Carlsberg Res. Commun. Vol. 52, p. 123–196, 1987

BARLEY : GENES AND CHROMOSOMES

by

BODIL SØGAARD[1] and PENNY von WETTSTEIN-KNOWLES[1,2]

[1] Department of Physiology, Carlsberg Laboratory
Gamle Carlsberg Vej 10, DK-2500 Copenhagen Valby

[2] Institute of Genetics, University of Copenhagen
Øster Farimagsgade 2A, DK-1353 Copenhagen K

Keywords: cDNA, chloroplast DNA, chloroplast map, chromosome map, genomic DNA, Giemsa C-bands, translocations

The information on barley genes and chromosomes assembled consists of:

INTRODUCTION TO TABLES AND FIGURES

In this compilation a gene is equated with a complementation (functional) group whose alternate forms are called alleles. At present this definition causes a problem only with respect to *cer-cqu*, a gene with seven complementation groups. The leftmost column contains the basic gene symbol plus a locus (gene) designation if more than one phenotypically similar complementation group has been identified. For clarity in Tables I and II, the symbol is separated from its locus designation by a space or dash although as shown in the figures and text the space is omitted in practice. Where a series of phenotypically distinguishable alleles exist, such as *K*, K^c and *k*, or where a consensus of opinion as to which allele should be regarded as the wild type has not been reached, for example *Sh* vs. *sh*, we have listed the two or more symbols in the first column separating them with a slashed line. The information in the subsequent columns is presented in an analogous fashion.

For many genes the basic symbol has changed with the passage of time or different symbols have been assigned to what has turned out to be the same complementation groups. The present table indubitably contains many additional, as yet unidentified, cases of the latter phenomenon. Whenever known, synonyms are presented in the second column. If the alternate symbols are in common use, the data we have assembled is presented under each one. For genes whose symbols either fail to conform to present day conventions or where none was assigned, an appropriate one has been intro-

0105-1938/87/0052/0123/$14.80

duced after consulting the pertinent individuals. In such cases all data is presented under the new designation. Symbols for chloroplast genes are those used in other plants. If alternatives existed, that from the plant most closely related to barley was chosen.

Until recently the existence of a gene was established only after an allele giving rise to a modified phenotype was identified. The figures in the column headed alleles in Table I represent the best estimate we can make of the number of such altered alleles of a gene. They are specified primarily for genes which form part of large mutant collections induced in one or several very closely related backgrounds. For many genes, especially those determining isoenzymes, we do not feel it is of any value to give an allele number, but have inserted a dash which represents one or more. Fourteen isoenzyme genes as well as the rDNA genes for which we have been unable to locate any mention of genetic variation in the literature have been localized to chromosomes, and are therefore included in Table I where they can be recognized by the presence of an * in the allele column. Such genes cannot be mapped by classic methods. Should their amino acid sequence or antibodies become available, however, they are theoretically isolatable and characterizable at the DNA level. In this connection it should be noted that no genetic variation is known for *Ale*, one of the first four isolated nuclear genes in barley (Table II, part B). Presumably many more similar situations will be encountered in the coming years.

In contrast to previous summaries of barley genetic literature (e.g. references 273, 308, 309, 310, 347, 395 and BGN 14:140), the chromosomal location of a gene is given in column 5 of Table I only when the assignment appears definitive. Arm designations have been excluded as the terminology has changed frequently and the genetic location of the centromeres is still more speculative than not. In Table III the letters p and q have been used to designate the arm above and below the cytologically placed centromere as diagrammed in Figures 8 and 10. While the same orientation of the chromosomes is used in the genetic maps of Figures 1 to 7, the arms remain unlabelled.

One of the five original purposes of the master list of barley genes (BGN 12:133) was to enable individuals to rapidly "determine the availability of seed stocks". In continued pursuit of this goal, the column headed stock source contains this information in code form and applies to the allele(s) specified in the rightmost column. Names and addresses corresponding to each symbol are given at the end of Table I. Sources for chloroplast DNA clones and translocation stocks are given in the text to Figure 8 and the heading to Table III, respectively. Questions concerning availability of genomic and cDNA clones should be directed to the specified authority.

Two types of literature citations have been used in the text and in the column headed authority(ies) of the tables: Firstly, numbers which refer to papers given in the literature list of this report. Secondly, references to articles in the Barley Genetics Newsletter which are specified as BGN volume number (1-15, 1971-1985, respectively): first page of article. We have been fortunate to receive preprints for a number of articles submitted for the much delayed BGN 16. These are all listed as BGN 16:--.

Under the authority(ies) column in Table I we have tried to include references to the genes' identification, symbol changes and mapping as well as to those detailing observations on its morphological, physiological and biochemical effects. Roughly speaking as the number of the later type of articles increases for a given gene, a decreasing proportion of them have been listed. Our goal has been to include not only studies reporting, what we believe are, the most significant results, but also those encompassing the full range of techniques and levels that have been exploited in trying to understand a gene's expression. References given in Table I are not reiterated when that gene occurs in Table II. Inclusion of similar references for the genes itemized only in Table II is a task for the future.

Table II presents the names of the plasmids containing the cloned genes. For those from the chloroplast in part A, the approximate length of the cloned fragment in kb is given. Whether or not the gene has been sequenced is detailed in the text of Figure 8. For the sequenced nuclear genes in part B, the bases sequenced upstream (-) and downstream (+) from the start codon are specified. For the cDNAs in part C, the best possible estimate of the number of bases has been made, and it has been noted whether they have been sequenced.

Figures 1-7 are a potpourri disclosing the state of chromosome map construction in barley today. We have not attempted to do any building ourselves, but have only assembled those results of others' endeavors which we deem reveal useful information in their existing state. Firstly, maps of chromosomes or segments thereof are presented which have been derived by a statistical treatment of available linkage data to give a best estimate of gene order and distances. The maps have been modified to make clear that the correctness of such summations is dependent upon the quality of the raw data used. Secondly, results from three- and multi-point crosses involving genes and/or C-bands are schematized. Only rarely has data from a 2-point cross been embraced and when so is noted in the figure texts. Finally, the preliminary fine structure maps are included for three of the four loci *(li, Reg6 (ml-o), wx* and *cer-cqu)* for which such an exercise has been undertaken. When more than one symbol is in use for a given gene both are listed side-by-side with the one farthest from the map being enclosed in brackets. Two different genes apparently located at the same position are separated by a comma.

Table I. Barley Genes.

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
A	Sh 2	spring habit of growth				
A	K,Lk 2	long awn or hooded				
a/A	r/R	smooth/rough awn				
a	kl,lk	short awn				
a	–	albino seedling	–	2		273,349
a 1	kl	short awn				
a 2	kl 2	short awn				
a 2	a 1	albino seedling	–	2	B53	273,349,BGN 1:113, 10:105
a 3	a 2,alb-za	albino seedling	3	–	C	273,349,BGN 12:93
a 4	a 3	albino seedling	–	2		273,349
a 5	a 4	albino seedling	–	2		273,349
a_b	cm	albino (cream) seedling	–	7		273,349
a_c	–	albino seedling	–	3	C,B106	273,368,378, BGN 1:128
a_c2	alb-m	albino seedling	2	1	C,B4	273,294,350,BGN 1:107,5:90,12:93, 13:26
a_c3	–	albino seedling	–	–		273,349
a_h	–	albino seedling	–	–		273,349
al	li	absence of ligules and auricles				
al	ebu	albino lemma (eburatum)	4	3	F,B108	118,273,368,378, BGN1:130,2:28,3:67, 10:111,12:42
a_n	–	albino seedling	–	3	C,B112	273,294,368,378, BGN 1:134
a_t	–	albino seedling	–	5	B207	149,273,BGN 1:152
a_t2	–	albino seedling	–	–		273,349
a_t3	alb^t	albino seedling	–	–		273,349
Aat 2	Got 1, Got-H2	aspartate aminotransferase	*	6		130

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
Aat 3	Got 2, Got 1	aspartate aminotransferase	–	3		46,49,187,271
abr 1	–	accordian basal rachis internodes	3	2		222,223,BGN 11:25
Aco 1	Fpd 1	aconitate hydratase	–	6	R	49,270,271, BGN 12:68,13:59
Aco 2	–	aconitate hydratase	–	–		49
Acp 1	Acph 1	acid phosphatase	–	–		50
Acp 2	Acph 2, Acph-H1	acid phosphatase	–	4		50,74,271,291
Acp 3	Acph 3, AcPh 1	acid phosphatase	–	6		49,50,187,270,271
Acp 4	–	acid phosphatase	–	–		271
Acph-H1	Acp 2	acid phosphatase				
AcPh 1	Acp 3	acid phosphatase				
Acph 1	Acp 1	acid phosphatase				
Acph 2	Acp 2	acid phosphatase				
Acph 3	Acp 3	acid phosphatase				
acr	ril	accordian rachis (lax rachis internode)	–	–		82,133,195,273
act	–	cold temperature albino	–	–		273,420
Adh 1	Adh 2, Adh-H1	alcohol dehydrogenase	–	4		47,50,74,130, BGN 10:26
Adh 2	Adh 1	alcohol dehydrogenase	–	4		47,50,74, BGN 10:26
Adh 3	–	alcohol dehydrogenase	–	6		129,131, BGN 14:28
Adh-H1	Adh 1	alcohol dehydrogenase				
adp	–	awned palea	–	–		BGN 7:8
aec 1	R906	resistance to S(2-aminoethyl) cysteine	2	–		41,44, BGN 13:37
ag	–	agropyroides (calcaroides)	–	6		195,273,416
alb	as	albostrians (white stripe)	–	–		36,78,125,273
alb^{t}	a$_{t}$3	albostrians				
alb-a	–	albino seedling	2	–	C	402,BGN 3:113
alb-b	–	albino seedling	4	–	C	402,BGN 3:113
alb-c	y,y$_{x}$	albino seedling	3	2	C	143,273,349, BGN 3:113,12:93
alb-d	–	albino seedling	–	–	C	BGN 3:113
alb-e	–	albino seedling	–	–	C	30,114,143, BGN 3:113
alb-f	–	albino seedling	–	–	C	30,143,278,BGN 3:113
alb-g	–	albino seedling	–	–	C	BGN 3:113
alb-h	–	albino seedling	–	–	C	BGN 3:113
alb-i	–	albino seedling	–	–	C	BGN 3:113
alb-j	–	albino seedling	–	–	C	BGN 3:113
alb-k	–	albino seedling	–	–	C	BGN 3:113
alb-m	a$_{c}$2	albino seedling	2	1	C	BGN 3:113
alb-n	–	albino seedling	–	–	C	BGN 3:113
alb-o	–	albino seedling	–	–	C	BGN 3:113
alb-p	–	albino seedling	–	–	C	BGN 3:113
alb, ,p	–	albino seedling	15	2		BGN 6:53,9:78

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
alb-q	–	albino seedling	–	–	C	BGN 3:113
alb, ,q	–	albino seedling	–	6		BGN 6:53
alb-r	–	albino seedling	–	–	C	BGN 3:113
alb-s	–	albino seedling	–	–	C	BGN 3:113
alb-t	–	albino seedling	–	–	C	BGN 3:113
alb, ,t	–	albino seedling	–	6		BGN 6:8,10:13
alb-u	–	albino seedling	–	–	C	BGN 3:113
alb-v	–	albino seedling	–	–	C	BGN 3:113
alb-x	–	albino seedling	–	–	C	BGN 3:113
alb-y	–	albino seedling	–	–	C	BGN 3:113
alb-z	–	albino seedling	–	–	C	BGN 3:113
alb-za	a 3	albino seedling	2	–	C	BGN 3:113
alb-zb	–	albino seedling	–	–	C	BGN 3:113
alb-zc	–	albino seedling	–	–	C	BGN 3:113
alb-zd	–	albino seedling	–	–	C	BGN 3:113
alb-ze	–	albino seedling	–	3	C	BGN 3:113
alp	–	aluminum toxicity	–	–		306a
als	–	absent lower laterals	–	3	F,B101	190,191,195, BGN 1:123,13:25
Ami	–	gramine synthesis (tryptophan to aminomethyl indole)	1	–		230
amo 1	–	high amylase	–	3		BGN 8:112,9:7
Amp	Amp 1	aminopeptidase				
Amp-A	–	aminopeptidase	2	1		BGN 8:31
Amp-C	–	aminopeptidase	2	–		BGN 8:31
Amp 1	Amp, Lap, Amp-H1	aminopeptidase	*	6		49,130
Amp-H1	Amp 1	aminopeptidase				
Amy 1	αAmy 1, Amy1Bi, Amy1Ke, αAmy^{c}, αAmy^{c1},	alpha amylase	–	6	R,B259	48,270,271, BGN 4:53,6:133
Amy 2	αAmy 2	alpha amylase	–	1		48,167
Ang	–	angustifolia	–	–		BGN 6:95
ant 1	rub-a	anthocyanin less (exrubrum)	4	1	C,S	118,241,284,BGN 8:57,14:76
ant 2	pr	anthocyanin less	30	2	C,S	95,BGN 8:57,14:76
ant 3	–	decreased in anthocyanin	3	–	C,S	4,BGN 8:57
ant 4	–	decreased in anthocyanin	10	–	C,S	BGN 8:57,14:76
ant 5	rs_2	anthocyanin less	4	–	C,S	95,BGN 8:57,14:76
ant 6	–	decreased in anthocyanin	2	–	C	BGN 8:57
ant 7	–	decreased in anthocyanin	–	–	C	BGN 8:57
ant 8	–	decreased in anthocyanin	–	–	C,S	BGN 8:57
ant 9	–	decreased in anthocyanin	–	–	C,S	BGN 8:57
ant 10	–	decreased in anthocyanin	–	–	C,S	BGN 8:57
ant 11	–	decreased in anthocyanin	–	–	C,S	BGN 8:57
ant 12	–	decreased in anthocyanin	–	–	C,S	BGN 8:57
ant 13	–	proanthocyanidin,catechin and anthocyanin less	112	6	C,S	4,173,174,403,BGN 8:57,14:76,15:27
ant 14	–	decreased in anthocyanin	–	–	C,S	BGN 8:57

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
ant 15	–	decreased in anthocyanin	1	–	C,S	BGN 14:76
ant 16	–	decreased in anthocyanin	1	–	C,S	BGN 14:76
ant 17	–	flavanone-3-hydroxylase	146	3	C	4,173,174,175, 176,BGN 14:76, 15:27
ant 18	–	dihydroquercitin reductase (proanthocyanidin,catechin and anthocyaninless)	110	–	C	4,173,174,175,176, 212,BGN 14:76
ant 19	–	leucocyanidin reductase	1	–	C	4,173,175,176,212, 213,BGN 14:76
ant 20	rub	anthocyanin rich	2	–	C	176,BGN 14:76
ant 21	–	proanthocyanidin,catechin and anthocyanin less	8	–	C	173,174,BGN 14:76
ant 22	–	flavanone-3-hydroxylase	5	–	C	173,175,BGN 14:76
ant 23	–	decreased in anthocyanin	1	–	C,S	BGN 14:76
ant 24	–	decreased in anthocyanin	1	–	C,S	BGN 14:76
ant 25	–	proanthocyanidin and catechin less; decreased in anthocyanin	6	–	C	174
ari-a	lk 7	breviaristatum (short awn)	18	3	S	118,215,284,285, BGN 4:80
ari-b	–	breviaristatum	8	–	S	118,215
ari-c	lk 5	breviaristatum	26	4	S	118,215,285,BGN 4:80, 10:119,14:61
ari-d	lk 8	breviaristatum	22	1	S	118,215,284,285, BGN 3:99,4:80
ari-e	lk 9	breviaristatum	4	7	S	118,284,285, BGN 3:99,4:80
ari-f	–	breviaristatum	16	–	S	118,215
ari-g	lk 10	breviaristatum	9	–	S	118,215,BGN 4:80
ari-h	lk 11	breviaristatum	1	–	S	118,215,BGN 4:80
ari-i	br	breviaristatum (brachytic)	1	–	S	118,215, BGN 4:80,14:33
ari-j	–	breviaristatum	2	–	S	118,215
ari-k	–	dearistatum (dehiscent)	4	–	S	118,215,284
ari-l	–	breviaristatum	6	–	S	215
ari-m	–	breviaristatum	5	–	S	215
ari-n	–	breviaristatum	11	–	S	215
ari-o	–	breviaristatum	2	–	S	215
ari-p	–	breviaristatum	5	–	S	215
ari-q	–	breviaristatum	3	–	S	215
ari-r	–	breviaristatum	3	–	S	215
as	alb	albino stripe				
aur-a	li	exauriculum (auricleless)	5	–	S	118,284
B	I^h	fertile intermedium				359,BGN 4:8
B_1		high protein and lysine	–	–		
$B/B^{mb}/$ B^g/b	Bk///bk	black/medium black/grey/ white lemma and pericarp	–	5	B203/ B204/ B205/ B206/	67,76,137,264, 273,349,400, BGN 1:148,1:149, 1:150,1:151
b	bt	non brittle rachis				
Bam 1	Bmy 1	beta amylase				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
bb	–	broad leaf (brodbladig)	–	7		273,395,396
Bb 2	Brl,Nlh	broad leaf	–	–		170,273,295
bb 3	wlh	broad leaf	–	–		273,295
bc	–	resistance to barban	–	–		136a,308
be	Nb	branched ear (rachis)	–	–		273,349
be 2	Nb 1	branched ear (rachis)	–	–		273,349
Bg	G	brown-yellow lemma	–	–		273,309
bh	–	bushy head (multiflorus)	–	–		273
bi	Ib	long basal rachis internode				
bir	s^i	branching, inflorescent rachilla	–	7		BGN 11:25,13:82
Bl/bl	Bl_1/bl_1, blx	blue/white aleurone (xenia)	–	4	/B15	95,128,137,163, 236,273,294,411, 420,BGN 2:109,5:11, 6:26,8:163,14:61
Bl_2/bl_2	Bl_1/bl_1	blue/white aleurone	–	1	/B19	74,95,400,BGN 5:100, 6:26,8:164
Bl_3/bl_3	bly	blue/white aleurone	–	4		95,BGN 8:165
Bl_4/bl_4	–	blue/pink aleurone	–	4		95,BGN 8:166
Bl_5/bl_5	–	blue/white aleurone	–	1		95,333, BGN 8:167
Bmy 1	Bam 1	β-amylase	2	4	R	27,111,184,239,271, 291,BGN 12:68, 13:55,14:61
Br 1	Bb 2	broad leaf				
br 1	br, ari-i	brachytic dwarf (breviaristatum)	3	1	B1	76,137,273,294,304, 367,BGN 1:104,4:80, 10:100,13:27
br 2	–	brachytic dwarf	2	4	B157	374,BGN 1:143, 10:115,14:61
bra-a	–	bracteatum	–	–	S	118
bra-b	–	bracteatum	–	–	S	118
bra-c	trd	bracteatum (third outer glume)	–	–	S	118
Bt/bt	–	brittle/non-brittle rachis from Mars	–	–		273
Bt/bt	/b,r	brittle/non-brittle rachis from Colsess IV	–	3	/B115	273,369, BGN 2:181
Bt 2/bt 2	√b,r	brittle/non-brittle rachis from Russian 82	–	3	/B116	273,369, BGN 2:182
Bt 3/bt 3	–	brittle/non-brittle rachis	–	–		273,349
C	Re	purple lemma, palea and pericarp				
C	Sh 3	spring habit of growth				
C_1	P_c	purple veined lemma	–	–		422,BGN 5:108
C_1	Clt	colored leaf tip				
C_2	Clt_2	colored leaf tip				
cal-a	–	calcaroides (hooded)	–	–	S	118,284
cal-b	–	calcaroides (hooded)	–	–	S	118
Cat 1	–	catalase	–	4		31,50
cat 2	Cat 2, Cat 3, RPr 79/4	catalase	–	6		194,280,348, BGN 15:7

Gene locus	Synonyms	Character			Alleles	Chromosome	Stock source	Authority(ies)
		eceriferum (surface wax)						
		ear	stem	leaf				
cer-a	gs 3	–	–	++	62	1	S	242,243,405,406, BGN 1:41,2:79,3:67, 4:9
cer-b	–	–	–	++	39	7	S,B398	242,243,BGN 4:9, 5:116
cer-c	cer-cqu	–	+/-	++	204	4	S	242,243,250,343, 351,404, 405,407, 408,429,BGN 3:57, 4:9
cer-cq	cer-cqu	–	–	++	1	4	S	351,407,408,BGN 5:88
cer-cqu	–	–	–	++	6	4	S	243,351,404,407,408, BGN 1:97,5:88
cer-cu	cer-cqu	–	–	++	4	4	S	243,351,404,407,408, BGN 1:97,5:88,7:92
cer-d	–	+	++	++	14		S,B399	242,243,BGN 5:117
cer-e	–	–	++	++	44	5	S,B400	93,242,243,405,406, BGN 5:118
cer-f	–	+	+	++	5	1	S,B401	242,243,BGN 1:41,4:9, 5:119
cer-g	–	+	+	++	41	2	S,B402	93,242,243,428,429, BGN 4:9,5:120
cer-h	–	–	++	++	6	–	S,B403	242,243,BGN 5:121
cer-i	–	–	++	++	68	7	S,B404	93,242,243,404,405, BGN 5:122
cer-j	gl 3,gl 4	++	++	–	69	4	S	93,108,242,243,351, 404,425,BGN 4:31
cer-k	–	+	++	++	1	–	S,B405	242,BGN 5:123
cer-l	–	+	++	++	1	–	S,B406	242,BGN 5:124
cer-m	–	+	+	++	1	–	S,B407	242,BGN 5:125
cer-n	cer-zm	–	+	++	56	2	S,B408	93,242,243,245,406, 429,BGN 4:9,5:126, 12:169
cer-o	–	–	++	++	5	–	S,B409	242,BGN 5:127
cer-p	–	++	++	+	37	–	S,B410	108,242,243,343, BGN 5:128
cer-q	gs,gs 1, cer-cqu	–	–	++	157	4	S	242,243,250,351,404, 405,407,408,BGN 3:57, 4:9
cer-qu	cer-cqu	–	–	++	2	4	S	243,351,407,408, BGN 1:97,3:110,5:88, 7:92
cer-r	–	–	+	++	9	3	S,B411	93,242,243,BGN 5:129
cer-s	gs 5	+	–	++	19	2	S	93,242,243,343, BGN 4:9
cer-t	–	+	++	++	50	7	S,B412	93,242,243,405, BGN 5:130
cer-u	cer-cqu	+	+	++	148	4	S,B413	242,243,250,351,404, 405,407,408,BGN 3:57, 4:9,5:131
cer-v	–	+/-	++	++	6	2	S,B414	242,BGN 1:41,5:132

Gene locus	Synonyms	Character			Alleles	Chromosome	Stock source	Authority(ies)
cer-w	–	+	++	++	19	7	S	242,243,BGN 3:57, 5:133
cer-x	–	++	++	–	34	7	S	93,243,405,406, BGN 5:134
cer-xa	–	++	++	+	3	–	S	BGN 15:89
cer-xb	–	–	++	++	2	–	S	241
cer-xc	–	+	+	++	2	–	S	241
cer-xd	–	+	+	++	2	–	S	241
cer-y	–	+	+/++	++	3	–	S,B417	243,BGN 4:9,5:135
cer-ya	–	++	++	–	1	–	S	BGN 3:110,5:162
cer-yb	–	++	++	–	5	–	S	BGN 3:110,5:163
cer-yc	–	–	++	++	5	–	S	406,BGN 3:110,5:164
cer-yd	–	–	++	++	1	–	S	BGN 3:110,5:165
cer-ye	–	++	++	–	5	–	S	BGN 3:110,5:166
cer-yf	–	++	++	+	2	–	S	BGN 3:110,5:167
cer-yg	–	–	–	–	1	–	S	BGN 3:110,5:168
cer-yh	–	–	++	++	2	–	S	BGN 3:110,5:169
cer-yi	–	++	++	–	4	–	S	BGN 7:92
cer-yj	–	++	++	–	5	–	S	BGN 7:92
cer-yk	–	+	+	++	1	–	S	BGN 7:92
cer-yl	–	–	–	++	4	–	S	406,BGN 7:92
cer-ym	–	–	–	–	2	–	S	BGN 7:92
cer-yn	–	+	+	++	1	–	S	BGN 7:92
cer-yo	–	++	++	–	1	–	S	BGN 9:135
cer-yp	–	++	++	+	2	–	S	BGN 9:135
cer-yq	–	++	++	–	1	–	S	BGN 12:169
cer-yr	–	+	+	++	2	–	S	BGN 12:169
cer-ys	–	++	++	–	5	–	S	BGN 12:169
cer-yt	–	–	++	++	11	–	S	BGN 12:169
cer-yu	–	++	++	–	7	–	S	BGN 15:89
cer-yx	–	+	+	++	4	–	S	BGN 15:89
Cer-yy	–	–	++	++	18	–	S	244,BGN 12:169
cer-yz	–	+	+	++	2	–	S	BGN 15:89
cer-z	–	–	–	++	9	–	S,B418	243,BGN 5:136
cer-za	–	++	++	–	78	–	S,B419	243,429,BGN 5:137
cer-zb	–	-	++	++	6	–	S,B420	243,429,BGN 5:138
cer-zc	–	+/-	++	++	16	–	S,B421	243,429,BGN 5:139
cer-zd	–	++	++	–	7	3	S,B422	93,243,425,429, BGN 5:140
cer-ze	–	++	++	–	73	–	S,B423	243,425,429,BGN 5:141
cer-zf	–	++	++	+	1	–	S,B424	243,429,BGN 5:142
cer-zg	–	++	++	+	2	4	S,B425	243,429,BGN 3:57, 5:143,14:61
cer-zh	gl, gl 2	++	++	–	11	4	S,B426	243,BGN 1:101,3:57, 5:144
cer-zi	–	+	+	++	18	5	S,B427	243,429,BGN 3:57, 4:9,5:145
cer-zj	–	++	++	–	57	7	S,B428	93,243,425,429, BGN 5:146
cer-zk	–	+	+	+/-	17	–	S,B429	243,425,BGN 5:147
cer-zl	–	–	–	++	3	–	S,B430	243,425,BGN 5:148

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
cer-zm	cer-n	– +/++ ++				
cer-zn	–	+/- ++ ++	6	3	S,B431	243,425,BGN 1:41, 5:149
cer-zo	–	– ++ ++	5	–	S,B432	243,425,BGN 5:150
cer-zp	–	++ ++ –	7	7	S,B433	243,425,BGN 1:41, 5:151
cer-zq	–	++ ++ –	4	–	S	243,425,BGN 5:152
cer-zr	–	+ ++ ++	2	–	S	243,425,BGN 5:153
cer-zs	–	+ ++ ++	4	–	S	BGN 7:92,5:154
cer-zt	–	+ ++ ++	2	–	S	BGN 1:97,5:155
cer-zu	–	– + ++	11	–	S	BGN 9:135,3:110, 5:156
cer-zv	–	– – –	4	–	S	BGN 9:135,5:157
cer-zw	–	+ + ++	1	–	S	343,BGN 3:110,5:158
cer-zx	–	+ + ++	1	–	S	BGN 3:110,5:159
cer-zy	–	++ ++ +	2	–	S	BGN 3:110,5:160
cer-zz	–	++ ++ –	1	–	S	BGN 3:110,5:161
cer-soh	cer-$^{\text{soh}}$	secondary alcohols in awn wax	–	–	C	BGN 9:75
Ch-a	–	chlorotic hybrids	–	–		372,BGN 6:71
Ch-e	–	chlorotic hybrids	–	4		372,BGN 6:71
C 1	K	hooded				
cl	–	curly lateral	–	7		273,396
clh	–	curly leaf dwarf	–	5		293a,308,BGN 7:89
clo-fc	f c	chlorina seedling	2	1	C, B2	273,349,341 BGN 1:105,3:71,13:27, 10:101
clo-f2	f 2	chlorina seedling	14	3	C, B117	18,30,144,246,341, 388,BGN 2:183,3:71, 5:56
clo-f7	f 7	chlorina seedling	2	5	C, B201	341,BGN 1:146,3:71, 10:120,14:9
clo-f8	f 8	chlorina seedling	1	1	C, B5	341,BGN 1:108,3:71, 6:10,10:102,13:28, 14:53,14:81
cls 1	–	concentric leaf spot	–	–		BGN 3:7
cls 2	–	concentric leaf spot	–	–		BGN 3:7
Clt	C_1	colored leaf tip	–	7		135,370
Clt_2	C_2, Pr	colored leaf tip	–	2		135,370,BGN 1:51
cm	a_b	cream seedling	–	7	B305	207,273,BGN 1:164
cm 2	c	cream seedling	–	5		273,274
Cma 1	CMa	CM-protein A (A hordein)	1	1		29,318,318a
Cmb 1	CMb	CM-protein B (A hordein)	2	4		29,318,318a
Cmc 1	CMc	CM-protein C (A hordein)	1	1		29,318,331
Cmd 1	CMd	CM-protein D (A hordein)	*	4		318,318a,331
Cme 1	CMe	CM-protein E (A hordein)	2	3		140,226,318
CMa	Cma 1	CM-protein A (A hordein)				
CMb	Cmb 1	CM-protein B (A hordein)				
CMc	Cmc 1	CM-protein C (A hordein)				
CMd	Cmd 1	CM-protein D (A hordein)				
CMe	Cme 1	CM-protein E (A hordein)				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
com 1	s^{l},bir	compositum	1	7		222,223,BGN 11:25, 13:82
cr	–	curved peduncle	–	–		273,349
cs	–	corn stalk	–	7		82,273
cu	–	curly	–	6	G395	273,310
cu 2	–	curly	–	3	B114	203,371,BGN 1:136, 4:82
cu 3	–	curly	–	6		136,BGN 8:50
cu 4	spn	curly	–	–		BGN 14:51,14:97
cud	–	curly dwarf	–	7		136,BGN 5:56,10:47
cud 2	–	curly dwarf	–	5		136
D	–	dwarf (sterile)	–	2		273,349
D	I_1	intermedium				
d	x	xantha seedling	–	–		273,396
D_1	–	dense spike	–	–		BGN 9:111
D_2	–	dense spike	–	–		BGN 9:111
De	L 7	lax spike				
da	lku	dehiscent awn	–	2		76,273,391
da 2	–	dehiscent awn	–	–		273,349
dct	RPr 79/2	dicarboxylate transport	3	–		327,393,BGN 15:7
ddt	–	resistance to DDT	–	7		273,415, BGN 14:95,14:96
des 1	lc	desynapsis	–	1	B12	273,349,BGN 2:65, 3:124
des 2	ds	desynapsis	–	3	B119	82,83,191,273, BGN 2:65,3:125
des 3	–	desynapsis	–	–	B386	BGN 3:126,6:116
des 4	–	desynapsis	–	1	B13	BGN 3:127,6:116
des 5	–	desynapsis	–	1	B14	BGN 3:128
des 6	–	desynapsis	–	5	B215	BGN 3:129
des 7	–	desynapsis	–	2	B64	BGN 3:130
des 8	–	desynapsis	–	–	B387	BGN 3:131
des 9	–	desynapsis	–	–	B388	BGN 4:137
des 10	–	desynapsis	–	–	B389	BGN 4:138
des 11	–	desynapsis	–	–	B390	BGN 4:139
des 12	–	desynapsis	–	–	B391	BGN 4:140
des 13	–	desynapsis	–	–	B392	BGN 4:141
des 14	–	desynapsis	–	–	B393	BGN 4:142
des 15	–	desynapsis	–	–	B394	BGN 5:113
dex 1	sex 2	defective endosperm, xenia	–	7		BGN 6:60,6:134, 8:109,8:114,11:30, 11:104,13:67
dex 2	–	defective endosperm, xenia	–	–		BGN 11:105,13:118
dex 3	–	defective endosperm, xenia	2	–		BGN 11:106,13:119
dex 4	–	defective endosperm, xenia	–	–		BGN 11:107,13:120
Dip	amy	high diastatic power	–	–		71,273
Dip 1	Pept 1	dipeptidase	–	6		49,50
Dip 2	Pept 2	dipeptidase	–	–		50
dn	m 3	many noded dwarf 3	–	3		273,396
ds	des 2	desynaptic chromosomes				
dsk	–	dusky	–	7		136,BGN 2:75,13:42
Dt	–	dented leaf margin	–	7		171

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
dw-1	–	light green dwarf	–	3		BGN 14:35
dwf	–	vegetative dwarf	–	–		BGN 12:69,12:106,13:121
E	Ea	early maturity				
E	Pe	purple veined lemma				
e	l	lax spike				
e	lep-e,w,ex,log	elongated outer glume awn (macrolepis)	–	2	B57	118,142,228,273,275,275b,349,383,BGN 2:28,4:76,4:82,5:101,14:140,16:—
e 2	gh	fine-awned glume	–	1		76,273
EA	Est 1	esterase				
EB	Est 2	esterase				
EC	Est 4	esterase				
ED	Est 5	esterase				
EE	Est 6	esterase				
EF	Est 7	esterase				
EG	Est 8	esterase				
Ea	E,X,Y,z,Ea 6	early maturity	–	–		76,103,273,310,420
Ea 2	–	early maturity	–	4		273,349
ea 4	–	early maturity	–	–		220,273,309
Ea 6	Ea	early maturity	–	–		310,420
Ea 5	Ea 3	early maturity	–	7		170,273
ea 7	Ea 5,ec	early heading	–	6	B252	28,273,BGN 1:155
ea-a	ea_k,mat-a	early maturity (praematurum)				
ea-b	mat-b	early maturity				
ea-c	mat-c	early maturity				
ea-d	mat-d	early maturity				
ea_c	ea, ,c	early maturity	–	4		427,BGN 8:127,10:74
ea_k	ea-a,mat-a	early heading (light insensitive)	–	5	S,B214	385,426,BGN 2:198,8:125,13:94
eb	–	eburatum	7	–		28,317
ebu	al	eburatum (albino lemma)	3	–	S	118,BGN 3:67,10:111
ec	ea 7	early maturity	–	6		273,296
Edp-A	–	endopeptidase	2	–		BGN 8:31
eh	–	erect early growth habit	–	–		170,273
en-min	–	enhancer for minute (min)	–	–	B160	273,375,376 BGN 2:185
en-Bl, ,b	ibl	enhancer of blue and pink aleurone color	–	–		95,BGN 6:26
Enp	Enp 1	endopeptidase				
Enp 1	Enp, En-H1	endopeptidase	*	1		130
En-H1	Enp 1	endopeptidase				
er	–	erectum base on grain	–	–		273,349
Er_1^a	Reg 1	reaction to Erysiphe graminis hordei				
ER_{cp}	Reg 2	reaction to Erysiphe graminis hordei				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
er	reg 6	reaction to Erysiphe graminis hordei				
er 2	–	erectum base on grain	–	–		273,349
ert-a	–	erectoides (dense spike)	42	1	S	121,231a,241,284, 285,286,350,360, 401
ert-b	–	erectoides	10	5	S	65,241,273,284,286, 360
ert-c	–	erectoides	40	3	S	65,121,231a,241,273, 284,286,360
ert-d	–	erectoides	27	1	S	65,121,241,273,284, 286,350,360,401
ert-e	–	erectoides	6	–	S	273,284,286,360
ert-f	–	erectoides	3	–	S	286
ert-g	–	erectoides	10	7	S	65,231a,273,284,285, 286,360
ert-h	–	erectoides	2	–	S	273,286
ert-i	–	erectoides	3	4	S	273,284,285,286
ert-ii	–	erectoides	1	3	S	65,273,284,285,286
ert-j	–	erectoides	3	–	S	241,273,286
ert-k	–	erectoides	8	–	S	241,273,286
ert-l	–	erectoides	10	–	S	241,273,286
ert-m	–	erectoides	20	1	S	65,273,284,285,286, 336,350,360
ert-n	–	erectoides	9	7	S	65,241,273,284,285, 286,360
ert-o	–	erectoides	1	–	S	273,286,360
ert-p	–	erectoides	6	–	S	241,273,286
ert-q	–	erectoides	3	–	S	241,273,286
ert-r	–	erectoides	4	–	S	65,241,273,286,360
ert-s	–	erectoides	1	–	S	273,286
ert-t	–	erectoides	2	–	S	241,273,286
ert-u	–	erectoides	1	–	S	273,286,360
ert-v	–	erectoides	2	–	S	273,286
ert-x	–	erectoides	1	–	S	273,286
ert-y	–	erectoides	1	–	S	273,286
ert-z	–	erectoides	1	–	S	273,286
ert-za	–	erectoides	2	–	S	241,BGN 6:80
ert-zb	–	erectoides	1	–	S	BGN 6:80
ert-zc	–	erectoides	2	–	S	241
ert-zd	–	erectoides	1	–	S	241
ert-ze	–	erectoides	1	–	S	241
Est 1	EA, Est 4	esterase	–	3	R	162,185,186,269a, 271,BGN 1:35,6:45, 14:28,15:16
Est 2	EB, Est 3	esterase	–	3	R	162,185,186,269a, 271,BGN 1:35,14:28
Est 3	–	esterase	–	1	R	46,162,270,271, BGN 12:68
Est 4	EC, Est 3	esterase	–	3	R	162,185,186,271, BGN 14:28,15:16

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
Est 5	ED, Est 4	esterase	–	1	R	162,185,186,271, BGN 12:68, 14:28
Est 6	EE	esterase	–	–		162,185
Est 7	EF	esterase	–	–		162,185
Est 8	EG	esterase	–	–		162,185
Est 9	–	esterase	–	7	R	162,270,271
Est 10	–	esterase	–	3	R	46,162,271
etw	M-737	endosperm thin walls	1	–	C	2,3
ex	e	elongated outer glume awn				
f	lg, lg 8, lg 10	chlorina seedling (viridis)	4	2	C	273,294,BGN 3:71, 4:79 10:106
F	P_f	purple veined lemma				
f c	clo-fc,f_c	chlorina seedling				
f 2	clo-f2	chlorina seedling				
f 3	–	chlorina seedling	1	5	C, B220	341,349,BGN 3:71, 8:89,9:132,14:9
f 4	yv	chlorina seedling	1	1	C, B17	341,396,BGN 3:71, 5:98,6:10,10:103
f 5	z,yv 2	chlorina seedling	1	1	C, B18	341,396,BGN 3:71, 5:99
f 6	yv	chlorina seedling	1	7	C, B313	172,341,390,BGN 3:71,3:91,7:89, 13:50,13:111,14:52
f 7	clo-f7	chlorina seedling				
f 8	clo-f8	chlorina seedling				
f 9	F_k	chlorina seedling	1	4	C, B151	341,374,BGN 1:137, 3:71,14:61
f 10	–	chlorina seedling	1	4		136,341,BGN 5:56, 14:93
f 11	pg	chlorina seedling	1	6	G357	341,BGN 9:17,9:133
F_k	f 9	chlorina				
F_o	–	flower opening (anther extrusion)	–	–		58a
fb	sc	reaction to Fusarium blight (scab)	–	–		273,310,349
fer	–	few roots	2	–	R	BGN 8:162,7:43
fgs	glu S	ferredoxin-dependent glutamate synthase	3	–		193,327,BGN 15:7
fl	–	funnel-shaped lemma	–	–	O	334,335
fla-a	fla-b	flavum (yellow spike)	1	–	S	118,BGN 5:64
fla-b	–	flavum (yellow spike)	1	–	S	118
flo-a	–	extra floret	1	4	S	118,241,284,BGN 6:28
flo-b	–	extra floret	1	7	S	118,241,284
flo-c	–	extra floret	1	2	S	118,241,284
fls	msg	floral sensitivity (sterility)	–	–		273,310
fol-a	–	angustifolium (narrow leaf; stunted grossy habit)	1	2	W20	97,134,BGN 6:28
Fpd 1	Aco 1	fructose phosphate dehydrogenase				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
fs	–	fragile stem	–	7	B301	273,297,383, BGN 1:160,13:42
fs 2	–	fragile stem	–	5	B208	191,273,396, BGN 1:153,2:192, 10:122,14:10
fs 3	–	fragile stem	–	1		BGN 15:47
G	–	teeth on lemma	–	2	B69	273,309,410 BGN 5:109,8:161
G	Bg	brown (gray) yellow lemma				
G 2	–	teeth on lemma	–	–		273,349
ga	–	gametophyte factor	–	1		273,364,365
gal	GA-less	gibberellin (GA_3)-less	–	–		90
gai	GA-ins	gibberellin (GA_3)-(insensitive)	–	2		155 90
Gdh 1	Gdh	glutamate dehydrogenase	–	5		31,49,78
Ge	wh	glaucous ear (white,waxy)	–	–		163,273
Gh	–	long glume hairs	–	–		204,273
gh	e 2	fine-awned glume				
gig	sf	gigas (vine; sterile female)	–	–	S	90,132,197, BGN 5:64,15:67
gl	wl,gl 2, cer-zh	glossy seedling (leaf) (waxless, eceriferum)	4	4	F,S, B155	76,163,243,273 347,411,420, BGN 2:79, 4:13,4:31, 10:114,14:61
gl 2	gl	glossy seedling (leaf)				
gl 3	gl 4, cer-j	glossy seedling (leaf) (eceriferum)	2	4	C, B165	374 BGN 1:55,3:66,4:13, 4:31,5:56,10:74, 10:117,14:61
gl 4	gl 3	glossy leaf				
gl 5	–	glossy leaf	–	1		136,BGN 8:48
Gle-1	–	glossy spike	–	5		BGN 12:13
gln	–	chloroplast glutamine synthetase	6	–		394
glo-a	–	globosum (globe shaped grain)	1	4	W10, B168	134,BGN 6:28,8:152, 10:30
glo-b	–	globosum (globe shaped grain)	5	7	W1-5	97,134,BGN 6:28, 10:30
glo-c	–	globosum (globe shaped grain)	1	2	W9	134,BGN 6:28,10:30
glo-d	–	globosum (globe shaped grain)	3	2	W6-8,S	97,BGN 10:30
glo-e	–	globosum (globe shaped grain)	1	5	W11,S	BGN 10:30
glo-f	–	globosum (globe shaped grain)	2	7	W12-13, S	97
glx	wx	high amylopectin endosperm (waxy endosperm)				
Got 1	Aat 2, Aat 3	glutamate oxaloacetate transaminase				
Got 2	Aat 3	glutamate oxaloacetate transaminase				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
Got-H2	Aat 2	glutamate oxaloacetate transaminase				
gp	gp 2	grandpa	3	2	C,B59	76,163,273,335,336, BGN 1:62,1:119, 10:107
Gpd 1	Gpd-H1	glucose-6-phosphate dehydrogenase	*	2		291
Gpd-H1	Gpd 1	glucose-6-phosphate dehydrogenase				
Gpi 1	Pgi-H1, Pgi	glucosephosphate isomerase	–	5		49,50,271,291
Gpi 2	–	glucosephosphate isomerase				46
Gr	–	growth factors	–	3		273,349
Gr 2	–	high yield (growth factor)	–	7		85,273,310
gra	gran-a	granum (small kernel, heavy tillering)	–	3	W19	97,134,BGN 6:28
Grb	Rsg 1	reaction to Schizaphis graminum Rondani				
Grb 2	Rsg 2	reaction to Schizaphis graminum Rondani				
Grb 3	Rsg 3	reaction to Schizaphis graminum Rondani				
Grt_S	–	growth retardation	–	–		BGN 10:20
Grt_T	–	growth retardation	–	–		BGN 10:20
gs 1	gs,cer-q	glossy sheath/spike (eceriferum)	14	4	C,S, B351	12,13,137,273,411, BGN 1:31,1:168, 3:28,4:9
gs 2	–	glossy sheath/spike (eceriferum)	5	3	C,B352	203,273,BGN 1:31 1:69,3:28,4:9
gs 3	vs 3,cer-a	glossy sheath/spike (eceriferum)	4	1	C,B353	273,396,397, BGN 1:31,1:169,3:28, 4:9, 13:27
gs 4	wh 1,wh 2	glossy sheath/spike (waxless head)	1	6	C,B354	273,349,BGN 1:31, 1:170,3:28,4:9
gs 5	gs 6,gs 7, gs 8	glossy sheath/spike	16	2	C,B355	374,BGN 1:31,1:51, 1:171,3:28
gs 6	gs 5	glossy sheath/spike			C,B356	371, BGN 1:31,1:172, 3:28
gs 7	gs 5	glossy sheath/spike				
gs 8	gs 5	glossy sheath/spike				
gs 9	–	glossy sheath and ear	–	2		136
H/h	U/u	high (tall)/short culm	–	2		12,165,217,273,420, BGN 5:102
H 2	–	high (tall)	–	7		273,349
H 4	–	high (tall)	–	4		310,410
H_l	–	high (tall), modifying factor	–	–		273,349
Ha	Ha 2	reaction to Heterodera avenae races 1 and 2				
Ha 1	Rha 1	reaction to Heterodera avenae race 1				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
Ha 2	Ha,Rha 2	reaction to Heterodera avenae races 1 and 2				
hap	–	haploid initiator	–	–	S	123,124,252, BGN 15:61
hex-v	v	hexastichon (six-row)	41	2	S	118,119,241,343
hf	–	hairy furrow of palea	–	–		57,273
Hg	Rhg 1	reaction to Helminthosporium gramineum (leaf stripe)	–	–		273,349,BGN 2:145
Hg 2	Rhg 2	reaction to Helminthosporium gramineum (leaf stripe)	–	–		273,349,BGN 2:145
Hg 3	Rhg 3	reaction to Helminthosporium gramineum (leaf stripe)	–	–		273,349,BGN 2:145
hl	–	reaction to Helminthosporium sativum (spot blotch)	–	2		273,349
hl 2	–	reaction to Helminthosporium sativum (spot blotch)	–	5		273,349
hl 3	–	reaction to Helminthosporium sativum (spot blotch)	–	7		273,349
hl 4	–	reaction to Helminthosporium sativum (spot blotch)	–	–		20,273
Hn	–	hairs on lemma nerves	–	4	B164	273,367,BGN 2:189
Hor 1	Hrd A, Pr-a	C hordeins	–	5		33,34,53,54,74,111, 209,271,292,329, 330,332,352,353, 392,BGN 11:43, 11:74,15:48,15:51,
Hor 2	Hrd B Risø 56	B hordeins	–	5		33,34,53,54,73,74, 111,209,210,226,271, 292,328,329,330, 352,353,392,BGN 11:43,11:74,13:35, 15:48,15:51
Hor 3	–	D hordeins	–	5		34,209,225,330, BGN 11:74,15:48
Hr	Pbr	hairy rachis	–	2		273,400
Hr 2	Pbr 2	hairy rachis	–	7		273,400
Hr 3	Pbr 3	hairy rachis	–	–		273,349
Hrd C	–	hordein	–	5		353
Hrd D	–	hordein	–	5		353
Hrd E	–	hordein	–	5		353
Hrd F	–	hordein	–	5		33,BGN 12:13, 13:35,15:51
Hrd G	–	hordein	–	5		BGN 14:4
Hs	–	hairy leaf sheath	–	4	F, B158	57,273,282,371, BGN 2:184,14:61, 16:--
Hyp 1	–	proline accumulating	3	–		216,BGN 13:37
I	R 2	rough awn				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
$I/I^h/i$	W,B, int-c	infertile intermedium/ fertile intermedium/ deficiens	–	4		191,273,420, BGN 7:34,9:106, 14:61
I^e	In^e	inhibitor of awns in e/e genotypes				
I_I	D	intermedium	–	4		12,273
ibl	en-Bl, ,b	intense blue aleurone layer				
Ica 1	–	inhibitor of chymotrypsin and Aspergillus protease (CI-1,SP-I)	*	5		27,140,184,BGN 13:53
Ica 2	–	inhibitor of chymotrypsin and Aspergillus protease (CI-2,SP-II)	*	5		27,140,184,303, BGN 13:53
Idh 1	–	isocitrate dehydrogenase	–	–		49
Idh 2	–	isocitrate dehydrogenase	–	2		49
In^e	I^e	inhibitor of awns in e/e genotypes	–	2		142,308
Inc	–	partial incompability with H. bulbosum	–	7		287,BGN 13:114
int-a	int-g, int-a´	intermedium spike	31	5	S	118,119,240,241,284, BGN 14:9
int-b	–	intermedium spike	3	–	S	118,119,240,241
int-c	I^h	intermedium spike	23	4	S	118,119,240,241,284, 285,BGN 7:34
int-d	–	intermedium spike	20	–	S	118,119,240,241
int-e	–	intermedium spike	14	3	S	118,119,240,241,284
int-f	–	intermedium spike	1	–	S	118,119,240
int-g	int-a	intermedium spike				
int-h	–	intermedium spike	4	–	S	119,240,241
int-i	–	intermedium spike	1	–	S	119,240
int-k	–	intermedium spike	1	–	S	240
int-l	–	intermedium spike	1	–	S	241
int-m	–	intermedium spike	1	–	S	241
Isa 1	–	inhibitor of subtilisin and α-amylase (BASI, ASI)	*	2	R	140,362,BGN 13:53
Itc 1	CMe	inhibitor of trypsin and chymotrypsin (TI-1)	–	3	R	140,226,270,276, BGN 13:53,15:16
j	–	inhibitor of red pericarp color	–	–		273,349
j 2	j 1	inhibitor of red pericarp color	–	–		273,349
JMl_g	Reg 2	reaction to Erysiphe graminis hordei				
JMl_h	Reg 3	reaction to Erysiphe graminis hordei				
JMl_k	Reg 4	reaction to Erysiphe graminis hordei				
JMl_p	Reg 5	reaction to Erysiphe graminis hordei				
JMl_r	Ml-at	reaction to Erysiphe graminis hordei				
JMl_{nn}	Ml-nn	reaction to Erysiphe graminis hordei				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
JMl$_{sn}$	Reg 1	reaction to Erysiphe graminis hordei				
K/K^{e}/k	A,C 1//	hooded/elevated hooded/ awned lemma	–	4	B152/ B153/ B154	12,228,236,237,273, 294,304,356,383,411, 420,421,423 BGN 1:138,1:139, 1:140,14:61
K 2	–	hooded (second factor)	–	–		12,273,420,BGN 1:139
k$_{r}$	–	hooded (calcaroides)	–	–		273,396
kl	a,v,al	short awned	–	1		273,349
kl 2	Kl 1,a 2	short awned	–	–		273,349
kw	–	heavy kernels (several factors)	–	–		25,266,267,273
l	log	long outer glume				
L/l	E/e, L 8/l 8	lax (long)/dense spike	–	1	B8/B9	76,273,366,383,420, BGN 2:173,2:174
L 2	L 1	lax spike	–	1		273,349
L 3	L 2	lax spike	–	7		25,273,309
L 4	L 3	lax spike	–	–		273,349
L 5	L 4	lax spike	–	2		273,349
L 6	L 5	lax spike	–	–		273,349
L 7	De	lax spike	–	1		273,396
L 8	L	lax spike	–	–		310,420
L$_{a}$	–	lax spike	–	1		273,349
L$_{c}$/l$_{c}$	–	lax/dense spike	–	3	B110/ B111	273,294,309, BGN 1:132,1:133, 13:91
L$_{d}$	–	lax spike	–	–		273,309
l 9	la	dense spike	–	6	F	BGN 3:31,6:132,8:71
lab	–	labile (lateral spikelets completely reduced to partly developed and fertile)	–	–		71a,275
Lap	Amp	aminopeptidase				
lax-a	–	laxatum (lax spike); five anthers	14	7	S	118,222,223,284,285, BGN 2:28
lax-b	–	laxatum (lax spike); xenia; shrunken endosperm	1	6	S	222,223
lax-c	–	laxatum (lax spike)	1	6	S	222,223
Lb/lb	Bi/bi, /rac-a, /rac-b	short/long basal rachis internode (rachisextensum)	–	7	B307/ B308	273,309,BGN 1:166, 1:167,4:82
lb 2	–	long weak basal rachis internode 2	–	4	B156	190,191,273, BGN 1:142,14:61
lb 3	–	long weak basal rachis internode 3	–	1		191,273
lb 3^{m}	–	moderately long weak rachis basal internode	–	1		190,191,273
lc	des 1	long chromosome (desynapsis)				
Ldh 1	–	lactate dehydrogenase	1	–		152,153
Ldh 2	–	lactate dehydrogenase	1	–		152,153
lep-a	lep-e	macrolepis				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
lep-e	lep-a, e,log	macrolepis (elongated or wide outer glume awn)	54	2	S	118,241,273,275,275b,284,BGN 4:82,14:40,16:--
let	–	pollen lethal	–	7		123,272,BGN 8:46,9:57,15:61
Lfb	–	leafy bract (bracteatum)	–	7		273,396
Lfl	–	leafless	–			BGN 5:67
lg	f, lg 8, lg 10	light green seedling	–	2		191,273,294,BGN 3:17,4:79,10:106
lg 2	lg 3	light green	–	4	B169	206,273,349,BGN 8:153,14:61
lg 3	lg 7	light green	–	4	B170	273,BGN 3:17,8:154
lg 4	lg 9	light green	2	4	B171	136,BGN 3:17,5:56 8:155,14:61
lg 5	–	light green	2	4		BGN 3:17
lg 7	lg 3	light green				
lg 8	lg 10,f,lg	light green				
lg 9	lg 4	light green				
lg 10	lg 8,f,lg	light green				
lgr	–	long shaped grain	–	–		BGN 12:4
li	al, aur-a	ligule and auricle less (exauriculum)	7	2	B60	202,273,294,324,383,420,BGN 1:120,3:67,10:36,10:39
lin	s,rin	lesser internode number	–	2	B57	BGN 14:91
lig-a	–	eligulum (liguleless)	4	–	S	118
lk	lk$_2$	short awn				
Lk 2/lk 2	A/a Lk/lk Lk$_4$/lk$_4$	long/short (fine) awn	9	1	B8/B9	273,349,383,BGN 2:175,2:176,3:119,13:28,14:59
lk 3	lk 2	short awn	–	–		273,349
lk 4	lk 3	short awn	–	–		273,349
lk 5	ari-c, lk 4	short awn (breviaristatum)	3	4	B172	236,273,BGN 8:156,10:119,14:20,14:61,15:22
lk 6	lk 5	short awn	–	4		236,276
lk 7	ari-a	short awn				
lk 8	ari-d	short awn				
lk 9	ari-e	short awn				
lk 10	ari-g	short awn				
lk 11	ari-h	short awn				
lku	da	dehiscent awn				
lnt	rnt	low number of tillers	–	3	B118	BGN 3:45,4:56,10:113
lo	–	small lodicule	–	–		273,308
log	e,l, lep-e	long outer glume	–	–		142,273,275b,349,BGN 4:5,4:76,14:140,16:--
log 2	–	long outer glume	–	–		273,349
lp	–	lethal seedling	–	–		273,349
lp 2	lp 1	lethal seedling	–	–		273,349
Lpx 1	–	lipoxygenase	–	4		131

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
lr	–	reduced lateral spikelet appendage on the lemma (awnless lateral floret)	–	2	B58	228,273,BGN 1:118
lr 2	lr 1	reduced lateral and central spikelet appendage on the lemma	–	–		236,273
ls	sh	light sensitive (spring habit of growth)				
Ltr 1	Lt 1	aspartate kinase II (resistance to lysine and threonine)	2	–		21,40,42,314, BGN 13:37
Ltr 2	Lt 2	aspartate kinase III (resistance to lysine and threonine)	2	–		21,40,314,327, BGN 13:37
lys	–	high lysine	1	7		1,27,184,189,226, 262,303,BGN 2:34, 2:54,9:33
lys 2	–	high lysine	1	1		84,BGN 9:33
lys 3	sex 3, Risø 1508, Risø 18, Risø 19	high lysine	3	7		1,53,54,156,180,209, 226,328,392,399, BGN 7:40,7:66,15:48 15:65,9:33
Lys 4	sex 5, Risø 8	high lysine	1	5		72,180,BGN 8:114, 9:33,11:45
lys 5	sex 1,sex 4, se 6 Risø 13, Risø 29, Risø 86	high lysine	4	6		72,180,BGN 9:33, 12:90
lys 6	Risø 527	high lysine	1	6		72,180,226, BGN 9:33
lzd	dw 4	dwarf	–	3		200,201,203 BGN 5:56,13:89
m	–	many noded dwarf	3	–		273,349
m 2	mnd	many noded dwarf 2	–	2	F	228,273
m 3	dn,mn 3	many noded dwarf 3	–	3		273,396
mat-a	ea$_k$,ea-a	praematurum (early maturity)	35	5	S	77,116,117,118,241, 284,385,BGN 2:198, 8:125
mat-b	ea-b	praematurum	36	–	S	77,116,117,118,241
mat-c	ea-c	praematurum	15	–	S	77,116,117,118,241
mat-d	ea-d	praematurum	2	–	S	117,118,241
mat-e	–	praematurum	7	–	S	118,241
mat-f	–	praematurum	4	–	S	118,241
mat-g	–	praematurum	3	–	S	118,241
mat-h	–	praematurum	2	–	S	118,241
mat-i	–	praematurum	4	–	S	118,241
Mdh 1	Mdh-H1	malate dehydrogenase	–	5		50,291
Mdh 2	–	malate dehydrogenase	–	3		49,50
Mdh-H1	–	malate dehydrogenase				
min	d	semi-minute (dwarf)	–	4	B161	273,375,376, BGN 2:186,14:61

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
Ml-a	Reg 1	reaction to Erysiphe graminis hordei				
Ml-at	JMl_r,Pm_7	reaction to Erysiphe graminis hordei (powdery mildew)	–	5	CI,J	149,258,273, BGN 14:173
Ml-b	Reg 1	reaction to Erysiphe graminis hordei				
Ml-(CP)	–	reaction to Erysiphe graminis hordei (powdery mildew)	–	4	R	413,BGN 14:173
ml-d	–	reaction to Erysiphe graminis hordei (powdery mildew)	–	5	CI	273,BGN 14:173
Ml-g	Reg 2	reaction to Erysiphe graminis hordei				
Ml-go	Reg 1	reaction to Erysiphe graminis hordei				
Ml-h	Reg 3	reaction to Erysiphe graminis hordei				
Ml-k	Reg 4	reaction to Erysiphe graminis hordei				
Ml-m	Reg 1	reaction to Erysiphe graminis hordei				
Ml-n	Pm 6	reaction to Erysiphe graminis hordei (powdery mildew)	–	5	CI,R	89,108,183,258, 273,BGN 14:173
Ml-nn	JMl_{nn}	reaction to Erysiphe graminis hordei (powdery mildew)	–	5	R	149,183
ml-o	reg 6	reaction to Erysiphe graminis hordei				
Ml-p	Reg 5	reaction to Erysiphe graminis hordei				
Ml-ra	Reg 7	reaction to Erysiphe graminis hordei				
Ml-(41/145)	Reg 7	reaction to Erysiphe graminis hordei				
Ml-(1063)	Reg 1	reaction to Erysiphe graminis hordei				
mlt	mul	multiflorous				
mn	–	many noded	5	–	0	338
mn 2	–	many noded	–	–	0	338
mnb	–	multi noded branched	–	–		BGN 15:10
mnd		multi noded dwarf	–	–		BGN 15:10
mo 1	mo 2,mo 3, mo 4,mo 5	multi-ovary	5	1		188a,253,273,BGN 10:69,12:18,12:86
ms 20	msg 20	male sterile				
ms 21	msg 21	male sterile				
msg	ms	male sterile	5	5	F	273,294,BGN 1:175, 13:9
msg 2	–	male sterile 2	2	2	F	273,349,BGN 1:175

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
msg 3	msg 10	male sterile (brachytic-like dwarf)	2	2	B359	190,191,273,BGN 1:176
msg 4	–	male sterile	–	–	F	273,310,BGN 1:177
msg 5	–	male sterile	2	3	F	273,310,BGN 1:178, 13:9,4:16
msg 6	–	male sterile	–	6	G370	86,273,310,BGN 1:189,10:137
msg 7	–	male sterile	2	–	F	273,310,BGN 1:179
msg 8	–	male sterile	–	6	F	101,273,310,BGN 1:180
msg 9	–	male sterile	–	–		273,310,BGN 1:181
msg 10	ms 3	male sterile	2	1	F	273,310,BGN 1:181
msg 11	ms 10, ms 12	male sterile	2	–		273,310,BGN 1:182
msg 12	ms 11, ms 10	male sterile	–	–		BGN 1:182
msg 13	–	male sterile	–	–		BGN 1:183
msg 14	–	male sterile	3	1		BGN 1:184
msg 15	–	male sterile	–	–		BGN 1:184
msg 16	–	male sterile	–	7		BGN 1:185
msg 17	–	male sterile	–	–		BGN 1:186
msg 18	–	male sterile	2	–		BGN 1:186
msg 19	–	male sterile	–	7	F	BGN 1:187
msg 20	ms 20	male sterile	–	5		BGN 1:188,12:107
msg 21	ms 21	male sterile	–	–		BGN 1:188,12:107
msg 22	–	male sterile	2	1	B383	BGN 2:178,3:121
msg 23	–	male sterile	3	1	B384	BGN 2:179,3:122
msg 24	–	male sterile	5	4	F, B385	BGN 2:191,3:123,13:9, 14:61
msg 25	–	male sterile	–	4	B166	BGN 4:135,5:112
msg 26	–	male sterile	–	–	B395	BGN 4:136,4:121, 5:170,10:138
msg 27	–	male sterile	–	2		101,BGN 9:124
msg 28	–	male sterile	–	–		BGN 9:124
msg 29	–	male sterile	–	6		101,BGN 9:124
msg 30	–	male sterile	–	–		BGN 9:124
msg 31	–	male sterile	–	–		BGN 9:124
msg 32	–	male sterile	–	–		BGN 9:124
msg 33	–	male sterile	–	–		BGN 13:70
msg 34	–	male sterile	–	6		101
msg, ,bk	–	male sterile	–	6		BGN 5:49
msm 1	–	male sterile maternal (cytoplasmic)	–	–	A	7,8,10
msm 2	–	male sterile maternal (cytoplasmic)	–	–	A	9,BGN 9:3,10:31, 12:86
mss	–	midseason stripe	–	2		273,396
mt	–	mottled leaves	–	2		191,273,396
mt 2	–	mottled leaves-2	–	7	B302	273,396,BGN 1:161
mt 3	–	mottled leaves-3	–	–		190,191,273
mt, ,e	–	mottled leaves	–	2		136
mt, ,f	–	mottled leaves	–	6		BGN 8:71
mu	–	multiploid sporocytes	–	–		273,349
mul	mlt	multiflorous	–	2		191,273,396
mul 2	mlt 2	multiflorous	–	6	B251	273,396,BGN 2:154, 8:61

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
N/n	H/h, S/s	covered (hulled)/naked (nudoides) caryopsis	–	1	/C, B6/B7	76,137,163,207,273, 294,383,BGN 1:109, 1:110,12:18,12:86
N182	–	resistance to Erysiphe graminis hordei (powdery mildew)	–	4		147,182,BGN 15:4
nar 1	Az, Chlo 29	NADH-nitrate reductase apoprotein	21	–	K	197,198,199,339,398, BGN 9:55
nar 2	R9401, Az	nitrate reductase and xanthine dehydrogenase deficient (molybdenum cofactor)	3	7	K	43,197,198,199,327, BGN 9:55
nar 3	Chlo 18, Chlo 19	nitrate reductase and xanthine dehydrogenase deficient (molybdenum cofactor)	2	–	K	198,339
nar 4	–	nitrate reductase and xanthine dehydrogenase deficient (molybdenum cofactor)	1	–	K	198
nar 5	–	nitrate reductase and xanthine dehydrogenase deficient (molybdenum cofactor)	3	–	K	198
nar 6	–	nitrate reductase and xanthine dehydrogenase deficient (molybdenum cofactor)	1	–	K	198
nar 7	–	NAD(P)H-nitrate reductase apoprotein	1	–	K	198
Nb	be	branched spike				
Nb 1	be 2	branched spike				
Nadhd 1	Ndh 1	NADH dehydrogenase				
Nadhd 2	Ndh 2	NADH dehydrogenase				
Ndh 1	Nadhd 1	NADH dehydrogenase	–	4		49,50,74,270,271
Ndh 2	Nadhd 2	NADH dehydrogenase	–	–		50
Ndh 3	–	NADH dehydrogenase	–	–		271
Ndh 4	–	NADH dehydrogenase	*	2		270,271
nec 1	sp, ,b	necrotic leaf	2	5	R,B222	91,179,BGN 3:25, 3:97,11:101
nec 2	–	necrotic leaf	–	6	R	179,BGN 11:102
nec 3	–	necrotic leaf	2	6	W14-15	97,134,BGN 6:28, 10:30
nec 4	–	necrotic leaf	2	3	W16-17	97,134,BGN 6:28, 10:30
nec 5	–	necrotic leaf	1	3	W18	97,134,BGN 6:28, 10:30
Nec-B$_1$	–	necrotic leaf	–	3		BGN 10:30
nld	–	narrow leafed dwarf	–	7		371,374,BGN 10:138, 13:42,14:52
Nlh	Bb 2	broad leaf				
nls	sid	nodeless dwarf				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
Nmt	–	gramine synthesis from (methyl)aminomethyl indole	1	–		230
No	–	high nitrogen content of caryopsis	–	–		70,273
notch 1	–	high lysine	1	–		26,328,BGN 2:21,3:10
notch 2	–	high lysine	1	–		26,328,BGN 2:21,3:10
Np	–	resistance to nonparasitic leaf spot	–	–		255,256,273
o	rob-o	orange lemma base and nodes (robiginosum)	–	6	C,B254	136,137,273,294, BGN 1:157,4:53, 8:48,8:61,8:71, 9:17,10:13,13:83
op	–	opposite spikelets	–	1		273,304,420
or	–	orange seedling	–	2	C	273,294,BGN 1:112, 10:104
ovl	–	ovaryless (male)	–	4	B176	BGN 6:95,10:118, 13:110
P	Re 2	purple lemma, palea and pericarp				
P	–	purple lemma	–	2		273,349
P 2	P 1	purple lemma	–	–		273,349
P 3	P 2	purple lemma	–	–		273,349
P_c	C_1	purple veined lemma	–	2	B68	135,273,349,BGN 5:108
P_e	E	purple veined lemma	–	–		135,273,349
P_f	F	purple veined lemma	–	–		135,273,349
Pa	C, Rph 1	reaction to Puccinia hordei				
Pa 2	Rph 1	reaction to Puccinia hordei				
Pa 3	A, Rph 3	reaction to Puccinia hordei				
Pa 4	D, Rph 4	reaction to Puccinia hordei				
Pa 5	B, Rph 5	reaction to Puccinia hordei				
Pa 7	Rph 7	reaction to Puccinia hordei				
Pa 9	Rph 9	reaction to Puccinia hordei				
Pa X	X, Rph X	reaction to Puccinia hordei				
Pau	Pr_a	purple auricle	–	2	C	76,95,228,265,273
Paz 1	–	protein Z4 (antigen 1a)	–	4		27,111,138,270, BGN 13:55,14:61
Paz 2	–	protein Z7 (antigen 1b)	*	7		138,270
Pbc 1	–	basic protein C (endochitinase)	*	1		139,227,270
Pbg	–	pubescence on outer glume	–	1		273,349
Pbn 1	–	basic protein N	*	3		139,270
Pbq 1		basic protein Q	*	2		139,270
Pbr	Hr	hairy rachis				
Pbr 2	Hr 2	hairy rachis				
Pbr 3	Hr 3	hairy rachis				
pco	–	phosphoglycollate phosphatase	1	–		126
Pd	–	pedicle on lateral spikelets	–	–		24,308
Pept 1	Dip 1	dipeptidase				
Pept 2	Dip 2	dipeptidase				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
pg	f 11	pale green (chlorina)				
Pgd 1	6Pgd 1	phosphogluconate dehydrogenase	–	–		50,74
Pgd 2	6Pgd 2, 6Pdgdh 1	phosphogluconate dehydrogenase	–	5	R	49,50,187,271, BGN 12:68,13:57
Pgi	Gpi 1	phosphoglucose isomerase				
Pgi H1	Gpi 1	phosphoglucose isomerase				
Pgm 1	–	phosphoglucomutase	–	4		49,50,270
phd	–	post-harvest dormancy	–	–		237,273
Pht	–	pH 3 soil tolerance	–	4		359a
Plm	–	anthocyanin rich	–	1		BGN 8:31
Pm 1	Reg 1	reaction to Erysiphe graminis hordei				
Pm 2	Reg 2	reaction to Erysiphe graminis hordei				
Pm 3	Reg 3	reaction to Erysiphe graminis hordei				
Pm 4	Reg 4	reaction to Erysiphe graminis hordei				
Pm 5	Reg 5	reaction to Erysiphe graminis hordei				
Pm 6	Ml-n	reaction to Erysiphe graminis hordei				
Pm 7	Ml-at	reaction to Erysiphe graminis hordei				
Pn	–	purple node	–	2		264,273
Pr/pr	Ant-2/ant-2 Clt_2/clt_2, C_2/c_2	purple/non-purple straw	–	2	C/, B53/	76,95,264,273,294, 383,420,BGN 1:51, 5:107,14:76
Pr-a	Hor 1	hordein				
Pr_a	Pau	purple auricle				
Prx 1	Per-H1 CPX_6	peroxidase	–	5		11,92
Prx 2	Per-H2 CPX_{4L} Perl	peroxidase	–	2		37,92
Prx 3	CPX_{4R}	peroxidase	–	–		92
Prx 4	Cpxe	peroxidase	*	1		270,271
Pt	Rpt 1	reaction to Pyrepophora teres				
Pt 2	Rpt 2	reaction to Pyrepophora teres				
Pt 3	Rpt 3	reaction to Pyrepophora teres				
Pt, ,d	–	reaction to Pyrepophora teres (net blotch)	–	–		BGN 1:25
r	bt 1	brittle rachis				
R/r	A/a	rough/smooth awn	–	7	B6/F /B312	BGN 3:20,8:158, 8:157,13:42,14:52
r, ,e	r_2,r 5	smooth awn	–	6	B257	BGN 1:25,6:131, 8:71
r_2	r 5, r, .e	smooth awn				

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
R 2	R 1,S,I	rough awn	–	7		22,273
R 3	R 2,A	rough awn	–	–		177,273,400
R 4	R 3	rough awn	–	1		273,349
r 5	r_2, r, ,e	smooth awn				
ra	–	short rachilla	–	2		273,349
ra 2	–	short rachilla	–	–		273,349
ra 3	–	short rachilla	–	–		273,349
rac-a	lb, rac-b	rachisextensum (long basal rachis internode)	–	–	S	118,284,BGN 4:82
rac-b	lb, rac-a	rachisextensum (long basal rachis internode)	–	–	S	118,BGN 4:82
rb	–	ribbon grass (white stripe on early leaves)	–	6	G397	76,82,273,396,420
rDNA	–	cytoplasmic ribosomal RNAs				19,BGN 8:99,9:9, 10:3
		:25-28S, 5.8S and 18S	*	6,7		
		:5S	*	–		
Re	C,P 1	red ear (purple lemma, palea and pericarp)	–	5		95,135,273,420,422
Re 2	R 1,P	red ear (purple lemma, palea and pericarp)	–	2		95,267,273,420,422
Reg 1	Ml-a,Ml-b, Ml-go,Ml-m, Ml-1063, Pm 1,Er_1^a, JMl_{snt}	reaction to Erysiphe graminis hordei (powdery mildew)	–	5	CI,R, HOR,W, J,B216	33,87,88,89,109,110, 149,150,168,169,178, 224,238,249,258,268, 273,389,413,418,419, BGN 5:87,6:127, 14:173
Reg 2	Ml-g, JMlg,PM 2, ER_{cp}	reaction to Erysiphe graminis hordei (powdery mildew)	–	4	CI	149,258,BGN 5:87, 6:124,14:173
Reg 3	Ml-h, JMl_h,PM 3	reaction to Erysiphe graminis hordei (powdery mildew)	–	6	CI,B452	149,258,BGN 6:143, 14:173,15:46
Reg 4	Ml-k, JMl_k,Pm 4	reaction to Erysiphe graminis hordei (powdery mildew)	–	5	CI,J	110,149,258,389,BGN 6:12,14:173
Reg 5	Ml-p, JMlp,Pm 5	reaction to Erysiphe graminis hordei (powdery mildew)	–	5	CI,B217	149,258,BGN 6:128, 14:173
reg 6	ml-o, er	reaction to Erysiphe graminis hordei (powdery mildew)	–	4	CI,R, S,HOR	145,224,424,BGN 8:168,9:37,14:173
Reg 7	Ml-ra, Ml-(41/145)	reaction to Erysiphe graminis hordei (powdery mildew)	–	5	R	75,BGN 14:173
Rfm 1	–	restoration of fertility in msm 1 and msm 2	4	–	A	8,9,10,BGN 12:26
Rh	Rrs 1, Rha	reaction to Rynchosporium secalis				
Rh 2	Rrs 2	reaction to Rynchosporium secalis (scald)	–	–		79,80,81,120,273, 354,BGN 2:145,8:17

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
Rh 3	Rrs 3	reaction to Rynchosporium secalis (scald)	–	3		79,80,81,120,273,354, BGN 2:145,8:17
Rh 4	Rrs 4	reaction to Rynchosporium secalis (scald)	–	3		79,80,81,120,273,354, BGN 2:145,8:17
Rh 5	Rrs 5	reaction to Rynchosporium secalis (scald)	–	–		79,80,81,120,273,354, BGN 2:145
rh 6	rrs 6	reaction to Rynchosporium secalis				
rh 7	rrs 7	reaction to Rynchosporium secalis (scald)	–	–		23,120,354,BGN 2:145, 8:17
rh 8	rrs 8	reaction to Rynchosporium secalis (scald)	–	–		23,120,BGN 2:145
Rh 9	rrs 9	reaction to Rynchosporium secalis				
Rh 10	rrs 10	reaction to Rynchosporium secalis (scald)	–	–		120,BGN 2:145
rh 11	rrs 11	reaction to Rynchosporium secalis (scald)	–	–		120,BGN 2:145
Rha	Rh	reaction to Rynchosporium secalis				
Rha 1	Ha 1	reaction to Heterodera avenae race 1 (cereal cyst nematode)	–	–		64,64a,BGN 2:145, 2:201
Rha 2	Ha 2	reaction to Heterodera avenae races 1 and 2 (cereal cyst nematode)	–	2		14,64,64a,BGN 2:145,2:201
rin	s,lin	low number of rachis internodes	–	2	B57	219,273,294, BGN 1:117
rin 2	–	low number of rachis internodes	–	4		273,349
rnt	lnt	reduced number of tillers				
rob-o	o	robiginosum (orange lemma)	5	–	S	118,241
Rpg 1	T	reaction to Puccinia graminis tritici (stem rust)	–	1		13,15,45,273,281, 282,BGN 2:145,15:68
Rpg 2	T 2	reaction to Puccinia graminis tritici (stem rust)	–	–		273,310, BGN 2:145
Rph 1	Pa,Pa 1, Pa 2,C	reaction to Puccinia hordei Otth (leaf rust)	–	2	B70	63,273,307,349,354, BGN 6:120
Rph 3	Pa 1,Pa 3, A	reaction to Puccinia hordei Otth (leaf rust)	–	3	B121	63,307,354, BGN 6:121
Rph 4	Pa 4,D	reaction to Puccinia hordei Otth (leaf rust)	–	5	B218	248,259,307, BGN 6:129
Rph 5	Pa 5,B	reaction to Puccinia hordei Otth (leaf rust)	–	3	B122	307,BGN 6:122
Rph 7	Pa 7	reaction to Puccinia hordei Otth (leaf rust)	–	–		63
Rph 9	Pa 9	reaction to Puccinia hordei Otth (leaf rust)	–	–		63
Rph X	Pa X, X	reaction to Puccinia hordei Otth (leaf rust)	–	–		307

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
rps 1	yr 1	reaction to Puccinia striiformis West (stripe rust)	–	–		258,275a
rps 2	yr 2	reaction to Puccinia striiformis West (stripe rust)	–	–		258,275a
rps 3	yr 3	reaction to Puccinia striiformis West (stripe rust)	–	–		258,275a
Rps 4	Yr4	reaction to Puccinia striiformis West (stripe rust)	–	5	B219	BGN 6:130,7:37,13:95
Rpt 1	Pt	reaction to Pyrenophora teres (net blotch)	–	3		251,273,320, BGN 7:11
Rpt 2	Pt 2	reaction to Pyrenophora teres (net blotch)	–	5		251,273, BGN 7:11
Rpt 3	Pt 3	reaction to Pyrenophora teres (net blotch)	–	2		251,273, BGN 7:11
Rrs 1	Rh, Rha	reaction to Rynchosporium secalis (scald)	–	3		52,79,80,81,120, 273,354,BGN 7:11, 8:17
rrs 6	rh 6	reaction to Rynchosporium secalis (scald)	–	4		23,120,354, BGN 7:11,8:17
Rrs 9	Rh 9	reaction to Rynchosporium secalis (scald)	–	4		23,354, BGN 7:11
Rs	–	red stem and leaf sheath	–	1	//B15	273,349,BGN 5:96
Rs_2/rs_2	Ant-5/ant-5	red stem/non-red stem				
Rsg 1	Grb	reaction to Schizaphis graminum Rondani (greenbug)	–	1	B22	66,105,273, BGN 6:119
Rsg 2	Grb 2	reaction to Schizaphis graminum Rondani (greenbug)	–	–		66,105,273, BGN 2:145
Rsg 3	Grb 3	reaction to Schizaphis graminum Rondani (greenbug)	–	–		66,273, BGN 2:145
Rt/Rt'/rt	–	normal/intermediate/ rattail spike	2	2	B51	273,349, BGN 1:111,6:74
rub-a	ant-1	exrubrum (anthocyanin-free)				
Run 1	Un	reaction to Ustilago nuda (Jens) Rostr (loose smut)	–	1	B21	15,16,BGN 6:118
Run 2	Un 2	reaction to Ustilago nuda (Jens) Rostr (loose smut)	–	–		273,349, BGN 2:145
Run 3	Un 3	reaction to Ustilago nuda (Jens) Rostr (loose smut)	–	–		273,349, BGN 2:145
Run 4	Un 4	reaction to Ustilago nuda (Jens) Rostr (loose smut)	–	–		273,349, BGN 2:145
Run 5	Un 5	reaction to Ustilago nuda (Jens) Rostr (loose smut)	–	–		273,349, BGN 2:145
Run 6	Un 6	reaction to Ustilago nuda (Jens) Rostr (loose smut)	–	–		248a,273,345, BGN 2:145

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
run 7	un 7	reaction to Ustilago nuda (Jens) Rostr (loose smut)	–	–		13,15,16,273, BGN 2:145
rvl	–	revoluted leaf	–	5		91,BGN 5:67
ryd 1	yd	reaction to yellow dwarf virus (BYDV)	–	–		258,273,361
Ryd 2	Yd 2	reaction to yellow dwarf virus (BYDV)	–	3	B123	258,273,306,321, BGN 6:123
Rym 1	Ym 1	reaction to barley yellow mosaic virus (BYMV)	–	4		373,BGN 6:125
Rym 2	Ym 2	reaction to barley yellow mosaic virus (BYMV)	–	1		373,BGN 6:117
rym 3	rym 3, Ea52	reaction to barley yellow mosaic virus (BYMV)	–	–		BGN 14:31,15:58
S	R 2	rough awn				
S/s	L/l, S^i/s^i	long/short rachilla hairs	–	7	/F, B6/ B312	71,76,237,273,294, 297,400,BGN 8:159, 8:160,11:25,13:42, 13:82
s	rin,lin	low number of rachis internodes				
s^i	bir	short haired, inflorescent rachilla (branching inflorescent rachilla)				
sb	–	subnodal bract	–	1		273,396
sbn	–	subnudoides (semi-naked caryopsis)	–	–		273,323
sc	–	short chromosome (desynaptic)				254,273
sca	–	short crooked awn	–	3		203,BGN 10:47
scs 1	SCS 1	segregating cytoplasmic streak	–	–	A	5,10a
scs 2	SCS 2	segregating cytoplasmic streak	–	–	A	5,10a
Sdh	Sdh 1	shikimate dehydrogenase				
Sdh 1	Sdh	shikimate dehydrogenase	–	7		46,49
sdw-b	–	bracteatum semidwarf	–	3		BGN 14:35
se 1	seg 1	shrunken endosperm				
se 2	seg 2	shrunken endosperm				
se 3	seg 3	shrunken endosperm				
se 4	seg 4	shrunken endosperm				
se 5	seg 5	shrunken endosperm				
se 6	seg 6, sex 1	shrunken endosperm (genetic, xenia)	–	–		BGN 13:67
se 7	seg 7	shrunken endosperm				
seg 1	se 1	shrunken endosperm, genetic	–	1	B377	BGN 1:22,1:190, 6:135,10:124
seg 2	se 2	shrunken endosperm, genetic	–	1	B378	BGN 1:22,1:190, 6:136,10:125
seg 3	se 3	shrunken endosperm, genetic	–	3	B379	BGN 1:22,1:191, 6:137,10:126
seg 4	se 4	shrunken endosperm, genetic	–	1	B380	BGN 1:22,1:192, 6:138,10:127

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
seg 5	se 5	shrunken endosperm, genetic	–	1	B381	BGN 1:22,1:192, 6:139,10:128
seg 6	se 6	shrunken endosperm, genetic	–	3		BGN 5:144,6:59, 6:141,13:64,13:115
seg 7	se 7	shrunken endosperm, genetic	–	–		BGN 5:115,6:59, 6:142,10:130
seg 8	–	shrunken endosperm, genetic	–	1		BGN 11:34,11:103, 13:64,13:116, 13:117
Sep	Rsp 1	reaction to Septoria avenae triticae (Septoria leaf blotch)	–	–		273,305,BGN 2:145
Sep 2	Rsp 2	reaction to Septoria avenae triticae (Septoria leaf blotch)	–	–		273,305,BGN 2:145
Sep 3	Rsp 3	reaction to Septoria avenae triticae (Septoria leaf blotch)	–	–		273,305,BGN 2:145
sex 1	se 6,lys 5	shrunken endosperm, xenia	3	6	F, B382	86,BGN 1:193,6:140, 7:28,8:109,8:114, 9:33,10:81,10:129, 12:90,13:67
sex 2	dex 1	shrunken endosperm, xenia (defective endosperm, xenia)				
sex 3	lys 3, Risø 1508	shrunken endosperm, xenia	–	7		BGN 7:66,8:109, 8:114,9:33,13:67
sex 4	lys 5, Risø 13	shrunken endosperm, xenia	–	–		BGN 8:114,9:33 13:67
sex 5	Lys 4, Risø 8	shrunken endosperm, xenia	–	–		BGN 8:114,9:33, 13:67
sex 6	–	shrunken endosperm	–	1		33
sf	gig	female sterile (gigas plant)				
sfa	–	silver fall off awnes	–	–	O	337
Sg	–	grooves on palea	–	–		57,273
Sh/sh	Ls/ls	winter/spring habit of growth	–	4	B310/ B163	273,380,384,385, 386,BGN 2:188,2:200, 11:38,16:––
Sh 2/sh 2	A/a	spring/winter habit of growth	–	7	B309/ B310	273,384,385, BGN 2:199,2:200, 11:38,13:30
Sh 3/sh 3	C/c	spring/winter habit of growth	–	5	B213/ B310	273,384,385, BGN 2:197,2:200, 11:38,13:30
Sh_4/sh_4	Sh/sh	spring/winter habit of growth	–	–		310
sid	nls	single elongated-internode dwarf	–	4		136,BGN 3:65,5:56
sk	–	subjacent hood	–	2	B62	273,371,383,BGN 1:122
sld	dw-1	dwarf	–	3		84,200,203,BGN 5:56, 13:89

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
sld 2	sld-2	culm short and slender	–	2		136
sln	sl	slender	1	–		358,BGN 7:24
sm	rsm 1	reaction to stripe mosaic virus	–	–		273,344,BGN 2:145
sm 2	rsm 2	reaction to stripe mosaic virus	–	–		273,344,BGN 2:145
sm 3	sm^3, rsm 3	reaction to stripe mosaic virus	–	–		258, BGN 2:145
Sm 4	Sm^4, Rsm 4	reaction to stripe mosaic virus	–	–		258, BGN 2:145
sm 5	sm^5, Rsm 5	reaction to stripe mosaic virus	–	–		258, BGN 2:145
smn	–	seminudoides (semi-naked caryopsis)	–	–		273,323
smn 2	–	semi-naked caryopsis	–	1		BGN 7:33
sp, ,b	nec 1	spotted leaf				
spn	cu 4	spiral neck				
Su-cer-cu	–	suppressor of cer-cu^{947}	–	–		351
Su 1-sex 3	Sse 1	suppressor 1 of sex 3	–	–	A	6,10a
Su 2-sex 3	Sse 2	suppressor 2 of sex 3	–	–	A	6,10a
st	–	striped	–	3		191,273
sts	–	breaking strength of straw	–	–		273,309
t	trd	third outer glume				
T	Rpg 1	reaction to Puccinia graminis tritici				
T 2	Rpg 2	reaction to Puccinia graminis tritici				
tg	ti	third inner glume	–	7		273,396
tig-a	–	tigrina-seedling	8	–	C	56,272,402, BGN 3:113
tig-b	infrared	tigrina to zonata seedling	4	–	C	56,115,272,402, BGN 3:113
tig-c	–	tigrina to zonata seedling	2	–	C	56,272,402,BGN 3:113
tig-d	infrared	tigrina-seedling	1	–	C	56,115,188,272,BGN 3:113
tig-e	–	tigrina-seedling	1	–	C	56,272,BGN 3:113
tig-f	–	tigrina to zonata seedling	1	–	C	56,272,BGN 3:113
tig-g	–	tigrina to zonata seedling	1	–	C	272,BGN 3:113
tig-h	–	zonata-seedling	1	–	C	272,BGN 3:113
tig-i	–	zonata-seedling	1	–	C	272,BGN 3:113
tig-j	–	zonata-seedling	1	–	C	56,272,BGN 3:113
tig-k	–	zonata to maculata seedling	1	–	C	272,BGN 3:113
tig-l	–	zonata-seedling	1	–	C	272,BGN 3:113
tig-m	infrared	zonata-seedling	1	–	C	56,272,BGN 3:113
tig-n	infrared	zonata-seedling	2	–	C	56,188,272,BGN 3:113
tig-o	infrared	tigrina to zonata seedling	1	7	C	56,115,154,157,188, 272,BGN 3:113,8:46
tl	–	tube leaves	–	–	O	337
Tpi 1	–	triosephosphate isomerase	–	3		131
tr	–	triple awned lemma	–	2	S	13,76,163,228,273, 324,420,BGN 1:121
Tr 2	–	triple awned lemma	–	–		273

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
tr 3	tr 2	triple awned lemma	–	–		273
trd	t,bra-c	third outer glume (bracteatum)	4	5	F	12,13,118,137,195, 205,273,383,396,BGN 1:147,2:28,4:82, 10:121,14:9
trd 2	–	third outer glume	–	–		273,308,310
tri	–	triploid inducer	–	–		BGN 7:4,12:22
tric	–	tricomposite floret	–	–		308
Ts	Un 6	reaction to Ustilago nuda				
tw	–	tweaky spike	–	–		82,273,309
u	–	unbranched style	–	7		273,309
U/u	H/h	tall high/short culm				
u 2	u 1	unbranched style	–	–		273,249
u 3	u 2	unbranched style	–	–		273,349
u 4	–	unbranched style	–	1	B11	273,382,BGN 2:177
uc	u	uniculm	–	–		273,420
uc 2	–	uniculm	–	6	B253	136,196,273,308, 310,BGN 1:156, 2:202
Uh	Ruh 1	reaction to Ustilago hordei (covered smut)	–	–		273,326,400,BGN 2:145
Uh 2	Ruh 2	reaction to Ustilago hordei (covered smut)	–	–		273,400,BGN 2:145
uh 3	ruh 3	reaction to Ustilago hordei (covered smut)	–	–		273,400,BGN 2:145
uh 4	ruh 4	reaction to Ustilago hordei (covered smut)	–	–		248a,273,400,BGN 2:145
Un	Run 1	reaction to Ustilago nuda				
Un 2	Run 2	reaction to Ustilago nuda				
Un 3	Run 3	reaction to Ustilago nuda				
Un 4	Run 4	reaction to Ustilago nuda				
Un 5	Run 5	reaction to Ustilago nuda				
Un 6	Ts,Run 6	reaction to Ustilago nuda				
un 7	run 7	reaction to Ustilago nuda				
Ung	–	reaction to Ustilago nigra Tapke (false loose smut)	–	–		248a
uz	uz 2,uz 3	"uzu" (semi-brachytic)	–	3	B102,F	231,247,273,294,310, 366,368,378,381,BGN 1:124,2:87,10:108, 12:42
uz 2	uz	"uzu" (semi-brachytic)				
uz 3	uz	"uzu" (semi-brachytic)				
v	kl	short awn				
$V/V^d/$ V^t/v	V^p,V^{M20} V_{1sa},a^s,a^f, a,z,hex-v	two rowed/two rowed/ deficiens/six rowed	–	2	///C, B203/ B66/ B67/ B6	76,104,119,127,163, 177,228,236,240,273, 275,294,349,383,400, 416,BGN 5:12,5:103, 5:104,5:105,5:106, 8:44
v_2	–	"six-row" (intermedium)	1	7	B314	104,374,BGN 5:12, 13:112
v_3	–	"six-row" (intermedium)	5	5	B315	104,BGN 5:12,13:113

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
v_4	–	"six-row" (intermedium)	3	3		104,BGN 5:12
v_5	–	"six-row" (intermedium)	1	4		104,BGN 5:12,12:29, 14:61
v_f	–	four-rowed	–	–		BGN 5:40
va	–	variegated	–	7	C,B306	273,395,BGN 1:165
va_2	–	variegated 2	–	–		395
va_3	–	variegated 3	–	7	C,B303	273,395,BGN 1:162
var	va	variegated				273
var 2	va 3	variegated 2				273
vbn	–	low number of vascular bundles	–	1		218,273,319,342
vir-a	–	viridis seedling	5	–	C	143,342,402
vir-b	–	viridis seedling	2	–	C	143,342,402
vir-c	–	viridis seedling	2	–	C	55,143,342,402
vir-d	–	viridis seedling	2	–	C	143,342,402
vir-e	–	viridis seedling	3	–	C	143,160,342,402
vir-f	–	viridis seedling	1	–	C	143,342
vir-g	–	viridis seedling	1	–	C	143,342
vir-h	–	viridis seedling	1	–	C	143,148,342
vir-i	–	viridis seedling	1	–	C	143,342
vir-j	–	viridis seedling	1	–	C	143,342
vir-k	–	viridis seedling	1	–	C	55,143,342
vir-l	x_c	viridis seedling	2	3	C	55,143,342,BGN 12:93
vir-m	–	viridis seedling	1	–	C	55,143,154,342
vir-n	–	viridis seedling	1	–	C	143,148,257,340,342
vir-o	–	viridis seedling	1	–	C	143,342
vir-p	–	viridis seedling	1	–	C	143,342
vir-q	–	viridis seedling	2	–	C	143,148,342
vir-r	–	viridis seedling	1	–	C	143,342
vir-s	–	viridis seedling	1	–	C	143,342
vir-t	–	viridis seedling	1	–	C	55,143,342
vir-u	–	viridis seedling	1	–	C	55,143,342
vir-v	–	viridis seedling	1	–	C	143,342
vir-w	–	viridis seedling	1	–	C	342
vir-x	–	viridis seedling	1	–	C	143,342
vir-y	ts 2	viridis seedling (± temp.sensitivity)	2	–	C	143,342,346
vir-z	–	viridis seedling	1	–	C	143,342
vir-za	–	viridis seedling	1	–	C	143,342
vir-zb	–	viridis seedling	1	–	C	55,144,148,158,159, 257
vir-zc	–	viridis seedling	1	–	C	143,342
vir-zd	–	viridis seedling	1	–	C	55,143,144,154,342
vir-ze	–	viridis seedling	1	–	C	143,342
vir-zf	ts 4	viridis seedling (temp. sensitive)	1	–	C	346
vir-zg	ts 9	viridis seedling (temp. sensitive)	1	–	C	346
vir-zh	ts 46	viridis seedling (temp. sensitive)	1	–	C	346
vir-zi	ts 49	viridis seedling (temp. sensitive)	1	–	C	346

Gene locus	Synonyms	Character	Alle-les	Chromo-some	Stock source	Authority(ies)
vir-zj	ts 57	viridis seedling (temp. sensitive)	1	–	C	346
vs 3	gs 3,cer-a	glossy sheath				
w	e	wide outer glume awn				
w	wlk	wide lateral kernels				
W	I	infertile intermedium				
Wek-a	–	hybrid weakness	–	–		BGN 15:39
Wek-t	–	hybrid weakness	–	–		BGN 15:39
wh 1	gs 4	waxless head (glossy sheath)				
wh 2	gs 4	waxless head (glossy sheath)				
wi	–	wide glume inhibitor	–	–		273,349
wl	gl	waxless (glossy leaf)				
wlh	bb 3	broad leaf				
wlk	w	wide lateral kernels	–	–		58,273
wnd	–	semi-dwarf with winding peduncles	–	1		BGN 5:56
Wr	–	weak rachis	–	–		192,273
Ws	–	weakly attached spikelet	–	–		273,349
wst	wst 3,st	white stripe	–	3	C,B107	310,377,BGN 1:125, 1:129,10:109,10:110
wst 2	wst$_2$	white stripe	–	7	B304	377,BGN 1:163
wst 3	wst,wst$_3$	white stripe			B103	
wst 4	wst$_4$	white stripe	–	2	B56	377,BGN 1:116
wst 5	–	white stripe	–	5	B221	183,BGN 3:19, 11:100,13:94
wst. ,j	–	white stripe	–	3		203,BGN 13:89
wx	glx	high amylopectin endosperm (waxy endosperm; starch synthase)	9	1	F, B16	197,203,207,273,364, 365,BGN 5:97,9:79
X	Ea	early maturity				
x	d	xantha seedling	–	–		273,349
X$_a$	–	xantha seedling	–	1		374,BGN 2:43
x$_c$	vir-l	xantha seedling	2	3	C, B105	208,273,293,294,368, 369,BGN 1:127,12:93
x$_c$2	–	xantha seedling	–	–		273,349
x$_n$	–	xantha seedling	–	6	C, B255	207,273,363,BGN 1:158
x$_s$	–	xantha seedling	–	3	C, B113	273,349,BGN 1:135, 10:112
x 4	lpy	yellow seedling 5	–	–		298,308
x 5	–	lethal pale yellow seedling 4	–	–		308
xan-a	–	albo-xantha seedling	15	–	C	143,402,BGN 3:113
xan-b	–	xantha seedling	6	–	C	143,160,402,BGN 3:113
xan-c	–	xantha seedling	2	–	C	55,143,402,BGN 3:113
xan-d	–	xantha seedling	2	–	C	55,143,160,402,BGN 3:113
xan-e	–	xantha seedling	2	–	C	143,160,402,BGN 3:113

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
xan-f	–	xantha seedling	8	–	C	30,114,143,188,402, BGN 3:113
xan-g	–	xantha seedling	5	–	C	30,114,143,188,402, BGN 3:113
xan, ,g	–	xantha seedling	–	5		BGN 6:53
xan-h	–	xantha seedling	4	–	C	143,402,BGN 3:113
xan, ,h	–	xantha seedling	–	3		BGN 6:53
xan-i	–	xantha seedling	2	–	C	143,402,BGN 3:113
xan, ,i	–	xantha seedling	–	1		BGN 6:53
xan-j	–	xantha seedling	3	–	C	143,402,BGN 3:113
xan-k	–	xantha seedling	1	–	C	143,402,BGN 3:113
xan-l	–	xantha seedling	1	–	C	30,114,143,188,402, BGN 3:113
xan-m	–	xantha seedling	5	–	C	55,143,402,BGN 3:113
xan-n	–	xantha seedling	3	–	C	143,402,BGN 3:113
xan-o	–	xantha seedling	2	–	C	143,402,BGN 3:113
xan-p	–	xantha seedling	1	–	C	143,402,BGN 3:113
xan-q	vir	xantha seedling	7	–	C	143,148,342,402,BGN 3:113
xan-s	–	xantha seedling	1	–	C	143,402,BGN 3:113
xan-t	–	xantha seedling	1	–	C	55,143,402,BGN 3:113
xan-u	–	xantha seedling	1	–	C	114,143,188,402,BGN 3:113
Y	Ea	early maturity				
y	y_x,alb-c	virescent seedling	2	2	B63	BGN 2:180,12:93
y_c	–	virescent seedling	–	1	C,B3	273,294,BGN 1:106
y_x	y,alb-c	yellow (xantha) seedling	2	2	B54	BGN 1:114,12:93
yd	yd 1, ryd 1	reaction to yellow dwarf virus				
Yd 2	Ryd 2	reaction to yellow dwarf virus				
yh	yh 2, cl	yellow spike	–	4	F, B158	273,310,367,371, BGN 1:144,14:61, 16:--
Ym 1	Rym 1	reaction to barley yellow mosaic virus				
Ym 2	Rym 2	reaction to barley yellow mosaic virus				
ym 3	Ea52, rym 3	reaction to barley yellow mosaic virus				
yr 1	rps 1	reaction to Puccinia striiformis				
yr 2	rps 2	reaction to Puccinia striiformis				
yr 3	rps 3	reaction to Puccinia striiformis				
Yr 4	Rps 4	reaction to Puccinia striiformis				
ys	yst	yellow stripe				
yst	ys	yellow stripe	–	3	B104	273,310,396,BGN 1:126
yst 2	yst_2	yellow stripe	–	3	B109	377,BGN 1:131

Gene locus	Synonyms	Character	Alleles	Chromosome	Stock source	Authority(ies)
yst 3	yst$_3$	yellow stripe	–	2		BGN 3:54,9:106
yv	f 4,f 6	yellow viable (chlorina)				
yv 2	f 5,z	yellow viable (chlorina)				
yw	–	yellow wavy	–	–		79,273
z	Ea	early maturity				
z	zd,zb$_c$,z$_c$, zb 2	zoned leaf				
z	f 5,yv 2	yellow viable				
z$_c$	z,zd,zb$_c$	zoned leaf	–	–		13,137,177,273,294
z$_w$	z,zd	zoned leaf	–	–		137,273,411,420
zb	–	zebra stripe (tigrina)	–	3	C, B120	191,273,BGN 5:64,5:110, 14:21
zb 2	z,z$_c$,zb$_c$, zd	zebra stripe	–	4		BGN 4:167,5:64, 14:21,14:98
zb 3	zb$_c$,zb$_c$2	zebra striped leaf	–	5	C	BGN 4:107,5:64,8:86, 12:78,13:85,14:10, 14:94,15:74
zb$_c$	z$_c$,zd,z	zebra stripe (tigrina)			C	
zb$_c$2	zb 3	zebra stripe	–	5		BGN 15:74
zb$_w$	z$_w$	zebra stripe (tigrina)	–	–		BGN 5:64
zd	zb 2,zb$_c$, z$_c$,z$_w$	zebra stripe (zoned leaf)				
zon	tig	zonata seedling (tigrina)	1	–		402

Addresses from which seeds of the stocks containing the gene in question can be obtained:

A : H. Ahokas, University of Helsinki, Department of Genetics, Arkadiankatu 7, SF-00100 Helsinki 7, Finland
B (number) = (BGS; Barley Genetics Stock number) T. Tsuchiya, Department of Agronomy. Colorado State University, Fort Collins, Colorado 80523, USA.
C : B. Søgaard, Department of Physiology, Carlsberg Laboratory, Gamle Carlsberg Vej 10, DK-2500 Copenhagen Valby, Denmark. Telex 15434.
CI : D.H. Smith, Jr., USDA Small Grains Collection, Beltsville, Maryland 20705, USA.
F : R.I. Wolfe, Agriculture Canada, Beaverlodge, Alberta, Canada.
G (number) = (GBC; Guelph Barley Collection number) K. Kasha, Department of Crop Science, University of Guelph, Ontario N16 2W1, Canada.
HOR : Chr. Lehmann, Gene Bank, Zentralinstitut für Genetik und Kulturpflanzenforschung, DDR-4325 Gatersleben, Germany (DDR). Telex kupfga 48558
J : T. Konishi, Barley Germ Plasm Center, Institute for Agricultural and Biological Sciences, Okayama University, Kurashiki, 710 Japan.
K : A. Kleinhofs, Department of Agronomy and Soils, Washington State University, Pullman, Washington 99164-3520, USA. Telex 5107741099 coll ag pman
R : J.H. Jørgensen, Agricultural Research Department, Risø, National Laboratory, DK-4000 Roskilde, Denmark. Telex 43116.
S : U. Lundqvist, Svalöf AB, S-26800 Svalöv, Sweden. Telex 72476.
O : G.G. Shvedov, All-Union Institute of Plant Breeding and Genetics, Ovidiopolskaya doroga 3, Odessa, 270036, USSR.
W (number): (Weihenstephan Barley Stock number) G. Fischbeck, Lehrstuhl für Pflanzenbau und Pflanzenzüchting der Technischen Universität München, 8050 Freising - Weihenstephan, F.R. Germany.

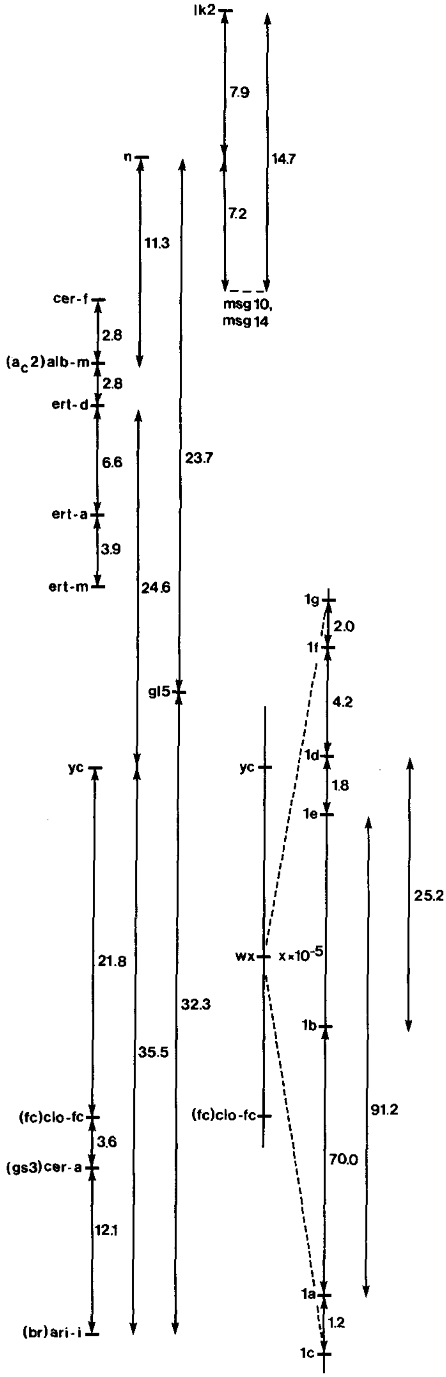

Figure 1. Chromosome 1.

The percent recombination values presented were selected from $F_2 \pm F_3$ 3-point cross data found in BGN 2:123 and references 136 and 350. The map of the *wx* locus expressed in recombination frequency is taken from BGN 9:79.

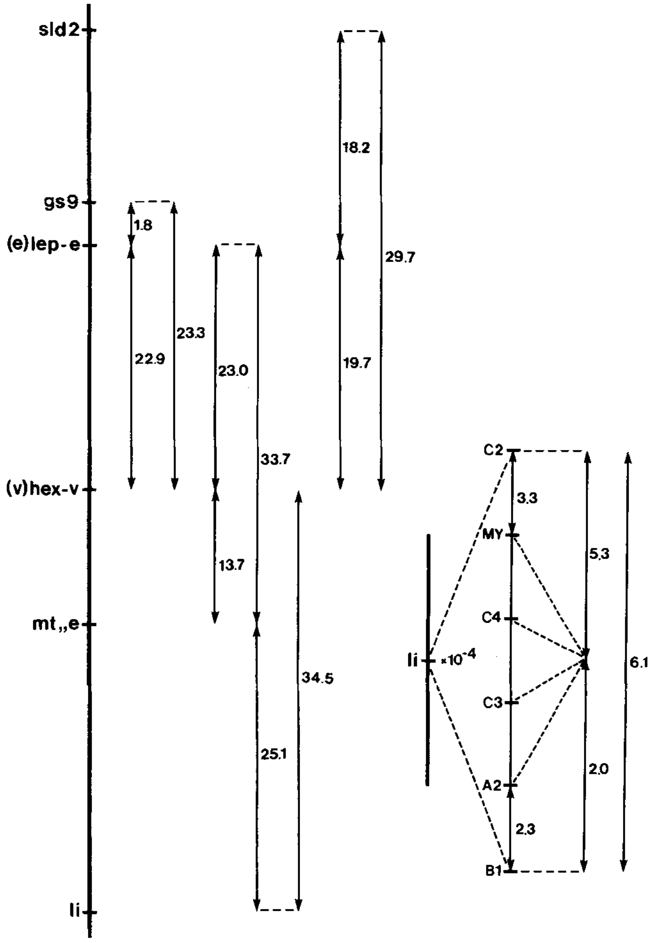

Figure 2. Chromosome 2.

The percent recombination values presented were selected from $F_2 \pm F_3$ multi-point cross data found in reference 136. The map of the *li* locus expressed in recombination frequency is modified from reference 202.

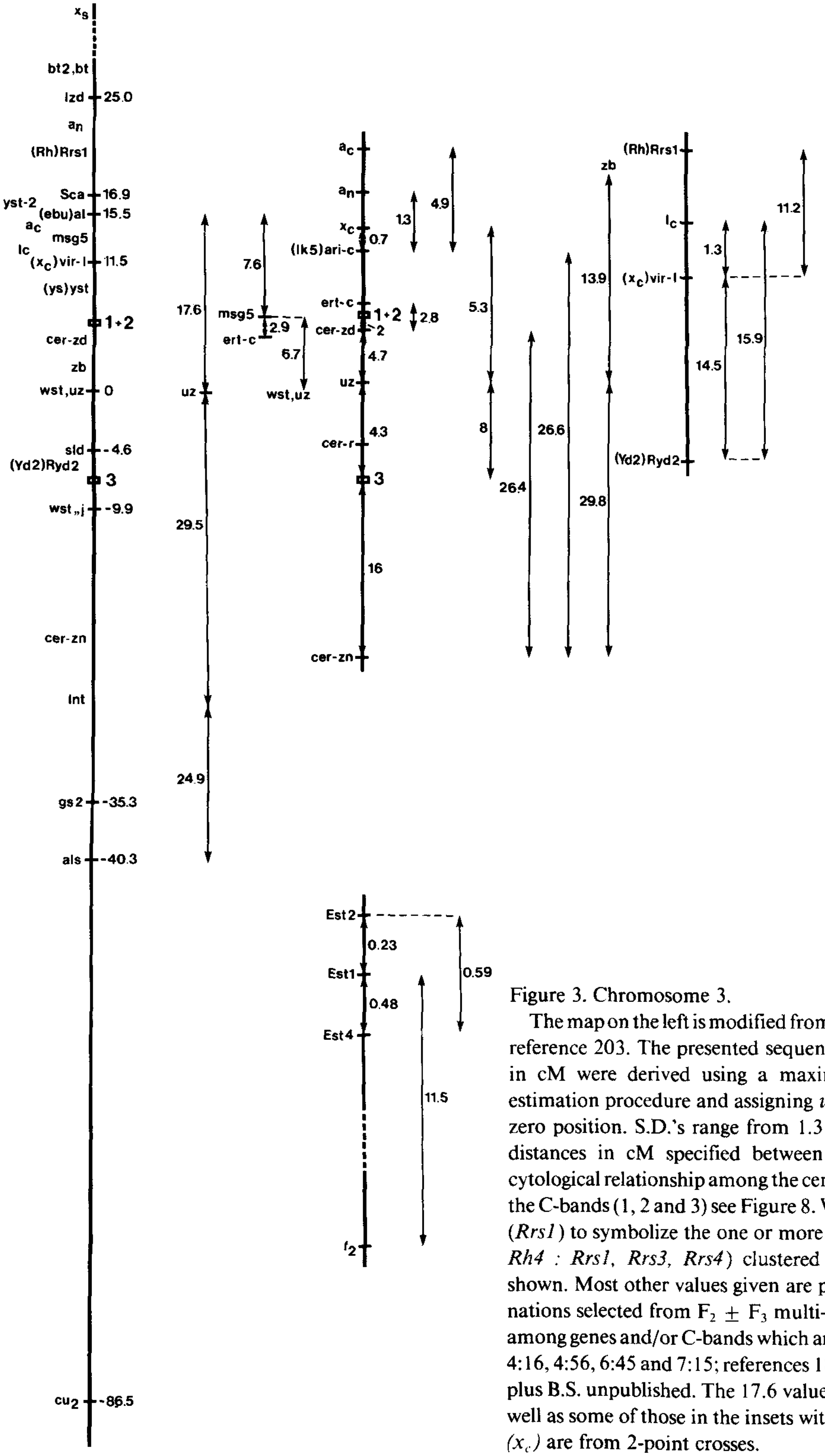

Figure 3. Chromosome 3.

The map on the left is modified from BGN 13:89 and reference 203. The presented sequence and distances in cM were derived using a maximum likelihood estimation procedure and assigning *uz* and *wst* to the zero position. S.D.'s range from 1.3 to 26.4% of the distances in cM specified between genes. For the cytological relationship among the centromere (C) and the C-bands (1, 2 and 3) see Figure 8. We have used *Rh* (*Rrs1*) to symbolize the one or more genes (*Rh, Rh3, Rh4 : Rrs1, Rrs3, Rrs4*) clustered at the position shown. Most other values given are percent recombinations selected from $F_2 \pm F_3$ multi-point cross data among genes and/or C-bands which are found in BGN 4:16, 4:56, 6:45 and 7:15; references 185, 234 and 321; plus B.S. unpublished. The 17.6 value from *uz* to *al* as well as some of those in the insets with *msg5* and *vir-l* (x_c) are from 2-point crosses.

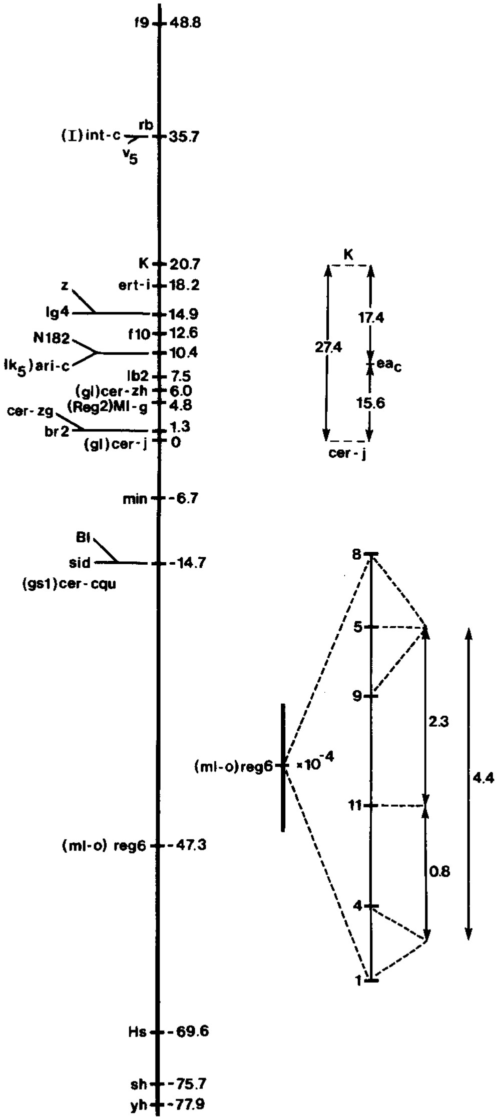

Figure 4. Chromosome 4.

The map is modified from reference 182. The presented sequence and distances in cM were derived using a maximum likelihood map estimation procedure and assigning *cer-j* (*gl*) to the zero position. Note that for markers from *yh* to *reg6* (*ml-o*) the S.D. ranges from 2.3 to 3.1 cM, and for markers *Bl* to *int-c* (*I*) from 0.7 to 1.3 cM except for *ari-c* (*lk5*) and *cer-zg* with S.D.s of 2.1 and 1.8, respectively. The S.D.'s of 5.8 and 6.9 for *cer-cqu* and *rb* preclude their being assigned a numerical position on the map. We have grouped together at their average position on the map all genes located within 0.8 cM of one another. The percent recombination values from $F_2 + F_3$ 3-point cross data from reference 427 locates ea_c between K and *cer-j* (*gl*). The map of the *reg6* (*ml-o*) locus expressed in recombination frequency is taken from BGN 9:37.

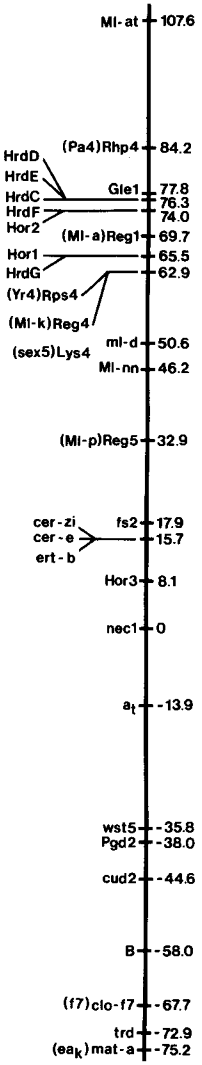

Figure 5. Chromosome 5.

The map is modified from BGN 16:—. The presented sequence and distances in cM were derived using a maximum likelihood map estimation procedure and assigning *nec1* to the zero position. Note that for markers from *Ml-at* to *cer-e* the S.D. is ≥ 3.0 cM, while from *ert-b* to ea_k the S.D. ranges from 1.5 to 2.9 cM. The S.D. of 8.6 for *Lys4* (*sex5*) precludes its being assigned a position on the map. We have grouped together at their average position on the map all genes located within 1.2 cM of one another.

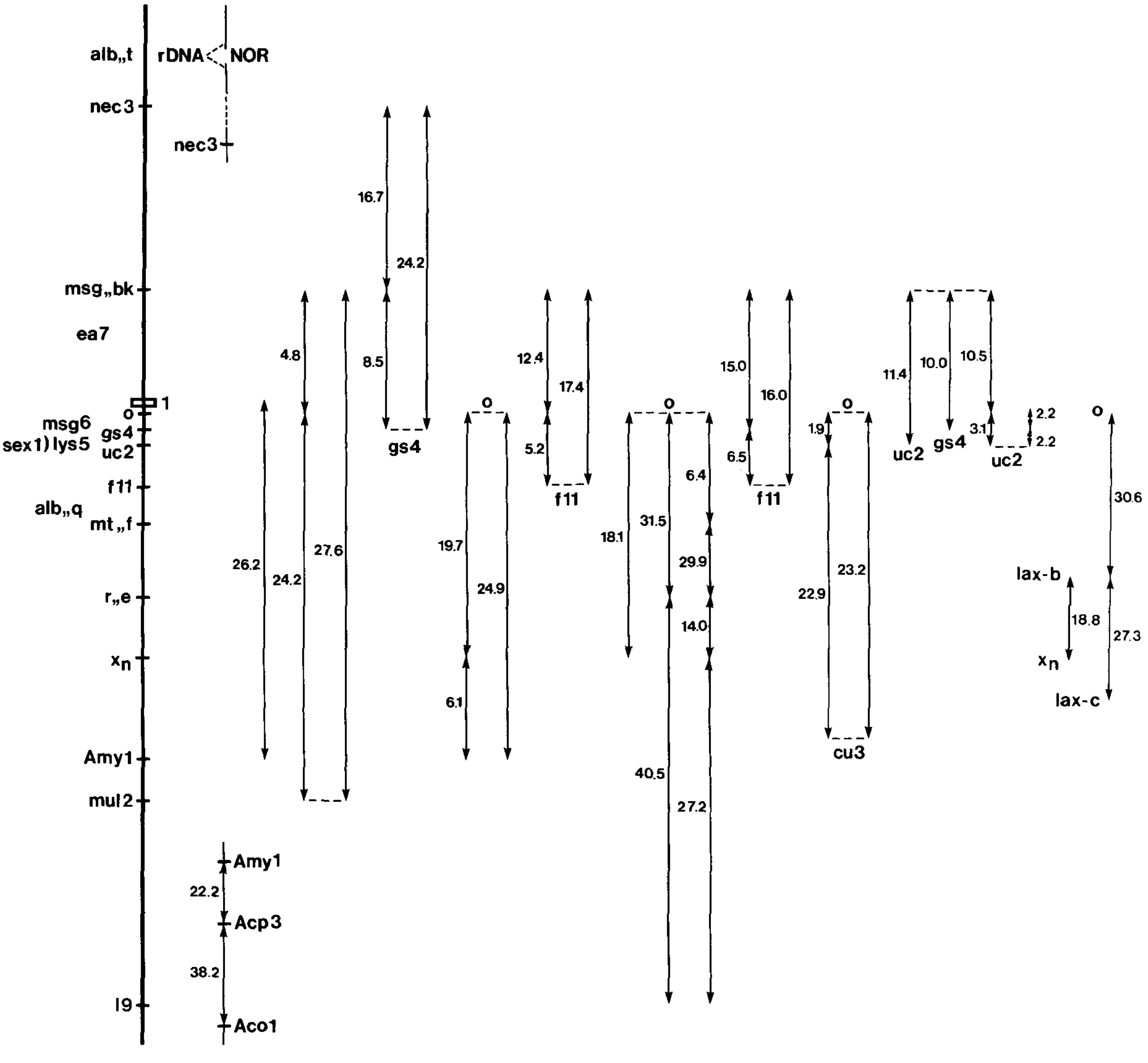

Figure 6. Chromosome 6.

One possible arrangement of *msg6* and *lys5* (*sex1*) with relation to *o* is shown. Should the reverse order prove true, *alb, ,q* and *alb, ,t* must be interchanged. For cytological relationship of C-band S1 to centromere see Figure 8. Relationship of *nec3* to the nucleolus organizer region (NOR) is unknown as indicated by the broken line. The percent recombination values presented were selected from $F_2 \pm F_3$ multi-point cross data found in BGN 4:53, 8:48, 8:61, 8:71, 9:17, 10:13 and 12:90 plus references 223, 232 and 270. The location of the *rDNA* genes is taken from reference 19.

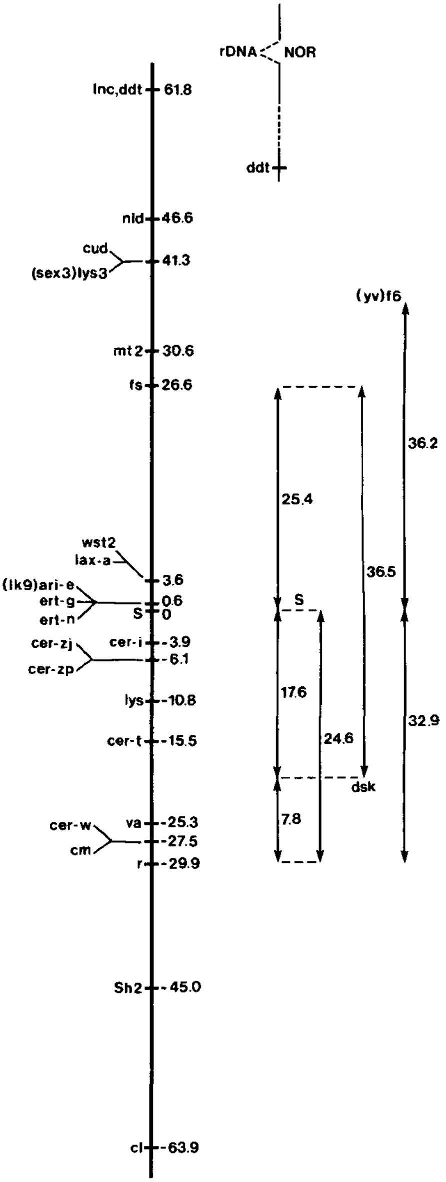

Figure 7. Chromosome 7.

The map on the left is modified from reference 181. The presented sequence and distances in cM were derived using a maximum likelihood map estimation procedure and assigning *s* to the zero position. Note that for markers from *wst2* to *ert-n* the S.D. ranges from 0.7 to 1.5 cM and for *cer-i* to *r* from 0.7 to 1.3 cM. We have grouped together at their average position on the map all genes located within 1.1 cM of one another. Relationship of *ddt* to the nucleolus organizer region (NOR) is unknown as indicated by the broken line. The location of the *rDNA* genes is taken from reference 19 and of *Inc* from 287. All other specified values are percent recombinations selected from F_2 + F_3 multipoint cross data in BGN 13:50 plus reference 136.

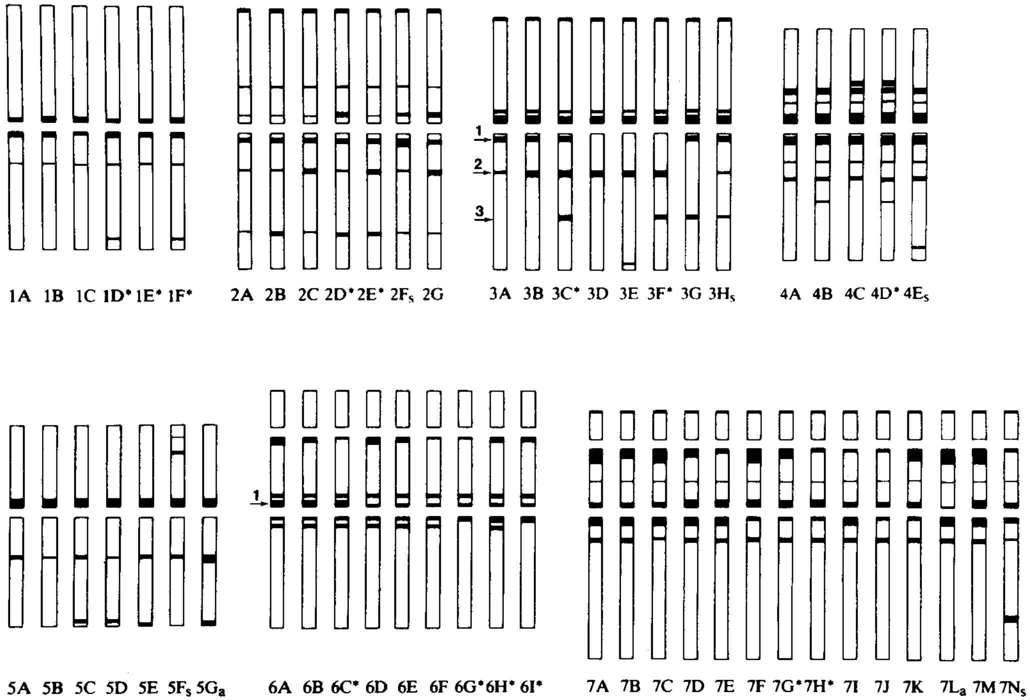

Figure 8. Idiograms of barley chromosomes illustrating the variation in C-banding patterns in cultivated H. vulgare and wild species. The latter are denoted by subscripts a and s for H. agriocrithon and spontaneum, respectively. Variants found only in six row types are indicated with an asterisk. The figure which is taken from reference 233 has been modified by labelling those bands on chromosomes 3 and 6 which have been used as genetic markers (see Figures 3 and 6).

Table II. Cloned genes.

		Plasmid		
A. Chloroplast	Character	Name	kb	Authority(ies)
atp A	α-subunit of CF$_1$-ATPase	pHvC 21	7.4	277
atp B	β-subunit of CF$_1$-ATPase	pHvC 209	10.0	289
		pHvu-SH13	37.0	430
atp E	ε-subunit of CF$_1$-ATPase	pHvC 209	10.0	289
		pHvu-SH13	3.7	430
atp H	subunit III of CF$_0$-ATPase	pHvC 174	1.7	277
pet A	cytochrome f	pHvC 186	3.5	277
pet D	subunit 4 of cytochrome b$_6$/f	pHvC 79	8.4	277
psa A	PSI P700 apoprotein A1	pHvC 238	2.7	211,289
psb A	PSII 32 kd protein	pHvC 147	1.6	269
psb C	PSII 44 kd protein	pHvC 35	4.3	269
		pHvC 101-2 (3' end)	0.9	
psb D	PSII D2 protein	pHvC 101-5	1.0	269
		pHvC 101-2 (5' end)	0.9	
psb E	PSII cytochrome b559 apoprotein I	pHvC 46	8.3	214
		pHvC 46-4.2	4.2	
psb F	PSII cytochrome b559 apoprotein II	pHvC 46	8.3	214
		pHvC 46-4.2	4.2	
rbc L	large subunit of ribulose bisphosphate carboxylase	pHvC 186	13.5	289,290
5SrDNA	5S ribosomal RNA	pHvC 203	5.6	289
23SrDNA	23S ribosomal RNA	pHvC 203	5.6	289
16SrDNA	16S ribosomal RNA	pHvC 205	8.4	289
trn D-GUC	tRNA-aspartate (GUC)	pHvC 208-1.6	1.6	32
trn E-UUC	tRNA-glutamate (UUC)	pHvC 208-1.6	1.6	32
trn G-GCC	tRNA-glycine (GCC)	pHvC 35	4.3	279
trn G-UCC	tRNA-glycine (UCC)	pHvC 35	4.3	279
trn M1-CAU	tRNA-formyl methionine (CAU)	pHvC 35	4.3	279
trn M2-CAU	tRNA-methionine (CAU)	pHvC 209	10.0	277
		pHvu-SH13	3.7	430
trn S-UGA	tRNA-serine (UGA)	pHvC 35	4.3	279
trn T-GGU	tRNA-threonine (GGU)	pHvC 35	4.3	279
trn V-UAC	tRNA-valine (UAC)	pHvC 209	10.0	277
		pHvu-SH13	3.7	430
trn Y-GUA	tRNA-tyrosine (GUA)	pHvC 208-1.6	1.6	32

B. Genomic	Character	Plasmid name	Bases sequenced	Authority(ies)
Ale	aleurain (thiol protease)	λ aleurain	-1399 to 3977	412
Amy 2	α-amylase (type A)	λ amy32b	-606 to 2144	313,412
Hor 2	B1 hordein	pBHR 184	-563 to 2337	99,327
		λhor 2-4	-550 to 1229	39
rDNA	25-28S, 5.8S and 18S cytoplasmic ribosomal RNA			107
	9.9 kb repeat	pHV 99	–	
		pHV 107	–	
		pHV 287	–	
	9.0 b repeat	pHV 29	–	
		pHV 103	–	
		pHV 132	–	
		pHV 144	–	
		pHV 158	–	
		pHV 256	–	
		pHV 279	–	
		pHV 294	–	
		pHV 309	–	
		pHV 361	–	

C. cDNA	Character	Plasmid			Authority(ies)
		Name	bp	Sequenced	
Amy 1	α-amylase (type B)	103	≃630	yes	161,265
		pHV19	1119	yes	59
		pM/C	1479	yes	311
Amy 2	α-amylase (type A)	E	1588	yes	312
Cab 1	photosystem II light harvesting chlorophyll a/b protein	pHvLF2	≃610	no	113
Chs	chalcone synthase	pcchs11	1477	yes	315,316
Cm-	endosperm CM- proteins	pUP-13	506	yes	283
		pUP-38	496	yes	
Glb 2	(1→3,1→4)-β-D-glucan 4-glucanohydrolase isoenzyme II	pA5	874	yes	96
		pBA170	287	yes	166
		pYBAG17	1088	yes	
Gld	glyceraldehyde-3-phosphate dehydrogenase	pc gld-1	1147	yes	61
H3	histone H3	pc h31-1	522	yes	62
Hor 1	C hordein	pc P387	475	yes	100,327
		pc hor1-3	362	yes	300
Hor 1+2	C + B1 hordein	pc-919	252	yes	300
Hor 2	B1 hordein	pc hor2-1	254	yes	301
	B1 hordein	pc hor2-2	153	yes	156,301
	B1 hordein	pc hor2-3	257	yes	
	B1 hordein	pc hor2-4	720	yes	
	B1 hordein	pc hor2-5	506	yes	38,39
	B1 hordein	pc hor2-7	390	yes	
	B1 hordein	pc hor2-8	398	yes	
	B1 hordein	pB11	884	yes	100,327
	B3 hordein	pB7	977	yes	

C. cDNA	Character	Plasmid			Authority(ies)
		Name	bp	Sequenced	
Hor 3	D hordein	pHvE-c135	–	no	98,327
		pHvE-c133	–	no	
		pHvE-c155	≃900	no	
Hth 1	α-hordothionin	pTH1	569	yes	288
Hth 2	β-hordothionin	pTH2	489	yes	146
		pTH3	471	yes	
Ica 2	inhibitor of chymotrypsin and Aspergillus protease				327,417
	A sub-family	pcIC 38	451	yes	
	B sub-family	pcIH 161	≃225	yes	
Ipa	probable α-amylase/ protease inhibitor	A1f	650	yes	263
Lth	leaf thionins				16a,35
	group 1	pHvDD3	543	yes	
		pHvDG3	428	yes	
	group 2	pHvDD4	641	yes	
		pHvDC4	650	yes	
		pHvDF2	456	yes	
Ml-p	mRNA and/or proteins induced upon infection with Erysiphe graminis hordei (powdery mildew)	pRP1 to 6	160 to 820	no	68
Nar 1	NADH-nitrate reductase	bNRp10	≃1100	no	60
Paz 1	protein Z4	pc paz1-1	360	partly	302
		pc paz1-2	325	yes	141
		pc paz1-3	409	yes	
Pcr	NADPH:protochlorophyllide oxidoreductase	pHvDF1	≃600	no	16a,17,357
Ub 1	ubiquitin	pKG3730	702	yes	106
Wx	starch synthase	pcwx27	2397	yes	315,316

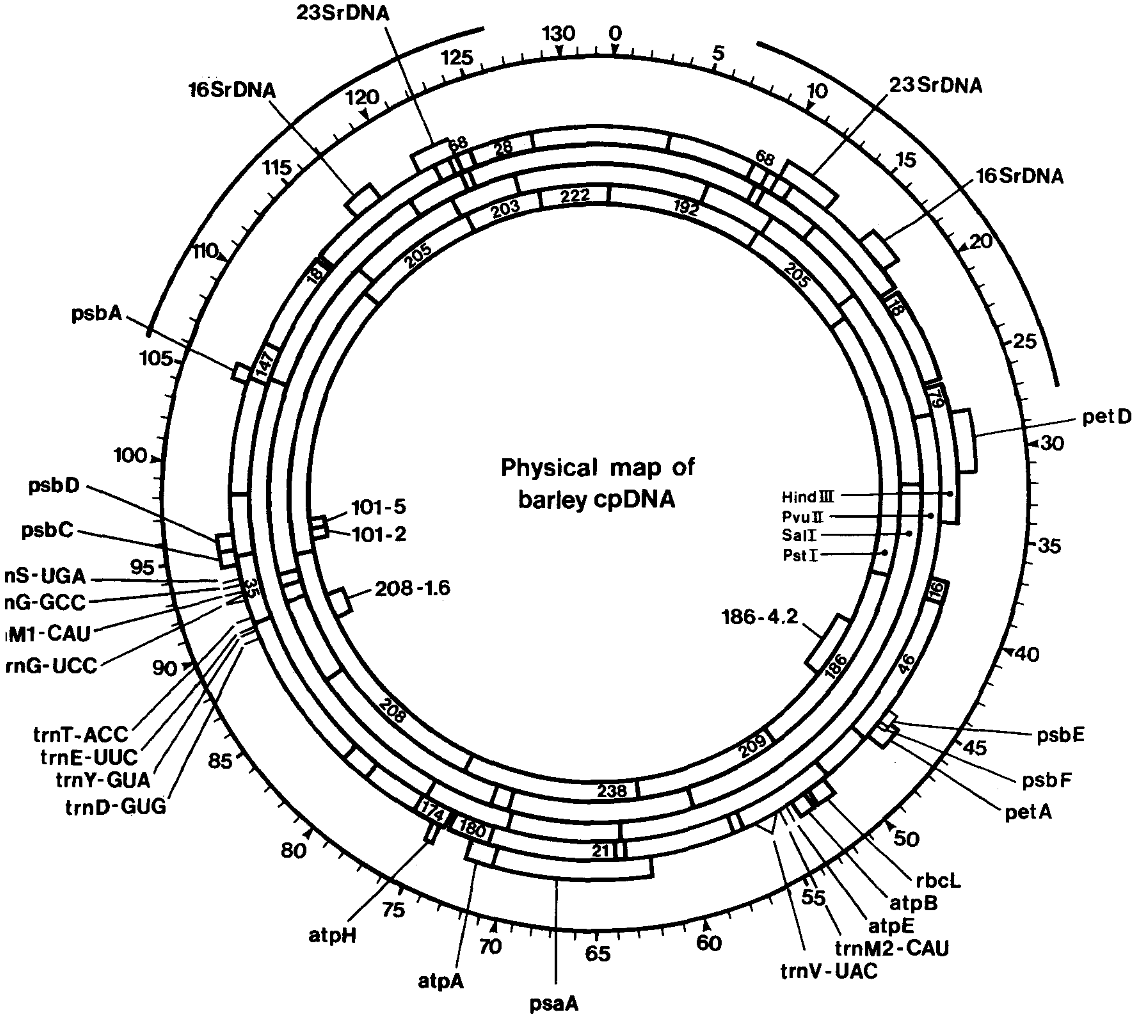

Figure 9. Physical map of barley cpDNA in kb derived from Hind III, Pvu II, Sal I and Pst I digests (269, 289). The zero position is located midway between the two inverted repeats designated by the two outermost lines. All numbered fragments are available as clones from C as are the subclones shown in the inner ring. Reference 69 contains restriction maps of barley cpDNA after Hpa I, Pst I, Pvu II, Sal GI, Sst I, Xho I and Bam HI digests. The genes *atpA, atpH, petA, petD, psaA, 16SrDNA* and *23SrDNA* have been located within the areas designated by heterologous hybridization. The precise position and sequence of the other genes is known from DNA sequencing.

Table III. Barley translocations.

x and y designate the two chromosomes involved in the interchange. p and q designate the arm in which the break has taken place if known, with p and q standing for the arm above and below the centromere, respectively, as diagrammed in Figures 8 and 10. cen = centromere, sat = satellite, NOR = nucleolus organizer region. When more than one symbol is given, that in brackets is the original one. Two symbols separated by a comma indicate both equally likely. Seeds of the translocations are available from R.T. Ramage, Agronomy Department, University of Arizona, Tucson, Arizona 85721, USA.

Translocation chromosome	Site of interchange(s)		Authority(ies)
x y	x	y	
T 1-2a	cen	cen	273,294,BGN 1:74
T 1-2b	cen		273,294,BGN 1:74
T 1-2c			229,BGN 1:74
T 1-2d			BGN 1:74
T 1-2e			BGN 1:74
T 1-2f			BGN 1:74
T 1-2g			285,BGN 1:74
T 1-2h			BGN 2:135
T 1-2i			BGN 2:135
T 1-2j			BGN 2:135
T 1-2k			BGN 2:135
T 1-2l			BGN 2:135
T 1-2m			BGN 2:135
T 1-2n			BGN 2:135
T 1-2o			BGN 2:135
T 1-2p			BGN 4:111
T 1-2q			BGN 5:76
T 1-2r			BGN 5:76
T 1-2s			BGN 5:76
T 1-2t			BGN 5:76
T 1-2u			BGN 5:76
T 1-2v			BGN 5:76
T 1-2w			BGN 5:76
T 1-3a	q	cen	273,285,294,BGN 1:74
T 1-3b	q		273,285,294,BGN 1:74
T 1-3c	p	cen	273,294,BGN 1:74
T 1-3d	cen		273,294,BGN 1:74
T 1-3e	q	q	273,285,294,BGN 1:74,14:12
T 1-3f	q	cen	273,284,285,294,BGN 1:74
T 1-3g			299,BGN 1:74
T 1-3h			298,BGN 1:74
T 1-3i			229,BGN 1:74
T 1-3j	p(q)	q(p,cen)	235,285,BGN 1:74,14:12
T 1-3k	p	q	235,285,BGN 1:74,14:12
T 1-3l			BGN 4:111
T 1-3m			BGN 4:111
T 1-3n			BGN 4:111
T 1-3o			BGN 4:111
T 1-3p			BGN 4:111
T 1-3q			BGN 5:76
T 1-3r			BGN 5:76
T 1-3s			BGN 5:76
T 1-3t			BGN 5:76
T 1-3u			BGN 5:76
T 1-3v			BGN 5:76
T 1-3w			BGN 5:76
T 1-3x			BGN 5:76
T 1-3y			BGN 5:76
T 1-3z			BGN 5:76
T 1-3aa			BGN 5:76
T 1-3ab			BGN 5:76
T 1-3ac			BGN 5:76

Translocation chromosome	Site of interchange(s)		Authority(ies)
x y	x	y	
T 1-3ad			BGN 5:76
T 1-3ae			BGN 5:76
T 1-3af			BGN 5:76
T 1-3ag			BGN 5:76
T 1-3ah			BGN 5:76
T 1-4a	cen	cen	273,294,BGN 1:74
T 1-4b	q	p	284,285,294,BGN 1:74
T 1-4c			294,BGN 1:74
T 1-4d			229,BGN 1:74
T 1-4e	q	p	229,285,BGN 1:74
T 1-4f		p	285,BGN 1:74
T 1-4g	q	p	284,285,BGN 1:74
T 1-4h			BGN 1:74
T 1-4i		p	285,BGN 1:74
T 1-4j		p	285,BGN 1:74
T 1-4k			285,BGN 1:74
T 1-4l			BGN 4:111
T 1-4m			BGN 5:76
T 1-4n			BGN 5:76
T 1-4o			BGN 5:76
T 1-4p			BGN 5:76
T 1-4q			BGN 5:76
T 1-4r			BGN 5:76
T 1-4s			BGN 5:76
T 1-4t			BGN 5:76
T 1-4u			BGN 5:76
T 1-4v			BGN 5:76
T 1-4w			BGN 5:76
T 1-4x			BGN 5:76
T 1-4y			BGN 5:76
T 1-4z			BGN 5:76
T 1-4aa			BGN 5:76
T 1-4ab			BGN 5:76
T 1-4ac			BGN 5:76
T 1-5a	q	cen(p)	235,273,284,285,294,BGN 1:74,14:12
T 1-5b	p?	q?	273,294,BGN 1:74
T 1-5c	(cen)p	p	273,294,BGN 1:74
T 1-5d	p?	q(p)	273,294,BGN 1:74
T 1-5e	q	p	273,284,285,294,BGN 1:74
T 1-5f	p	q	273,284,285,294,BGN 1:74
T 1-5g	cen		273,285,294,BGN 1:74
T 1-5h	q?	p?	273,285,294,BGN 1:74
T 1-5i	q(p)		273,285,294,BGN 1:74
T 1-5j	q	p	273,284,285,294,BGN 1:74,14:12
T 1-5k			BGN 1:74
T 1-5l	q		285,BGN 1:74
T 1-5m	q		285,BGN 1:74
T 1-5n			BGN 1:74
T 1-5o		q	BGN 4:111
T 1-5p			BGN 4:111
T 1-5q			BGN 5:76
T 1-5r			BGN 5:76
T 1-5s			BGN 5:76
T 1-5t			BGN 5:76
T 1-5u			BGN 5:76
T 1-5v	p	q	94,BGN 5:76
T 1-5w			BGN 5:76
T 1-5x			BGN 5:76
T 1-5y			BGN 5:76
T 1-5z			BGN 5:76
T 1-5aa			BGN 5:76
T 1-5ab			BGN 5:76
T 1-5ac			BGN 5:76
T 1-5ad			BGN 5:76

T 1-5ae			BGN 5:76
T 1-5af			BGN 5:76
T 1-6a	p	sat	273,294,BGN 1:74
T 1-6b	cen	q	273,294,BGN 1:74
T 1-6c		q	273,294,BGN 1:74
T 1-6d	p	q	273,294,BGN 1:74
T 1-6e	q	p	273,285,294,BGN 1:74
T 1-6f			298,BGN 1:74
T 1-6g			BGN 1:74
T 1-6h	q		285,BGN 1:74
T 1-6i	q(p)	q	235,284,BGN 1:74,14:12
T 1-6j	q	sat	285,BGN 1:74
T 1-6k			BGN 1:74
T 1-6l			BGN 1:74
T 1-6n			BGN 4:111
T 1-6o		sat	BGN 4:111
T 1-6p			BGN 5:76
T 1-6q			BGN 5:76
T 1-6r			BGN 5:76
T 1-6s			BGN 5:76
T 1-6t			BGN 5:76
T 1-6u			BGN 5:76
T 1-6v			BGN 5:76
T 1-6w			BGN 5:76
T 1-6x			BGN 5:76
T 1-6y			BGN 5:76
T 1-6z			BGN 5:76
T 1-6aa			BGN 5:76
T 1-6ab			BGN 5:76
T 1-6ac			BGN 5:76
T 1-6ad			BGN 5:76
T 1-6ae			BGN 5:76
T 1-6af			BGN 5:76
T 1-7a	q	p	273,294,BGN 1:74
T 1-7b	cen	cen	273,294,BGN 1:74
T 1-7c	p	sat	273,284,294,BGN 1:74
T 1-7d	cen	p	273,294,BGN 1:74
T 1-7e	q	q	273,284,285,294,BGN 1:74
T 1-7f	q	q	273,284,285,294,BGN 1:74
T 1-7g			298,BGN 1:74
T 1-7h	q	q	285,BGN 1:74
T 1-7i	q	sat	BGN 1:74
T 1-7j			BGN 1:74
T 1-7k	q	q	285,BGN 1:74
T 1-7l			BGN 1:74
T 1-7m		q?	BGN 1:74
T 1-7n		p	BGN 4:111
T 1-7o			BGN 5:76
T 1-7p			BGN 5:76
T 1-7q			BGN 5:76
T 1-7r			BGN 5:76
T 1-7s			BGN 5:76
T 1-7t			BGN 5:76
T 1-7u			BGN 5:76
T 1-7v			BGN 5:76
T 1-7w			BGN 5:76
T 1-7x			BGN 5:76
T 1-7y			BGN 5:76
T 1-7z			BGN 5:76
T 1-7aa			BGN 5:76
T 1-7ab			BGN 5:76
T 2-3a	p(cen)	q(p)	273,284,285,294,BGN 1:74
T 2-3b	cen	p	273,294,BGN 1:74
T 2-3c	p(q,cen)	p(q,cen)	235,273,284,294,BGN 1:74,14:12
T 2-3d		cen	273,294,BGN 1:74
T 2-3e	q(cen)	q	273,284,285,294,BGN 1:74,14:12
T 2-3f	q	p(cen)	235,273,284,285,294,BGN 1:74,14:12
T 2-3g	q		273,284,285,294,BGN 1:74
T 2-3h	q(cen)	p(q?)	235,273,294,BGN 1:74,14:12
T 2-3i			298,BGN 1:74
T 2-3j	q	p	235,298,BGN 1:74,14:12
T 2-3k			285,BGN 1:74
T 2-3l			BGN 1:74
T 2-3m			BGN 1:74

Translocation chromosome x y	Site of interchange(s) x	y	Authority(ies)
T 2-3n			285,BGN 1:74
T 2-3o			285,BGN 1:74
T 2-3p			285,BGN 1:74
T 2-3q			BGN 2:135
T 2-3r			BGN 2:135
T 2-3s			BGN 2:135
T 2-3t			BGN 2:135
T 2-3u			BGN 4:111
T 2-3v			BGN 4:111
T 2-3w			BGN 5:76
T 2-3x			BGN 5:76
T 2-3y			BGN 5:76
T 2-3z			BGN 5:76
T 2-3aa			BGN 5:76
T 2-3ab			BGN 5:76
T 2-3ac			BGN 5:76
T 2-3ad			BGN 5:76
T 2-3ae			BGN 5:76
T 2-3af			BGN 5:76
T 2-4a	cen	cen	273,294,BGN 1:74
T 2-4b	cen		273,294,BGN 1:74
T 2-4c	cen	p	273,285,294,BGN 1:74
T 2-4d	p?	p(q)	273,285,294,BGN 1:74
T 2-4e			298,BGN 1:74
T 2-4f			BGN 1:74
T 2-4g			BGN 1:74
T 2-4h			BGN 1:74
T 2-4i		p	285,BGN 1:74
T 2-4j		p	285,BGN 1:74
T 2-4k			BGN 2:135
T 2-4l			BGN 2:135
T 2-4m			BGN 2:135
T 2-4n			BGN 2:135
T 2-4o			BGN 2:135
T 2-4p			BGN 2:135
T 2-4q			BGN 2:135
T 2-4r			BGN 2:135
T 2-4s			BGN 2:135
T 2-4t			BGN 4:111
T 2-4u			BGN 4:111
T 2-4v			BGN 4:111
T 2-4w			BGN 5:76
T 2-4x			294,BGN 5:76
T 2-4y			BGN 5:76
T 2-4z			BGN 5:76
T 2-4aa			BGN 5:76
T 2-4ab			BGN 5:76
T 2-4ac			BGN 5:76
T 2-5a	p(q)	q(p)	235,273,284,285,294,BGN 1:74,14:12
T 2-5b	q(cen)		273,284,294,BGN 1:74
T 2-5c			229,BGN 1:74
T 2-5d			229,BGN 1:74
T 2-5e			BGN 1:74
T 2-5f			BGN 1:74
T 2-5g			BGN 1:74
T 2-5h			BGN 2:135
T 2-5i			BGN 2:135
T 2-5j			BGN 2:135
T 2-5k			BGN 2:135
T 2-5l			BGN 2:135
T 2-5m			BGN 2:135
T 2-5n			BGN 2:135
T 2-5o			BGN 2:135
T 2-5p	q	q	BGN 4:111

T 2-5q			BGN 4:111
T 2-5r			BGN 4:111
T 2-5s			BGN 4:111
T 2-5t			BGN 4:111
T 2-5u			BGN 5:76
T 2-5v			BGN 5:76
T 2-5w			BGN 5:76
T 2-5x			BGN 5:76
T 2-5y			BGN 5:76
T 2-5z			BGN 5:76
T 2-5aa			BGN 5:76
T 2-5ab			BGN 5:76
T 2-5ac	cen,p	cen,q	BGN 6:43, BGN 15:79
T 2-6a	cen	q	273,294
T 2-6b	p(cen)	q?	273,284,294
T 2-6c	cen		273,299
T 2-6d			298
T 2-6e			298
T 2-6f	p	p	BGN 1:74
T 2-6g			BGN 1:74
T 2-6h	p	q	BGN 1:74
T 2-6i			BGN 1:74
T 2-6j		q?	BGN 1:74
T 2-6k			BGN 1:74
T 2-6l			BGN 2:135
T 2-6m			BGN 2:135
T 2-6n			BGN 2:135
T 2-6o			BGN 2:135
T 2-6p			BGN 2:135
T 2-6q			BGN 2:135
T 2-6r			BGN 2:135
T 2-6s	p	p	BGN 4:111
T 2-6t	p?	p?	BGN 4:111
T 2-6u	q	p	BGN 4:111
T 2-6v			BGN 5:76
T 2-6w			BGN 5:76
T 2-6x			BGN 5:76
T 2-6y	p	q	94,235,BGN 5:76
T 2-6z			BGN 5:76
T 2-6aa			BGN 5:76
T 2-6ab			BGN 5:76
T 2-6ac			BGN 5:76
T 2-7a			273,294,BGN 1:74
T 2-7b	p	q	273,284,285,294,BGN 1:74,14:12
T 2-7c	p(cen)	q	273,284,285,294,BGN 1:74
T 2-7d	p	p	273,284,285,294,BGN 1:74,14:12
T 2-7e			298,BGN 1:74
T 2-7f			BGN 1:74
T 2-7g			BGN 1:74
T 2-7h		q?	BGN 1:74
T 2-7i			BGN 2:135
T 2-7j			BGN 2:135
T 2-7k			BGN 2:135
T 2-7l			BGN 2:135
T 2-7m	p?	sat	BGN 4:111
T 2-7n	p?	p?	BGN 4:111
T 2-7o	p?	q?	BGN 4:111
T 2-7p			BGN 5:76
T 2-7q			BGN 5:76
T 2-7r			BGN 5:76
T 2-7s			BGN 5:76
T 2-7t			BGN 5:76
T 2-7u			BGN 5:76
T 2-7v			BGN 5:76
T 2-7w			BGN 5:76
T 2-7x			BGN 5:76
T 2-7y			BGN 5:76
T 2-7z			BGN 5:76
T 2-7aa			BGN 5:76
T 2-7ab			BGN 5:76
T 3-4a	cen	q	273,294,BGN 1:74
T 3-4b	cen	p	273,294,BGN 1:74
T 3-4c			273,294,BGN 1:74
T 3-4d	q		273,285,294,BGN 1:74

Translocation chromosome x y	Site of interchange(s) x	Site of interchange(s) y	Authority(ies)
T 3-4e			BGN 1:74
T 3-4f			BGN 1:74
T 3-4g		p	285,BGN 1:74
T 3-4h		p	285,BGN 1:74
T 3-4i		p	285,BGN 1:74
T 3-4j			BGN 1:74
T 3-4k			BGN 1:74
T 3-4l			BGN 1:74
T 3-4m		p	285,BGN 1:74
T 3-4n			BGN 1:74
T 3-4o			BGN 2:135
T 3-4p			BGN 2:135
T 3-4q			BGN 5:76
T 3-4r			BGN 5:76
T 3-4s			BGN 5:76
T 3-4t			BGN 5:76
T 3-4u			BGN 5:76
T 3-4v			BGN 5:76
T 3-4w			BGN 5:76
T 3-4x			BGN 5:76
T 3-4y			BGN 5:76
T 3-4z			BGN 5:76
T 3-4aa			BGN 5:76
T 3-5a	cen	cen	273,294,BGN 1:74
T 3-5b	cen	q	273,294,BGN 1:74
T 3-5c	cen	p(q)	235,273,284,285,294,BGN 1:74
T 3-5d	p(q)	q(p)	235,273,284,285,294,BGN 1:74
T 3-5e	q	p	235,BGN 1:74
T 3-5f	p	p	235,BGN 1:74
T 3-5g	cen	cen	235,285,BGN 1:74
T 3-5h	q	p	BGN 4:111
T 3-5i			BGN 4:111
T 3-5j			BGN 4:111
T 3-5k			BGN 4:111
T 3-5l	q	q	BGN 4:111
T 3-5m			BGN 5:76
T 3-5n	p	q	235,BGN 5:76
T 3-5o			BGN 5:76
T 3-5p			BGN 5:76
T 3-5q	q	q	235,BGN 5:76
T 3-5r	q	q	235,BGN 5:76
T 3-5s	q	p	235,BGN 5:76
T 3-5t	p	p	235,BGN 5:76
T 3-5u	cen	q	235,BGN 5:76
T 3-5v	q	q	235,BGN 5:76
T 3-5w	p	p	235,BGN 5:76
T 3-5x			BGN 5:76
T 3-5y			BGN 5:76
T 3-5z			BGN 5:76
T 3-5aa	p	p	235,BGN 5:76
T 3-5ab			BGN 5:76
T 3-6a			273,294,BGN 1:74
T 3-6b		q?	273,284,294,BGN 1:74
T 3-6c	p?	q?	273,284,285,294,BGN 1:74
T 3-6d	p?	q?	273,284,285,294,BGN 1:74
T 3-6e		q	273,284,285,294,BGN 1:74
T 3-6f			298,BGN 1:74
T 3-6g			298,BGN 1:74
T 3-6h			285,BGN 1:74
T 3-6i			BGN 1:74
T 3-6j	p	p	285,BGN 1:74
T 3-6k			BGN 1:74
T 3-6l	q	p	BGN 2:135
T 3-6m	q(p)	q(p)	BGN 2:135

T 3-6n	q	q	BGN 2:135
T 3-6o			BGN 5:76
T 3-6p			BGN 5:76
T 3-6q			BGN 5:76
T 3-6r			BGN 5:76
T 3-6s			BGN 5:76
T 3-6t			BGN 5:76
T 3-6u			BGN 5:76
T 3-6v			BGN 5:76
T 3-7a	cen,q	q	273,294,BGN 1:74
T 3-7b	cen,q	q	273,294,BGN 1:74
T 3-7c	q(p)	q	273,284,285,294,BGN 1:74.14:12
T 3-7d	p(q)	p	235,273,285,294,BGN 1:74,14:12
T 3-7e			298,BGN 1:74
T 3-7f			298,BGN 1:74
T 3-7g			BGN 1:74
T 3-7h		q	285,BGN 1:74
T 3-7i			285,BGN 1:74
T 3-7j			BGN 1:74
T 3-7k	q	q	BGN 2:135
T 3-7l			BGN 5:76
T 3-7m			BGN 5:76
T 3-7n			BGN 5:76
T 3-7o			BGN 5:76
T 3-7p			BGN 5:76
T 3-7q			BGN 5:76
T 3-7r			BGN 5:76
T 3-7s			BGN 5:76
T 3-7t			BGN 5:76
T 3-7u			BGN 5:76
T 3-7v			BGN 5:76
T 3-7w			BGN 5:76
T 3-7x			BGN 5:76
T 3-7y			BGN 5:76
T 3-7z			BGN 5:76
T 3-7aa			BGN 5:76
T 3-7ab			BGN 5:76
T 4-5a	q	p	273,294,BGN 1:74
T 4-5b	p	q	273,294,BGN 1:74
T 4-5c	q(p)		273,284,294,BGN 1:74
T 4-5d	q(p?)	q?	273,284,294,BGN 1:74
T 4-5e	q	q	273,284,285,294,BGN 1:74,14:12
T 4-5f			BGN 1:74
T 4-5g			BGN 1:74
T 4-5h	p		285,BGN 1:74
T 4-5i	p		285,BGN 1:74
T 4-5j	p		285,BGN 1:74
T 4-5k			BGN 1:74
T 4-5l			BGN 2:135
T 4-5m			BGN 4:111
T 4-5n			BGN 4:111
T 4-5o	q	p	BGN 4:111
T 4-5p			BGN 4:111
T 4-5q			BGN 5:76
T 4-5r			BGN 5:76
T 4-5s			BGN 5:76
T 4-5t			BGN 5:76
T 4-5u			BGN 5:76
T 4-5v			BGN 5:76
T 4-5w			BGN 5:76
T 4-5x			BGN 5:76
T 4-5y			BGN 5:76
T 4-5z			BGN 5:76
T 4-5aa			BGN 5:76
T 4-5ab			BGN 5:76
T 4-6a	p(q)	q	179,273,285,294,BGN 1:74
T 4-6b			BGN 1:74
T 4-6c	p		285,BGN 1:74
T 4-6d			BGN 1:74
T 4-6e	p		285,BGN 1:74
T 4-6f	p	q	285,BGN 1:74
T 4-6g			BGN 1:74
T 4-6h	p		285,BGN 1:74
T 4-6i			BGN 2:135

Translocation chromosome x y	Site of interchange(s) x	y	Authority(ies)
T 4-6j			BGN 4:111
T 4-6k	p	q	BGN 4:111
T 4-6l			BGN 5:76
T 4-6m			BGN 5:76
T 4-6n			BGN 5:76
T 4-6o			BGN 5:76
T 4-6p			BGN 5:76
T 4-6q			BGN 5:76
T 4-6r			BGN 5:76
T 4-6s			BGN 5:76
T 4-6t			BGN 5:76
T 4-6u			BGN 5:76
T 4-6v			BGN 5:76
T 4-7a			273,284,285,294,BGN 1:74
T 4-7b	p	sat	273,284,285,294,BGN 1:74,14:12
T 4-7c	p	q	273,294,BGN 1:74
T 4-7d			298,BGN 1:74
T 4-7e			298,BGN 1:74
T 4-7f	p	q	285,BGN 1:74
T 4-7g		q	BGN 1:74
T 4-7i	p	q	BGN 4:111
T 4-7j			BGN 5:76
T 4-7k			BGN 5:76
T 4-7l			BGN 5:76
T 4-7m			BGN 5:76
T 4-7n			BGN 5:76
T 4-7o			BGN 5:76
T 4-7p			BGN 5:76
T 4-7q			BGN 5:76
T 4-7r			BGN 5:76
T 4-7s			BGN 5:76
T 5-6a		p	273,284,285,294,BGN 1:74,4:111
T 5-6b	q?	q?	273,285,294,BGN 1:74,4:111
T 5-6c	p	p	273,284,294,BGN 1:74,4:111
T 5-6d			284,298,BGN 1:74,4:111
T 5-6e			BGN 1:74,4:111
T 5-6f		q	BGN 1:74,4:111
T 5-6g			285,BGN 1:74,4:111
T 5-6h			BGN 1:74,4:111
T 5-6i			BGN 4:111
T 5-6j			BGN 4:111
T 5-6k			BGN 4:111
T 5-6l			BGN 4:111
T 5-6m			BGN 4:111
T 5-6n			BGN 4:111
T 5-6o			BGN 4:111
T 5-6p			BGN 4:111
T 5-6q			BGN 4:111
T 5-6r			BGN 4:111
T 5-6s			BGN 4:111
T 5-6t			BGN 4:111
T 5-6u			BGN 4:111
T 5-6v			BGN 4:111
T 5-7a		cen	273,294,BGN 1:74
T 5-7b	p?	q?	273,285,294,BGN 1:74
T 5-7c			BGN 1:74
T 5-7d		q	BGN 1:74
T 5-7e			BGN 1:74
T 5-7f	q?	q	285,BGN 1:74
T 5-7g		q	285,BGN 1:74
T 5-7h	q	q	BGN 1:74
T 5-7i		q	285,BGN 1:74
T 5-7j			BGN 1:74
T 5-7k	q?	q?	BGN 4:111

T 5-7l	p	q	BGN 4:111
T 5-7m			BGN 5:76
T 5-7n			BGN 5:76
T 5-7o			BGN 5:76
T 5-7p			BGN 5:76
T 5-7q			BGN 5:76
T 5-7r			BGN 5:76
T 5-7s			BGN 5:76
T 5-7t			BGN 5:76
T 5-7u			BGN 5:76
T 5-7v			BGN 5:76
T 5-7w			BGN 5:76
T 5-7x			BGN 5:76
T 5-7y			BGN 5:76
T 5-7z			BGN 5:76
T 5-7aa			BGN 5:76
T 6-7a	cen	cen	122,273,284,285,294,BGN 1:74,14:12
T 6-7b	q	q	122,273,284,285,294,BGN 1:74,14:12
T 6-7c	p,cen	p,cen(q)	122,273,284,285,294
T 6-7d	NOR(p)	q(cen)	122,235,273,284,285,294,BGN 1:74,14:12
T 6-7e	q	p(q)	122,273,294,BGN 1:74
T 6-7f	cen	p	122,298,BGN 1:74
T 6-7g	q	q	122,229,BGN 1:74
T 6-7h	q	q	122,BGN 1:74
T 6-7i	q	p	122,285,BGN 1:74
T 6-7j			BGN 1:74
T 6-7k	p	sat	122,BGN 1:74,14:12
T 6-7l	p(cen)	p,sat	122,BGN 1:74
T 6-7m	p(cen)	q	122,235,BGN 1:74,14:12
T 6-7n	q	q	BGN 1:74
T 6-7o	q,cen?	cen?	122,BGN 2:135
T 6-7p	sat	q	122,BGN 2:135
T 6-7q	sat?	sat?	122,BGN 2:135
T 6-7r	sat?	sat?	122,BGN 2:135
T 6-7s	sat?	sat?	122,BGN 2:135
T 6-7t	q	q	122,BGN 4:111
T 6-7u			BGN 4:111
T 6-7v	p	q	122,BGN 5:76
T 6-7w	p	sat	122,BGN 5:76,14:12
T 6-7x	p	p	122,BGN 5:76
T 6-7y	q,cen	p	122,BGN 5:76
T 6-7z	q	q	122,BGN 5:76
T 6-7aa	p	p	122,BGN 5:76
T 6-7ab	p	sat?	122,BGN 5:76
T 6-7ac	p	q	122,BGN 5:76
T 6-7ad	q	q	122,BGN 5:76
T 6-7ae	sat	p	122,BGN 5:76
T 6-7af	p	q	122,BGN 5:76
T 6-7ag	p	q	122,BGN 5:76
T 6-7ah	p	q	122,BGN 5:76
T 6-7ai	p	q	122,BGN 5:76
T 6-7aj	q	q	122,BGN 5:76
T 6-7ak	sat	q	122,BGN 5:76,14:12
T 6-7al	q	p	122,BGN 5:76
T 6-7am			BGN 5:76
T 6-7an	p	sat	122,BGN 5:76
T 6-7ao			BGN 5:76
T 6-7ap	p	p	122,BGN 5:76

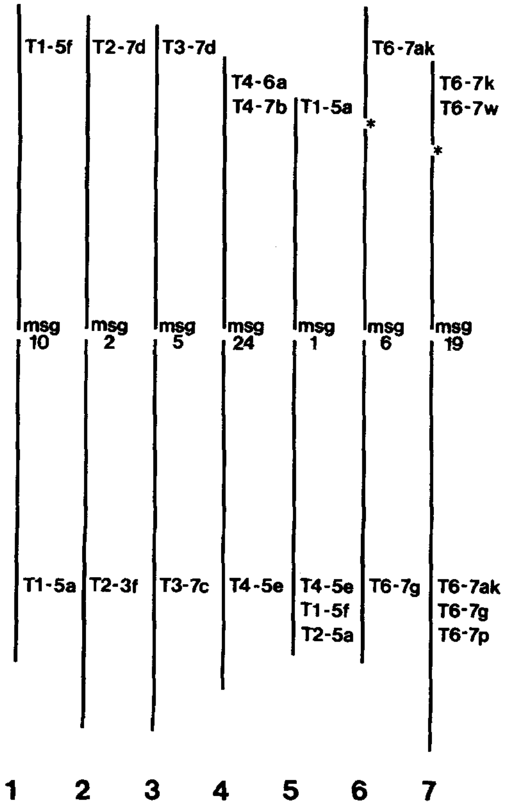

Figure 10. Idiogram of barley chromosomes. The central break in each line represents the centromere region and the distal breaks marked with asterisks represent the nucleolus organizer regions (NOR). Of the translocations in Table III those with the most distally located breakpoints according to references 94, 122 and 179 are given in this figure. They are the most suitable for assigning a mutant to the region between a breakpoint and the centromere. The set of male sterile genes (*msg*) closely linked to the centromeres (BGN 14:20) can be used to localize a mutant to the centromeric region of a chromosome.

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