

Descriptions of barley genetic stocks for 2005.

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In this volume of the Barley Genetics Newsletter twenty-three new and revised Barley Genetic Stock descriptions are published (Table 1). The current list of new and revised BGS descriptions, including those in Table 1, are again presented by BGS number order (Table 2) and by locus symbol in alphabetic order (Table 3) in this issue. Information on the description location, recommended locus name, chromosomal location, previous gene symbols, and the primary genetic stock (GSHO number) are included in these lists. The GSHO stocks are held in the USDA-ARS Barley Genetic Stocks collection at the National Small Grains Germplasm Research Facility, Aberdeen, Idaho 83210, USA. This information is available through the Internet at the following addresses:

(1) <http://www.ars.usda.gov/pwa/aberdeen>

(2) <http://www.ars-grin.gov/npgs/>

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

Table 1. A listing of Barley Genetic Stock (BGS) descriptions published in this issue of the Barley Genetics Newsletter, giving recommended locus symbols and names, and stock location information.

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
43	mov1	mo5,mo6b	7HL	Multiovary 1	35:185	
96	Rph15	Rph15	2HS	Reaction to <i>Puccinia hordei</i> 15	35:186	1586
122	Rph5	Pa ₅	3HS	Reaction to <i>Puccinia hordei</i> 5	35:188	1865
147	mov2	mo, mo7a	3HS	Multiovary 2	35:190	
176	ovl1	ovl	4H	Ovaryless 1	35:191	610
623	eli-a	lig-a		Eligulum-a	35:192	
636	tst2			Tip sterile 2	35:193	2280
637	nar1		6HS	NADH nitrate reductase-deficient 1	35:194	2413
638	nar2		5HL	NADH nitrate reductase-deficient 2	35:196	2415
639	nar3		7HS	NADH nitrate reductase-deficient 3	35:197	
640	nar4		2HL	NADH nitrate reductase-deficient 4	35:198	
641	nar5		5HL	NADH nitrate reductase-deficient 5	35:199	
642	nar6		2HL	NADH nitrate reductase-deficient 6	35:200	
643	nar7		6HL	NADH nitrate reductase-deficient 7	35:201	2418
644	nar8		6HS	NADH nitrate reductase-deficient 8	35:202	
645	bsp1			Bushy spike 1	35:203	
646	ovl2			Ovaryless 2	35:204	
647	tst1			Tip sterile 1	35:205	
648	mov4	mo8		Multiovary 4	35:206	
649	asp1			Aborted spike 1	35:207	
650	sun1			Sensitivity to <i>Ustilago nuda</i> 1	35:208	
651	lam1			Late maturity 1	35:209	
652	ylf1			Yellow leaf 1	35:210	

* 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.

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

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
1	brh1	br, ari-i	7HS	Brachytic 1	26: 44	25
2	fch12	f _c , clo-fc	7HS	Chlorina seedling 12	26: 45	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	26: 48	40
6	vrs1	v, Int-d	2HL	Six-rowed spike 1	26: 49	196
7	nud1	n, h	7HL	Naked caryopsis 1	26: 51	115
9	dsp1	l	7HS	Dense spike 1	26: 53	1232
10	lks2	lk2, lk4	7HL	Short awn 2	26: 54	566
11	ubs4	u4, ari-d	7HL	Unbranched style 4	26: 56	567
12	des1	lc	7H	Desynapsis 1	26: 57	592
13	des4	des4	7H	Desynapsis 4	26: 58	595
14	des5	des5	7H	Desynapsis 5	26: 59	596
15	blx1	bl	4HL	Non-blue aleurone xenia 1	26: 60	185
16	wax1	wx, glx	7HS	Waxy endosperm 1	26: 61	908
17	fch4	f4, yv	7HL	Chlorina seedling 4	26: 63	1214
18	fch5	f5, yv2	7HS	Chlorina seedling 5	26: 64	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 <i>Ustilago nuda</i> 1	26: 67	1324
22	Rsg1	Grb	7H	Reaction to <i>Schizaphis graminum</i> 1	26: 68	1317
23	wnd1	wnd	7HS	Winding dwarf 1	26: 69	2499
24	fst3	fs3	7HS	Fragile stem 3	26: 70	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	26: 73	536
28	ert-a	ert-a	7HS	Erectoides-a	26: 74	468
29	ert-d	ert-d	7HS	Erectoides-d	26: 76	475
30	ert-m	ert-m	7HS	Erectoides-m	26: 78	487
31	sex6	sex6	7HS	Shrunken endosperm xenia 6	26: 80	2476
32	Rph9	Pa9	5HL	Reaction to <i>Puccinia hordei</i> 9	26: 81	1601
33	ant1	rs, rub-a	7HS	Anthocyanin-less 1	26: 82	1620
34	msg50	msg,,hm	7HL	Male sterile genetic 50	26: 83	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	7HS	Seminudoides 1	32: 78	1602

Table 2. (continued)

BGS no.	Locus symbol [*]		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec.	Prev.				
39	mss2	mss2	7HS	Midseason stripe 2	32: 79	2409
40	prm1	prm	7HS	Premature ripe 1	32: 80	2429
41	brh7	brh.w	7HS	Brachytic 7	32: 81	1687
42	Pyr1	Pyr1	7HS	Pyramidatum 1	32: 82	1581
43	mov1	mo5	7HL	Multiovary 1	35:185	
51	rtt1	rt	2HS	Rattail spike 1	26: 87	216
52	fch15	or	2HS	Chlorina seedling 15	26: 88	49
53	abo2	a2	2HS	Albino seedling 2	26: 89	70
55	fch1	f, lg	2HS	Chlorina seedling 1	26: 90	112
56	wst4	wst4	2HL	White streak 4	26: 91	568
57	eog1	e, lep-e	2HL	Elongated outer glume 1	26: 92	29
58	vrs1	lr, v ^{lr}	2HL	Six-rowed spike 1	26: 94	153
59	gpa1	gp, gp2	2HL	Grandpa 1	26: 95	1379
60	lig1	li, aur-a	2HL	Liguleless 1	26: 96	6
61	trp1	tr	2HL	Triple awned lemma 1	26: 97	210
62	sbk1	sk, cal-a	2HS	Subjacent hood 1	32: 83	267
63	yvs1	y _x , alb-c2	2HS	Virescent seedling 1	26: 99	68
64	des7	des7	2H	Desynapsis 7	26:100	598
65	Eam1	Ea, Ppd-H1	2HS	Early maturity 1	26:101	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	26:105	132
69	Gth 1	G	2HL	Toothed lemma 1	26:106	309
70	Rph1	Pa	2H	Reaction to <i>Puccinia hordei</i> 1	26:107	1313
71	com2	bir2	2HS	Compositum 2	26:108	1703
72	glo-c	glo-c	2H	Globosum-c	26:109	1329
73	fol-a	fol-a	2HL	Angustifolium-a	26:110	1744
74	flo-c	flo-c	2HS	Extra floret-c	26:111	1743
75	Lks1	Lk	2HL	Awnless 1	26:112	44
76	Pre2	Re2, P	2HL	Red lemma and pericarp 2	26:113	234
77	hcm1	h	2HL	Short culm 1	26:115	2492
78	mtt4	mt ₂ ,e, mt	2HL	Mottled leaf 4	26:116	1231
79	wst7	rb	2HL	White streak 7	26:117	247
80	ant2	pr, rub	2HL	Anthocyanin-less 2	26:118	1632
81	gsh7	gs7		Glossy sheath 7	26:119	1759
82	Zeol	Knd	2HL	Zeocriton 1	26:120	1613
83	sld2	sld2	2HS	Slender dwarf 2	26:121	2491
84	mss1	mss	2H	Midseason stripe 1	26:122	1404
85	yst4	yst4	2HL	Yellow streak 4	26:123	2502
86	fch13	fl3		Chlorina seedling 13	26:124	16

Table 2. (continued)

BGS	Locus symbol*		Chr.	Locus name or phenotype	Descr.	GSHO
no.	Rec.	Prev.	loc. [†]		vol. p.	no. [‡]
87	fch14	f14	2HL	Chlorina seedling 14	26:125	1739
88	Rph2	Pa2, A	5HS	Reaction to <i>Puccinia hordei</i> 2	26:126	1593
89	ari-g	ari-g, lk10		Breviaristatum-g	26:128	1655
90	ert-j	ert-j	2H	Erectoides-j	26:129	484
91	ert-q	ert-q	2H	Erectoides-q	26:130	1562
92	ert-u	ert-u, br5	2H	Erectoides-u	26:131	496
93	ert-zd	ert-zd, br7	2H	Erectoides-zd	26:132	504
94	abo4	a4	2H	Albino seedling 4	26:133	167
95	abo13	alb.,p	2HL	Albino seedling 13	26:134	585
96	Rph15	Rph15	2HS	Reaction to <i>Puccinia hordei</i> 15	35:186	1586
97	acr1	acr	2HL	Accordion rachis 1	32: 85	1617
98	Eam6	Ea6, Ea	2HS	Early maturity 6	32: 86	
99	lin1	s, rin	2HL	Lesser internode number 1	32: 88	2492
100	sld4	sld4	2HL	Slender dwarf 4	32: 89	2479
101	als1	als	3HL	Absent lower laterals 1	26:135	1065
102	uzu1	uz, u	3HL	Uzu or semi brachytic 1	26:136	1300
104	yst1	yst, ys	3HS	Yellow streak 1	26:138	1140
105	xnt3	x _c , vir-l	3HS	Xantha seedling 3	26:139	66
106	abo6	a _c	3HS	Albino seedling 6	26:140	30
107	wst1	wst, wst3	3HL	White streak 1	26:141	159
108	alm1	al, ebu-a	3HS	Albino lemma 1	26:143	270
109	yst2	yst2	3HS	Yellow streak 2	26:144	570
111	dsp10	l _c	3HS	Dense spike 10	26:145	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	26:148	274
115	btr1	bt1	3HS	Non-brittle rachis 1	26:149	1233
116	btr2	bt2	3HS	Non-brittle rachis 2	26:150	842
117	fch2	f2, lg5	3HL	Chlorina seedling 2	26:151	107
118	Int1	rnt, int-l	3HL	Low number of tillers 1	26:153	833
119	des2	ds	3H	Desynapsis 2	26:154	593
120	zeb1	zb	3HL	Zebra stripe 1	26:155	1279
121	Rph3	Pa3	7HL	Reaction to <i>Puccinia hordei</i> 3	26:156	1316
122	Rph5	Pa5, Pa6	3HS	Reaction to <i>Puccinia hordei</i> 5	35:188	1597
123	Ryd2	Yd2	3HL	Reaction to BYDV 2	26:158	1315
124	vrs4	mul, int-e	3HL	Six-rowed spike 4	26:159	775
125	lzd1	lzd, dw4	3HS	Lazy dwarf 1	26:161	1787
126	sld1	dw1	3HL	Slender dwarf 1	26:162	2488
127	Pub1	Pub	3HL	Pubescent leaf blade 1	26:163	1576
128	sca1	sca	3HS	Short crooked awn 1	26:164	2439

Table 2. (continued)

BGS	Locus symbol*		Chr.	Locus name or phenotype	Descr.	GSHO
no.	Rec.	Prev.	loc. [†]		vol. p.	no. [‡]
129	wst6	wst ₂ j	3HL	White streak 6	26:165	2500
130	eam10	ea _{sp}	3HL	Early maturity 10	26:166	2504
131	gra-a	gran-a	3HL	Granum-a	26:167	1757
132	ari-a	ari-a	3HS	Breviaristatum-a	26:168	1648
133	sdw2	sdw-b	3HL	Semidwarf 2	26:169	2466
134	ert-c	ert-c	3HL	Erectoides-c	26:170	471
135	ert-ii	ert-ii	3HL	Erectoides-ii	26:172	483
136	Rph7	Pa7, Pa5	3HS	Reaction to Puccinia hordei 7	26:173	1318
137	Rph10	Rph10	3HL	Reaction to Puccinia hordei 10	26:174	1588
138	nec4	nec4	3H	Necrotic leaf spot 4	26:175	
139	nec5	nec5	3H	Necrotic leaf spot 5	26:176	
140	xnt8	xan ₂ h	3HS	Xantha seedling 8	26:177	582
141	rym5	Ym	3HL	Reaction to Barley yellow mosaic virus5	32: 90	
142	brh8	brh.ad	3HS	Brachytic 8	32: 92	1671
143	sex8	sex.j	3HS	Shrunken endosperm 8	32: 93	2471
144	sld5	sld5	3HS	Slender dwarf 5	32: 94	2483
146	cal-d	cal-d	3H	Calcaroides-d	32: 95	1697
147	mov2	mo	3HS	Multiovary 2	35:190	
151	fch9	f9	4HS	Chlorina seedling 9	26:178	571
152	Kap1	K	4HS	Hooded lemma 1	26:179	985
155	glf1	gl, cer-zh	4HL	Glossy leaf 1	26:181	98
156	lbi2	lb2, ert-i	4HL	Long basal rachis internode 2	26:183	572
157	brh2	br2, ari-l	4HL	Brachytic 2	26:184	573
158	yhd1	yh	4HL	Yellow head 1	26:185	574
160	min2	en-min		Enhancer of minute 1	26:186	266
161	min1	min	4HL	Semi-minute dwarf 1	26:187	987
163	sgh1	sh1	4HL	Spring growth habit 1	26:188	575
164	Hln1	Hn	4HL	Hairs on lemma nerves 1	26:189	576
165	glf3	gl3, cer-j	4HL	Glossy leaf 3	26:190	577
166	msg25	msg ₂ r	4HL	Male sterile genetic 25	26:192	744
167	rym1	Ym	4HL	Reaction to barley yellow mosaic virus 1	32: 96	
168	glo-a	glo-a	4HS	Globosum-a	26:194	1328
170	lgn3	lg3	4HL	Light green 3	26:195	171
171	lgn4	lg4, lg9	4HL	Light green 4	26:196	681
172	lks5	lk5, ari-c	4HL	Short awn 5	26:197	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	
178	int-c	i, v5	4HS	Intermedium spike-c	26:200	776
179	Hsh1	Hs	4HL	Hairy leaf sheath 1	26:202	986

Table 2. (continued)

BGS	Locus symbol*		Chr.	Locus name or phenotype	Descr.	GSHO
no.	Rec.	Prev.	loc. [†]		vol. p.	no. [‡]
180	sid1	nls	4HL	Single internode dwarf 1	26:203	2477
181	eam9	ea,,c	4HL	Early maturity 9	26:204	1732
182	flo-a	flo-a		Extra floret-a	26:205	1741
183	Ynd1	Yn	4HS	Yellow node 1	32:98	
184	Zeo3	Zeo.h	4HL	Zeocriton 3	32:99	1611
185	brh5	brh.m	4HS	Brachytic 5	32:100	1678
186	sld3	ant17.567	4HS	Slender dwarf 3	32:101	2480
201	fch7	f7	1HL	Chlorina seedling 7	26:206	4
202	trd1	t, bra-c	1HL	Third outer glume 1	26:207	227
203	Blp1	B	1HL	Black lemma and pericarp 1	26:209	988
207	abo1	a _i	1HL	Albino seedling 1	26:210	51
208	fst2	fs2	1HL	Fragile stem 2	26:211	578
213	Sgh3	Sh3	1HL	Spring growth habit 3	26:212	764
214	eam8	ea _k , mat-a	1HL	Early maturity 8	26:213	765
215	des6	des6		Desynapsis 6	26:216	597
218	Rph4	Pa4	1HS	Reaction to <i>Puccinia hordei</i> 4	26:217	1314
220	fch3	f3	1HS	Chlorina seedling 3	26:218	851
221	wst5	wst5	1HL	White streak 5	26:219	591
222	nec1	sp,,b	1HL	Necrotic leaf spot 1	26:220	989
223	zeb3	zb3, zb _c	1HL	Zebra stripe 3	26:221	1451
224	ert-b	ert-b	1HL	Erectoides-b	26:222	470
225	clh1	clh	1HL	Curled leaf dwarf 1	26:223	1212
226	rvl1	rvl	1HL	Revoluted leaf 1	26:224	608
227	sls1	sls	1HS	Small lateral spikelet 1	26:225	2492
228	Sil1	Sil	1HS	Subcrown internode length 1	26:226	1604
229	cud2	cud2	1HL	Curly dwarf 2	26:227	1712
230	glo-e	glo-e	1HL	Globosum-e	26:228	1755
231	cur5	cu5	1HS	Curly 5	26:229	1710
232	Lys4	sex5	1HS	High lysine 4	26:230	2475
233	xnt7	xan,,g	1HL	Xantha seedling 7	26:231	581
234	mov3	mo-a	1H	Multiovary 3	32:102	
235	lel1	lel	1HL	Leafy lemma 1	32:103	1780
251	mul2	mul2	6HL	Multiflorus 2	26:232	1394
252	eam7	ea7, ec	6HS	Early maturity 7	26:233	579
253	cul2	uc2	6HL	Unicula 2	26:234	531
254	rob1	o, rob-o	6HS	Orange lemma 1	26:235	707
255	xnt5	x _n	6HL	Xantha seedling 5	26:237	43
257	raw5	r,,e	6HL	Smooth awn 5	26:238	785
258	dsp9	l9, ert-e	6HL	Dense spike 9	26:239	1774
260	fch11	fl1	6HL	Chlorina seedling 11	26:240	1738

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
261	nec2	nec2	6HS	Necrotic leaf spot 2	26:241	1224
262	cur1	cu1	6HL	Curly 1	26:242	1705
263	cur3	cu3	6HL	Curly 3	26:243	1707
264	mtt5	mt,,f	6HL	Mottled leaf 5	26:244	2410
265	nec3	nec3	6HS	Necrotic leaf spot 3	26:245	1330
266	ert-e	ert-e	6HL	Erectoides-e	26:246	477
267	Rph11	Rph11	6HL	Reaction to <i>Puccinia hordei</i> 11	26:247	1589
268	lax-b	lax-b	6HL	Laxatum-b	26:248	1776
269	lys6	lys6	6H	High lysine 6	26:249	1786
270	abo14	alb,,q	6HL	Albino seedling 14	26:250	586
271	abo15	alb,,t	6HS	Albino seedling 15	26:251	
301	fst1	fs	5HL	Fragile stem 1	26:252	629
302	mtt2	mt2	5HL	Mottled leaf 2	26:253	1398
303	var3	va3	5HL	Variegated 3	26:254	1277
304	wst2	wst2	5HL	White streak 2	26:255	766
305	crm1	cm	5HL	Cream seedling 1	26:256	20
306	var1	va	5HL	Variegated 1	26:257	1278
308	lbi1	lb, rac-a	5HL	Long basal rachis internode 1	26:258	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	26:261	27
313	fch6	f6, yv	5HL	Chlorina seedling 6	26:262	1390
314	vrs2	v2	5HL	Six-rowed spike 2	26:263	773
315	vrs3	v3, int-a	1HL	Six-rowed spike 3	26:264	774
317	ddt1	ddt	5HS	Reaction to DDT 1	26:266	331
319	rpg4	rpg4	5HL	Reaction to <i>Puccinia graminis</i> 4	26:267	2438
320	int-b	int-b	5HL	Intermedium spike-b	26:268	1764
321	srh1	s, l	5HL	Short rachilla hair 1	26:269	27
322	dsk1	dsk	5HL	Dusky 1	26:270	1714
323	nld1	nld	5HL	Narrow leafed dwarf 1	26:271	769
324	cud1	cud	5HL	Curly dwarf 1	26:272	1711
325	crl1	crl, cl		Curly lateral 1	26:273	1211
326	blf1	bb	5HL	Broad leaf 1	26:274	1393
327	flo-b	flo-b	5HL	Extra floret-b	26:275	1742
328	ari-e	ari-e	5HL	Breviaristatum-e	26:276	1653
329	ari-h	ari-h	5HL	Breviaristatum-h	26:277	1656
330	ert-g	ert-g, br3	5HL	Erectoides-g	26:278	479
331	ert-n	ert-n	5HL	Erectoides-n	26:279	488
332	Ert-r	Ert-r		Erectoides-r	26:280	492
333	Rph12	Rph12	5HL	Reaction to <i>Puccinia hordei</i> 12	26:281	1590

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec.	Prev.				
334	raw6	r6	5HL	Smooth awn 6	26:282	2437
335	msg49	msg,,jw	5HL	Male sterile genetic 49	26:283	2402
336	glo-b	glo-b	5HL	Globosum-b	26:284	1326
337	blf2	bb2, nlh	5HL	Broad leaf 2	26:285	1667
338	lys1	lys	5HL	High lysine 1	26:286	1784
339	lys3	sex3	5HL	High lysine 3	26:287	1785
340	raw2	r2	5HL	Smooth awn 2	26:289	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	28: 30	1577
344	var2	va2	5HL	Variegated 2	32:104	2496
345	rym3	ym3	5HS	Reaction to barley yellow mosaic virus 3	32:105	
346	yst5	yst5	5HL	Yellow streak 5	32:107	2501
347	mnd4	m4	5HL	Many noded dwarf 4	32:108	1798
348	Eam5	Ea5	5HL	Early maturity 5	32:109	
349	brh4	brh.j	5HL	Brachytic 4	32:110	1675
350	brh6	brh.s	5HL	Brachytic 6	32:111	1684
351	gsh1	gs1, cer-q	2HS	Glossy sheath 1	26:292	735
352	gsh2	gs2, cer-b	3HL	Glossy sheath 2	26:294	736
353	gsh3	gs3, cer-a	7HS	Glossy sheath 3	26:296	737
354	gsh4	gs4, cer-x	6HL	Glossy sheath 4	26:298	738
355	gsh5	gs5, cer-s	2HL	Glossy sheath 5	26:300	739
356	gsh6	gs6, cer-c	2HS	Glossy sheath 6	26:302	740
357	msg1	ms1	1HL	Male sterile genetic 1	26:304	1810
358	msg2	ms2	2HL	Male sterile genetic 2	26:306	2371
359	msg3	ms3	2HS	Male sterile genetic 3	26:307	1130
360	msg4	ms4	1H	Male sterile genetic 4	26:308	2392
361	msg5	ms5	3HS	Male sterile genetic 5	26:309	2403
362	msg6	ms6	6HS	Male sterile genetic 6	26:310	2405
363	msg7	ms7	5HL	Male sterile genetic 7	26:311	2406
364	msg8	ms8	5HL	Male sterile genetic 8	26:312	2407
365	msg9	ms9	2HS	Male sterile genetic 9	26:313	2408
366	msg10	ms10	7HS	Male sterile genetic 10	26:314	1811
367	msg11	ms11		Male sterile genetic 11	26:315	1812
368	msg13	ms13		Male sterile genetic 13	26:316	1813
369	msg14	ms14	7HS	Male sterile genetic 14	26:317	1814
370	msg15	ms15		Male sterile genetic 15	26:318	1815
371	msg16	ms16	5HS	Male sterile genetic 16	26:319	1816
372	msg17	ms17		Male sterile genetic 17	26:320	1817
373	msg18	ms18	5HL	Male sterile genetic 18	26:321	1818

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
374	msg19	ms19	5HS	Male sterile genetic 19	26:322	1819
375	msg20	ms20	1H	Male sterile genetic 20	26:323	2372
376	msg21	ms21		Male sterile genetic 21	26:324	2373
377	seg1	se1	7HL	Shrunken endosperm 1	26:325	750
378	seg2	se2	7HS	Shrunken endosperm 2	26:326	751
379	seg3	se3	3H	Shrunken endosperm 3	26:327	752
380	seg4	se4	7HL	Shrunken endosperm 4	26:328	753
381	seg5	se5	7HS	Shrunken endosperm 5	26:329	754
382	sex1	lys5	6HL	Shrunken endosperm xenia 1	26:330	755
383	msg22	ms22	7H	Male sterile genetic 22	26:331	741
384	msg23	ms23	7HL	Male sterile genetic 23	26:332	2375
385	msg24	ms24	4HL	Male sterile genetic 24	26:333	2376
386	des3	des3		Desynapsis 3	26:334	594
387	des8	des8		Desynapsis 8	26:335	599
388	des9	des9		Desynapsis 9	26:336	600
389	des10	des10		Desynapsis 10	26:337	601
390	des11	des11		Desynapsis 11	26:338	602
391	des12	des12		Desynapsis 12	26:339	603
392	des13	des13		Desynapsis 13	26:340	604
393	des14	des14		Desynapsis 14	26:341	605
394	des15	des15		Desynapsis 15	26:342	606
395	msg26	msg,,u	7HS	Male sterile genetic 26	26:343	745
396	seg6	se6	3HL	Shrunken endosperm 6	26:344	2467
397	seg7	se7		Shrunken endosperm 7	26:345	2468
399	cer-d	cer-d		Eceriferum-d	26:346	425
400	cer-e	cer-e	1HL	Eceriferum-e	26:347	1518
401	cer-f	cer-f	7HS	Eceriferum-f	26:348	427
402	cer-g	cer-g	2HL	Eceriferum-g	26:349	428
403	cer-h	cer-h		Eceriferum-h	26:351	429
404	cer-i	cer-i	5HL	Eceriferum-i	26:352	430
405	cer-k	cer-k	7HS	Eceriferum-k	26:354	432
406	cer-l	cer-l		Eceriferum-l	26:355	433
407	cer-m	cer-m		Eceriferum-m	26:356	434
408	cer-n	gs9	2HL	Eceriferum-n	26:357	435
409	cer-o	cer-o		Eceriferum-o	26:359	436
410	cer-p	cer-p		Eceriferum-p	26:360	437
411	cer-r	cer-r	3HL	Eceriferum-r	26:361	439
412	cer-t	cer-t	5HL	Eceriferum-t	26:362	441
413	gsh8	cer-u, gs8	2HS	Glossy sheath 8	26:364	442
414	cer-v	cer-v	2HS	Eceriferum-v	26:366	443

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec.	Prev.				
415	cer-w	cer-w	5HL	Eceriferum-w	26:367	1519
417	cer-y	cer-y		Eceriferum-y	26:368	446
418	cer-z	cer-z	7HS	Eceriferum-z	26:369	447
419	cer-za	cer-za	5HL	Eceriferum-za	26:370	1521
420	cer-zb	cer-zb		Eceriferum-zb	26:371	1522
421	cer-zc	cer-zc		Eceriferum-zc	26:372	450
422	cer-zd	cer-zd	3HL	Eceriferum-zd	26:373	451
423	cer-ze	gl5	7HS	Eceriferum-ze	26:374	452
424	cer-zf	cer-zf		Eceriferum-zf	26:376	453
425	cer-zg	cer-zg	4HL	Eceriferum-zg	26:377	454
427	cer-zi	cer-zi	1HL	Eceriferum-zi	26:378	456
428	cer-zj	cer-zj	5HL	Eceriferum-zj	26:379	457
429	cer-zk	cer-zk	2H	Eceriferum-zk	26:381	458
430	cer-zl	cer-zl		Eceriferum-zl	26:382	459
431	cer-zn	cer-zn	3HL	Eceriferum-zn	26:383	1523
432	cer-zo	cer-zo		Eceriferum-zo	26:384	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		Eceriferum-zr	26:387	1525
436	cer-zs	cer-zs		Eceriferum-zs	26:388	1526
437	cer-zt	cer-zt		Eceriferum-zt	26:389	1527
438	cer-zu	cer-zu		Eceriferum-zu	26:390	1528
439	cer-zv	cer-zv		Eceriferum-zv	26:391	1529
440	cer-zw	cer-zw		Eceriferum-zw	26:392	1530
441	cer-zx	cer-zx		Eceriferum-zx	26:393	1531
442	cer-zy	cer-zy		Eceriferum-zy	26:394	1532
443	cer-zz	cer-zz		Eceriferum-zz	26:395	1533
444	cer-ya	cer-ya	3HS	Eceriferum-ya	26:396	1534
445	cer-yb	cer-yb	2HL	Eceriferum-yb	26:397	1535
446	cer-yc	cer-yc		Eceriferum-yc	26:398	1536
447	cer-yd	cer-yd	3HS	Eceriferum-yd	26:399	1537
448	cer-ye	cer-ye	5HL	Eceriferum-ye	26:400	1538
449	cer-yf	cer-yf		Eceriferum-yf	26:401	1539
450	cer-yg	cer-yg	7HS	Eceriferum-yg	26:402	1540
451	cer-yh	cer-yh	3HS	Eceriferum-yh	26:403	1541
454	blx5	bl5	7HL	Non-blue aleurone xenia 5	26:404	2509
455	seg8	seg8	7H	Shrunken endosperm 8	26:405	2469
460	cur4	cu4, glo-d	2HL	Curly 4	26:406	1708
461	zeb2	zb2, fl0	4HL	Zebra stripe 2	26:407	93
462	yst3	yst,,c	3HS	Yellow streak 3	26:409	48

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
463	gig1	gig, sf	2H?	Gigas 1	26:410	1650
464	msg27	msg,,ae	2HL	Male sterile genetic 27	26:411	2379
465	msg28	msg,,as	6H	Male sterile genetic 28	26:412	2380
466	msg29	msg,,a	5HL	Male sterile genetic 29	26:413	2381
467	msg30	msg,,c	7HL	Male sterile genetic 30	26:414	2382
468	msg31	msg,,d	1HS	Male sterile genetic 31	26:415	2383
469	msg32	msg,,w	7H	Male sterile genetic 32	26:416	2384
470	msg33	msg,,x	2HS	Male sterile genetic 33	26:417	2385
471	msg34	msg,,av	6H	Male sterile genetic 34	26:418	2386
472	abr1	abr	2HL	Accordion basal rachis internode 1	26:419	1563
473	com1	bir1	5HL	Compositum 1	26:420	1702
474	lax-a	lax-a	5HL	Laxatum-a	26:421	1775
475	lax-c	lax-c	6HL	Laxatum-c	26:423	1777
498	msg35	msg,,dr	2HL	Male sterile genetic 35	26:424	2387
499	msg36	msg,,bk	6HS	Male sterile genetic 36	26:425	2388
500	msg37	msg,,hl		Male sterile genetic 37	26:426	2389
501	msg38	msg,,jl		Male sterile genetic 38	26:427	2390
502	msg39	msg,,dm	6H	Male sterile genetic 39	26:428	2391
503	msg40	msg,,ac	6H	Male sterile genetic 40	26:429	2393
504	msg41	msg,,aj		Male sterile genetic 41	26:430	2394
505	msg42	msg,,db	3H	Male sterile genetic 42	26:431	2395
506	msg43	msg,,br		Male sterile genetic 43	26:432	2396
507	msg44	msg,,cx		Male sterile genetic 44	26:433	2397
508	msg45	msg,,dp		Male sterile genetic 45	26:434	2398
509	msg46	msg,,ec		Male sterile genetic 46	26:435	2399
510	msg47	msg,,ep		Male sterile genetic 47	26:436	2400
511	Rpg1	T	7HS	Reaction to <i>Puccinia graminis</i> 1	26:437	701
512	Rpg2	T2		Reaction to <i>Puccinia graminis</i> 2	26:439	187
513	xnt2	x _b		Xantha seedling 2	26:440	2
515	Rsp1	Sep		Reaction to <i>Septoria passerinii</i> 1	26:441	2510
516	Rsp2	Sep ₂		Reaction to <i>Septoria passerinii</i> 2	26:442	2511
517	Rsp3	Sep ₃		Reaction to <i>Septoria passerinii</i> 3	26:443	2512
518	sdw1	denso	3HL	Semidwarf 1	26:444	2513
519	mnd1	m		Many-noded dwarf 1	26:446	253
520	msg48	msg,,jt	2H	Male sterile genetic 48	26:447	2401
521	mtt1	mt	1HS	Mottled leaf 1	26:448	622
522	cer-yi	cer-yi		Eceriferum-yi	26:449	1542
523	cer-yj	cer-yj		Eceriferum-yj	26:450	1543
524	cer-yk	cer-yk		Eceriferum-yk	26:451	1544
525	cer-yl	cer-yl		Eceriferum-yl	26:452	1545

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec.	Prev.				
526	cer-ym	cer-ym	1HS	Eceriferum-ym	26:453	1546
527	cer-yn	cer-yn		Eceriferum-yn	26:454	1547
528	cer-yo	cer-yo		Eceriferum-yo	26:455	1548
529	cer-yp	cer-yp		Eceriferum-yp	26:456	1549
530	cer-yq	cer-yq		Eceriferum-yq	26:457	1550
531	cer-yr	cer-yr		Eceriferum-yr	26:458	1551
532	cer-ys	cer-ys		Eceriferum-ys	26:459	1552
533	cer-yt	cer-yt		Eceriferum-yt	26:460	1553
534	cer-yu	cer-yu		Eceriferum-yu	26:461	1554
535	cer-yx	cer-yx		Eceriferum-yx	26:462	1555
536	Cer-yy	Gle1		Eceriferum-yy	26:463	1556
537	cer-yz	cer-yz		Eceriferum-yz	26:464	1557
538	cer-xa	cer-xa		Eceriferum-xa	26:465	1558
539	cer-xb	cer-xb		Eceriferum-xb	26:466	1559
540	cer-xc	cer-xc		Eceriferum-xc	26:467	1560
541	cer-xd	cer-xd		Eceriferum-xd	26:468	1561
542	Dwf2	Dwf2		Dominant dwarf 2	24:170	
543	int-f	int-f		Intermedium spike-f	26:469	1767
544	int-h	int-h		Intermedium spike-h	26:470	1768
545	int-i	int-i		Intermedium spike-i	26:471	1769
546	int-k	int-k		Intermedium spike-k	26:472	1770
547	int-m	int-m		Intermedium spike-m	26:473	1772
548	Fol-b	Ang		Angustifolium-b	26:474	17
549	Lga1	Log		Long glume awn 1	26:475	835
550	ari-b	ari-b		Breviaristatum-b	26:476	1649
551	ari-f	ari-f		Breviaristatum-f	26:477	1654
552	ari-j	ari-j		Breviaristatum-j	26:478	1658
553	ari-k	ari-k		Breviaristatum-k	26:479	1659
554	ari-m	ari-m		Breviaristatum-m	26:480	1661
555	ari-n	ari-n		Breviaristatum-n	26:481	1662
556	ari-o	ari-o		Breviaristatum-o	26:482	
557	ari-p	ari-p		Breviaristatum-p	26:483	1664
558	ari-q	ari-q		Breviaristatum-q	26:484	1665
559	ari-r	ari-r		Breviaristatum-r	26:485	1666
560	ert-f	ert-f		Erectoides-f	26:486	478
561	ert-h	ert-h		Erectoides-h	26:487	481
562	ert-k	ert-k		Erectoides-k	26:488	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

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
566	ert-t	ert-t		Erectoides-t	26:492	494
567	ert-v	ert-v		Erectoides-v	26:493	497
568	ert-x	ert-x		Erectoides-x	26:494	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		Erectoides-za	26:497	501
572	ert-zb	ert-zb		Erectoides-zb	26:498	502
573	ert-zc	ert-zc		Erectoides-zc	26:499	503
574	ert-ze	ert-ze		Erectoides-ze	26:500	505
575	Rph6	Pa6		Reaction to <i>Puccinia hordei</i> 6	26:501	1598
576	Rph8	Pa8		Reaction to <i>Puccinia hordei</i> 8	26:502	1600
577	Rsg2	Rsg2		Reaction to <i>Schizaphis graminum</i> 2	26:503	2513
578	mat-b	mat-b		Praematurum-b	26:504	1788
579	mat-c	mat-c		Praematurum-c	26:506	1789
580	mat-d	mat-d		Praematurum-d	26:507	1790
581	mat-e	mat-e		Praematurum-e	26:508	1791
582	mat-f	mat-f		Praematurum-f	26:509	1792
583	mat-g	mat-g		Praematurum-g	26:510	1793
584	mat-h	mat-h		Praematurum-h	26:511	1794
585	mat-i	mat-i		Praematurum-i	26:512	1795
586	bra-d	bra-d		Bracteatum-d	26:513	1696
587	abo3	a2, alb-za		Albino seedling 3	26:514	165
588	abo10	a2		Albino seedling 10	26:515	57
589	abo11	a3, alb ^t		Albino seedling 11	26:516	233
590	Rph13	Rph13		Reaction to <i>Puccinia hordei</i> 13	28: 31	1591
591	Rph14	Rph14		Reaction to <i>Puccinia hordei</i> 14	28: 32	1592
592	yhd2	yh2		Yellow head 2	28: 33	757
593	adp1	adp		Awned palea 1	28: 34	1618
594	ant3	rub		Anthocyanin-deficient 3	29: 82	1641
595	ant4	ant4		Anthocyanin-deficient 4	29: 83	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	3HL	Proanthocyanin-free 17	29: 88	1628
600	ant18	ant18	7HL	Proanthocyanin-free 18	29: 90	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	7HL	Proanthocyanin-free 22	29: 95	1635
605	ant25	ant25		Proanthocyanin-free 25	29: 96	1638

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec.	Prev.				
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	29: 99	
609	ant29	ant29		Proanthocyanin-free 29	29:100	
610	ant30	ant30		Proanthocyanin-free 30	29:101	
611	Nec6	Sp		Necrotic leaf spot 6	32:112	2424
612	gig2	gig2		Gigas 2	32:113	1750
613	brc1	brc-5	2HS	Branched 1	32:114	
614	Zeo2	Zeo2		Zeocriton 2	32:115	637
615	wxs1	wxs1		Waxy spike 1	32:116	
616	cul3	cul3		Uniculme 3	32:117	2494
617	cul4	uc-5		Uniculme 4	32:118	2493
618	mnd3	mn3, m3	3H	Many noded dwarf 3	32:119	1797
619	bra-a	bra-a	7HS	Bracteatum-a	32:120	1693
620	cal-b	cal-b	5H	Calcaroides-b	32:121	1697
621	Cal-c	Cal-c	5HL	Calcaroides-c	32:122	1567
622	cal-e	cal-23	5HS	Calcaroides-e	32:123	
623	eli-a	lig-a		Eligulum-a	35:192	
624	ops1	op-3		Opposite spikelets 1	32:125	2427
625	sci-a	sci-3		Scirpoides 1	32:126	
626	scl-a	scl-6		Scirpoides leaf-a	32:127	
627	viv-a	viv-5		Viviparoides-a	32:128	2498
628	sex7	sex.i	5HL	Shrunken endosperm 7	32:129	2470
629	mtt6	mtt6		Mottled leaf 6	32:130	2411
630	Ari-s	ari-265		Breviaristatum-s	32:131	
631	brh3	brh.g		Brachytic 3	32:132	1672
632	mnd5	mnd5		Many noded dwarf 5	32:133	
633	mnd6	den-6		Many noded dwarf 6	32:134	1713
634	pmr2	nec-50		Premature ripe 2	32:135	2421
635	nec7	nec-45		Necroticans 7	32:136	2420
636	tst2	lin2		Tip sterile 2	35:193	1781
637	nar1	nar1	6HS	NADH nitrate reductase-deficient 1	35:194	
638	nar2	nar2	5HL	NADH nitrate reductase-deficient 2	35:196	
639	nar3	nar3	7HS	NADH nitrate reductase-deficient 3	35:197	
640	nar4	nar4	2HL	NADH nitrate reductase-deficient 4	35:198	
641	nar5	nar5	5HL	NADH nitrate reductase-deficient 5	35:199	
642	nar6	nar6	2HL	NADH nitrate reductase-deficient 6	35:200	
643	nar7	nar7	6HL	NADH nitrate reductase-deficient 7	35:201	2418
644	nar8	nar8	6HS	NADH nitrate reductase-deficient 8	35:202	
645	bsp1	bsp1		Bushy spike 1	35:203	

Table 2. (continued)

BGS no.	Locus symbol [*]		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec.	Prev.				
646	ovl2	ovl2		Ovaryless 2	35:204	
647	tst1	tst1		Tip sterile 1	35:205	
648	mov4	mo8		Multiovary 4	35:206	
649	asp1	asp1		Aborted spike 1	35:207	
650	sun1	sun1		Sensitivity to <i>Ustilago nuda</i> 1	35:208	
651	lam1	lam1		Late maturity 1	35:209	
652	ylf1	ylf1		Yellow leaf 1	35:210	

* 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 Small Grains Germplasm Research Facility, Aberdeen, Idaho, USA.

Table 3. An alphabetic listing of recently published Barley Genetic Stock (BGS) descriptions for loci in barley (*Hordeum vulgare*), including information on chromosomal locations, recommended locus names, 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	26:140	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	32:85	Burma Girl
adp1	adp	593		Awned palea 1	28:34	Unknown cultivar
alm1	al	108	3HS	Albino lemma 1	26:143	Russia 82
als1	als	101	3HL	Absent lower laterals 1	26:135	Montcalm
ant1	rs	33	7HS	Anthocyanin-less 1	26:82	Bonus
ant2	pr	80	2HL	Anthocyanin-less 2	26:118	Foma
ant3		594		Anthocyanin-deficient 3	29:82	Bonus
ant4		595		Anthocyanin-deficient 4	29:83	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	3HL	Proanthocyanidin-free 17	29:88	Nordal
ant18		600	7HL	Proanthocyanidin-free 18	29:90	Nordal
ant19		601		Proanthocyanidin-free 19	29:92	Alf
ant20		602		Anthocyanidin-rich 20	29:93	Foma
ant21		603	6H	Proanthocyanidin-free 21	29:94	Georgie
ant22		604	7HS	Proanthocyanidin-free 22	29:95	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	29:99	Grit
ant29		609		Proanthocyanidin-free 29	29:100	Ca 708912
ant30		610		Proanthocyanidin-free 30	29:101	Gunhild
ari-a		132	3HS	Breviaristatum-a	26:168	Bonus

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
ari-b		550		Breviaristatum-b	26:476	Bonus
ari-e		328	5HL	Breviaristatum-e	26:276	Bonus
ari-f		551		Breviaristatum-f	26:477	Bonus
ari-g		89		Breviaristatum-g	26:128	Bonus
ari-h		329	5HL	Breviaristatum-h	26:277	Foma
ari-j		552		Breviaristatum-j	26:478	Bonus
ari-k		553		Breviaristatum-k	26:479	Bonus
ari-m		554		Breviaristatum-m	26:480	Bonus
ari-n		555		Breviaristatum-n	26:481	Bonus
ari-o		556		Breviaristatum-o	26:482	Bonus
ari-p		557		Breviaristatum-p	26:483	Foma
ari-q		558		Breviaristatum-q	26:484	Kristina
ari-r		559		Breviaristatum-r	26:485	Bonus
Ari-s	ari-265	630		Breviaristatum-s	32:131	Kristina
asp1		649		Aborted spike 1	35:207	Steptoe
blf1	bb	326	5HL	Broad leaf 1	26:274	Bonus
blf2	bb2	337	5HL	Broad leaf 2	26:285	Hannchen
Blp1	B	203	1HL	Black lemma and pericarp 1	26:209	Nigrinudum
blx1	bl	15	4HL	Non-blue aleurone xenia 1	26:60	Goldfoil
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	7HS	Bracteatum-a	32:120	Bonus
bra-d		586		Bracteatum-d	26:513	Foma
brc1	brc-5	613	2HS	Branched 1	32:114	
brh1	br	1	7HS	Brachytic 1	26:44	Himalaya
brh2	br2	157	4HL	Brachytic 2	26:184	Svanhals
brh3	brh.g	631		Brachytic 3	32:132	Birgitta
brh4	brh.j	349	5HL	Brachytic 4	32:110	Birgitta
brh5	brh.m	185	4HS	Brachytic 5	32:100	Birgitta
brh6	brh.s	350	5HL	Brachytic 6	32:111	Akashinriki
brh7	brh.w	41	7HS	Brachytic 7	32:81	Volla
brh8	brh.ad	142		Brachytic 8	32:92	Birgitta
bsp1		645		Bushy spike 1	35:203	Morex
btr1	bt	115	3HS	Non-brittle rachis 1	26:149	A 222
btr2	bt2	116	3HS	Non-brittle rachis 2	26:150	Sakigoke
cal-b		620	5H	Calcaroides-b	32:121	Bonus
Cal-c		621	5HL	Calcaroides-c	32:122	Bonus
cal-d		146	3H	Calcaroides-d	32:95	Foma

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
cal-e		622	5HS	Calcaroides-e	32:123	Semira
cer-d		399		Eceriferum-d + + + +	26:346	Bonus
cer-e		400	1HL	Eceriferum-e -/+ + + +	26:347	Bonus
cer-f		401	7HS	Eceriferum-f + + + +	26:348	Bonus
cer-g		402	2HL	Eceriferum-g + + + +	26:349	Bonus
cer-h		403		Eceriferum-h - + + +	26:351	Bonus
cer-i		404	5HL	Eceriferum-i - + + +	26:352	Bonus
cer-k		405	7HS	Eceriferum-k + + + +	26:354	Bonus
cer-l		406		Eceriferum-l + + + +	26:355	Bonus
cer-m		407		Eceriferum-m +/+ + + +	26:356	Bonus
cer-n	gs9	408	2HL	Eceriferum-n - - + + & - +/- + +	26:357	Bonus
cer-o		409		Eceriferum-o -/+ + + +	26:359	Bonus
cer-p		410		Eceriferum-p + + + +	26:360	Bonus
cer-r		411	3HL	Eceriferum-r +/- + + +	26:361	Bonus
cer-t		412	5HL	Eceriferum-t +/- + + +	26:362	Bonus
cer-v		414	2HS	Eceriferum-v +/- + + +	26:366	Bonus
cer-w		415	5HL	Eceriferum-w +/- + + +	26:367	Bonus
cer-y		417		Eceriferum-y + +/+ + +	26:368	Bonus
cer-z		418	7HS	Eceriferum-z - - + +	26:369	Bonus
cer-za		419	5HL	Eceriferum-za + + + -	26:370	Foma
cer-zb		420		Eceriferum-zb - + + +	26:371	Bonus
cer-zc		421		Eceriferum-zc +/- + + +	26:372	Bonus
cer-zd		422	3HL	Eceriferum-zd + + + -	26:373	Bonus
cer-ze	gl5	423	7HS	Eceriferum-ze + + + -	26:374	Bonus
cer-zf		424		Eceriferum-zf + + + +	26:376	Bonus
cer-zg		425	4HL	Eceriferum-zg + + + +	26:377	Foma
cer-zi		427	1HL	Eceriferum-zi + + + +	26:378	Bonus
cer-zj		428	5HL	Eceriferum-zj + + + -	26:379	Bonus
cer-zk		429	2H	Eceriferum-zk + + +/-	26:381	Bonus
cer-zl		430		Eceriferum-zl - - + +	26:382	Bonus
cer-zn		431	3HL	Eceriferum-zn +/- + + +	26:383	Foma
cer-zo		432		Eceriferum-zo - + + +	26:384	Foma
cer-zp		433	5HL	Eceriferum-zp + + + -	26:385	Bonus
cer-zq		434		Eceriferum-zq + + + -	26:386	Foma
cer-zr		435		Eceriferum-zr +/- + + +	26:387	Foma
cer-zs		436		Eceriferum-zs + + + +	26:388	Foma
cer-zt		437		Eceriferum-zt + + + +	26:389	Foma
cer-zu		438		Eceriferum-zu - + + +	26:390	Bonus
cer-zv		439		Eceriferum-zv - - -	26:391	Foma
cer-zw		440		Eceriferum-zw + + + +	26:392	Foma

Table 3. (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc. [†]			
cer-zx		441		Eceriferum-zx + + ++	26:393	Bonus
cer-zy		442		Eceriferum-zy ++ ++ +	26:394	Bonus
cer-zz		443		Eceriferum-zz ++ ++ -	26:395	Bonus
cer-ya		444	3HS	Eceriferum-ya ++ ++ -	26:396	Bonus
cer-yb		445	2HL	Eceriferum-yb ++ ++ -	26:397	Bonus
cer-yc		446		Eceriferum-yc - ++ ++	26:398	Bonus
cer-yd		447	3HS	Eceriferum-yd - ++ ++	26:399	Bonus
cer-ye		448	5HL	Eceriferum-ye ++ ++ -	26:400	Foma
cer-yf		449		Eceriferum-yf ++ ++ +	26:401	Foma
cer-yg		450	7HS	Eceriferum-yg - - -	26:402	Carlsberg II
cer-yh		451	3HS	Eceriferum-yh - ++ ++	26:403	Bonus
cer-yi		522		Eceriferum-yi ++ ++ -	26:449	Foma
cer-yj		523		Eceriferum-yj ++ ++ -	26:450	Bonus
cer-yk		524		Eceriferum-yk + + ++	26:451	Bonus
cer-yl		525		Eceriferum-yl - - ++	26:452	Bonus
cer-ym		526		Eceriferum-ym - - -	26:453	Bonus
cer-yn		527		Eceriferum-yn + + ++	26:454	Kristina
cer-yo		528		Eceriferum-yo ++ ++ +	26:455	Bonus
cer-yp		529		Eceriferum-yp ++ ++ +	26:456	Bonus
cer-yq		530		Eceriferum-yq ++ ++ -	26:457	Kristina
cer-yr		531		Eceriferum-yr -/+ + ++	26:458	Foma
cer-ys		532		Eceriferum-ys ++ ++ -	26:459	Bonus
cer-yt		533		Eceriferum-yt - ++ ++	26:460	Bonus
cer-yu		534		Eceriferum-yu ++ ++ -	26:461	Bonus
cer-yx		535		Eceriferum-yx + + ++	26:462	Foma
Cer-yy	Gle1	536	1HS	Eceriferum-yy - ++ ++	26:463	Bonus
cer-yz		537		Eceriferum-yz + + ++	26:464	Bonus
cer-xa		538		Eceriferum-xa ++ ++ -	26:465	Foma
cer-xb		539		Eceriferum-xb - ++ ++	26:466	Bonus
cer-xc		540		Eceriferum-xc + + ++	26:467	Bonus
cer-xd		541		Eceriferum-xd + + ++	26:468	Bonus
clh1	clh	225	1HL	Curled leaf dwarf 1	26:223	Hannchen
com1	bir1	473	5HL	Compositum 1	26:420	Foma
com2	bir2	71	2HS	Compositum 2	26:108	CIMMYT freak
crl1	cl	325		Curly lateral 1	26:273	Montcalm
crm1	cm	305	5HL	Cream seedling 1	26:256	Black Hulless
cud1	cud	324	5HL	Curly dwarf 1	26:272	Akashinriki
cud2		229	1HL	Curly dwarf 2	26:227	Akashinriki
cul2	uc2	253	6HL	Uniculm 2	26:234	Kindred
cul3		616		Uniculme 3	32:117	Donaria

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
cul4	uc-5	617		Uniculme 4	32:118	Bonus
cur1	cu1	262	6HL	Curly 1	26:242	48-cr cr-17
cur2	cu2	114	3HL	Curly 2	26:148	Choshiro
cur3	cu3	263	6HL	Curly 3	26:243	Akashinriki
cur4	cu4	460	2HL	Curly 4	26:406	Asahi 5
cur5	cu5	231	1HS	Curly 5	26:229	Glenn
ddt1	ddt	317	5HS	Reaction to DDT 1	26:266	Spartan
des1	lc	12	7H	Desynapsis 1	26:57	Mars
des2	ds	119	3H	Desynapsis 2	26:154	Husky
des3		386		Desynapsis 3	26:334	Betzes
des4		13	7H	Desynapsis 4	26:58	Betzes
des5		14	7H	Desynapsis 5	26:59	Betzes
des6		215	1H	Desynapsis 6	26:216	Betzes
des7		64	2H	Desynapsis 7	26:100	Betzes
des8		387		Desynapsis 8	26:335	Betzes
des9		388		Desynapsis 9	26:336	Betzes
des10		389		Desynapsis 10	26:337	Betzes
des11		390		Desynapsis 11	26:338	Betzes
des12		391		Desynapsis 12	26:339	Betzes
des13		392		Desynapsis 13	26:340	Betzes
des14		393		Desynapsis 14	26:341	Betzes
des15		394		Desynapsis 15	26:342	Ingrid
dex1	sex2	311	5HS	Defective endosperm xenia 1	26:260	BTT 63-j-18-17
dsk1	dsk	322	5HL	Dusky 1	26:270	Chikurin-Ibaraki 1
dsp1	l	9	7HS	Dense spike 1	26:53	Honen 6
dsp9	l9	258	6HL	Dense spike 9	26:239	Akashinriki
dsp10	lc	111	3HS	Dense spike 10	26:145	Club Mariout
Dwf2		542		Dominant dwarf 2	24:170	Klages/Mata
Eam1	Ea	65	2HS	Early maturity 1	26:101	Estate
Eam5	Ea5	348	5HL	Early maturity 5	32:109	Higuerilla*2/ Gobernadora
eam6	Ea6, Ea	98	2HS	Early maturity 6	32:86	Morex
eam7	ea7	252	6HS	Early maturity 7	26:233	California Mariout
eam8	ea _k , ert-o	214	1HL	Early maturity 8	26:213	Kinai 5
eam9	ea _{,c}	181	4HL	Early maturity 9	26:204	Tayeh 8
eam10	ea _{sp}	130	3HL	Early maturity 10	26:166	Super Precoz
eli-a	lig-a	623		Eligulum-a	35:192	Foma
eog 1	e	57	2HL	Elongated outer glume 1	26:92	Triple Bearded Club Mariout

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
ert-a	ert-6	28	7HS	Erectoides-a	26:74	Gull
ert-b	ert-2	224	1HS	Erectoides-b	26:222	Gull
ert-c	ert-1	134	3HL	Erectoides-c	26:170	Gull
ert-d	ert-7	29	7HS	Erectoides-d	26:76	Gull
ert-e	ert-17	266	6HL	Erectoides-e	26:246	Bonus
ert-f	ert-18	560		Erectoides-f	26:486	Bonus
ert-g	ert-24	330	5HL	Erectoides-g	26:278	Bonus
ert-h	ert-25	561		Erectoides-h	26:487	Bonus
ert-ii	ert-79	135	3HL	Erectoides-ii	26:172	Bonus
ert-j	ert.31	90	2H	Erectoides-j	26:129	Bonus
ert-k	ert-32	562		Erectoides-k	26:488	Bonus
ert-l	ert-12	563		Erectoides-l	26:489	Maja
ert-m	ert-34	30	7HS	Erectoides-m	26:78	Bonus
ert-n	ert-51	331	5HL	Erectoides-n	26:279	Bonus
ert-p	ert-44	564		Erectoides-p	26:490	Bonus
ert-q	ert-101	91	2H	Erectoides-q	26:130	Bonus
Ert-r	Ert-52	332		Erectoides-r	26:280	Bonus
ert-s	ert-50	565		Erectoides-s	26:491	Bonus
ert-t	ert-55	566		Erectoides-t	26:492	Bonus
ert-u	ert-56	92	2H	Erectoides-u	26:131	Bonus
ert-v	ert-57	567		Erectoides-v	26:493	Bonus
ert-x	ert-58	568		Erectoides-x	26:494	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		Erectoides-za	26:497	Bonus
ert-zb	ert-132	572		Erectoides-zb	26:498	Bonus
ert-zc	ert-149	573		Erectoides-zc	26:499	Bonus
ert-zd	ert-159	93	2H	Erectoides-zd	26:132	Bonus
ert-ze	ert-105	574		Erectoides-ze	26:500	Bonus
fch1	f	55	2HS	Chlorina seedling 1	26:90	Minn 84-7
fch2	f2	117	3HL	Chlorina seedling 2	26:151	28-3398
fch3	f3	220	1HS	Chlorina seedling 3	26:218	Minn 89-4
fch4	f4	17	7HL	Chlorina seedling 4	26:63	Montcalm
fch5	f5	18	7HS	Chlorina seedling 5	26:64	Gateway
fch6	f6	313	5HL	Chlorina seedling 6	26:262	Himalaya
fch7	f7	201	1HL	Chlorina seedling 7	26:206	Smyrna
fch8	f8	5	7HS	Chlorina seedling 8	26:48	Comfort
fch9	f9	151	4HS	Chlorina seedling 9	26:178	Ko A
fch11	f11	260	6HL	Chlorina seedling 11	26:240	Himalaya
fch12	f _c	2	7HS	Chlorina seedling 12	26:45	Colsess

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
fch13	f13	86		Chlorina seedling 13	26:124	Niggrinudum
fch14	f14	87	2HL	Chlorina seedling 14	26:125	Shyri
fch15	or	52	2HS	Chlorina seedling 15	26:88	Trebi IV
flo-a		182		Extra floret-a	26:205	Foma
flo-b		327	5HL	Extra floret-b	26:275	Foma
flo-c		74	2HS	Extra floret-c	26:111	Foma
fol-a		73	2HL	Angustifolium-a	26:110	Proctor
Fol-b	Ang	548		Angustifolium-b	26:474	Unknown
fst1	fs	301	5HL	Fragile stem 1	26:252	Kamairazu
fst2	fs2	208	1HL	Fragile stem 2	26:211	Oshichi
fst3	fs3	24	7HS	Fragile stem 3	26:70	Kobinkatagi 4
gig1	gig	463	2H?	Gigas 1	26:410	Tochigi Golden Melon
gig2		612		Gigas 2	32:113	ND12463
glf1	gl	155	4HL	Glossy leaf 1 ++ ++ -	26:181	Himalaya
glf3	gl3	165	4HL	Glossy leaf 3 ++ ++ -	26:190	Goseshikoku
glo-a		168	4HS	Globosum-a	26:194	Proctor
glo-b		336	5HL	Globosum-b	26:284	Villa
glo-c		72	2H	Globosum-c	26:109	Villa
glo-e		230	1HL	Globosum-e	26:228	Foma
glo-f		342	5HL	Globosum-f	26:291	Damazy
gpa1	gp	59	2HL	Grandpa 1	26:95	Lyallpur
gra-a	gran-a	131	3HL	Granum-a	26:167	Donaria
gsh1	gs1	351	2HS	Glossy sheath 1 - - ++	26:292	Clho 5818
gsh2	gs2	352	3HL	Glossy sheath 2 - - ++	26:294	Atlas
gsh3	gs3	353	7HS	Glossy sheath 3 - - ++	26:296	Mars
gsh4	gs4	354	6HL	Glossy sheath 4 - - ++	26:298	Gateway
gsh5	gs5	355	2HL	Glossy sheath 5 + - ++	26:300	Jotun
gsh6	gs6	356	2HS	Glossy sheath 6 - - ++	26:302	Betzes
gsh7	gs7	81		Glossy sheath 7 - - ++	26:119	Akashinriki
gsh8	cer-u	413	2HS	Glossy sheath 8 + + ++	26:364	Bonus
Gth1	G	69	2HL	Toothed lemma 1	26:106	Machine (Wexelsen)
hcm1	h	77	2HL	Short culm 1	26:115	Morex
Hln1	Hn	164	4HL	Hairs on lemma nerves 1	26:189	Kogane-mugi
Hsh1	Hs	179	4HL	Hairy leaf sheath 1	26:202	Kimugi
int-b		320	5HL	Intermedium spike-b	26:268	Bonus
int-c	i	178	4HS	Intermedium spike-c	26:200	Gamma 4
int-f		543		Intermedium spike-f	26:469	Foma
int-h		544		Intermedium spike-h	26:470	Kristina

Table 3. (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc. [†]		vol. p.	
int-i		545		Intermedium spike-i	26:471	Kristina
int-k		546		Intermedium spike-k	26:472	Kristina
int-m		547		Intermedium spike-m	26:473	Bonus
Kap1	K	152	4HS	Hooded lemma 1	26:179	Colsess
lam1		651		Late maturity 1	35:209	Steptoe
lax-a		474	5HL	Laxatum-a	26:421	Bonus
lax-b		268	6HL	Laxatum-b	26:248	Bonus
lax-c		475	6HL	Laxatum-c	26:423	Bonus
lbi1	lb	308	5HL	Long basal rachis internode 1	26:258	Wisconsin 38
lbi2	lb2	156	4HL	Long basal rachis internode 2	26:183	Montcalm
lbi3	lb3	27	7HL	Long basal rachis internode 3	26:73	Montcalm
lel1	lel	235	1HL	Leafy lemma 1	32:103	G7118
Lfb1	Lfb	343	5HL	Leafy bract 1	28:30	Montcalm
Lga1	Log	549		Long glume awn 1	26:475	Guy Mayle
lgn3	lg3	170	4HL	Light green 3	26:195	No 154
lgn4	lg4	171	4HL	Light green 4	26:196	Himalaya/ Ingrescens
lig1	li	60	2HL	Liguleless 1	26:96	Muyoji
lin1	s, rin	99	2HL	Lesser internode number 1	32:88	Natural occurrence
Lks1	Lk	75	2HL	Awnless 1	26:112	<i>Hordeum inerme</i>
lks2	lk2	10	7HL	Short awn 2	26:54	Honen 6
lks5	lk5	172	4HL	Short awn 5	26:197	CIho 5641
lnt1	lnt	118	3HL	Low number of tillers 1	26:153	Mitake
lys1	lys	338	5HL	High lysine 1	26:286	Hiproly
lys3	sex3	339	5HL	High lysine 3	26:287	Bomi
Lys4	sex5	232	1HS	High lysine 4	26:230	Bomi
lys6		269	6H	High lysine 6	26:249	Bomi
lzd1	lzd	125	3HS	Lazy dwarf 1	26:161	Akashinriki
mat-b		578		Praematurum-b	26:504	Bonus
mat-c		579		Praematurum-c	26:506	Bonus
mat-d		580		Praematurum-d	26:507	Bonus
mat-e		581		Praematurum-e	26:508	Bonus
mat-f		582		Praematurum-f	26:509	Bonus
mat-g		583		Praematurum-g	26:510	Bonus
mat-h		584		Praematurum-h	26:511	Bonus
mat-i		585		Praematurum-i	26:512	Bonus
min1	min	161	4HL	Semi-minute dwarf 1	26:187	Taisho-mugi
min2	en-min	160		Enhancer of minute 1	26:186	Kaiyo Bozu
mnd1	m	519		Many-noded dwarf 1	26:446	Mesa
mnd3	m3	618	3H	Many noded dwarf 3	32:119	Montcalm

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
mnd4	m4	347	5HL	Many noded dwarf 4	32:108	Akashinriki
mnd5		632		Many noded dwarf 5	32:133	C2-95-199
mnd6	den-6	633	5HL	Many noded dwarf 6	32:134	Bonus
mov1	mo6b	43	7HL	Multiovary 1	35:185	Steptoe
mov2	mo7a	147	3HS	Multiovary 2	35:190	Steptoe
mov3	mo-a	234	1H	Multiovary 3	32:102	Akashinriki
mov4		648		Multiovary 4	35:206	Steptoe
msg1		357	1HL	Male sterile genetic 1	26:304	CIho 5368
msg2		358	2HL	Male sterile genetic 2	26:306	Manchuria
msg3		359	2HS	Male sterile genetic 3	26:307	Gateway
msg4		360	1H	Male sterile genetic 4	26:308	Freja
msg5		361	3HS	Male sterile genetic 5	26:309	Carlsberg II
msg6		362	6HS	Male sterile genetic 6	26:310	Hanna
msg7		363	5HL	Male sterile genetic 7	26:311	Dekap
msg8		364	5HL	Male sterile genetic 8	26:312	Betzes
msg9		365	2HS	Male sterile genetic 9	26:313	Vantage
msg10		366	7HS	Male sterile genetic 10	26:314	Compana
msg11		367		Male sterile genetic 11	26:315	Gateway
msg13		368		Male sterile genetic 13	26:316	Haisa II
msg14		369	7HS	Male sterile genetic 14	26:317	Unitan
msg15		370		Male sterile genetic 15	26:318	Atlas/2*Kindred
msg16		371	5HS	Male sterile genetic 16	26:319	Betzes
msg17		372		Male sterile genetic 17	26:320	Compana
msg18		373	5HL	Male sterile genetic 18	26:321	Compana
msg19		374	5HS	Male sterile genetic 19	26:322	CIho 14393
msg20		375	1H	Male sterile genetic 20	26:323	Hannchen
msg21		376		Male sterile genetic 21	26:324	Midwest Bulk
msg22		383	7H	Male sterile genetic 22	26:331	Glacier/Compana
msg23		384	7HL	Male sterile genetic 23	26:332	Betzes
msg24		385	4HL	Male sterile genetic 24	26:333	Betzes
msg25		166	4HL	Male sterile genetic 25	26:192	Betzes
msg26		395	7HS	Male sterile genetic 26	26:343	Unitan
msg27		464	2HL	Male sterile genetic 27	26:411	Firlbecks III
msg28		465	6H	Male sterile genetic 28	26:412	York
msg29		466	5HL	Male sterile genetic 29	26:413	Ackermans MGZ
msg30		467	7HL	Male sterile genetic 30	26:414	Compana
msg31		468	1HS	Male sterile genetic 31	26:415	51Ab4834
msg32		469	7H	Male sterile genetic 32	26:416	Betzes
msg33		470	2HS	Male sterile genetic 33	26:417	Betzes
msg34		471	6H	Male sterile genetic 34	26:418	Paragon

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
msg35		498	2HL	Male sterile genetic 35	26:424	Karl
msg36		499	6HS	Male sterile genetic 36	26:425	Betzes
msg37		500		Male sterile genetic 37	26:426	Clermont
msg38		501		Male sterile genetic 38	26:427	Ingrid
msg39		502	6H	Male sterile genetic 39	26:428	CIho 15836
msg40		503	6H	Male sterile genetic 40	26:429	Conquest
msg41		504		Male sterile genetic 41	26:430	Betzes
msg42		505	3H	Male sterile genetic 42	26:431	Betzes
msg43		506		Male sterile genetic 43	26:432	Betzes
msg44		507		Male sterile genetic 44	26:433	HA6-33-02
msg45		508		Male sterile genetic 45	26:434	RPB439-71
msg46		509		Male sterile genetic 46	26:435	Hector
msg47		510		Male sterile genetic 47	26:436	Sel 12384CO
msg48		520	2H	Male sterile genetic 48	26:447	Simba
msg49		335	5HL	Male sterile genetic 49	26:283	ND7369
msg50		34	7HL	Male sterile genetic 50	26:83	Berac
mss1	mss	84	2H	Midseason stripe 1	26:122	Montcalm
mss2		39	7HS	Midseason stripe 2	32:79	ND11258
mtt1	mt	521	1HS	Mottled leaf 1	26:448	Montcalm
mtt2	mt2	302	5HL	Mottled leaf 2	26:253	Montcalm
mtt4	mt,,e	78	2HL	Mottled leaf 4	26:116	Victorie
mtt5	mt,,f	264	6HL	Mottled leaf 5	26:244	Akashinriki
mtt6		629		Mottled leaf 6	32:130	ND6809
mul2		251	6HL	Multiflorus 2	26:232	Montcalm
nar1		637	6HS	NADH ntrate reductase-deficient 1	35:194	Steptoe
nar2		638	5HL	NADH ntrate reductase-deficient 2	35:196	Steptoe
nar3		639	7HS	NADH ntrate reductase-deficient 3	35:197	Winer
nar4		640	2HL	NADH ntrate reductase-deficient 4	35:198	Steptoe
nar5		641	5HL	NADH ntrate reductase-deficient 5	35:199	Steptoe
nar6		642	2HL	NADH ntrate reductase-deficient 6	35:200	Steptoe
nar7		643	6HL	NADH ntrate reductase-deficient 7	35:201	Steptoe
nar8		644	6HS	NADH ntrate reductase-deficient 8	35:202	Steptoe
nec1		222	1HL	Necrotic leaf spot 1	26:220	Carlsberg II
nec2		261	6HS	Necrotic leaf spot 2	26:241	Carlsberg II
nec3		265	6HS	Necrotic leaf spot 3	26:245	Proctor
nec4		138	3H	Necrotic leaf spot 4	26:175	Proctor
nec5		139	3H	Necrotic leaf spot 5	26:176	Diamant
Nec6	Sp	611		Necrotic leaf spot 6	32:112	Awnless Atlas
nec7	nec-45	635		Necroticans 7	32:136	Kristina
nld1	nld	323	5HL	Narrow leafed dwarf 1	26:271	Nagaoka

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
nud1	n, nud	7	7HL	Naked caryopsis 1	26:51	Himalaya
ops1	op-3	624		Opposite spikelets 1	32:125	Bonus
ovl1		176	4H	Ovaryless 1	35:191	Kanto Bansei Gold
ovl2		646		Ovaryless 2	35:204	Harrington
pmr1	pmr	40	7HS	Premature ripe 1	32:80	Glenn
pmr2	nec-50	634		Premature ripe 2	32:135	Bonus
Pre2	Re2	76	2HL	Red lemma and pericarp 2	26:113	Buckley 3277
Pub1	Pub	127	3HL	Pubescent leaf blade 1	26:163	Multiple Dominant
Pvc1	P _c	68	2HL	Purple veined lemma 1	26:105	Buckley 2223-6
Pyr1		42	7HS	Pyramidatum 1	32:82	Pokko/Hja80001
raw1	r	312	5HL	Smooth awn 1	26:261	Lion
raw2	r2	340	5HL	Smooth awn 2	26:289	Lion
raw5	r ₅ ,e	257	6HL	Smooth awn 5	26:238	Akashinriki
raw6	r6	334	5HL	Smooth awn 6	26:282	Glenn
rob1	o	254	6HL	Orange lemma 1	26:235	Clho 5649
Rpg1	T	511	7HS	Reaction to <i>Puccinia graminis</i> 1	26:437	Chevron
Rpg2	T2	512		Reaction to <i>Puccinia graminis</i> 2	26:439	Hietpas 5
rpg4		319	5HL	Reaction to <i>Puccinia graminis</i> 4	26:267	Q21861
Rph1	Pa	70	2H	Reaction to <i>Puccinia hordei</i> 1	26:107	Oderbrucker
Rph2	Pa2	88	5HS	Reaction to <i>Puccinia hordei</i> 2	26:126	Peruvian
Rph3	Pa3	121	7HL	Reaction to <i>Puccinia hordei</i> 3	26:156	Estate
Rph4	Pa4	218	1HS	Reaction to <i>Puccinia hordei</i> 4	26:217	Gull
Rph5	Pa5	122	3HS	Reaction to <i>Puccinia hordei</i> 5	35:188	Magnif 102
Rph6	Pa6	575	3HS	Reaction to <i>Puccinia hordei</i> 6	26:501	Bolivia
Rph7	Pa7	136	3HS	Reaction to <i>Puccinia hordei</i> 7	26:173	Cebada Capa
Rph8	Pa8	576		Reaction to <i>Puccinia hordei</i> 8	26:502	Egypt 4
Rph9	Pa9	32		Reaction to <i>Puccinia hordei</i> 9	26:81	HOR 2596
Rph10		137	3HL	Reaction to <i>Puccinia hordei</i> 10	26:174	Clipper C8
Rph11		267	6HL	Reaction to <i>Puccinia hordei</i> 11	26:247	Clipper C67
Rph12		333	5HL	Reaction to <i>Puccinia hordei</i> 12	26:281	Triumph
Rph13		590		Reaction to <i>Puccinia hordei</i> 13	28:31	PI 531849
Rph14		591		Reaction to <i>Puccinia hordei</i> 14	28:32	PI 584760
Rph15		96	2HL	Reaction to <i>Puccinia hordei</i> 15	35:186	PI 355447
Rsg1	Grb	22	7H	Reaction to <i>Schizaphis raminum</i> 1	26:68	Omugi
Rsg2		577		Reaction to <i>Schizaphis raminum</i> 2	26:503	PI 426756
rsm1	sm	35	7HS	Reaction to BSMV 1	26:84	Modjo 1
Rsp1	Sep	515		Reaction to <i>Septoria passerinii</i> 1	26:441	Clho 14300
Rsp2	Sep ₂	516		Reaction to <i>Septoria passerinii</i> 2	26:442	PI 70837
Rsp3	Sep ₃	517		Reaction to <i>Septoria passerinii</i> 3	26:443	Clho 10644
rtl1	rt	51	2HS	Rattail spike 1	26:87	Goldfoil

Table 3. (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc. [†]			
Run1	Un	21	7HS	Reaction to <i>Ustilago nuda</i> 1	26:67	Trebi
rvl1	rvl	226	1HL	Revoluted leaf 1	26:224	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	32:83	Tayeh 13
sca1	sca	128	3HS	Short crooked awn 1	26:164	Akashinriki
sci-a	sci-3	625		Scirpoides-a	32:126	Bonus
scl-a	scl-6	626		Scirpoides leaf-a	32:127	Foma
sdw1	sdw	518	3HL	Semidwarf 1	26:444	M21
sdw2	sdw-b	133	3HL	Semidwarf 2	26:169	Mg2170
seg1	se1	377	7HL	Shrunken endosperm 1	26:235	Betzes
seg2	se2	378	7HS	Shrunken endosperm 2	26:326	Betzes
seg3	se3	379	3H	Shrunken endosperm 3	26:327	Compana
seg4	se4	380	7HL	Shrunken endosperm 4	26:328	Compana
seg5	se5	381	7HS	Shrunken endosperm 5	26:329	Sermo/7*Glacier
seg6	se6	396	3HL	Shrunken endosperm 6	26:344	Ingrid
seg7	se7	397		Shrunken endosperm 7	26:345	Ingrid
seg8		455	7H	Shrunken endosperm 8	26:405	60Ab1810-53
sex1	lys5	382	6HL	Shrunken endosperm xenia 1	26:330	Compana
sex6		31	7HS	Shrunken endosperm xenia 6	26:80	K6827
sex7	sex.i	627	5HL	Shrunken endosperm xenia 7	32:129	I90-374
sex8	sex.j	143	6HS	Shrunken endosperm xenia 8	32:93	I89-633
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	26:203	Akashinriki
Sil1	Sil	228	1HS	Subcrown internode length 1	26:226	NE 62203
sld1	dw-1	126	3HL	Slender dwarf 1	26:162	Akashinriki
sld2		83	2HS	Slender dwarf 2	26:121	Akashinriki
sld3	ant-567	186	4HS	Slender dwarf 3	32:101	Manker
sld4		100	2HL	Slender dwarf 4	32:89	Glacier
sld5		144	3HS	Slender dwarf 5	32:94	Indian Dwarf
sls1	sls	227	1HS	Small lateral spikelet 1	26:225	Morex
smn1	smn	38	7HS	Seminudoides 1	32:225	Haisa
snb1	sb	26	7HS	Subnodal bract 1	26:72	L50-200
srh1	s	321	5HL	Short rachilla hair 1	26:269	Lion
sun1		650		Sensitivity to <i>Ustilago nuda</i> 1	35:208	Steptoe

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
trd1	trd	202	1HL	Third outer glume 1	26:207	Valki
trp1	tr	61	2HL	Triple awned lemma 1	26:97	CIho 6630
tst1		647		Tip sterile 1	35:205	Steptoe
tst2	lin2	636		Tip sterile 2	32:137	Donaria
ubs4	u4	11	7HL	Unbranched style 4	26:56	Ao-Hadaka
uzu1	uz	102	3HL	Uzu or semi brachytic 1	26:136	Baitori
var1	va	306	5HL	Variegated 1	26:257	Montcalm
var2	va2	344	5HL	Variegated 2	32:104	Montcalm
var3	va3	303	5HL	Variegated 3	26:254	Montcalm
viv-a	viv-5	627		Viviparoides-a	32:128	Foma
vrs1	v	6	2HL	Six-rowed spike 1	26:49	Trebi
vrs1	lr	58	2HL	Six-rowed spike 1	26:94	Nudihaxtoni
vrs1	V ^d	66	2HL	Two-rowed spike	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	26:264	Hadata 2
vrs4	v4	124	3HL	Six-rowed spike 4	26:159	MFB 104
wax1	wx	16	7HS	Waxy endosperm 1	26:61	Oderbrucker
wnd1	wnd	23	7HS	Winding dwarf 1	26:69	Kogen-mugi
wst1	wst	107	3HL	White streak 1	26:141	CIho 11767
wst2		304	5HL	White streak 2	26:255	Manabe
wst4		56	2HL	White streak 4	26:91	Kanyo 7
wst5		221	1HL	White streak 5	26:219	Carlsberg II
wst6	wst _{5,j}	129	3HL	White streak 6	26:165	Akashinriki
wst7	rb	79	2HL	White streak 7	26:117	GS397
Xnt1	X _a	25	7HL	Xantha seedling 1	26:71	Akanshinriki
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 _{5,g}	233	1HL	Xantha seedling 7	26:231	Erbet
xnt8	xan _{5,h}	140	3HS	Xantha seedling 8	26:177	Carlsberg II
xnt9	xan _{5,i}	37	7HL	Xantha seedling 9	26:86	Erbet
yhd1	yh	158	4HL	Yellow head 1	26:185	Kimugi
yhd2	yh2	592		Yellow head 2	28:34	Compana
ylf1		652		Yellow leaf 1	35:210	Villa
Ynd1	Yn	183	4HS	Yellow node 1	32:98	Morex
yst1	yst	104	3HS	Yellow streak 1	26:138	Gateway

Table 3. (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.	no.	loc. [†]			
yst2		109	3HS	Yellow streak 2	26:144	Kuromugi 148/ Mensury C
yst3	yst,,c	462	3HS	Yellow streak 3	26:409	Lion
yst4		85	2HL	Yellow streak 4	26:123	Glenn
yst5		346	5HL	Yellow streak 5	32:107	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	26:155	Mars
zeb2	zb2	461	4HL	Zebra stripe 2	26:407	Unknown
zeb3	zb3	223	1HL	Zebra stripe 3	26:221	Utah 41
Zeo1	Knd	82	2HL	Zeocriton 1	26:120	Donaria
Zeo2		614		Zeocriton 2	32:115	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.

BGS 43, Multiovary 1, *mov1*

Stock number: BGS 43
Locus name: Multiovary 1
Locus symbol: *mov1*

Previous nomenclature and gene symbolization:

Multiovary 5 = *mo5* (4).

Multiovary 6 = *mo6b* (2, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HL [1L] in Bin 7H-07, near the *Amy2* (alpha-amylase 2) locus (2), co-segregation with molecular markers *Hsp17* and JS192.5 (3).

Description:

The *mov1.f* (*mov6b*) mutant has four carpels and two sepal-like structures where the lodicules should be. Stamens and lodicules are absent. It is presumed that the three stamens found in wild-type flowers have been converted into three additional carpels and that the lodicules have become leaf-like structures (3). The plant appears normal, but is completely sterile. The stock must be maintained as a heterozygote (1). This mutant appears morphologically similar to the *mo5* mutant (4), which was reported to map to the same region of chromosome 7HL (5). A seed stock was, however, not available for allelism tests (3).

Origin of mutant:

A fast neutron induced mutant in Steptoe (Clho 15229) (2).

Mutational events:

mov1.f (*mo6b*, FN1) in Steptoe (1); *mov1.e* (*mo5*) (3, 4); *mov1.i* (5102, *mo6c*); *mov1.j* (5103, *mo6d*) from the Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany (3).

Mutant used for description and seed stocks:

mov1.f in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).
2. Soule, J., I. Skodova, D. Kudrna, A. Kilian, and A. Kleinhofs. 1995. Molecular and genetic characterization of barley flower development mutants. BGN 25:76-80.
3. Soule, J.D., D.A. Kudrna, and A. Kleinhofs. 2000. Isolation, mapping, and characterization of two barley multiovary mutants. J. Hered. 91:483-487.
4. Tazhin, O.T. 1980. The linkage of the genes *mo5* and *n* in barley. BGN 10:69-72.
5. Tazhin, O.T. 1982. Value of crossing-over between linked genes *mo5* and *n* in barley. BGN 12:18-21.

Prepared:

A. Kleinhofs. 2005. BGN 35:185.

BGS 96, Reaction to *Puccinia hordei* 15, *Rph15*

Stock number: BGS 96
Locus name: Reaction to *Puccinia hordei* 15 (barley leaf rust)
Locus symbol: *Rph15*

Previous nomenclature and gene symbolization:

Rph16 = Reaction to *Puccinia hordei* 16 (4, 7).

Inheritance:

Monofactorial dominant (1, 2).

Located in chromosome 2HS (1, 4), in bin 2H-6 near molecular markers MWG2133 and MWG874 (4, 7); about 25.2cM distal from the centromere (7), about 14cM proximal from the *Eam1* (Early maturity 1) locus (Falk, personal communications), over 32.3 cM proximal from the *vrs1* (six-rowed spike 1) locus (1).

Description:

The seedling reaction to most isolates of *Puccinia hordei* is a relatively large necrotic fleck (1). The seedling reaction of heterozygotes is indistinguishable from that of homozygous resistant seedlings. Alleles at this locus were found in six of the first seven *Rph* genes from *Hordeum vulgare* subsp. *spontaneum* evaluated in Bowman backcross-derived lines (1, 2). Only one of 350 leaf rust isolates (90-3 from Israel) was found to be virulent on *Rph15* lines (6, 7).

Origin of mutant:

Natural occurrence in accession PI 355447 of *Hordeum vulgare* subsp. *spontaneum*, but isolated in a selection that contained one *Rph* gene from the original accession crossed to Bowman (PI 483237) (1, 5).

Mutational events:

Rph15.ad in PI 355447 (1, 2, 3), PI 354937, PI 391024, PI 391069, PI 391089, and PI 466245 (1, 2); *Rph15.ae* from HS084 (4, 7); PI 466245 has at least two genes for leaf rust resistance (5).

Mutant used for description and seed stocks:

Rph15.ad in selection from a cross to Bowman (GSHO 1586); *Rph15.ad* in Bowman*4 (GSHO 2330).

References:

1. Chicaiza, O. 1996. Genetic control of leaf rust in barley. Ph.D. dissertation, North Dakota State Univ., Fargo.
2. Chicaiza, O., J.D. Franckowiak, and B.J. Steffenson. 1996. New sources of resistance to leaf rust in barley. pp. 706-708. In A.E. Slinkard, G.J. Scoles, and B.G. Rosnagel (eds.). Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp., Saskatoon. Univ. of Saskatchewan, Saskatoon.
3. Franckowiak, J.D., Y. Jin, and B.J. Steffenson. 1997. Recommended allele symbols for leaf rust resistance genes in barley. BGN 27:36-44.
4. Ivandic, V., U. Walther, and A. Graner. 1998. Molecular mapping of a new gene in wild barley conferring complete resistance to leaf rust (*Puccinia hordei* Otth). Theor. Appl. Genet. 97:1235-1239.
5. Jin, Y., and B.J. Steffenson. 1994. Inheritance of resistance to *Puccinia hordei* in cultivated and wild barley. J. Hered. 85:451-454.
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Prepared:

J.D. Franckowiak and O. Chicaiza. 1998. BGN 28:29.

Revised:

J.D. Franckowiak. 2005. BGN 35:186-187.

BGS 122, Reaction to *Puccinia hordei* 5, *Rph5*

Stock number: BGS 122
Locus name: Reaction to *Puccinia hordei* 5 (barley leaf rust)
Locus symbol: *Rph5*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth 5 = *Pa₅* (4, 5).

Resistance to *Puccinia hordei* B = *B* (3).

Resistance to *Puccinia hordei* 6 = *Rph6.f* (BGS 575).

Inheritance:

Monofactorial incomplete dominant (1, 4).

Located in chromosome 3HS; about 6.0 cM distal from *Rph7*, about 1.0 cM proximal from RFLP marker CDO549, about 2.0 cM distal from RFLP marker MWG2021 (2, 8).

Description:

The seedling reaction type is 0 - 0;^c with race 4 culture 57-19 (1). Incomplete dominance is observed in segregating progenies (1, 3, 4).

Origin of mutant:

Natural occurrence in Quinn (PI 39401) (4, 7).

Mutational events:

Rph5.e in Magnif 102 (PI 337140) (7); *Rph5.f* (formerly *Rph6.f*) in Bolivia (PI 36360) (8);

Rph5.ai in Quinn along with *Rph2.q* (3, 4).

Mutant used for description and seed stocks:

Rph5.e in Malteria Heda*4/Quinn (Magnif 102, GSHO 1597) (7); *Rph5.e* in Bowman (PI 483237)*8 (GSHO 1865); *Rph5.f* in Bowman*8 (GSHO 2323).

References:

1. Jin, Y., G.H. Cui, B.J. Steffenson, and J.D. Franckowiak. 1996. New leaf rust resistance genes in barley and their allelic and linkage relationships with other *Rph* genes. *Phytopathology* 86:887-890.
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4. Roane, C.W., and T.M. Starling. 1967. Inheritance of reaction to *Puccinia hordei* in barley. II. Gene symbols for loci in differential cultivars. *Phytopathology* 57:66-68.
5. Roane, C.W., and T.M. Starling. 1970. Inheritance of reaction to *Puccinia hordei* in barley. III. Genes in the cultivars Cebada Capa and Franger. *Phytopathology* 60:788-790.
6. Starling, T.M. 1956. Sources, inheritance, and linkage relationships of resistance to race 4 of leaf rust (*Puccinia hordei* Otth), race 9 of powdery mildew (*Erysiphe graminis hordei* El. Marchal), and certain agronomic characters in barley. *Iowa State Coll. J. Sci.* 30:438-439.
7. Yahyaoui, A.H., and E.L. Sharp. 1987. Virulence spectrum of *Puccinia hordei* in North Africa and the Middle East. *Plant Dis.* 71:597-598.
8. Zhong, S., R.J. Effertz, Y. Jin, J.D. Franckowiak, and B.J. Steffenson. 2003. Molecular mapping of the leaf rust resistance gene *Rph6* in barley and its linkage relationships with *Rph5* and *Rph7*. *Phytopathology* 93:604-609.

Prepared:

C.W. Roane. 1976. BGN 6:122.

Revised:

J.D. Franckowiak and Y. Jin. 1997. BGN 26:157.

Revised:

B.J. Steffenson and J.D. Franckowiak. 2005. BGN 35:188-189.

§BGS 147, Multiovary 2, *mov2*

Stock number: BGS 147
Locus name: Multiovary 2
Locus symbol: *mov2*

Previous nomenclature and gene symbolization:

Multi-ovary = *mo* (4).
Multiovary 7 = *mo7a* (5, 6).

Inheritance:

Monofactorial recessive (2, 4, 5, 6).
Located in chromosome 3HS in Bin 3H-02, co-segregation with molecular markers ABC171A and JS001B (6).

Description:

The *mov2.g* (*mov7a*) mutant has between five and seven carpel-like structures and normal lodicules. Stamens are not present, but some carpels are terminated with stamen-like structures. Pollination using wild-type flowers results in a few seeds (6). The plant appears abnormal with a twisted and compact spike and reduced awn length. The frequency of mutant plants in the two F₂ progenies examined was much lower than expected (6). The stock must be maintained as a heterozygote (3). The mutants reported by Moh and Nilan (4) and Kamra and Nilan (2) may be alleles, but seed stocks were unavailable for testing (6).

Origin of mutant:

A fast neutron induced mutant in Steptoe (Clho 15229) (5).

Mutational events:

mov2.g (*mo7a*) in Steptoe (5, 6); *mov2.a* (*mo1*) (4, 6); *mov2.c* (*mo3*) (1, 2, 6).

Mutant used for description and seed stocks:

mov2.g in Steptoe.

References:

1. Kamra, P. 1966. Genetic control of the development of floral organs in *Hordeum vulgare*. p. 213-215. In A. Lengerova (ed.) Mechanisms of Mutation and Inducing Factors. Academia, Prague.
2. Kamra, O.P., and R.A. Nilan 1959. Multi-ovary in barley. Floral anatomy and embryo-sac development. J. Hered. 50:159-165.
3. Kleinhofs, A. (Unpublished).
4. Moh, C.C., and R.A. Nilan. 1953. Multi-ovary in barley. A. mutant induced by atomic radiation. J. Hered. 44:183-184.
5. Soule, J., I. Skodova, D. Kudrna, A. Kilian, and A. Kleinhofs. 1995. Molecular and genetic characterization of barley flower development mutants. BGN 25:76-80.
6. Soule, J.D., D.A. Kudrna, and A. Kleinhofs. 2000. Isolation, mapping, and characterization of two barley multiovary mutants. J. Hered. 91:483-487.

Prepared:

A. Kleinhofs. 2005. BGN 35:190.

BGS 176, Ovaryless 1, *ovl1*

Stock number: BGS 176
Locus name: Ovaryless 1
Locus symbol: *ovl1*

Previous nomenclature and gene symbolization:

Ovaryless = *ovl* (2, 3).

Inheritance:

Monofactorial recessive with very weak co-dominance (3).

Location in chromosome 4H (1, 5).

Description:

The homozygous recessive plant shows nonfunctional female reproductive parts, but anthers are well developed and pollen is viable. Spikes are nearly normal length but are awnless and completely sterile. Due to the lack of a midvein, the second and later leaves droop noticeably. Leaf length is slightly short than normal and leaf blades are somewhat narrower. The heterozygous plant has a midvein present in the basal half of the leaf, but it disappears toward the tip. As a result, some drooping is observed, but it is less apparent than in homozygous plants. Leaf length and width is nearly normal and the plant is fertile (2, 3). A viable source of this mutant has not been identified.

Origin of mutant:

A gamma ray induced mutant in Kanto Bansei Gold (Kanto Bansei Gall) (OUJ818) (2, 3).

Mutational events:

ovl1.a (Kmut 21b) in Kanto Bansei Gold (GSHO 610) (1).

Mutant used for description and seed stocks:

ovl1.a in Kanto Bansei Gold (GSHO 610). The original stock carried both *ovl1.a* and a reciprocal translocation (T4-6) (3, 4).

References:

1. Seip, L., and T. Tsuchiya. 1979. Trisomic analysis of a mutant gene *ovl* for ovaryless or male in barley. BGN 9:89-90.
2. Tsuchiya, T. 1962. Radiation breeding in two-rowed barley. Seiken Zihō 14:21-34.
3. Tsuchiya, T. 1969. p. 573-580. *In* Induced Mutations in Plants. (Proc: FAO/IAEA Symposium on the Nature, Induction and Utilization of Mutations in Plants, Pullman, Washington, 1969). Int. Atomic Energy Agency, Vienna.
4. Tsuchiya, T. 1972. Cytological identification of a translocation accompanied by a gene mutation. BGN 2:107-108.
5. Tsuchiya, T., S.D. Tanksley, and R. Ward. 1976. Trisomic analysis of three mutant genes in barley. BGN 6:95-96.

Prepared:

T. Tsuchiya and L. Seip. 1980. BGS 168, Ovaryless (male), *ovl*. BGN 10:118.

Revised:

T. Tsuchiya. 1983. BGN 13:110. (The BGS number was changed to BGS 176.)

Revised:

J.D. Franckowiak. 2005. BGN 35:191.

BGS 623, Eligulum-a, *eli-a*

Stock number: BGS 623
Locus name: Eligulum-a
Locus symbol: *eli-a*

Previous nomenclature and gene symbolization:

Eligulum-a = *lig-a* (2).

Eligulum-3 = *eli-3* (4).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Plants do not have ligules in the junction between the sheath and leaf blade, auricles are rudimentary and asymmetrically displaced. Plants are about 2/3 of normal height and have very wide leaves (3, 4). The peduncle is short and spike emergence from the sheath of the flag leaf is poor. Spikes have a compact arrangement of spikelets and are extremely compacted near the tip (1, 3). The culm breaks very easily just below the nodes. The Bowman backcross-derived lines have glume awns that are nearly twice as long as those of Bowman (1).

Origin of mutant:

An ethylene imine induced mutant in Foma (Clho 11333) (2, 3).

Mutational events:

eli-a.3 (NGB 115390), *-a.7* (NGB 115392), *-a.9* (NGB 115393), *-a.10* (NGB 115394) in Foma (3); *eli-a.11* (NGB 115395), *-a.14* (NGB 115397) in Kristina (NGB 1500); *eli-a.15* (NGB 115398), *-a.16* (NGB 151399) in Bonus (PI 189763 (4), *-a.216* (FN216) in Steptoe (Clho 15229) (1, 3).

Mutant used for description and seed stocks:

eli-a.3 in Foma (NGB 115390); *eli-a.3* in Bowman (PI 483237)*3.

References:

1. Franckowiak, J.D. (Unpublished).
2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
3. Kleinhofs, A. (Unpublished).
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2002. BGN 32:126.

Revised:

J.D. Franckowiak and A. Kleinhofs. 2005. BGN 35:192.

BGS 636, Tip sterile 2, *tst2*

Stock number: BGS 636
Locus name: Tip sterile 2
Locus symbol: *tst2*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Location is unknown.

Description:
Spikes of *tst2.b* plants are 1/4 to 1/2 of normal length because seed set fails in the upper portion of the spike. Slow or poor development of the spike reduces both the number of rachis internodes and number of fertile spikelets (1, 4). Most spikes of the Bowman backcross-derived line set less than 10 seeds. Plants are shorter than are normal sibs because peduncles fail to elongate normally. Both rachis internode length and awn length are reduced in *tst2* plants (1).

Origin of mutant:
An X-ray induced mutant in Donaria (PI 161974) (3, 4).

Mutational events:
tst2.b in Donaria (Mut. 2249, DWS1337) (2, 3).

Mutant used for description and seed stocks:
tst2.b in Haisa (GSHO 1781); *tst2.b* in Bowman (PI 483237)*5 (GSHO 2280).

References:
1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. BGN 21:116-127.
3. Scholz, F. 1956. Mutationsversuche an Kulturpflanzen. V. Die Vererbung zweier sich variabel manifestierender Übergangsmerkmale von bespelzter zu nackter Gerste bei röntgeninduzierten Mutanten. Kulturpflanze 4:228-246.
4. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l.l. Kulturpflanze 6:123-166.

Prepared:
J.D. Franckowiak and U. Lundqvist. 2002. BGN 32:137.

Revised:
J.D. Franckowiak. 2005. BGN 35:193 (Locus symbol was changed.)

BGS 637, NADH nitrate reductase-deficient 1, *nar1*

Stock number: BGS 637
Locus name: NADH nitrate reductase-deficient 1 (EC1.6.6.1; Acc. No. X57844 and X57845)
Locus symbol: *nar1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial co-dominant based on enzyme assay (4).
Located in chromosome 6HS (2) in Bin 6H-01 (3), about 0.8 cM proximal from molecular marker ABG466 (3).

Description:
Mutants are characterized by low in vivo nitrate reductase activity and low in vitro NADH nitrate activity. FMNH₂ and cytochrome c reductase activity is variable among the different alleles. All mutants have elevated nitrate reductase activity and accumulate nitrate to variable degrees (1, 8). All *nar1* mutants have normal xanthine dehydrogenase activity. All *nar1* mutants are viable and morphologically normal except some alleles are slightly light green. Yields are slightly depressed (6). The mutant Xno29 (*nar1.j*) does not grow well in field plots probably due to other associated mutations (1).

Origin of mutant:
A sodium azide induced mutant in Steptoe (Clho 15229) (4).

Mutational events:
nar1.a (Az12, GSHO 2413), *nar1.b* (Az13, GSHO 2414), *nar1.c* (Az23), *nar1.d* (Az28), *nar1.e* (Az29), *nar1.f* (Az30), *nar1.g* (Az31), *nar1.h* (Az32), *nar1.i* (Az33) in Steptoe (5); *nar1.j* (Xno29) in Winer (7); *nar1.k* (EMS29), *nar1.l* (EMS31) in Steptoe (5); *nar1.m* (Az56), *nar1.n* (Az57), *nar1.p* (Az63), *nar1.q* (Az64), *nar1.r* (Az65), *nar1.t* (Az67), *nar1.ab* (Az76), *nar1.ac* (Az77), *nar1.ai* (Az79), *nar1.aj* (Az80) in Steptoe (5); *nar1.ao* (BSMV1) in Vantage (Clho 7324) (1).

Mutant used for description and seed stocks:
nar1.a (Az12) in Steptoe (GSHO 2413).

References:
1. Kleinhofs, A. (Unpublished).
2. Kleinhofs, A., S. Chao, and P.J. Sharp. 1988. Mapping of nitrate reductase genes in barley and wheat. p. 541-546. *In* T.E. Miller and R.M.D. Koebner (eds.) Seventh Int. Wheat Genetics Symposium.
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. *Theor. Appl. Genet.* 86:705-712.
4. Kleinhofs, A., T. Kuo, and R.L. Warner. 1980. Characterization of nitrate reductase-deficient barley mutants. *Molec. Gen. Genet.* 177:421-425.
5. Kleinhofs, A., R.L. Warner, J.M. Lawrence, J.M. Melzer, J.M. Jeter, and D.A. Kudrna. 1989. Molecular genetics of nitrate reductase in barley. p. 197-211. *In* J.L. Wray and J.R. Kinghorn (eds.) *Molecular and Genetic Aspects of Nitrate Assimilation*, Chapter 13. *Proc. 2nd Int. Symp. on Nitrate Assimilation - Molecular and Genetic Aspects*, St. Andrews, July, 1987. Oxford Univ. Press, New York.

6. Oh, J.Y., R.L. Warner, and A. Kleinhofs. 1980. Effects of nitrate reductase deficiency upon growth, yield, and protein in barley. *Crop Sci.*20:487-490.
7. Tokarev, B.I., and V.K. Shumny. 1977. Detection of barley mutants with low level of nitrate reductase activity after seed treatment with ethylmethane sulphonate. *Genetika (Moskva)* 13:2097-2103.
8. Warner, R.L., C.J. Lin, and A. Kleinhofs. 1977. Nitrate reductase-deficient mutants in barley. *Nature* 269:406-407.

Prepared:

A. Kleinhofs. 2005. *BGN* 35:194-195.

BGS 638, NADH nitrate reductase-deficient 2, *nar2*

Stock number: BGS 638
Locus name: NADH nitrate reductase-deficient 2 (molybdenum cofactor)
Locus symbol: *nar2*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Location in chromosome 5HL [7L] in Bin 5H-06, near molecular marker ABC324 (2).
Morphological marker data placed *nar2* about 8.4 cM proximal from the *nld1* (narrow leafed dwarf 1) locus, about 23.0 cM distal from the *mtt2* (mottled leaf 2) locus (5).

Description:
The *nar2* mutants are characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity due to defective molybdenum cofactor synthesis or insertion (4). Some alleles are viable (*nar2.a2*), but they have a definite light green color and loss of vigor (3). The *nar2.ad* and *nar2.ag* homozygotes are not viable, and they must be maintained as heterozygotes (1).

Origin of mutant:
A sodium azide induced mutant in Steptoe (CIho 15229) (4).

Mutational events:
nar2.a2 (Az34, GSHO 2415) in Steptoe (4); *nar2.ad* (R9401), *nar2.ag* (R9201) in Maris Mink (PI 467824) (1).

Mutant used for description and seed stocks:
nar2.a2 in Steptoe (GSHO 2415).

References:
1. Bright, S.W.J. P.B. Norbury, J. Franklin, D.W. Kirk, and J.L. Wray. 1983. A conditional lethal *cnx*-type nitrate reductase-deficient barley mutant. *Mol. Gen. Genet.* 189:240-244.
2. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. *BGN* 27:105-112.
3. Kleinhofs, A. (Unpublished).
4. Kleinhofs, A., T. Kuo, and R.L. Warner. 1980. Characterization of nitrate reductase-deficient barley mutants. *Molec. Gen. Genet.* 177:421-425.
5. Melzer, J.M., A. Kleinhofs, D.A. Kudrna, R.L. Warner, and T.K. Blake. 1988. Genetic mapping of barley nitrate reductase-deficient *nar1* and *nar2* loci. *Theor. Appl. Genet.* 75:767-771.

Prepared:
A. Kleinhofs. 2005. *BGN* 35:196.

BGS 639, NADH nitrate reductase-deficient 3, *nar3*

Stock number: BGS 639
Locus name: NADH nitrate reductase-deficient 3 (molybdenum cofactor)
Locus symbol: *nar3*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Location in chromosome 7HS [1S] in Bin 7H-05, near molecular marker MWG836 (1).

Description:
The *nar3* mutants are characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity due to defective molybdenum cofactor synthesis or insertion (3). The *nar3* mutants are lethal and must be maintained as heterozygotes (2).

Origin of mutant:
An ethyl methanesulphonate induced mutant in Winer (4).

Mutational events:
nar3.a3 (Xno18) in Winer (3); *nar3.b2* (Xno19) in Winer (4); *nar3.x* (Az71) in Steptoe (Clho 15229) (2).

Mutant used for description and seed stocks:
nar3.x in Steptoe.

References:
1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. BGN 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., R.L. Warner, J.M. Lawrence, J.M. Melzer, J.M. Jeter, and D.A. Kudrna. 1989. Molecular genetics of nitrate reductase in barley. p. 197-211. In J.L. Wray and J.R. Kinghorn (eds.) Molecular and Genetic Aspects of Nitrate Assimilation, Chapter 13. Proc. 2nd Int. Symp. on Nitrate Assimilation - Molecular and Genetic Aspects, St. Andrews, July, 1987. Oxford Univ. Press, New York.
4. Tokarev, B.I., and V.K. Shumny. 1977. Detection of barley mutants with low level of nitrate reductase activity after seed treatment with ethylmethane sulphonate. Genetika (Moskva) 13:2097-2103.

Prepared:
A. Kleinhofs. 2005. BGN 35:197.

BGS 640, NADH nitrate reductase-deficient 4, *nar4*

Stock number: BGS 640
Locus name: NADH nitrate reductase-deficient 4 (molybdenum cofactor)
Locus symbol: *nar4*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Location in chromosome 2HL in Bin 2H-13, co-segregating with *Gln2* (glutamine synthetase 2) (1).

Description:
The *nar4* mutant is characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity (3). It is lethal under field conditions, but can be grown to maturity in the greenhouse with a reduced nitrogen source (2).

Origin of mutant:
A sodium azide induced mutant in Steptoe (Clho 15229) (2).

Mutational events:
nar4.y (Az72) in Steptoe (2).

Mutant used for description and seed stocks:
nar4.y in Steptoe.

References:
1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. BGN 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. Theor. Appl. Genet. 86:705-712.

Prepared:
A. Kleinhofs. 2005. BGN 35:198.

BGS 641, NADH nitrate reductase-deficient 5, *nar5*

Stock number: BGS 641
Locus name: NADH nitrate reductase-deficient 5 (molybdenum cofactor)
Locus symbol: *nar5*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Location in chromosome 5HL [7L] in Bin 5H-06, near molecular marker ABC324 (1).

Description:
The *nar5* mutants are characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity (3). All alleles are somewhat light green and viable as homozygotes (1).

Origin of mutant:
A sodium azide induced mutant in Steptoe (Clho 15229) (2).

Mutational events:
nar5.o (Az62), *nar5.s* (Az66), *nar5.u* (Az68, GSHO 2417) in Steptoe (2).

Mutant used for description and seed stocks:
nar5.o in Steptoe.

References:
1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. BGN 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. Theor. Appl. Genet. 86:705-712.

Prepared:
A. Kleinhofs. 2005. BGN 35:199.

BGS 642, NADH nitrate reductase-deficient 6, *nar6*

Stock number: BGS 642
Locus name: NADH nitrate reductase-deficient 6 (molybdenum cofactor)
Locus symbol: *nar6*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Location in chromosome 2HL in Bin 2H-13, co-segregating with *nar4* and *Gln2* (glutamine synthetase 2) (1).

Description:
The *nar6* mutant is characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity (3). Homozygotes are not viable and the *nar6* gene must be maintained as a heterozygote (2).

Origin of mutant:
A sodium azide induced mutant in Steptoe (Clho 15229) (2).

Mutational events:
nar6.v (Az69) in Steptoe (2).

Mutant used for description and seed stocks:
nar6.v in Steptoe.

References:
1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. BGN 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. Theor. Appl. Genet. 86:705-712.

Prepared:
A. Kleinhofs. 2005. BGN 35:200.

BGS 643, NADH nitrate reductase-deficient 7, *nar7*

Stock number: BGS 643
Locus name: NADH nitrate reductase-deficient 7 [NAD(P)H nitrate reductase-deficient EC1.6.6.2, Acc. No. X60173]
Locus symbol: *nar7*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Location in chromosome 6HL in Bin 6H-09, approximately 4.2 cM proximal from the *Amy1* (alpha-amylase 1) locus (2, 3).

Description:
The *nar7* mutant lacks root NAD(P)H-bispecific nitrate reductase activity (4). All other reductase associated activities, xanthine dehydrogenase and nitrate reductase are normal. The mutant is viable and appears morphologically normal in all respects (1). The *nar7.w* mutant was selected for very low nitrate reductase activity in a *nar1.a* stock. The double mutant was crossed to Steptoe and the two mutants were separated by enzyme analysis of the progeny (1).

Origin of mutant:
A sodium azide induced mutant in Steptoe (Clho 15229) mutant *nar1.a* (Az12) (3, 4).

Mutational events:
nar7.w (Az70, GSHO 2418) in Steptoe (3).

Mutant used for description and seed stocks:
nar7.w in Steptoe (GSHO 1418).

References:
1. Kleinhofs, A. (Unpublished).
2. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. Theor. Appl. Genet. 86:705-712.
3. Warner, R.L., D.A. Kudrna, and A. Kleinhofs. 1995. Association of the NAD(P)H-bispecific nitrate reductase structural gene with the *Nar7* locus in barley. Genome 38:743-746.
4. Warner, R.L., K.R. Narayanan, and A. Kleinhofs. 1987. Inheritance and expression of NAD(P)H nitrate reductase in barley. Theor. Appl. Genet. 74:714-717.

Prepared:
A. Kleinhofs. 2005. BGN 35:201.

BGS 644, NADH nitrate reductase-deficient 8, *nar8*

Stock number: BGS 644
Locus name: NADH nitrate reductase-deficient 8 (molybdenum cofactor))
Locus symbol: *nar8*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Location in chromosome 6HS in Bin 6H-01, close to molecular marker ABG378 (1).

Description:
The *nar8* mutant is characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity (3). The homozygote is not viable and mutant must be maintained as a heterozygote (2).

Origin of mutant:
A sodium azide induced mutant in Steptoe (Clho 15229) (2).

Mutational events:
nar8.z (Az73) in Steptoe (2).

Mutant used for description and seed stocks:
nar8.z in Steptoe.

References:
1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. BGN 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. Theor. Appl. Genet. 86:705-712.

Prepared:
A. Kleinhofs. 2005. BGN 35:202.

BGS 645, Bushy spike 1, *bsp1*

Stock number: BGS 645
Locus name: Bushy spike 1
Locus symbol: *bsp1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive, homozygotes do not produce anthers or ovaries (1).

Location is unknown.

Description:

The mutant appears normal except for a very bushy spike caused by many awn-like structures. Spikelets lack reproductive tissue and are completely sterile. The mutant must be maintained as a heterozygote (1).

Origin of mutant:

A fast neutron induced mutant in Morex (Clho 15773).

Mutational events:

bsp1.a in Morex (FN346) (1).

Mutant used for description and seed stocks:

bsp1.a in Morex (FN346).

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2005. BGN 35:203.

BGS 646, Ovaryless 2, *ov/2*

Stock number: BGS 646
Locus name: Ovaryless 2
Locus symbol: *ov/2*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1).
Location is unknown.

Description:
Mutant plants appear normal except carpels are rudimentary and female sterile. Plant development appears normal. Anther development is normal and pollen is viable (1).
The *ov/1.a* (BGS 176, GSHO 610) mutant was not available for allelism tests.

Origin of mutant:
A fast neutron induced mutant in Harrington (1).

Mutational events:
ov/2.b in Harrington (FN347) (1).

Mutant used for description and seed stocks:
ov/2.b in Harrington (FN347).

References:
1. Kleinhofs, A. (Unpublished).

Prepared:
A. Kleinhofs. 2005. BGN 35:204.

BGS 647, Tip sterile 1, *tst1*

Stock number: BGS 647
Locus name: Tip sterile 1
Locus symbol: *tst1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1, 2).
Location is unknown.

Description:
Mutant plants and spikes appear normal except there is no seed set in the tip of the spike (2). In the Bowman backcross-derived line, seed set is 40 to 60% with no fertile spikelets at the terminal 4 to 6 nodes of the rachis. The *tst1* mutant differs from *lin1* (BGS 99) and *tst2* (BGS 636) plants because *lin1* is not associated with tip sterility and *tst2* produces more sterility and reduces height and vigor (1).

Origin of mutant:
A fast neutron induced mutant in Steptoe (Clho 15229) (2).

Mutational events:
tst1.c (FN43) in Steptoe (2).

Mutant used for description and seed stocks:
tst1.c in Steptoe; *tst1.c* in Bowman (PI 483237)*4.

References:
1. Franckowiak, J.D. (Unpublished).
2. Kleinhofs, A. (Unpublished).

Prepared:
A. Kleinhofs and J.D. Franckowiak. 2005. BGN 35:205.

BGS 648, Multiovary 4, *mov4*

Stock number: BGS 648
Locus name: Multiovary 4
Locus symbol: *mov4*

Previous nomenclature and gene symbolization:

Multiovary 8 = *mo8* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

The mutant spikelet has two carpels, two anthers, and two lodicules. One of the anthers appears to have been converted to a carpel; however, this conversion does not occur in all spikelets. Spikelets with two carpels often set two seeds. Mutant plants are often difficult to identify (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (Clho 15229) (1).

Mutational events:

mov4.k (FN315, *mo8*) in Steptoe (1).

Mutant used for description and seed stocks:

mov4.k in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2005. BGN 35:206.

BGS 649, Aborted spike 1, *asp1*

Stock number: BGS 649
Locus name: Aborted spike 1
Locus symbol: *asp1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1).
Location is unknown.

Description:
Mutant plants appear normal except the spike is rudimentary or missing. A few spikelets are formed occasionally, but they are mostly sterile. The stock must be maintained as a heterozygote (1).

Origin of mutant:
A fast neutron induced mutant in Steptoe (Clho 15229) (1).

Mutational events:
asp1.a (FN222) in Steptoe (1).

Mutant used for description and seed stocks:
asp1.a in Steptoe.

References:
1. Kleinhofs, A. (Unpublished).

Prepared:
A. Kleinhofs. 2005. BGN 35:207.

BGS 650, Sensitivity to *Ustilago nuda* 1, *sun1*

Stock number: BGS 650
Locus name: Sensitivity to *Ustilago nuda* 1
Locus symbol: *sun1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1).
Location is unknown.

Description:
Mutant plants appear extremely susceptible to loose smut, *Ustilago nuda* (Jensen) Rostr. Spikes become entirely smutted under field conditions at Pullman, WA, USA where loose smut is rare and confined to one or a few florets (1).

Origin of mutant:
A fast neutron induced mutant in Steptoe (Clho 15229) (1).

Mutational events:
sun1.a (FN395) in Steptoe (1).

Mutant used for description and seed stocks:
sun1.a in Steptoe.

References:
1. Kleinhofs, A. (Unpublished).

Prepared:
A. Kleinhofs. 2005. BGN 35:208.

BGS 651, Late maturity 1, *lam1*

Stock number: BGS 651
Locus name: Late maturity 1
Locus symbol: *lam1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1).
Location is unknown.

Description:
Mutant plants have a very prostrate growth habit and heading is delayed to very late in the season, and sometimes they do not head. During juvenile stages before the reproductive phase is induced, plants have very narrow, long leaf blades. Leaves produced during the reproductive phase have wide, short leaf blades (1). The cultivar Steptoe in which the mutant was induced has a winter growth pattern. Several other late heading mutants in Steptoe have been isolated following treatment with mutagenic agents, but allelism test have not been completed. The mutants and their temporary gene symbols are: *lam.b* = FN197, *lam.c* = FN208, *lam.d* = FN209, *lam.e* = FN212, and *lam.f* = FN229 in cv. Steptoe (1).

Origin of mutant:
A fast neutron induced mutant in Steptoe (Clho 15229) (1).

Mutational events:
lam1.a (FN2) in Steptoe (1).

Mutant used for description and seed stocks:
lam1.a in Steptoe.

References:
1. Kleinhofs, A. (Unpublished).

Prepared:
A. Kleinhofs. 2005. BGN 35:209.

BGS 652, Yellow leaf 1, *y1f1*

Stock number: BGS 652
Locus name: Yellow leaf 1
Locus symbol: *y1f1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1).
Location is unknown.

Description:
Mutant plants show a gradual yellowing or loss of chlorophyll starting in the margins of leaf blades. Dying or necrosis of the leaf blade or its margins is not observed. The leaves gradually become a yellowish or golden in color with midrib region remaining green. Expression of *y1f1* gene is variable and is dependent on light intensity, temperature, moisture stress, and the age of the leaf blade. Mutant expression is often better under low light conditions in the greenhouse. High temperatures can induce yellowing of the leaf blade margins in seedlings; however, yellowing is often not expressed until after heading (1). The Bowman backcross-derived line with the *y1f1* gene can have slightly smaller kernels and lower grain yields than normal Bowman (1).

Origin of mutant:
An X-ray induced mutant in Villa (PI 399506) (2).

Mutational events:
y1f1.a (6002) in Villa (1, 2).

Mutant used for description and seed stocks:
y1f1.a in Villa; *y1f1.a* in Bowman (PI 483237)*8.

References:
1. Franckowiak, J.D. (Unpublished).
2. Gaul, H. (Personal communications).

Prepared:
J.D. Franckowiak. 2005. BGN 35:210.