observed between Bowman and its backcross-derived line BW411 (3). The *Gsh8* (*Cer-u*) locus is a member of the β-diketone synthase polyketide pathway for synthesis of β-diketone aliphatics, which are part of the complex of epicuticular or surface waxes present in Triticeae species (17). The *Cer-u* (*AK373499*) gene is a P450 hydroxylase with five exons and is positioned between the *Cer-q* (*Gsh1*) and *Cer-c* (*Gsh6*) loci (17). CER-U hydroxylates carbon 25 of the C_{31} β-diketone chain, as do most of its homologs in the β-diketone polyketide pathway in Triticeae species (17). The β-diketone biosynthesis *Cer-cqu* locus of barley is similar to the wheat *W1* locus, which contains a metabolic gene cluster mediating β-diketone biosynthesis (4).

Origin of mutant:

A gamma-ray induced mutant in Bonus (NGB 14657, PI 189763) (7). More information on the origins of *cer-u* mutants is presented in www.nordgen.org/bgs and in Schneider et al. (17).

Mutational events:

cer-u.21 (NGB 110905, GSHO 442), *-u.58* (NGB 110942) in Bonus (NGB 14657, PI 189763) (7, 8); *cer-u.69* (NGB 110953), *-u.76h* (NGB 110960), *-u.76l* (NGB 110985), *-u.80* (NGB 110964), *-u.99* (NGB 110983), *-u.107* (NGB 110992), *-cu.108* (NGB 110993), *-u.119* (NGB 111004), *-u.120* (NGB 111005) in Bonus, *-u.204* (NGB 111091), *-u.237* (NGB 111124), *-u.258* (NGB 111145), *-u.265* (NGB 111152), *-u.281* (NGB 111168), *-u.304* (NGB 111191), *-u.305* (NGB 111192), *-u.307* (NGB 111194), *-u.324* (NGB

111211), *-u.330* (NGB 111217), *-u.338* (NGB 111225), *-u.344* (NGB 111231), *-u.371* (NGB 111258), *-u.376* (NGB 111263), *-u.387* (NGB 111274), *-cqu.416* (NGB 111304), *-cqu.420* (NGB 111308), *-u.443* (NGB 111331), *-u.446* (NGB 111334), *-u.452* (NGB 111340), *-u.464* (NGB 111352), *-u.466* (NGB 111354), *-u.468* (NGB 111356), *-u.472* (NGB 111360),*-u.485* (NGB 111373), *-u.491* (NGB 111379), *-u.497* (NGB 111385), *-u.498* (NGB 111386), *-u.505* (NGB 111393), *-qu.510* (NGB 111398) in Foma (NGB 14659, CIho 11333) (8, 16); *cer-cqu.124* (NGB 111009), *-u.177* (NGB 111063), *-u.178* (NGB 111064), *-u.189* (NGB 111075) in Bonus, *-u.525* (NGB 111413), *-u.538* (NGB 111426), *-u.542* (NGB 111430), *-u.543* (NGB 111431), *-u.556* (NGB 111444), *-u.570* (NGB 111458), *-u.581* (NGB 111469), *-u.600* (NGB 111488), *-u.605* (NGB 111493), *-u.606* (NGB 111494) in Foma, *-u.677* (NGB 111565), *-u.686* (NGB 111574), *-u.689* (NGB 111577), *-u.697* (NGB 111585), *-cqu.724* (NGB 111612), -cqu.733 (NGB 111621) in Bonus, *-u.1003* (NGB 111891), *-u.1009* (NGB 111897), *-u.1042* (NGB 111930), *-u.1043* (NGB 111931), *-u.1048* (NGB 111936), *-u.1060* (NGB 111948), *-u.1076* (NGB 111964), *-u.1078* (NGB 111966) in Carlsberg II (NGB 5085, CIho 10114) (8); *cer-u.610* (NGB 111498), *-u.613* (NGB 111501) in Foma, *-u.737* (NGB 111625), *-u.766* (NGB 111654), *-u.775* (NGB 111663), *-u.779* (NGB 111667), *-u.784* (NGB 111672), *-u.789* (NGB 111677), *-u.798* (NGB 111686), *-qu.813* (NGB 111701), *-u.823* (NGB 111711), *-u.825* (NGB 111713), *-u.830* (NGB 111718), *-u.835* (NGB 111723), *-u.839* (NGB 111727), *-u.840* (NGB 111728), *-u.842* (NGB 111730), *-u.843* (NGB 111731), *-u.844* (NGB 111732), *-u.855* (NGB 111743), *-u.861* (NGB 111749) in Bonus, *-u.1091* (NGB 111979), *-u.1096* (NGB 111984), *-u.1101* (NGB 111989), *-u.1107* (NGB 111995), *-u.1108* (NGB 111996), *-u.1111* (NGB 111999), *-u.1114* (NGB 112002), *-u.1120* (NGB 112008), *-u.1137* (NGB 112025), *-u.1146* (NGB 112034), *-u.1148* (NGB 112036) in Kristina (NGB 14661, NGB 1500) (9); *cer-cu.644* (NGB 111532), *-u.695* (NGB 111583), *-u.850* (NGB 111738), *-u.887* (NGB 111775), *-u.892* (NGB 111780), *-u.895* (NGB 111783), *-u.901* (NGB 111789), *-cqu.925* (NGB 111813), *-cqu.944* (NGB 111832), *-cu.947* (NGB 111835) in Bonus, *-u.1177* (NGB 112065) in Kristina (10); *cer-u.699* (NGB 111587), *-u.776* (NGB 111664), *-u.986* (NGB 111874) in Bonus, *-u.1165* (NGB 112053), *-u.1184* (NGB 112072), *-u.1188* (NGB 112076), *-u.1202* (NGB 112090), *-u.1215* (NGB 112103), *-u.1227* (NGB 112115), *-u.1232* (NGB 112120), *-u.1237* (NGB 112125), *-u.1253* (NGB 112141), *-u.1272* (NGB 112160) in Kristina (11); *cer-u.1208* (NGB 112096), *-u.1261* (NGB 112149), *-u.1268* (NGB 112156), *-u.1282* (NGB 112170), *-u.1288* (NGB 112176), *-u.1295* (NGB 112183), *-u.1306* (NGB 112194), *-u.1309* (NGB 112197), *-u.1310* (NGB 112198) in Kristina, *-u.1327* (NGB 112215), *-u.1340* (NGB 112228), *-u.1341* (NGB 112229) in Bonus (12); *cer-u.457* (NGB 111345), *-u.578* (NGB 111466) in Foma, *-u.1364* (NGB 112252), *-u.1370* (NGB 112258), *-u.1372* (NGB 112260), *-u.1373* (NGB 112261), *-u.1390* (NGB 112278), *-u.1402* (NGB 112290), *-u.1409* (NGB 112297), *-u.1411* (NGB 112299), *-u.1420* (NGB 112308), *-u.1429* (NGB 112317) in Bonus (13); *cer-u.1496* (NGB 112384), *-u.1500* (NGB 112388), *-u.1734* (NGB 112547), *-u.1759* (NGB 112574), *-u.1763* (NGB 112567) in Bonus, *-u.1540* (NGB 112428), *-u.1541* (NGB 112429) in Nordal (NGB 13680, NGB 4704) (14); *cer-u.678* (NGB 111566), *-u.1825* (NGB 117373) in Bonus, *-u.602b* (NGB 111490) in Foma, *-u.1870* (NGB 117418) in Sv 79353 (15); *gsh8.ag* (OUM024, GSHO 1760), *gsh8.am* (OUM031) in Akashinriki (PI 467400, OUJ659) (5, 6).

Mutant used for description and seed stocks:

cer-u.21 (NGB 110905, GSHO 442) in Bonus; *cer-u.69* (NGB 110953) in Bonus is used for wax chemistry and wax structure studies (21, 23); *gsh8.ag* (OUM024, GSHO 1760) in Akashinriki; *gsh8.ag* in Bowman (PI 483237)*4 (GSHO 1870); *gsh8.ag* in Bowman*5

(BW411, NGB 20644).

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BGS 439, Eceriferum-zv, *cer-zv*

Stock number:	BGS 439
Locus name:	Eceriferum-zv
Locus symbol:	*cer-zv*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (6).

Located in chromosome 4HL (1, 3, 4); *cer-zv.268* is associated with SNP markers 2_1122 to 1_0568 (positions 47.80 to 78.18 cM) in 4H bins 05 to 06 of the Bowman backcross-derived line BW177 (1); *cer-ym.753*, a possible allele (4), is associated with SNP markers 2_0289 to 1_1513 (positions 69.62 to 101.44 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW144 (1); *cer-zv.268* and *cer-ym.753* are in a 0.8 cM interval between EST markers AK370363 and AK251484 in pericentromeric region of 4H (3, 4).

Description:

Surface wax coating on the spike, the leaf sheath and stem, and the leaf blade appears absent (wax code - - -) (6). Plants are semidwarf, very weak, and head late, and the hull is poorly attached to the kernel. The Bowman backcross-derived line for *cer-zv.268*, BW177, is a semidwarf (2/3 normal height) with a kinked upper peduncle and a strong wax coating on the nodes (2). Compared to Bowman, BW177 plants headed 2 to 10 days later in various environments. Plant height, peduncle length, and leaf blade length measurements were 1/2 to 2/3 those for Bowman. Awns were slightly shorter, but rachis internodes were slightly longer. Kernels of BW177 were shorter and thinner and weighed less, 3.5 vs. 5.8 mg, compared to Bowman kernels. Grain yields of BW177 averaged 10% those of Bowman (2). The *cer-ym.753* plants are weak, culms have a kinked peduncle, nodes are wax covered, and kernels are small, globe shaped, and nearly hulless (2, 5). Plants of the Bowman backcross-derived line for *cer-ym.753*, BW144, were phenotypically similar to BW177 plants, but they were more vigorous (2, 3, 4). Detached leaves of the mutant *cer-ym.753* lost 41.8% of their initial weight after 1 hour of dehydration under laboratory conditions, while that of the wild type Bowman plants lost only 7.1%. Stomata function was not affected by the mutation, but the mutant leaves showed increased cuticular permeability to water, suggesting a defective leaf cuticle, which was confirmed by toluidine blue staining. The *cer-ym.753* leaf blades showed a substantial reduction in the amounts of the major cutin monomers and a slight increase in the main wax component, suggesting that the enhanced cuticle permeability was a consequence of cutin deficiency (3, 4). Allelism tests demonstrated that mutants at the *cer-zv* and *cer-ym* loci are not alleles (5).

Origin of mutant:

An ethylene imine induced mutant in Foma (NGB 14659, CIho 11333) (5).

Mutational events:

cer-zv.268 (NGB 111155, GSHO 1529)*, -zv.342* (NGB 111229)*, -zv.576* (NGB 111464) in Foma (NGB 14659, CIho 11333) (6); *cer-zv.1256* (NGB 112144) in Kristina (NGB 1500, NGB 14661) (8); *cer-ym.130,* (NGB 111015, GSHO 1546), *-ym.753* (NGB 111641) in Bonus (NGB 14657, PI 189763) (7).

Mutant for description and seed stocks:

cer-zv.268 (GSHO 1529, NGB 111158) in Foma; *cer-zv.268* in Bowman (PI 483237)*5 (GSHO 2207); *cer-zv.268* in Bowman *7 (BW177, NGB 22009); *cer-ym.753* (GSHO 1546, NGB 111015) in Bonus; *cer-ym.753* in Bowman (PI 483237)*5 (GSHO 2217); *cer-ym.753* in Bowman*7 (BW144, NGB 20550).

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Revised:

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BGS 441, Eceriferum-zx, *cer-zx*

Stock number: BGS 441
Locus name: Eceriferum-zx
Locus symbol: *cer-zx*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3H (1); *cer-zx.100* is associated largely with SNP markers 1_0728 to 2_0523 (positions 96.85 to 173.82 cM) in 3H bins 06 to 11 of the Bowman backcross-derived line BW179 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem appears reduced (wax code + + ++) (4). The noted differences between the Bowman backcross-derived line for *cer-zx.100*, BW179, were the reduction in surface waxes on the spike and leaf sheath and the strong presence of wax on the nodes (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bonus (NGB14657, PI 189763) (3).

Mutational events:

cer-zx.100 (NGB 110984, GSHO 1531) in Bonus (PI 189763, NGB14657) (4).

Mutant used for description and seed stocks:

cer-zx.100 (NGB 110984, GSHO 1531) in Bonus; *cer-zx.100* in Bowman (PI 483237)*2 (GSHO 2209); *cer-zx.100* in Bowman*5 (BW179, NGB 22011).

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BGS 453, Few roots 1, *fer1*

Stock number: BGS 453
Locus name: Few roots 1
Locus symbol: *fer1*

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (1).
Location is unknown.
Description:
Mutant plants produce one to three seminal roots as six-day old seedlings while normal segregates produce four to nine seminal roots. Older plants grown in gravel do not develop a secondary root system (1). Older plants are phenotypically normal, but inclined to overturn or lodge easily (1).
Origin of mutant:
An ethyl methanesulfonate induced mutant in Bomi Abed (NGB 5096. PI 43371) (1).
Mutational events:
fer1.a (GSHO 2538, 2076/04-10) in Bomi Abed (NGB 5096, PI 43371) (1).
Mutant used for description and seed stocks:
fer1.a (GSHO2538, 2076/04-10) in Bomi Abed.
References:
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BGS 474, Laxatum-a, *lax-a*

Stock number:	BGS 474
Locus name:	Laxatum-a
Locus symbol:	*lax-a*

Previous nomenclature and gene symbolization:

Laxatum-01 = *lax-01* (5, 10, 15).
Laxatum-a = *lax-a*^{01} (16).
Hordeum vulgare laxatum-a = *HvLax-a* (8).

Inheritance:

Monofactorial recessive (11, 15).

Located in chromosome 5HL (11, 14); *lax-a.8* is about 2.4 cM proximal from the *ari-e* (breviaristatum-e) locus (7, 17); *lax-a.8* is about 3.1 cM from the *ert-g* (erectoides-g) locus (7, 16, 17); *lax-a.8* is associated with SNP markers 2_1065 to 2_1275 (positions 40.91 to 104.73 cM) in 5H of the Bowman backcross-derived line BW457; *lax-a.ap* is associated with SNP markers 1_0621 to 2_1275 (positions 56.40 to 104.73 cM) in 5H of the Bowman backcross-derived line BW458 (2), the deletion associated with the *lax-a.8* mutant mapped near SNP marker 2_0524 (8), in 5H bin 04.

Description:

Florets have five anthers with two developing from transformed lodicules (5, 19); however, the extra anthers are deficient in having two rather than four microsporangia (1). The grain is thin and angular and caryopses are exposed between the lemma and palea. The awn has a very wide base, without a distinct notch in the lemma attachment region. Rachis internodes are about 15% longer than normal. Tillers arise at oblique angles giving isolated plants an appearance of a tufty growth habit (10). Treatment of leaves after tillering with GA_3 increases rachis internode length (18). Plants of Bowman backcross-derived line for *lax-a.8*, BW457 were 4/5 the height of Bowman and anthesis was delayed by 3 to 4 days. Awns were slightly shorter than normal. Kernels were short and thin and highly variable in size. Compared to Bowman, BW457 plants had kernel weights about 60% of normal, test weights were low, and grain yields were about half of normal (4). The thinner grains are largely exposed due to reduced marginal growth of the palea and lemma. Flowers of the *lax-a.8* mutants can open without the impetus force of lodicule swelling (8). The *lax-a* locus was identified as a homolog of the Arabidopsis genes *BLADE-ON-PETIOLE1* (*BOP1*) and *BOP2*. The *HvLax-a* gene and its paralog *HvCul4* are involved in primarily regulating spike morphology and tiller number, respectively (8). Evaluation of natural alleles at the *Lax-a* locus identified one predominant haplotype and nine minor haplotype variants (8).

Origin of mutant:

A gamma-ray induced mutant in Bonus (NGB 14657, PI 189763) (3, 10, 13). More information about the origins and nature of mutants *lax-a* locus is presented in www.nordgen.org/bgs and by Jost et al. (8).

Mutational events:

lax-a.01 (NGB 116334), *-a.4* (NGB 116338), *-a.8* (NGB 116342, GSHO 1775), *-a.20* (NGB 116354), *-a.37* (NGB 116372), *-a.39* (NGB 116374), *-a.54* (NGB 116388) in Bonus (NGB 14657, PI 189763) (11, 12); *lax-a.92* (NGB 116425) in Bonus (12); *lax-a.208* (NGB 116435), *-a.218* (NGB 116446), *-a.222* (NGB 116450), *-a.229* (NGB 116457), *-a.256* (NGB 116483), *-a.278* (NGB 116503), *-a.286* (NGB 116510) in Foma (NGB 14659, CIho 11333) (10, 12); *-a.353* (NGB 116559) *-a.369* (NGB 116578, 116579), *-a.373* (NGB 116583), *-a.398* (NGB 116608), *-a.405* (NGB 116613), *-a.406* (NGB 116614) in Kristina (NGB 14661, NGB 1500) (11); *-a.413* (NGB 116621), *-a.434* (NGB 116647), *-a.437* (NGB 116650), *-a.444* (NGB 116658), *-a.448* (NGB 116664), *-a.450* (NGB 116667), *-a.455* (NGB 116674), *-a.472* (NGB 116695) in Bonus (12); a *lax-a* mutant (Mut 2100/61) in Proctor (PI 280420) (6); *lax-a.ap* (FN50) in Steptoe (CIho 15229) (9).

Mutant used for description and seed stocks:

lax-a.8 (NGB 116342, GSHO 1775) in Bonus; *lax-a.8* in Bowman (PI 483237)*7 (GSHO 2103, BW457, NGB 20689); *lax-a.ap* from Steptoe in Bowman*4 (BW458, NGB 22153).

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Barley Genetics newsletter (2016) 46:47-145.

BGS 525, Eceriferum-yl, *cer-yl*

Stock number:	BGS 525
Locus name:	Eceriferum-yl
Locus symbol:	*cer-yl*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 4HL (1); *cer-yl.187* is associated with SNP markers 2_0411 to 1_0062 (positions 52.11 to 91.93 cM) in 4H bins 04 to 06 of the Bowman backcross-derived line BW143 (1).

Description:

Surface wax coating on the spike, the leaf sheath, and the stem appears absent (wax code - - ++) (4). The original mutant stock produces weak plants (about 3/4 normal height) with a high level of sterility (4). Plants of the Bowman backcross-derived line for *cer-yl.187*, BW143, are semidwarf with waxy nodes, coiled peduncles, globose shaped seeds, and poor hull attachment. Reduced seed set can be caused by adverse environmental conditions (2). The BW143 plants headed 1 to 2 days later than Bowman and were shorter, 67 v. 89 cm. Peduncles and leaf blades were about 2/3 normal length. Kernels were thinner and weighed less, 4.4 vs. 5.9 mg and grain yields were 1/4 to 1/3 those of Bowman (2). Although not as extreme, the phenotypic characteristics of BW143 are similar to those of the Bowman backcross-derived lines for *cer-zv.268* (BW177) and *cer-ym.753* (BW144). Since all three loci retain donor parent markers in the same region of 4HL, they might have mutations in the same gene (1, 2). However, allelism tests demonstrated that the mutants at these loci are not alleles (3).

Origin of mutant:

A propane disulfonic acid diethyl ester induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

cer-yl.187 (NGB 111073, GSHO 1545), *-yl.188* (NGB 111074) in Bonus (NGB 14657, PI 189763) (4); *cer-yl.407* (NGB 111295) in Foma (NGB 14659¸ CIho 11333), *-yl.821* (NGB 111709) in Bonus (5).

Mutant used for description and seed stocks:

cer-yl.187 (NGB 111073, GSHO 1545) in Bonus; *cer-yl.187* in Bowman (PI 483237)*6 (GSHO 2216); *cer-yl.187* in Bowman*7 (BW143, NGB 20549).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:452.

Revised:

U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:116-117.

Barley Genetics newsletter (2016) 46:47-145.

BGS 526, Eceriferum-ym, *cer-ym*

Stock number: BGS 526
Locus name: Eceriferum-ym
Locus symbol: *cer-ym*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (7).

Located in chromosome 4HL (1, 3, 4); *cer-ym.753* is associated with SNP markers 2_0289 to 1_1513 (positions 69.62 to 101.44 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW144 (1); *cer-zv.268*, a possible allele (4), is associated with SNP markers 2_1122 to 1_0568 (positions 47.80 to 78.18 cM) in 4H bins 05 to 06 of the Bowman backcross-derived line BW177 (1); *cer-ym.753* and *cer-zv.268* are in a 0.8 cM interval between EST markers AK370363 and AK251484 in pericentromeric region of 4H (3, 4).

Description:

Surface wax coating on the spike, the leaf sheath and stem, and the leaf blade appears absent (wax code - - -) (7). Plants are weak, culms have a kinked peduncle, nodes are wax covered, and kernels are small, globe shaped, and nearly hull-less (2, 5). Plants of the Bowman backcross-derived line for *cer-ym.753*, BW144, averaged about 2/3 the height of Bowman with peduncles and leaf blades about 2/3 normal length. Awns of BW144 were slightly shorter and kernels were smaller and lighter, 4.2 vs. 6.1 mg. The grain yields of BW144 were less than 1/3 that of Bowman. Plants of the Bowman backcross-derived line for *cer-zv.268* (BW177) were phenotypically similar to BW144 (*cer-ym.753*) plants, but they were weaker (2, 3). Detached leaves of the mutant *cer-ym.753* lost 41.8% of their initial weight after 1 hour of dehydration under laboratory conditions, while that of the wild type Bowman plants lost only 7.1%. Stomata function was not affected by the mutation, but the mutant leaves showed increased cuticular permeability to water, suggesting a defective leaf cuticle, which was confirmed by toluidine blue staining (3, 4). The *cer-ym.753* leaf blades showed a substantial reduction in the amounts of the major cutin monomers and a slight increase in the main wax component, suggesting that the enhanced cuticle permeability was a consequence of cutin deficiency (3, 4). Allelism tests demonstrated that mutants at the *cer-ym* and *cer-zv* loci are not alleles (5).

Origin of mutant:

An ethylene oxide induced mutant in Bonus (NGB 14657¸ PI 189763) (5).

Mutational events:

cer-ym.130, (NGB 111015, GSHO 1546), *-ym.753* (NGB 111641) in Bonus (NGB 14657, PI 189763) (7); *cer-zv.268* (NGB 111158, GSHO 1529)*, -zv.342* (NGB 111229)*, -zv.576* (NGB 111464) in Foma (NGB 14659, CIho 11333) (6); *cer-zv.1246* (NGB 112144) in Kristina (NGB 14661, NGB 1500) (8).

Mutant used for description and seed stocks:

cer-ym.753 (NGB 111015, GSHO 1546) in Bonus*; cer-ym.753* in Bowman (PI 483237)*5 (GSHO 2217); *cer-ym.753* in Bowman*7 (BW144, NGB 20550).

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Revised:
U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:118-119.

Barley Genetics newsletter (2016) 46:47-145.

BGS 557, Breviaristatum-p, *ari-p*

Stock number:	BGS 557
Locus name:	Breviaristatum-p
Locus symbol:	*ari-p*

Previous nomenclature and gene symbolization:

Breviaristatum-27 = *ari-27* (3).

Inheritance:

Monofactorial recessive (3).

Location is unknown, no SNP markers were retained in the Bowman backcross-derived line BW054 for *ari-p.27* (1); the late heading trait observed in early backcrosses to Bowman might have reflected a repulsion linkage to the Early maturity 6 (*Eam6.h*) gene of Bowman (2).

Description:

Awns are about 3/4 normal length, and sterile spikelets occur at random in the original stocks (3). Initially during backcrossing to Bowman, short awned plants headed later than Bowman. In the Bowman backcross-derived line for *ari-p.27*, BW054, plants head about one day later than Bowman and have awn length from the tip of the spike of 6 vs. 11 cm. No other morphological differences were observed (2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (4).

Mutational events:

ari-p.27 (NGB 115875, GSHO 1664) in Bonus (NGB 14657, PI 189763) (4); *ari-p.108* (NGB 115920)*, -p.172* (NGB 115982)*, -p.208* (NGB 116016)*, -p.209* (NGB 116017)*, -p.223* (NGB 116032) in Foma (NGB 14659, CIho 11333) (3); *ari-p.278* (NGB 116091) in Kristina (NGB 1500, NGB 14661) (4).

Mutant used for description and seed stocks:

ari-p.27 (NGB 115875, GSHO 1664) in Bonus; *ari-p.27* in Bowman (PI 483237)*3 (GSHO 2163), in Bowman*7 (BW054, NGB 20462).

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Revised:

U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:132.

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BGS 562, Erectoides-k, *ert-k*

Stock number:	BGS 562
Locus name:	Erectoides-k
Locus symbol:	*ert-k*

Previous nomenclature and gene symbolization:

Erectoides-32 = *ert-32* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 6H (3, 5, 10), *ert-k.32* is associated with SNP markers 1_0061 to 1_0040 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 of the Bowman backcross-derived line BW314 (2); *ert-k.32* is in a 15.7-cM interval between markers 2_0291 (50.4 cM) and 1_0040 (66.1 cM) (8).

Description:

Spikes of *ert-k* mutants are semicompact with rachis internode length values varying from 2.4 to 2.8 mm compared to 3.1 for Bonus (12). Culm length was 3/4 to 5/6 of normal (12). The improved straw strength of this mutant has potential agronomic value as indicated by the release of the *ert-k.32* stock as the cultivar Pallas (1, 7). In the Bowman backcross-derived line for *ert-k.32*, BW314, plants were about 15% shorter, kernels were 10 to 15% lighter, and rachis internodes were shorter, 3.5 vs. 4.5 mm, than those of Bowman (4). The grain yields of BW314 and Bowman were similar (4). In comparison with Bowman as grown under greenhouse conditions, BW314 plants had shorter culms (78.4 ± 7.7 cm vs. 63.7 ± 4.6 cm) and denser spikes (7.3 ± 3.4 cm vs. 6.1 ± 2.5 cm) (8), Compared to Bowman, the 1000-kernel weight of BW314 was reduced by approximately 9.5% (46.2 ± 2.3 g and 41.9 ± 3.2 g) (8). The *ert-k* region of 6H was associated with a plant height QTL, QTL16_PHT, in a genome-wide association mapping study of spring barley accessions (11).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (6).

Mutational events:

ert-k.32 (NGB 112633, GSHO 485) in Bonus (NGB 14657, PI 189763) (6); *ert-k.76* (NGB 112675) in Bonus (7); *ert-k.93* (NGB 112692) in Bonus, *-k.309* (NGB 112825) in Foma (NGB 14659, CIho 11333) (12); *ert-k.302* (NGB 112819), *-k.435* (NGB 112951), *-k.459* (NGB 112974), *-k.477* (NB 112993) in Foma (9).

Mutant used for description and seed stocks:

ert-k.32 (NGB 112633, GSHO 485) in Bonus; *ert-k.32* in Bowman (PI 483237)*6 (GSHO 2253, BW314, NGB 20589).

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U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:121-122.

BGS 578, Praematurum-b, *mat-b*

Stock number: BGS 578
Locus name: Praematurum-b
Locus symbol: *mat-b*

Previous nomenclature and gene symbolization:

Early 7 = *ea-b7* (3).
Early maturity-b = *ea-b* (10).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7HL (9), *mat-b.7* is in a 5.74 cM interval between morex_contig_67392 and morex_contig_1561399 (positions 126.27 to132.01 cM) in 7H bin 13, but close to morex_contig_1561399 (9).

Description:

Early heading mutants at the *mat-b* locus show a rather drastic increase in earliness (heading 7 days earlier than the parents) under field cultivation in Sweden (3, 9). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and are classified as a pronounced long-day type (1, 2, 5). Early heading is also associated with decreased culm length, kernels per spike, and grain yield. Mutant plants are generally more productive in field trials than *mat-a* (*eam8*) mutants, but less resistant to lodging, partially caused by a modified culm structure. Compared with the original cultivars, they have one internode less per culm, a longer first internode, and a short basal rachis internode (3). At an early stage of development, *mat-b* mutants are characterized by pale green color when grown at 15 to 20ºC, but they are bright green in color at lower temperatures (1, 2, 5). Earliness of the *mat-b* mutants was observed to be day length responsive averaging 9 days earlier than their mother cultivars under long days, but they failed to head under short days (9).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

mat-b.7 (NGB 110007, GSHO 1788), *-b.10* (trans) (NGB 110010), *-b.13* (NGB 110013) in Bonus (3); *mat-b.34* (NGB 110034), *-b.35* (NGB 110035), *-b.38* NGB 110038), *-b.66* (NGB 110066) in Bonus (NGB 14657, PI 189763),*-b.106* (NGB 110106), *-b.108* (NGB 110108), *-b.134* (NGB 110134), *-b.137* (NGB 110137), *-b.145* (NGB 110145), *-b.214* (NGB 110214), *-b.216* (NGB 110216), *-b.237* (NGB 110237), *-b.244* (NGB 110244), *-b.261* (NGB 110261), *-b.279* (NGB 110279), *-b.286* (NGB 110286), *-b.313* (NGB 110313), *-b.337* (NGB 110337), *-b.403* (NGB 110403) in Foma (NGB 14659, CIho 11333), *-b.852* (NGB 110852), *-b.853* (NGB 110853), *-b.855* (NGB 110855), *-b.859* (NGB 110859), *-b.861* (NGB 110861), *-b.867* (NGB 110867), *-b.869* (NGB 110869), *-b.870* (NGB 110870), *-b.871* (NGB 110871), *-b.904* (NGB 116859), *-b.920* (NGB 117451), *-b.922* (NGB 117453) in Bonus, *-b.963* (NGB 117954), *-b.977* (NGB 117508), *-b.980* (NGB 117511), *-b.986* (NGB 117517), *-b.991* (NGB 117522), *-b.992* (NGB 117523), *-b.1008* (NGB 117539) in Sv 79353, *-b.1082* (NGB 117613) in Sv Vg74233, *-b.1103* (NGB 117634) in Sv Semira (NGB NSL 206731), *-b.1110* (NGB 119558), *-b.1112* (NGB 119560), *-b.1116* (NGB 119564) in Sv Frida (NGB 1519) (6, 7, 8); *mat-b.1401* (NGB 110408) in Bonus (3, 8); *mat-b.1404* (NGB 110411), *-b.1405* (NGB 110412) in Bonus (8).

Mutant used for description and seed stocks:

mat-b.7 (NGB 110007, GSHO 1788) in Bonus; *mat-b.7* in Bowman (PI 483237)*3 (GSHO 2282); *mat-b.7* in Bowman*7 (BW507, NGB 20735). The Bowman backcross-derived stock developed for *mat-b.7* (BW507) was demonstrated to have only the *mat-c.19* mutant (9).

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Revised:

U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl 46:123-124.

BGS 579, Praematurum-c, *mat-c*

Stock number:	BGS 579
Locus name:	Praematurum-c
Locus symbol:	*mat-c*

Revised locus symbol:

The *mat-c* mutants were demonstrated to be alleles at the Early maturity 6 (*Eam6*) locus (1). However, continued use of the *mat-c* nomenclature as the locus and allele symbols is recommended because the large phenotypic differences occur between the early alleles at the *Eam6* locus (see BGS 098) and the *mat-c* mutants.

Previous nomenclature and gene symbolization:

Early 16 = *ea-c16* (6).
Praematurum-c = *mat-c* (16).
Earliness per se 2S = *eps2S* (9)
Hordeum vulgare CENTRORADIALIS = *HvCEN* (1, 14).
Early maturity 6 = *Ea6* (1, 15).

Inheritance:

Monofactorial recessive (6, 7).

Located in chromosome 2H (3); *mat-c.19* is associated with SNP markers 1_0525 to 2_0781 (positions 46.10 to 135.19 cM) in 2H bins 05 to 09 of the Bowman backcross-derived line BW508 (3); the praematurum-c (*mat-c*) mutants mapped at 57.5 cM and were determined to be the structural gene *Hordeum vulgare* CENTRORADIALIS (*HvCEN*) (1, 14); the *mat-c.19* deletion is in a 0.27 cM segment of 2H near SNP markers 2_887, 2_0537, and 2_0390 (14), in 2H bin 07.

Description:

Early heading mutants at the *mat-c* locus show a rather drastic increase in earliness (heading 7 days earlier than the parents) under field cultivation in Sweden (6). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and are classified as a pronounced long-day type (2, 5, 8). Slightly later heading of some *mat-c* alleles is reported (8, 13). Early heading is also associated with decreased culm length, kernels per spike, and grain yield. Mutants have reduced culm length, caused by the reduction in internode number, and the length of the peduncle is increased. Spike length and spikelet number are markedly reduced (2, 6). The *mat-c* mutants are variant in the barley homolog of *Antirrhinum CENTORADIALIS* (*HvCEN*) (1).The *mat-c.19* deletion and seven additional *mat-c* mutants affect the barley ortholog of *Arabidopsis thaliana TERMINAL FLOWER 1* (*AtTFL1*) and *Antirrhinum majus CENTRORADIALIS* (*AmCEN*) gene (14). Not all mutant assigned to the *mat-c* allelic group have deletions or other structure change in the *HvCEN* gene (1, 14). In comparison to Bowman, the Bowman backcross-derived line for *mat-c.19* (BW508) headed 5 to 8 days earlier, were 5 to 10% shorter, and 4 to 10 fewer fertile spikelets. Kernels were slightly larger and heavier, but grain yield was only 15 to 35% of that for Bowman (4).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (6).

Mutational events:

mat-c.16 (NGB 110016) in Bonus (NGB 14657, PI 189763) (6); *mat-c.19* (NGB 110019, GSHO 1789)*, -c.32* (NGB 110032)*, -c.93* (NGB 110093)*, -c.94* (NGB 110094) in Bonus, *-c.101* (NGB 110101)*, -c.122* (NGB 110122)*, -c.400* (NGB 110400) in Foma (NGB

14659, CIho 11333), *-c.745* (NGB 110745) in Kristina (NGB 14661, NGB 1500), *-c.758* (NGB 110758), *-c.760* (NGB 110760), *-c.770* (NGB 110770), *-c.865* (NGB 110865), *-c.881* (NGB 110881), *-c.907*116862), *-c.910* (NGB 117441), *-c.913* (NGB 117444, *-c.926* (NGB 117457), *-c.943* (NGB 117474) in Bonus, *-c.966* (NGB 117497) in Sv 79353, *-c.1091* (NGB 117622) in Sv Vg74233, *-c.1096* (NGB 117627) in Sv Frida (NGB 1519), *-c.1102* (NGB 117633) in Sv Semira (NGB 10716, NSL 206731), *-c.1107* (NGB 119555), *-c.1108* (NGB 119556), *-c.1109* (NGB 119557), *-c.1111* (NGB 119559), *-c.1114* (NGB 119562), *-c.1115* (NGB 119563) in Sv Frida, *-c.1118* (NGB 119566), *-c.1120* (NGB 119568) in Sv Semira (11, 12, 13). The early variant (haplotype II) at the *Eam6* (*HvCEN*) locus is present in many domesticated winter barley accessions (1); Bowman (PI 483237) has .the *Eam6.h* allele (haplotype I) at the *mat-c* or *Eam6* locus (1). The late allele (haplotype III) at the *HvCEN* locus is present in European barley cultivars (1).

Mutant used for description and seed stocks:

mat-c.19 (NGB 110019, GSHO 1789) in Bonus; *mat-c.19* in Bowman (PI 483237)*2 (GSHO 2283); *mat-c.19* in Bowman*6 (BW508, NGB 20736); *Eam6.h* (haplotype I) from Nordic (CIho 15216) is present in Bowman (1, 4).

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Revised:
U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:125-127.

BGS 599, Proanthocyanidin-free 17, *ant17*

Stock number:	BGS 599
Locus name:	Proanthocyanidin-free 17
Locus symbol:	*ant17*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (6, 7).

Located in chromosome 3HS (1); *ant17.148* is associated with SNP markers 2_0607 to 1_0601 (positions 52.41 to 71.29 cM) in 3H bins 04 to 05 in Bowman backcross-derived line BW016 (2); the *ant17.148* mutant has been shown to be an allele at the *seg3* (shrunken endosperm genetic 3, see BGS 379) locus (3). The seed stock for the Bowman backcross derived line for *ant17.567*, BW017, is incorrect because the same SNP markers were retained in both BW016 and BW017 (2, 3). The correct seed lot for BW017 has been increased as NGB 20425.

Description:

Under normal growing conditions no anthocyanin pigmentation is observed in the *ant17* mutant plants. The testa layers of the grain of the *ant17* mutants lack proanthocyanidins and catechins, but accumulate homoeriodictyol and chrysoeriol (9, 12). A full length cDNA clone from barley, coding for a protein consisting of 377 amino acids (42 kDa), has been isolated. It shows a homology of 71% to the flavanone-3-hydroxylase enzyme protein from *Antirrhinum majus* (14). It is likely that the *ant17* gene codes for one subunit and the *ant22* gene for the other subunit of the dimeric flavanone 3-hydroxylase enzyme, which catalyzes the conversion of flavanones into dihydroflavanols (9, 14). The mutant line *ant17.148* was released as cultivar Galant (13). Alleles at the *seg3* locus in the Bowman backcross-derived lines BW016 (*ant17.148*) and BW836 (*seg3.c*) showed variable reductions in kernel weight: Kernels of BW016 and BW836 were 1/3 to 1/2 normal weight while those of BW017, the backcross-derived line for *ant17.567*, were about 3/4 normal (3). Grain yields of BW017 were about 3/4 those of Bowman (3). Grain weight was reduced by 20% in some ant17 mutants, but grain dormancy was unaltered (4). The low anthocyanin content of *ant17* mutants was quantified using the *ant17.469* mutant (4). Sequencing of three independent *ant17* alleles detected point mutations within the coding regions of *flavanone-3-hydroxylase* (*F3H*), which are predicted to cause a premature stop codon at different sites (4).

Origin of mutant:

A sodium azide induced mutant in Nordal (NGB 13680, NGB 4704) (5, 6).

Mutational events:

ant17.103, *17.104*, *17.105*, *17.139* (NGB 13697), *17.140*, *17.142*, *17.143*, *17.145* in Nordal (NGB 13680, NGB 4704) (5, 6); *ant17.107* in Alf (NGB13682) (5, 6); *ant17.147*, *17.148* (Galant) (NGB 24787, NGB 13698, GSHO 1628), *17.150*, *17.151*, *17.153*, *17.154*, *17.180*, *17.185* in Triumph (NGB 13678, PI 268180) (6); *ant17.352* in Triumph (7); *ant17.160* in Gula Abed (NGB 13681) (6); *ant17.165*, *17.167*, *17.169*, *17.171*, *17.174*, *17.182* in Ark Royal (PI 447006) (6); *ant17.192*, *17.193* in Georgie (NGB 13683, PI 447012) (6); *ant17.199* in Secobra 4681 (6); *ant17.200* in Secobra 4681 (7); *ant17.208* in Hege 876 (6); *ant17.210*, *17.211*, *17.217* in Hege 802 (6); *ant 17.216* in Hege 802 (6); *ant17.220*, *17.221*, *17.224*, in Secobra 4743 (NGB 13679) (6); *ant17.227* in Ca 59995 (7); *ant17.231* in Tron (6); *ant17.237*, *17.239*, *17.241*, *17.242*, *17.247*, *17.249* in Gunhild (NGB 13690, PI 464655) (6); *ant17.243*, *17.246* in Gunhild (7); *ant17.250*, *17.251*, *17.252*, *17.253*, *17.255* in Tokak (PI 264251) (6); *ant17.267*, *17.268*, *17.269* in Secobra 18193 (NGB 13684) (6); *ant17.270* in Secobra 18193 (7); *ant17.280* in Hege 550/75 (NGB 13692) (11); *ant17.288*, *17.289*, *17.290* in Hege 550/75 (6); *ant17.293*, *17.294, 17.295*, *17.296* in Bonus (NGB 14597, PI 189763) (6); *ant17.297*, *17.298*, 17.300, *17.301*, *17.307* in Ca 41507 (6); *ant17.306*, *17.340* in Ca 41507 (7); *ant17.316* in Ca 33787 (NGB 13693) (7); *ant17.318*, *17.321*, *17.326* in Harry (PI 491575) (7); *ant17.331* in Hege A2/A4 (7); *ant17.335*, *17.336*, *17.338* in Ackermann 724/5/7 (7); *ant17.359* in Hege15/74-1A (7); *ant17.370* in Ackermann 72/440 (7); *ant17.372*, *17.413*, *17.414*, *17.417*, *17.418*, *17.419*, *17.444* in Kaya (7); *ant17.375* in Fanette (8); *ant17.379*, 17.382, *17.383*, 17.386, *17.387*, *17.388*, *17.389*, *17.390*, *17.391*, *17.464*, 17.465 in Irene (7); *ant17.405* in Odin (8); *ant17.408* in KMJ 326 (7); *ant17.410*, *17.447* in Catrin (7); *ant17.421* in VBS 18707 (7); *ant17.422*, *17.423*, *17.424*, *17.426* in NZ 3789 (7); *ant17.432* in NZ 1836-3 (7); *ant17.438*, *17.439* in NZ 732.01 (7); *ant17.440* in Nordal (NGB 13680, NGB 4704) (7); *ant17.450* in Ca 601427 (7); *ant17.453*, *17.455*, *17.457*, *17.458* in Ackermann 1734/5 (7); *ant17.462* in Pamela (7); *ant17.469* (NGB 23018), *17.470* (NGB 23019) in Grit (NGB 13685, PI 548764) (7); *ant17.475* in Zenit (NGB 13686, PI 564447) (7); *ant17.476* in Zenit (8); *ant17.480* in Secobra 9709 (7); ant17.501 in Advance (CIho 15804) (6); *ant17.504* in Karla (CIho 15860) (6); *ant17.506*, *17.507*, *17.508*, *17.509* in OR 9114 (6); *ant17.515*, *17.516*, *17.518* in WA9037-75 (6); *ant17.520* in WA9044-75 (6); *ant17.530* in Morex (CIho15773) (6); *ant17.537*, *17.595*, *17.619*, *17.620* in Advance (7); *ant17.560*, *17.561*, *17.563*, *17.565*, *17.567* (NGB 23018, GSHO 1629) in Manker (CIho 15549) (7); *ant17.597* in Morex (8); *ant17.598* in Morex (7); *ant17.600* in S 80351 (7); *ant17.601* in Moravian 111 (CIho 15812) (7); *ant17.604* in Harrington (8); *ant17.612* in Andre (PI 469107) (7); *ant17.624* in Klages (CIho 15478) (7); *ant17.625* in Robust (M36, PI 476976) (7); *ant17.630* in Azure (CIho 15865) (15); *ant17.636*, *17.658* in Cougbar (PI 496400) (15); *ant17.637* in 8892-78 (15); *ant17.661* in Crest (PI 561409) (15); *ant17.1502*, *17.1505*, *17.1519* in Amagi-Nijo (6); *ant17.1510*, *17.1511* in Haruna-Nijo (6); *ant17.1515* in Nirakei 61 (6); *ant17.1537* in Nirakei 62 (7); *ant17.1544* in Nirakei 63 (7); *ant17.1534* in Nirasaki-Nijo 14 (7); *ant17.2022*, *17.2067* in Natasha (PI 592171) (8); *ant17.2084* in Hege 694/82 (11); *ant17.2106* in Ca 708912 (10); *ant17.5019* in Sonja (NGB 6324, PI 302047) (11); *ant17.5024* in Ackermann 72/27/4 (8); *ant17.5028* in Trigger (PI 473541) (11); *ant17.5034* in Kaskade (11); *ant17.5035*, *17.5036*, *17.5037* in Video (8); *ant17.5038*, 17.*5039*, *17.5040*, *17.5042* in Sonja (8); *ant17.5044* in Ackermann 27/220/8 (8).

Mutant used for description and seed stock:

ant17.139 (NGB 13697) in Nordal; *ant17.148* (Galant, NGB 24787, NGB 13698, GSHO 1628) in Triumph; *ant17.148* in Bowman (PI 483237)*4 (GSHO 1973, BW016, NGB 20424); *ant17.567* (GSHO 1629) in Manker; *ant17.567* in Bowman*5 (GSHO 1974); *ant17.567* in Bowman*7 (BW017, NGB 20425); *seg3.c* from Compana in Bowman (PI 483237)*7 (GSHO 1957, BW836, NGB 22273).

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BGS 608, Proanthocyanidin-free 28, *ant28*

Stock number:	BGS 608
Locus name:	Proanthocyanidin-free 28
Locus symbol:	ant28

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 3HL, *ant28.484* is close to the *Est4* (Esterase 4) locus (1); *ant28.494* mapped about 11 cM proximal from microsatellite marker EBmag0705 in the distal region of 3HL (2).

Description:

Mutant plants synthesize a wild type amount of anthocyanins in their vegetative parts. The testa layers of the mutant grains lack catechins and proanthocyanidins. The *ant28* gene affects the proanthocyanidin specific branch of the flavonoid pathway, but the exact nature of the gene action is not known (4). The gene for the *R2R3 MYB* domain protein, which regulates proanthocyanidin accumulation in developing grains, was isolated by PCR from the barley mutant *ant28.494* and named *Hvmyb10* due to its similarity to *Tamyb10* or *R-1* of wheat (2). The *ant28* mutants evaluated had reduced grain dormancy indicating that *Hvmyb10* is a key factor in grain dormancy in barley (2).

Origin of mutant:

A sodium azide induced mutant in Grit (NGB 13685, PI 548764) (3).

Mutational events:

ant28.484 (NGB 13711) in Grit (NGB 13685, PI 548764) (5); *ant28.493* (NGB 21978), *28.494*, *28.495* (NGB 21979) in Catrin (5); *ant28.2092* (NGB 21980), *28.2093* (NGB 21981), *28.2095* (NGB 22827) in Nairn (5); *ant28.2131* (NGB 13712), *28.2132* (NGB 21982) in Alexis (NGB 13688, PI 564487) (5).

Mutant used for description and seed stock:

ant28.484 (NGB 13711) in Grit; *ant28.2131* (NGB 13712) in Alexis.

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Prepared:

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Revised:

J. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:131.

BGS 617, Uniculme 4, *cul4*

Stock number:	BGS 617
Locus name:	Uniculme 4
Locus symbol:	*cul4*

Previous nomenclature and gene symbolization:

Uniculme-5 = *uc-5* (4).
Uniculme-3 = *uc-3* (4).
Hordeum vulgare Uniculme 4 = *HvCul4* (6).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HL (8); *cul4.3* is near AFLP marker E4143-4 in subgroup 32 of the Proctor/Nudinka map (5); *cul4.3*, *cul4.5*, *cul4.15*, and *cul4.16* mapped near RFLP markers CDO0394a and CDO105 (9); *cul4.5* is associated with SNP markers 1_0646 to 2_0339 (positions 239.73 to 248.51 cM) in 3H bin 15 of the Bowman backcross-derived line BW212 (2); *cul4.3* is associated with SNP markers 2_0136 to 1_0044 (positions 138.00 to 190.80) in 3H bins 08 to 13 and with markers 1_0646 to 2_1362 (positions 239.73 to 255.13 cM) in 3H bins 15 and 16 of the Bowman backcross-derived line BW211 (2), likely in 3HL bin 15.

Description:

Plants produce 1 to 4 tillers that are twisted and have slightly bowed culm internodes. All secondary tillers are shorter than the primary tiller and have a curly appearance. Often secondary tillers are trapped at the base of the primary tiller (3, 7). Compared to Bowman, *cul4* plants of the Bowman backcross-derived lines for *cul4.3* (BW211) and *cul4.5* (BW212) had peduncles that were slightly to 50% longer. Rachis internodes were slightly elongated, and kernels were slightly longer. Plant height varied from 2/3 normal to slightly taller than Bowman (3). The BW212 line with the *cul4.15* mutant exhibited more variation in height over environments (3). Under greenhouse conditions, the Bowman backcross-derived line for *cul4.5* (BW212) developed only two axillary tillers, and it was uniculm when combined with the *cul2.b* (uniculm 2) gene (1). The *cul4* mutants cause reduced tillering, deregulation of the number of axillary buds in an axil, and alterations in leaf proximal-distal patterning (10). Only one or two axils of BW212 plants contained axillary buds, but often two buds instead of one bud were present. These axillary buds were sometimes associated with the development of leafy shoots. All *cul4* mutants had a liguleless phenotype (10). The *Cul4* gene was isolated by positional cloning and shown to encode a BTB-ankyrin protein closely related to Arabidopsis *BLADE-ON-PETIOLE1* (*BOP1*) and *BOP2* (10). Morphological, histological, and in situ RNA expression analyses indicated that the dominant allele at the *Cul4* locus acts at axil and leaf boundary regions to control axillary bud differentiation, as well as development of the ligule (10). The *Cul4* locus was confirmed to be a homolog of the Arabidopsis genes *BLADE-ON-PETIOLE1* (*BOP1*) and *BOP2* (6). The *HvCul4* gene and its paralog *HvLax-a* are involved in primarily in regulating tiller number and spike morphology, respectively. Analysis of natural alleles at the *Cul4* locus identified 31 haplotype variants (6).

Origin of mutant:

An ethylene oxide induced mutant in Bonus (NGB 14657, PI 189763) (7). More information about the origins and nature of mutants at the *cul4* locus is presented in www.nordgen.org/bgs and by Jost et al. (6).

Mutational events:

cul4.3 (NGB 115062, GSHO 2495), *cul4.5* (NGB 115063, GSHO 2493) in Bonus (NGB 14657, PI 189763), *cul4.15* (NGB 115064) in Foma (NGB 14659, CIho 11333), *cul4.16* (NGB 115065) in Bonus (7, 9); *cul4.24* (NGB 119360) in Flare (NGB 1518) (7, 10, 11).

Mutant used for description and seed stocks:

cul4.3 (NGB 115062, GSHO 2495) in Bonus; *cul4.5* (NGB 115063, GSHO 2493) in Bonus; *cul4.3* in Bowman (PI 483237)*3 (GSHO 2360); *cul4.3* in Bowman*4 (BW211, NGB 22038); *cul4.5* in Bowman*4 (GSHO 2361); *cul4.5* in Bowman*7 (BW212, NGB 22039); *cul4.15* in Bowman*3 (BW208, NGB 22036); *cul4.16* in Bowman*2 (BW209, NGB 20559); *cul4.24* in Bowman*3 (BW210, NGB 22037).

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Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. Barley Genet. Newsl. 32:118.

Revised:

J.D. Franckowiak and U. Lundqvist. 2007. Barley Genet. Newsl. 37:289.
J.D. Franckowiak and U. Lundqvist. 2013. Barley Genet. Newsl. 43:162-163.
J.D. Franckowiak and U. Lundqvist. 2014. Barley Genet. Newsl. 44:192-193.
J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:132-133.

BGS 663, semidwarf 3, *sdw3*

Stock number:	BGS 663
Locus name:	Semidwarf 3
Locus symbol:	*sdw3*

Previous nomenclature and gene symbolization:

Gibberellin insensitive = GA-ins (8).
GA-insensitive = *gai* (5).
Elongation mutants = *elo* (6).
Hordeum vulgare semidwarf 3 = *Hv_sdw3* (11).

Inheritance:

Monofactorial recessive (2, 8, 10).

Located in chromosome 2HS (10); *sdw3.az* is linked to the six-rowed spike 1 *(vrs1*) locus (3, 8, 10); *sdw3.az* is about 9.0 cM from RFLP marker MWG557 (3); *sdw3.az* is located in 2HS close to the centromere and RFLP markers MWG2058 and MWG2278 (5); the RFLP markers flanking *sdw3.az*, MWG557 and cMWG658*,* were located 1.8 cM distal and 1.8 cM proximal, respectively (5); *sdw3.az* was genetically assigned to a 0.55 cM interval close to the centromere (10); the *sdw3.az* mutant mapped a 0.04 cM interval (11); *sdw3.az* is associated with SNP markers 1_1059 to 1_1061 (positions 17.96 to 81.50 cM) in 2H bins 02 to 06 of the Bowman backcrossed-derived line BW830 (7), in 2H bin 07.

Description:

Hv287 plants, which likely have both the *sdw3.az* and *sdw1.d* (semidwarf 1) genes, are semidwarfs (40 to 50 cm tall) compared to Monte Cristo (90 to 100 cM). Hv287 seedlings are insensitive to gibberellic acid (1, 2, 8). The height reduction in *sdw3.az* segregants without the *sdw1.d* gene was much less and other plant organs appeared unaffected (5, 9). Several GA_3 insensitive mutants, which were isolated after sodium azide treatment of Himalaya (6), were shown to be *sdw3* alleles (11). BW830 (NGB 22267), an F4 selection from a cross between Hv287 and Bowman, has retained SNP markers 1_1059 to 1_1061 (positions 17.96 to 81.50 cM) in 2H bins 02 to 06, which overlaps the *Eam1* (early maturity 1) gene from HV287 (7, 9). BW830 has the *Eam1* gene, but it may not have the *sdw3.az* allele (9).

Origin of mutant:

M.C. 90 is a gibberellin insensitive mutant induced by X-ray treatment of Mutante de Cebada 20 (M.C. 20, PI 346389) (1, 4), which is a mutant from Malteria Hede (PI 346380).

Mutational events:

sdw3.az in Hv287 is a double mutant selected from M.C. 90 backcrossed to Triumph (PI 548762, GSHO 2465) (1, 4); the sodium azide mutant M671 in Himalaya (probably CIho2448) is allelic at the *sdw3* locus (11); a group of allelic mutants (M12, M13, M102, M107, M119, M127, M130, M651, M671, M680) of Himalaya, of which only some originated as independent events (11).

Mutant used for description and seed stocks:

sdw3.az in Hv287 is a double mutant selected from M.C. 90 backcrossed to Triumph; possibly *sdw3.az* from HV287 in Bowman/Hv287 (BW830, NGB22267).

References:

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Prepared:

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:134-135.

BGS 716, Intense blue aleurone 1, *ibl1*

Stock number:	BGS 716
Locus name:	Intense blue aleurone 1
Locus symbol:	*ibl1*

Previous nomenclature and gene symbolization:

Intense blue aleurone = *ibl* (1, 2).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

The *ibl1.a* variant was identified based on mature aleurone color. Two new colors, brick red and intense blue, were found in the Abyssinian lines, Ethiopian 637 and Ab 2231, respectively. Aleurone color expression is influenced by the environment in much the same way as that of normal blue, but they are reasonably distinct from normal blue and white aleurones in well grown material (1). The *ibl1.a* gene intensifies the red anthocyanin pigmentation of base of seedlings and on the culms of maturing plants (3, 4). The leaf sheath anthocyanin content of the *ibl.a* variant [BW418 (NGB 20651)] having the dominant allele *Ant1.a* at the *Ant1* (Anthocyanin-less 1) or *HvMpc1* locus as measured by OD_{530} (anthocyanin content spectrophotometry at 530 nm) was about three times greater than that of Bowman backcross-derived lines with *Ant1.a*, but lacking *ibl1.a* (4).

Origin of mutant:

Natural occurrence in Ethiopian 637 (GSHO 2508) (1).

Mutational events:

ibl1.a in Ethiopian accessions Ethiopian 637 (GSHO 2508) and in Ab 2231 (1, 2).

Mutant used for description and seed stocks:

ibl1.a in Ethiopian 637; *ibl1.a* with *blx4.d* (blue aleurone 4) and *nud1.a* (naked caryopsis 1) in Bowman*4/ICARDA Green//Ethiopian 637 (BW417, NGB20650) produces red aleurone color; *ibl1.a* with *Blx1.a* (Blue aleurone 1) and *nud1.a* (naked caryopsis 1) in Bowman*4/ICARDA Green//Ethiopian 637 (BW418, NGB 20651) produces deep blue aleurone color.

References:

1. Finch, R.A., and G.E. Porter. 1976. A single gene determining two new aleurone colours in barley. Barley Genet. Newsl. 6:26-27.
2. Finch, R. A., and E. Simpson. 1978. New colours and complementary colour genes in barley. Z. Pflanzenzücht. 81:40-53.
3. Franckowiak, J.D. (Unpublished).
4. Shoeva, O.Y., T.V. Kukoeva, A. Börner, and E.K. Khlestkina. 2015. Barley *Ant1* is a homolog of maize C1 and its product is part of the regulatory machinery governing anthocyanin synthesis in the leaf sheath. Plant Breed. 134:400-405.

Prepared:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:241.

Revised:

J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:136.

BGS 730, Labile 1, *lab1*

Stock number: BGS 730
Locus name: Labile 1
Locus symbol: *lab1*

Previous nomenclature and gene symbolization:

Hordeum irregulare (2, 7).

Hordeum vulgare L. convar. *labile* (Schiem.) Mansf. (10, 11).

Inheritance:

Monofactorial recessive, but the *vrs1.a* (six-rowed spike 1) allele is required for expression (5, 10).

Located in chromosome 5HL (10); *lab1.a* is at approximately 80 cM of 5HL in an interval of 5.7 cM between closely linked markers BAR and ge00066s01 (10), likely in 5H bins 08 or 09.

Description:

The *lab1.a* variant causes variable spikelet development at rachis nodes and is characterized by missing kernels or a variable number fertile of spikelets at each rachis node in six-rowed spikes (2, 7). The lateral spikelets are missing more often than the central spikelets (4, 8, 9). All *lab1.a* (*labile*) accessions tested have the *vrs1.a* allele at the six-rowed spike 1 locus (8). The genetic background for *labile* phenotype is based on a six-rowed genotype with the six-rowed spike 1 with a recessive allele, *vrs1.a1* or *vrs1.a3*, at the six-rowed spike 1 locus and dominant *Int-c.a* allele present at the intermedium spike-c loci (11). Suppression of lateral spikelet development starts in late stamen primordium (10).

Origin of mutant:

Natural occurrence in barley accessions from Ethiopia (1, 2, 3, 6, 7).

Mutational events:

lab1.a in PI 95306 and PI 25672 from Ethiopia (2).

Mutant used for description and seed stocks:

lab1.a in HOR2573 and HOR5465 from Ethiopia (10).

References:

1. Abay, F., and A. Bjørnstad. 2009. Specific adaptation of barley varieties in different locations in Ethiopia. Euphytica 167:181-195.
2. Åberg, E., and G.A. Wiebe. 1945. Irregular barley, *Hordeum irregulare*, sp. nov. J. Wash. Acad. Sci. 35:161-164.
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Prepared:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:242.

Revised:
J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:137-138.

BGS 731, Required for *Puccinia graminis* resistance 2, *rpr2*

Stock number: BGS 731
Locus name: Required for *Puccinia graminis* resistance 2
Locus symbol: *rpr2*

Previous nomenclature:

ɣ08-118; R43-22#1 (4).

Inheritance:

Monofactorial recessive (2, 3, 4)

Location in chromosome 6H (2, 3); mapped to a 0.6 cM interval in 6H between markers Locus_6H_331 and GMS006 (2, 3).

Description:

The *rpr2.b* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in the cultivar, Morex, which has the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr2.b* mutant has been partially characterized (2, 3) with an infection type (IT) range of 21; to 3; with a mode 32 (rated by 1), or IT of 3-2 to 3 (rated by 2, 3), or IT of 2,3- to 3,3- (rated by 6). The *rpr2.b* mutant is not allelic to *rpr1.a*, *rpr3.c*, *rpr4.d; rpr5.e*, or *rpr6.f* (2, 3, 4). Barley often exhibits mesothetic reactions with two or more ITs on a single leaf; therefore, ITs observed are recorded in order of their prevalence (5). Overall the *rpr2.b* mutant stock is moderately susceptible as opposed to the parent line Morex, which is typically rated as moderately resistant. (4, 5). The RPG1 protein is present in the *rpr2.b* line and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3, 4). [Infection type (IT) for wheat stem rust (*Puccinia graminis* f. sp. *tritici*) seedling reaction is based on a 0-4 scale, defined by Stakman et al. (5), where 0 is highly resistant and 4 is highly susceptible with the in between numbers representing intermediate reactions which are further modified by + or – and a fleck (symbol = ;), which indicates a small necrotic area. IT1 indicates minute uredinia; IT2 small uredinia with chlorosis; IT3 medium uredinia often with chlorosis; and IT4 indicates large uredinia with chlorosis (5).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (3, 4).

Mutational events:

rpr2.b (ɣ08-118; R43-22#1, GSHO 3693) in Morex (CIho 15773) (2, 3, 4).

Mutant used for description and seed stocks:

rpr2.b (ɣ08-118; R43-22#1, GSHO 3693) in Morex; *rpr2.b* in F_2 seed lots GSHO 3694 and GSHO 3695 (4).

References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Gill, U., R. Brueggeman, J. Nirmala, Y. Chai, B. Steffenson, and A. Kleinhofs. 2016. Molecular and genetic characterization of barley mutants and genetic mapping of mutant *rpr2* required for *Rpg1*-mediated resistance against stem rust. Theor. Appl. Genet. 129 (8):1519-1529.
4. Kleinhofs, A. (Unpublished).

5. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
6. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:243.

Revised:

A. Kleinhofs. 2016. Barley Genet. Newsl. 46:139-140.

BGS 732, Required for *Puccinia graminis* resistance 3, *rpr3*

Stock number:	BGS 732
Locus name:	Required for *Puccinia graminis* resistance 3
Locus symbol:	*rpr3*

Previous nomenclature:

ɣ08-112; R12-31#3 (3, 4).

Inheritance:

Monofactorial recessive (2, 3, 4).

Location is unknown.

Description:

The *rpr3.c* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in the cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr3.c* mutant has been partially characterized (2, 3) with an infection type (IT) of moderately susceptible (MS): range of 3- to 3+ (rated by 2, 3); or MR with an IT range of 12 to 2 (rated by 1); or an IT of 2,3- (rated by 6) based on a 0-4 scale, defined by Stakman et al. (5). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpg3.c* mutant is not allelic to *rpr1.a, rpr2.b, rpr4.d, rpr5.e, or rpr6.f* (2, 3, 4). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3, 4).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (3, 4).

Mutational events:

rpr3.c (γ08-112; R12-31#3, GSHO 3696) in Morex (CIho 15773) (2, 3, 4).

Mutant used for description and seed stocks:

rpr3.c (γ08-112; R12-31#3, GSHO 3696) in Morex (4).

References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Gill, U., R. Brueggeman, J. Nirmala, Y. Chai, B. Steffenson, and A. Kleinhofs. 2016. Molecular and genetic characterization of barley mutants and genetic mapping of mutant *rpr2* required for *Rpg1*-mediated resistance against stem rust. Theor. Appl. Genet. 129 (8):1519-1529.
4. Kleinhofs, A. (Unpublished).
5. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
6. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:244.

Revised:

A. Kleinhofs. 2016. Barley Genet. Newsl. 46:141.

BGS 733, Required for *Puccinia graminis* resistance 4, *rpr4*

Stock number:	BGS 733
Locus name:	Required for *Puccinia graminis* resistance 4
Locus symbol:	*rpr4*

Previous nomenclature:

γ08-114; R36-37#1 (3, 4).

Inheritance:

Monofactorial recessive (2, 3, 4).

Location is unknown.

Description:

The *rpr4.d* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in the cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr4.d* mutant has been partially characterized (2, 3) with an infection type (IT) of moderately susceptible (MS): IT range of 21 to 32 with a mode 32 (rated by 1); IT range of 3- to 3+ (rated by 2, 3), or IT range of 3,3+ to 3,3- (rated by 6) based on a 0-4 scale, defined by Stakman et al. (5). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr4.d* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr5.e*, or *rpr6.f* (2, 3, 4). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3, 4).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (3, 4).

Mutational events:

rpr4.d (γ08-114; R36-37#1, GSHO 3697) in Morex (CIho 15773) (2, 3, 4).

Mutant used for description and seed stocks:

rpr4.d (γ08-114; R36-37#1, GSHO 3697) in Morex (4).

References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Gill, U., R. Brueggeman, J. Nirmala, Y. Chai, B. Steffenson, and A. Kleinhofs. 2016. Molecular and genetic characterization of barley mutants and genetic mapping of mutant *rpr2* required for *Rpg1*-mediated resistance against stem rust. Theor. Appl. Genet. 129 (8):1519-1529.
4. Kleinhofs, A. (Unpublished).
5. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
6. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:245.

Revised:

A. Kleinhofs. 2016. Barley Genet. Newsl. 46:142.

Barley Genetics newsletter (2016) 46:47-145.

BGS 734, Required for *Puccinia graminis* resistance 5, *rpr5*

Stock number:	BGS 734
Locus name:	Required for *Puccinia graminis* resistance 5
Locus symbol:	*rpr5*

Previous nomenclature and gene symbolization:

γ08-117; R42-33#5 (same as γ08-116) (3, 4).

Inheritance:

Monofactorial recessive (2, 3, 4).

Location is unknown.

Description:

The *rpr5.e* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in the cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr5.e* mutant has been partially characterized (2, 3) with an infection type (IT) of moderately susceptible (MS): IT range of 2 to 32 with a mode 23 to 32 (rated by 1); IT range of 3- to 3 (rated by 2. 3), or 3, 3-, and 2 rated by 6) based on a 0-4 scale, defined by Stakman et al. (5). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr5.e* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, or *rpr6.f* (2, 3, 4). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3, 4).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (3, 4).

Mutational events:

rpr5.e (γ08-117; R42-33#5, GSHO 3699) in Morex (CIho 15773) (2, 3, 4).

Mutant used for description and seed stocks:

rpr5.e (γ08-117; R42-33#5, GSHO 3699) in Morex (4).

References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Gill, U., R. Brueggeman, J. Nirmala, Y. Chai, B. Steffenson, and A. Kleinhofs. 2016. Molecular and genetic characterization of barley mutants and genetic mapping of mutant *rpr2* required for *Rpg1*-mediated resistance against stem rust. Theor. Appl. Genet. 129 (8):1519-1529.
4. Kleinhofs, A. (Unpublished).
5. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
6. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:246.

Revised:

A. Kleinhofs. 2016. Barley Genet. Newsl. 46:143.

BGS 735, Required for *Puccinia graminis* resistance 6, *rpr6*

Stock number:	BGS 735
Locus name:	Required for *Puccinia graminis* resistance 6
Locus symbol:	*rpr6*

Previous nomenclature:

γ08-119; R47-23#1 (1, 2).

Inheritance:

Monofactorial recessive (1, 2. 3).

Location is unknown.

Description:

The *rpr6.f* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in the cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr6.f* mutant has been partially characterized (2, 3) with an infection type (IT) of moderately susceptible (MS): IT range of 2,3- to 3+ (rated by 1, 2) or IT range of 2,3- to 3,3- (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr6.f* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, or *rpr5.e* (1, 2, 3) The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (1, 2, 3).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (2, 3).

Mutational events:

rpr6.f (γ08-119; R47-23#1, GSHO 3700) in Morex (CIho 15773) (1, 2, 3).

Mutant used for description and seed stocks:

rpr6.f (γ08-119; R47-23#1, GSHO 3700) in Morex (3).

References:

1. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
2. Gill, U., R. Brueggeman, J. Nirmala, Y. Chai, B. Steffenson, and A. Kleinhofs. 2016. Molecular and genetic characterization of barley mutants and genetic mapping of mutant *rpr2* required for *Rpg1*-mediated resistance against stem rust. Theor. Appl. Genet. 129 (8):1519-1529.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:247.

Revised:

A. Kleinhofs. 2016. Barley Genet. Newsl. 46:144.

Barley Genetics newsletter (2016) 46:47-145.

BGS 736, Required for *Puccinia graminis* resistance 7, *rpr7*

Stock number:	BGS 736
Locus name:	Required for *Puccinia graminis* resistance 7
Locus symbol:	*rpr7*

Previous nomenclature:

γ08-115; R3-18#3 (2, 3).

Inheritance:

Monofactorial recessive (2, 3, 4).

Location is unknown.

Description:

The *rpr7.g* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in the cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr7.g* mutant has been partially characterized (2, 3) with an infection type (IT) of moderately susceptible (MS): IT range of 1,2 to 3 with a mode 23,32 (rated by 1); IT of 3 (rated by 2, 3), or IT range of 2,3 to 3,3- (rated by 6) based on a 0-4 scale, defined by Stakman et al. (5). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr7.g* mutant was not tested for allelism to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, *rpr5.e*, or *rpr6.f* (2, 3, 4). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3, 4).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (3, 4).

Mutational events:

rpr7.g (γ08-115; R3-18#3, GSHO 3701) in Morex (CIho 15773) (2, 3, 4).

Mutant used for description and seed stocks:

rpr7.g (γ08-115; R3-18#3, GSHO 3701) in Morex (4).

References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Gill, U., R. Brueggeman, J. Nirmala, Y. Chai, B. Steffenson, and A. Kleinhofs. 2016. Molecular and genetic characterization of barley mutants and genetic mapping of mutant *rpr2* required for *Rpg1*-mediated resistance against stem rust. Theor. Appl. Genet. 129 (8):1519-1529.
4. Kleinhofs, A. (Unpublished).
5. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
6. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:348.

Revised:

A. Kleinhofs. 2016. Barley Genet. Newsl. 46:145.