

REPORTS OF THE COORDINATORS

Overall coordinator's report

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Since the latest overall coordinator's report in Barley Genetics Newsletter Volume 33, not many important changes of the coordinators have been reported. I do hope that most of you are willing to continue with this work and provide us with new important information and literature search in the future. Unhappily some of the coordinators have definitely retired from their positions or they do not find the time to prepare reports because of other commitments, or they have stopped working on barley research. The coordinator for Chromosome 3H, Roger Ellis, has retired from his position at the Scottish Crop Research Institute, United Kingdom, and we need to find a replacement. Diter von Wettstein, the coordinator for Chloroplast genes has desired to pass over this duty to Mats Hansson at the Department of Biochemistry, Lund University, Lund, Sweden. He promised to make this coordination as he intensively works on these problems. The coordinators for the Inversions, Bengt-Olle Bengtsson and Torbjörn Säll, both from the Institute of Genetics at the University of Lund, Sweden, asked to resign as they are not working with barley genetic research any more. I want to take the opportunity to thank all of them for their good corporation and their reliability of sending informative reports during all the years.

At the end of June, many of us met at the 9th International Barley Genetics Symposium in Brno, Czech Republic, and during a 'Barley Genetic Linkage Workshop' where it got intensively discussed if the current system and trait coordination should continue in this manner. I became decided to do so but with a view towards whole genome coordination in the future. The report of this workshop will be published in this or next BGN Volume.

Problems of minor modifications of Rule 6 and 7 of Gene Nomenclature were discussed and accepted at the Barley Genetic Linkage Workshop of the 9th International Barley Genetics Symposium in Brno, Czech republic, on June 19, 2004. Rules for Nomenclature and Gene Symbolization in Barley with the additional amendments will be published in this volume. Revised lists of BGS descriptions by BGS number (Table 1) and by locus symbols in alphabetic order (Table 2) are also published in this volume.

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Coordinator's Report: Barley Chromosome 1H (5)

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Long *et al.*, 2003 performed a marker regression based on a segregating population of 110 doubled haploid lines, derived from the cross 'Mundah/Keel'. Grain yield and early dry matter production were associated with the chromosome 1H fragment containing the SSR markers Bmac32 and Ebmac501. For the chromosome 1H fragment with the AFLP markers P13/M49-251 and the SSR marker Awbma35, they found associations with growth habit, early maturity, kernel yield, kernel weight and kernel screening fractions.

Read *et al.*, 2003 localised a QTL for heading date on chromosome 1H in 166 DH lines from a cross between the varieties 'Sloop' and 'Halicon'. The QTL was localised between the SNP locus SOUISC4 and the microsatellite locus Bmac0382. The marker explained 28 % of the phenotypic variance.

Pillen *et al.*, 2003 searched for associations between microsatellite markers and agronomic traits in 136 BC₂F₂ lines from an advanced backcross involving the wild barley (*Hordeum vulgare* ssp. *spontaneum*) line '101-23' and the barley variety 'Apex'. They found the following associations as expression of putative QTLs on chromosome 1H: an association between the SSR marker GMS21 and heading date, kernels per ear and kernel yield, an association between heading date and the SSR marker Bmac0213, an association between the traits heading date, plant height and lodging with the microsatellites HvALAAT, HVM20 and HVM64 and finally between the same traits and Bmag0211. For all QTLs, apart from the kernel yield related ones mentioned first, the alleles from the wild line were more favourable in relation to common breeding goals.

Mickelson *et al.*, 2003 studied nitrogen storage and remobilization in barley leaves in a RI-population based on a cross between the two barley varieties 'Karl' and 'Lewis'. On chromosome 1H, two regions of interest were detected: one QTL for "total leaf nitrogen at mid-grain fill" near the RFLP marker ABG53 and one QTL near the AFLP marker TB2122 for the traits "total leaf nitrogen at anthesis", "total leaf nitrogen at maturity" and yield.

Teulat *et al.*, 2003 found a locus with QTL x environment interaction for relative water content near the locus for black pericarp colour (*bpc*) on the long arm of chromosome 1H. The localisation was carried out in 167 recombinant inbred lines (RILs) from the cross 'Tadmor/Er-Apm', and based on data of humid as well as drought environments.

Also targeting towards genes of interest for barley cultivation under drought conditions, Baum *et al.*, 2003 were localising QTL for agronomic traits under mild and heavy drought stress. The analysis was based on 194 RIL lines from a cross between the ICARDA-variety 'Arta' and a *Spontaneum* line. Five QTLs were found on chromosome 1H: one QTL near the SSR marker Bmag0105 for biological yield and plant height, on just beside for growth habit and kernel weight, but only under favourable conditions, one for biological yield and tiller number, one for growth habit and finally one QTL for kernel weight, biological yield and tiller number.

In 150 DH lines from 'Steptoe/Morex', Han *et al.*, 2003 localised a QTL for acid detergent fibre (ADF). The locus was detected in the interval between the markers AGA006 and *Hor2* and accounted for 23.6 % of the variation for this trait.

Three QTLs for resistance against *Fusarium* head blight on chromosome 1H were localised by Dahleen *et al.*, 2003 in a DH population (75 lines) resulting from the three-way cross 'Zhedar 2/ND9712//Foster'. Those three QTLs were environment-specific.

In an attempt to analyse the relation of stoma density and "avoidance" against *Puccinia hordei*, Vaz Patto *et al.*, 2003 localised QTLs for the respective QTLs in a population of 100 F₂ plants derived from a cross between two *Hordeum chilense* accessions. On chromosome 1H, they detected a QTL for "avoidance". There was no correlation between stoma density and "avoidance".

Madsen *et al.*, 2003 described the development and localisation of Resistance Gene Analogues (RGAs) for barley. On chromosome 1H, three RGAs were localized: two (S-9217 and S-112, both between the RFLP locus MWG55 and the SSR locus Bmag0211) in the mapping population '1B-87/Vada' (Backes, *et al.*, 2003) and one (S-9240B, between the RFLP markers PSB67 and WG518) in the mapping population 'Igri/Triumph' (Laurie *et al.*, 1995).

In the above mentioned mapping population derived from a cross between the *Spontaneum*-line '1B-87' and the barley variety 'Vada' (121 RI lines), Backes *et al.*, 2003 localised a QTL for quantitative resistance against powdery mildew (caused by *Blumeria graminis*) acting additively in the field experiment at or nearby the *Mla* locus conferring qualitative resistance against the same disease.

Collins *et al.* used four different mapping populations for the localisation of QTLs for malt extract: a DH-population from the cross 'Sloop/Alexis' (Barr *et al.*, 2003), a RI-population from the cross 'Sloop-sibling/Alexis' (Barr *et al.*, 2003), a DH-population from the cross 'Galleon/Haruna Nijo' (Karakousis *et al.*, 2003) and a DH-population from the cross 'Chebec/Harrington' (Barr *et al.*, 2003). On chromosome 1H, they detected two QTLs: one near the centromere in the mapping populations 'Sloop/Alexis' (near the microsatellite locus Ebmac0501) and 'Sloop-sibling/Alexis' and one on the long arm in 'Chebec/Harrington' (near the RFLP locus BCD508).

Clancy *et al.*, 2003 localised QTLs for beta-amylase activity simultaneously in the three segregating populations derived from the crosses 'Steptoe/Morex', 'TR306/Harrington' and 'Harrington/Morex', ranging from 144 to 150 doubled haploid (DH) lines. In two of the three crosses, they found a major QTL for beta-amylase activity on the short arm of chromosome 1H close by the *Hor1* locus. An additional minor QTL for beta-amylase activity and diastatic power was detected on the same chromosome, but only in 'Steptoe/Morex'.

In a DH population of 65 lines from the cross 'Tallon/Kaputar', Cakir *et al.*, 2003 localised a QTL for diastatic power on chromosome 1H.

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Coordinator's report: Chromosome 2H (2)

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Dahleen *et al.*, 2003 and Mesfin *et al.* 2003 published papers on the inheritance of resistance to Fusarium head blight (FHB), incited primarily by *Fusarium graminearum* Schwabe), in crosses between two- and six-rowed barley. Quantitative trait loci (QTL) for FHB resistance were again reported to occur in chromosome 2H. The reports identified three QTLs for FHB resistance and two coincident QTLs for deoxynivalenol (DON) accumulation in chromosome 2H. One QTL is near the *vrs1* (six-rowed spike 1) locus and another is near the *Eam6* (early maturity 6) locus. The late two-rowed parents had QTLs for FHB resistance. Mesfin *et al.*, 2003 reported that the largest heading date effect associated with the *Eam6* gene was observed in a fall greenhouse nursery.

Krasheninnik and Franckowiak, 2003 studied that FHB resistance in the Harrington/Morex (HM) doubled-haploid population and found the largest QTL for FHB resistance in chromosome 2H. The map developed for the HM population by Marquez-Cedillo *et al.*, 2001 was used in the analysis of data. A QTL for early heading in China, a short-day environment, was at the same position in chromosome 2H as the heading date QTL reported for long-day response. This suggests that *Eam6* influences heading date in both long- and short-day environments. A preliminary report by Franckowiak *et al.*, 2003 suggests that *Eam6* is ineffective in New Zealand where days are slightly longer than 12 hours at planting.

Tanno *et al.*, 2002 used molecular marker cMWG699, which is very close (01. cM) to the *vrs1* locus, to study the origins of cultivated six-rowed barley. Based on marker differences, they divided six-rowed barleys into two distinct groups, types I and II. Type I is widely distributed while Type II is found only in the Mediterranean region. Since both types exist among two-rowed barley cultivars, six-rowed barley probably originated from at least two independent mutations at the *vrs1* locus.

Ayoub *et al.*, 2002 studied kernel size and shape in the HM doubled-haploid population. They found a large QTL for kernel size associated with the *vrs1* locus. The two-rowed cultivar, Harrington, had larger kernels than the six-rowed cultivar, Morex. Similar results on 1000-kernel weights were reported by Hori *et al.*, 2003 using another two- by six-rowed population of F₉ recombinant inbred lines. These results with previous studies that found pleiotropic effects of *vrs1* alleles on kernel size.

Weerasena *et al.*, 2003 reported on the conversion of amplified fragment length polymorphism (AFLP) marker P13M40 to a co-dominant marker for *Rph15* (reaction to *Puccinia hordei* 15) locus in chromosome 2HS. This gene conferred resistance all expect one isolate in a collection of over 350 *P. hordei* isolates (Fetch *et al.*, 1998). The leaf rust resistance gene *Rph15.ad* was shown to be an allele of the gene *Rph16.ae*, which was identified by Ivandic *et al.*, 1998 in wild barley (*Hordeum vulgare* ssp. *spontaneum*).

Backes *et al.*, 2003 identified a QTL for resistance to powdery mildew (*Blumeria graminis* f. sp. *hordei*) in chromosome 2HS and a QTL for leaf rust (*Puccinia hordei*) resistance in chromosome 2HL. The study was conducted using the progeny of a cross between 'Vada' and wild barley accession 1B-87 from Israel.

Decousset *et al.*, 2000 reported on the development of sequence tagged site (STS) primer pairs for the *Ppd-H1* or *Eam1* locus in chromosome 2HS. Plants with the *Eam1* gene are very early when grown under long-day conditions (Tohno-oka *et al.*, 2000).

Canci *et al.*, 2003 identified a minor QTL for kernel discoloration in chromosome 2H. However, two major QTLs for kernel color were found in chromosome 6H and one of these was coincident with a major QTL for high grain protein from 'Chevron'.

Li *et al.*, 2003 mapped 127 new microsatellite markers in barley. One of the four large clusters of makers that they found was in chromosome 2H.

Arru *et al.*, 2003 mapped a QTL for resistance to leaf stripe (*Pyrenophora graminea*) in chromosome 2H of 'Steptoe'. The QTL is at a different position in chromosome 2H than the *Rdg1* locus, which also confers resistance to leaf stripe of barley.

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The seed dormancy loci SD1 and SD2 of Steptoe barley have previously been mapped to chromosome 7 (5H) (Han *et al.*, 1996). SD2 had been mapped to a 8cM interval between markers ABC 309 and MWG851 at the distal end of the long arm (Ullrich *et al.*, 1996). This locus was subsequently fine mapped to a 0.8cM interval using a substitution mapping approach. The flanking markers were MWG 851D and MWG 851B (Gao *et al.*, 2003). There was probably another dormancy QTL in the ABG 496 - MWG 851C interval of 5H that reduced the dormancy effect of SD2.

The locus Ba YMV/Ba YMV-2, that provides resistance to the two strains of barley yellow mosaic virus from the barley variety Chikurin Ibaraki was mapped to chromosome 5H. Three SSR markers, Bmac 0306, Bmac 0163 and Bmac 0113 cosegregated with the resistance locus. It was concluded that the resistance locus is included in a 4.3cM interval spanned by the three markers (Werner *et al.*, 2003).

It is interesting to note that the barley yellow mosaic resistance locus *rym3* has previously been mapped to chromosome 5H (Saeki *et al.*, 1999). The resistance locus was obtained from barley line Ea52. The latter is a gamma ray induced mutant of the variety Chikurin Ibaraki.

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Coordinator's report: Chromosome 7H

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Three studies examined polymorphisms among various genotype collections. Russell *et al.*, 2003 sampled landraces from Syria and Jordan and tested polymorphism with 21 SSRs. One of the chromosome 7H SSRs tested showed three alleles while the other SSR locus had 31 different alleles in the 125 landrace accessions genotyped. Sjakste *et al.*, 2003 examined microsatellite allele inheritance in the 37 European ancestors of seven Latvian varieties. The 14 SSRs tested from chromosome 7H two to seven alleles, and an average polymorphism information content (PIC) value of 0.62, a bit above the overall PIC average of 0.57. Allelic pedigrees were constructed to trace the genetic route of each current allele back to the specific ancestral source. Lund *et al.*, 2003 used SSRs to evaluate potential duplicate groups in gene bank collections. The 35 primer pairs tested, six from chromosome 7H, identified 22 homogeneous groups among the 36 groups studied, providing a rapid method for identifying duplicates.

Pillen *et al.*, 2003 conducted a QTL analysis of a BC₂F₂ population between an *H. v. spontaneum* and the recurrent spring barley Apex. QTLs for heading date, harvest index, malt tenderness, yield, height, thousand-grain weight, water absorption, and above ground biomass were located on chromosome 7H. Many of the favorable alleles for these important traits were from *H. v. spontaneum*. Matus *et al.*, 2003 developed recombinant chromosome substitution lines by backcrossing an *H. vulgare* subsp. *spontaneum* accession to Harrington barley. They then used 47 SSR markers to determine the percentage of *spontaneum* introgressed into the lines. The average length of the donor segment in chromosome 7H was 39.0 cM, with segregation distorted towards the donor's DNA. Baum *et al.*, 2003 tested recombinant inbred lines from another *H. v. spontaneum* cross, with Arta. They developed a linkage map on 189 markers, including 24 on chromosome 7H. QTLs located on this chromosome included those for grain yield, 1000-kernel weight, days to heading, plant height, beta-glucan content, biological yield, and cold damage. Only the QTL for cold damage was significant in more than one environment. SSRs were used with genomic in situ hybridization (GISH) to evaluate wheat x barley backcross-derived lines (Malysheva *et al.*, 2003). One BC₁ plant contained only two small 7H fragments which were not transmitted to the progeny. The other plant contained the complete chromosome 7H. Only the end of the short arm was detected in BC₂ progeny. Similar patterns of elimination were observed for other chromosomes.

Several groups reported on the development of additional markers. Li *et al.*, 2003 developed 127 new SSR markers from genomic clones. Nine of the SSRs were located on chromosome 7H. Thiel *et al.*, 2003 developed 76 new SSR markers from EST database information; seven were on chromosome 7H. Kota *et al.*, 2003 also used EST collections to identify single nucleotide polymorphisms (SNPs) in barley. Of the 28 SNPs mapped in this study, three were on chromosome 7H. Another type of marker, based on NBS-LRR class resistance gene analogs (RGAs), was developed and mapped by Madsen *et al.*, 2003. Three of these RGAs mapped to chromosome 7H.

Placement of morphological markers on the molecular maps continued. Pozzi *et al.*, 2003 mapped 29 developmental mutants using RFLP-AFLP techniques. Both the *lks2* gene for short awns and the *sld4* gene for slender dwarf 4 were placed on the Proctor x Nudinka AFLP map of chromosome 7H. Dahleen *et al.*, 2003 identified linkages between SSR markers on chromosome 7H and the *lks.o* and *bra-a.001* morphological genes. Kikuchi *et al.*, 2003 fine-mapped the naked caryopsis gene, *nud*, using bulked segregant analysis and AFLP markers. The *nud* locus was mapped within a 1.5 cM region and cosegregated with two AFLP markers. Their data show that *nud* is further from the centromere than previously reported.

Gene mapping reports also included those involved in disease response. Chen *et al.*, 2003 compared genomic locations of rice and barley QTLs for resistance to rice blast. The 12 QTLs in barley included three on chromosome 7H. One of these loci was syntenic to a locus on rice chromosome 8. One of the QTL maps for Fusarium head blight (FHB), developed by Mesfin *et al.*, 2003, identified several FHB QTLs, but only detected one small QTL for resistance in the greenhouse on chromosome 7H. Rostoks *et al.*, 2003 isolated and mapped genes homologous to

maize hypersensitive-induced reaction (*HIR*) genes. *Hv-hir4* was located on the short arm of chromosome 7H in bin 03. This genes was similar to the other three *HIR* genes at the amino acid level, but not at the sequence level.

QTL analysis of recombinant inbred lines from a 2-rowed by 6-rowed spring barley cross was conducted using a map developed using the high efficiency genome scanning system (Hori *et al.*, 2003). This system allowed map construction in six months, and QTLs for plant height and spike exertion were located on chromosome 7H. Teulat *et al.*, 2003 located QTLs for relative water content in field-grown barley. One QTL representing main and QTL x E effects and one QTL that was detected only in one environment were located on chromosome 7H. Clancy *et al.*, 2003 conducted comparative mapping of beta-amylase activity QTLs among the three mapping populations from the North American Barley Genome Project. Both populations involving Morex showed coincident QTLs for beta amylase and diastatic power on chromosome 7H. This region contains several other QTL for malting quality. QTLs for kernel discoloration and grain protein content were located by Canci *et al.*, 2003. Two QTLs for kernel discoloration located on chromosome 7H were detected in a single environment, explaining 6.4-10.1 % of the variation for this trait. No regions on this chromosome were associated with grain protein content.

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Integrating Molecular and Morphological/Physiological Marker Maps

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During the past year I have attempted to integrate the Morphological /Physiological/ Disease resistance markers into the molecular Bin map. The results were sent to Grain Genes to produce an integrated map. My goal is to produce an interactive map that would incorporate pictures of markers that are “photogenic”, descriptions of markers, high resolution maps where available, BAC clone addresses, etc. The results can be viewed at <http://ceres.plbr.cornell.edu/cgi-bin/gbrowse>. This is obviously a work in progress, but to date it is not very viewer friendly or easy to navigate through, but the information is there. For those who would prefer the information in a less cumbersome form I reproduce it her, minus the pictures and high resolution maps, of course.

Please advise me if you have additions or corrections to this information.

Bin Assignments for Morphological Map Markers and closest molecular marker

Chr.1(7H)

BIN1	Rpg1	RSB228	Brueggeman et al., PNAS 99:9328, '02
	Run1		
	Rdg2a	MWG851A	Bulgarelli et al., TAG 108:1401-1408, '04
	Rrs2	MWG555A	Schweizer et al., TAG 90:920, '95
	mlt		
	brh1	MWG2074B	Li et al., 8th IBGS 3:72, '00
BIN2	Est5	iEst5	Kleinhofs et al., TAG 86:705, '93
	wax	Wax	Kleinhofs BGN32:152, '02
	gsh3	His3A	Kleinhofs BGN32:152, '02
BIN3	fch5	ABC167A	Kleinhofs BGN32:152, '02
	Rcs5	KAJ185	Johnson & Kleinhofs, unpublished
	yvs2		
	cer-ze	ABG380	Kleinhofs BGN27:105, '96
BIN4	wnd		
	Lga	BE193581	Johnson & Kleinhofs, unpublished
	abo7		
BIN5	ant1		
	nar3	MWG836	Kleinhofs BGN32:152, '02
	ert-m		
	ert-a		
BIN6	ert-d		
	fch8		
	fst3		
	cer-f		
	dsp1		
	msg14		
BIN7	msg10		
	rsm1	BC455	Edwards & Steffenson, Phytopath. 86:184, '96
	sex6		
	seg5		
	seg2		
	pmr	ABC308	Kleinhofs BGN27:105, '96
	mo6b	Hsp17	Soule et al., J Her. 91:483, '00
	nud	CDO673	Heun et al., Genome 34:437, '91
	fch4	MWG003	Kleinhofs BGN27:105, '96
BIN8	Amy2	Amy2	Kleinhofs et al., TAG 86:705, '93
	lks2	WG380B	Costa et al., TAG 103:415, '01
	Rpt4	Psr117D	Williams et al., TAG 99:323, '99
	ubs4		
	blx2		
BIN9	lbi3		
	xnt4		
	lpa2	?	Larson et al., TAG 97:141, '98
	msg50		
	Rym2		
	seg4		
BIN10	Xnt1	BF626025	Hansson et al., PNAS 96:1744, '99
	xan-h	BF626025	Hansson et al., PNAS 96:1744, '99
BIN11	Rph3	Tha2	Toojinda et al., TAG 101:580, '00
BIN12	Mlf		
	xnt9		
	seg1		
	msg23		
BIN13	none		
BIN14	none		

Chr.2(2H)

BIN1	sbk		
BIN2	none		
BIN3	gsh6	MWG878A	Kleinhofs BGN32:152, '02
	gsh1		
	gsh8		
BIN4	Eam1		
	Ppd-H1	MWG858	Laurie et al., Heredity 72:619, '94
	sld2		
	rtt		
	flo-c		
	sld4		
BIN5	fch15		
	brc1		
	com2		
BIN6	msg9		
	abo2		
	rph16	MWG874	Drescher et al., 8thIBGS II:95, '00
BIN7	yst4	CDO537	Kleinhofs BGN32:152, '02
	Az94	CDO537	Kleinhofs BGN32:152, '02
	gai	MWG2058	Börner et al., TAG 99:670, '99
	msg33		
	msg3		
	fch1		
BIN8	Eam6	ABC167b	Tohno-oka et al., 8thIBGS III:239, '00
	gsh5		
	msg2		
	eog	ABC451	Kleinhofs BGN27:105, '96
	abr		
	cer-n		
BIN9	Gth		
	hcm1		
	wst4		
	vrs1	MWG699	Komatsuda et al., Genome 42:248, '00
BIN10	cer-g		
	Lks1		
	mtt4		
	Pre2		
	msg27		
	ant2		
BIN11	Rha2	AWBMA21	Kretschmer et al., TAG 94:1060, '97
	Rar1	AW983293B	Freialdenhoven et al., Plt. Cell 6:983, '94
	fö1-a		
	gal	MWG581A	Börner et al., TAG 99:670, '99
	fch14		
	Pau		
BIN12	Pvc		
BIN13	lig	BCD266	Pratchett & Laurie Hereditas 120:35, '94
	nar4	Gln2	Kleinhofs BGN27:105, '96
	Zeo1	cnx1	Costa et al., TAG 103:415, '01
	lpa1	ABC157	Larson et al., TAG 97:141, '98
BIN14	none		
BIN15	gpa	CDO036	Kleinhofs BGN27:105, '96
	wst7	MWG949A	Costa et al., TAG 103:415, '01
	MIa	Ris16	Giese et al., TAG 85:897, '93
	trp		

Chr. 3(3H)

BIN1	Rph5 Rph6 Rph7	MWG848	Brunner et al., TAG 101:783, '00
BIN2	ant17 sld5 mo7a brh8	ABC171A	Soule et al., J. hered. 91:483, '00
BIN3	xnt6		
BIN4	btr1 btr2 lzd		
BIN5	alm abo9 sca yst2 dsp10	ABG471	Kleinhofs BGN27:105, '96
BIN6	Rrs1 Rrs.B87 Rh/Pt abo6 xnt3 msg5 ari-a yst1 zebl ert-c ert-ii cer-zd Ryd2	BCD828 ABG396 WG889B	Graner et al., TAG 93: 421 '96 Williams et al., Plant Breed. 120:301, '01 Smilde et al., 8th IBGS 2:178, '00 Collins et al., TAG 92:858, '96
BIN7	uzu cer-r		
BIN8	wst6 cer-zn sld1		
BIN9	wst1		
BIN10	vrs4 lnt1 gsh2		
BIN11	als sdw1	PSR170	Laurie et al., Plant Breed. 111:198, '93
BIN12	sdw2		
BIN13	Pub	ABG389	Kleinhofs et al., TAG 86:705, '93'
BIN14	cur2		
BIN15	Rph10 fch2		
BIN16	eam10 Est1/2/3 rym4 rym5 Est4 ant28	MWG010 MWG838	Graner & Bauer TAG 86:689, '93 Graner et al., TAG 98:285, '99

Chr.4(4H)

BIN1	none		
BIN2	fch9 sln		
BIN3	int-c Zeo3 Dwf2	Ole1	Ivandic et al., TAG 98:728, '99
	Ynd glo-a rym1	?	Konishi et al., TAG 94:871, '97
BIN4	Kap lbi2 zeb2 lgn3	X83518	Muller et al., Nature 374:727, '95
BIN5	lgn4 lks5 eam9 msg24		
BIN6	glf1 rym11 Mlg cer-zg brh2	MWG2134 MWG032	Bauer et al., TAG 95:1263, '97 Kurth et al., TAG 102:53, '01
BIN7	glf3 frp min1 blx4 sid blx3		
BIN8	blx1		
BIN9	ert1		
BIN10	mlo	P93766	Bueschges et al., Cell 88:695, '97
BIN11	none		
BIN12	Hsh Hln sgh1 yhd1	HVM067	Costa et al., TAG 103:415, '01
BIN13	Bmy1 rym8 rym9 Wsp3	pcbC51 MWG2307 MWG517	Kleinhofs et al., TAG 86:705, '93 Bauer et al., TAG 95:1263, '97 Bauer et al., TAG 95:1263, '97

Chr. 5(1H)

BIN1	Rph4 Mlra Cer-yy Sex76	Hor2	Netsvetaev BGN27:51, '97
	Hor5	Hor5	Kleinhofs et al., TAG 86:705, '93
BIN2	Hor2	Hor2	Kleinhofs et al., TAG 86:705, '93
	Rrs14	Hor2	Garvin et al., Plant Breed. 119:193-196, '00
	Mla6	AJ302292	Halterman et al., Plt J. 25:335, '01
BIN3	Hor1	Hor1	Kleinhofs et al., TAG 86:705, '93
	Rps4 Mlk		
BIN4	Lys4		
BIN5, 6, 7.		Mlnn; msg31; sls; msg4; fch3;	
BIN6	am01		
BIN7	clh vrs3		
BIN8	fst2 cer-zi cer-e ert-b MlGa msg1 xnt7		
BIN9	nec1		
BIN10	abo1 Glb1		
BIN11	wst5 cud2		
BIN12	rlv lel1		
BIN13	Blp	ABC261	Costa et al., TAG 103:415, '01
BIN14	fch7 trd eam8		

Chr. 6(6H)

BIN1	Nar1 abo15	X57845	Kleinhofs et al., TAG 86:705, '93
BIN2	nar8 nec3 Rrs13	ABG378B	Kleinhofs BGN27:105, '96
BIN3	none		
BIN4	msg36		
BIN5	nec2 ant21 msg6 eam7		
BIN6	rob sex1 gsh4 ant13 cul2 fch11 mtt5 abo14	HVM031 Crg4(KFP128)	Costa et al., TAG 103:415, '01 Babb & Muehlbauer BGN31:28, '01
BIN7	none		
BIN8	none		
BIN9	Amy1 Nar7 Nir mul2 cur3	JR115 X60173 pCIB808	Kleinhofs et al., TAG 86:705, '93 Warner et al., Genome 38:743, '95 Kleinhofs et al., TAG 86:705, '93
BIN10	lax-b raw5 cur1		
BIN11	none		
BIN12	xnt5 Aat2		
BIN13	Rph11 lax-c	Acp3	Feuerstein et al., Plant breed. 104:318, '90'
BIN14	dsp9		

Chr. 7(5H)

BIN1	abo12 msg16 ddt		
BIN2	dex1 msg19 nld fch6 glo-b		
BIN3	cud1 lys3 fst1 blf1 vrs2	ABG705A	
BIN4	cer-zj cer-zp msg18 wst2 Rph2 lax-a com1 ari-e ert-g ert-n	ITS1 PSR118	Borovkova et al., Genome 40:326, '97 Laurie et al., TAG 93:81, '96
BIN5	rym3	MWG028	Saeki et al., TAG 99:727, '99
BIN6	none		
BIN7	none		
BIN8	none		
BIN9	srh cer-I mtt2 lys1 cer-t dsk var1 cer-w Eam5	ksuA1B	Kleinhofs et al., TAG 86:705, '93
BIN10	raw1 msg7		
BIN11	Rph9/12 Sgh2 lbi1 Rha4 raw2	ABG712	
BIN12	none		
BIN13	rpg4 RpgQ	ARD5303 ARD5304	Druka et al., Mol.Gen.Genet. 264:283-290, '00 Sun et al., Phytopath. 86:1299-1302, '96
BIN14	var3		

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Coordinator's report: Barley Genetic Stock Collection

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Over 100 barley genetic male sterile stocks were planted in the greenhouse for seed increase. One hundred seventy-eight barley translocation stocks were increased in the field. In collaboration with Dr. Jerry Franckowiak, over 780 barley genetic stocks derived from crossing with cultivar 'Bowman' were planted in the field at Aberdeen in two-rowed single plot for seed increase and for agronomic evaluation.

Over one hundred-thirty barley genetic stocks were shipped to researchers in 2003.

Thirty-eight nitrate reductase deficient mutants obtained from Dr. Andy Kleinhofs (Table 1) were increased in the field in 2003.

Eleven globosum mutants from Dr. G. Fischbeck: glo-b.1 (W1), glo-b.2 (W2), glo-b.3 (W3), glo-b.4 (W4), glo-b.5 (W5), glo-d.1 (W6), glo-d.2 (W7), glo-d.3 (W8), glo-c (W9), glo-a (W10), and glo-e (W11) were increased in the field in 2003.

Ten translocation lines from Dr. Andreas Houben: T1-al, T1-6ai, T1-7ao, T2-5ah, T2-6aq, T2-7aj, T3-4ae, T3-7ax, T3-7aaa, and T5-6 ap, are being increased in the greenhouse, 2004.

Table 1. Nitrate reductase deficient mutants received from Dr. Andy Kleinhofs.

Entry	Gene Symbol	Line No.		Function or Chemical Pathway
1	nar1a	AZ12	84-151	NADH NR structural gene
2	nar1b	AZ13	Spillman 6758	NADH NR structural gene
3	nar1c	AZ23	84-155	NADH NR structural gene
4	nar1d	AZ28	85-101	NADH NR structural gene
5	nar1e	AZ29	77-5-2	NADH NR structural gene
6	nar1f	AZ30	85-102	NADH NR structural gene
7	nar1g	AZ31	85-103	NADH NR structural gene
8	nar1h	AZ32	85-104	NADH NR structural gene
9	nar1i	AZ33	85-105	NADH NR structural gene
10	nar1j	Xno29	G84-1020-1034	NADH NR structural gene
11	nar1k	EMS29	86-117 (1-4)	NADH NR structural gene
12	nar1l	EMS31	86-128-6	NADH NR structural gene
13	nar1m	AZ56	87-160-4	NADH NR structural gene
14	nar1n	AZ57	87-161-14	NADH NR structural gene
15	nar1p	AZ63	87-162-11	NADH NR structural gene
16	nar1q	AZ64	87-163-4	NADH NR structural gene
17	nar1r	AZ65	89-144-5	NADH NR structural gene
18	nar1t	AZ67	88-324-3	NADH NR structural gene
19	nar1ab	AZ76	87-165-3	NADH NR structural gene
20	nar1ac	AZ77	87-166-6	NADH NR structural gene
21	nar1ai	AZ79	87-167-3	NADH NR structural gene
22	nar1aj	AZ80	87-168-7	NADH NR structural gene
23	nar1ao	BSMV1	88-272-1	NADH NR structural gene
24	nar2a	AZ34	85-106	molybdenum cofactor
25	nar2ad	R9401	91-393-2 (het)	molybdenum cofactor
26	nar2ag	R9201	92-195-2 (het)	molybdenum cofactor
27	nar3a	Xno18	G84-996-1004 (het)	molybdenum cofactor
28	nar3b	Xno19	G84-1005-1019(het)	molybdenum cofactor
29	nar3x	AZ71	92-29-2	molybdenum cofactor
30	nar4y	AZ72	90-43-6 (het)	molybdenum cofactor
31	nar5o	AZ62	88-59-5	molybdenum cofactor
32	nar5s	AZ66	93-161-2	molybdenum cofactor
33	nar5u	AZ68	91-378-4	molybdenum cofactor
34	nar6v	AZ69	90-59-8 (het)	molybdenum cofactor
35	nar7w	AZ70	86-230	NAD(P)H NR structural gene
36	nar8z	AZ73	90-86-10 (het)	molybdenum cofactor
37	nar9ap	AZ94	90-113-6 (het)	nitrate toxicity
38	-	AZ86	90-92-2 (het)	nitrate toxicity

Coordinator's report: Trisomic and aneuploid stocks

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There is no new information about trisomic and aneuploid stocks. A list on these stocks are available in BGN 25:104. Seed request for these stocks should be sent to the coordinator.

Coordinator's report: Autotetraploids

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The collection of barley autotetraploids (exclusively spring types) described in former issues of BGN is maintained at the Giessen Field Experiment Station of our institute. The set of stocks, i.e. autotetraploids (4n) and corresponding diploid (2n) progenitors (if available) have last been grown in the field for seed multiplication in summer 2000. Limited seed samples of the stocks are available for distribution.

Coordinator's report: The Genetic Male Sterile Barley Collection

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The GMSBC has been at Brandon since 1992. If there are any new sources of male-sterile genes that you are aware of, please advice me, as this would be a good time to add any new source to the collection. For a list of the entries in the collection, simply E-mail me at the above adress. I can send the file (14Mb) in Excel format. We continue to store the collection at -20°C and will have small (5 g) samples available for the asking. Since I have not received any reports or requests the last years, there is absolutely no summary in my report.

Coordinator's report: Translocations and balanced tertiary trisomics

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Different translocation lines have been used to evaluate the influence of recombinantly-elongated chromosome arms on nuclear divisions in barley. Hudokova *et al.*, 2002 confirmed a rule according to which half the length of the average spindle axis defines the upper tolerance limit for chromosome arm length. A slightly longer chromosome arm caused incomplete separation of sister chromatids in similar to 70% of mitotic telophase cells and >2.5% of daughter cells showing a micronucleus, due to disruption of non-separated sister chromatids by the newly forming cell wall. In homozygous condition, this elongated chromosome mediated a slower growth and reduced fertility of the carrier plants. Its meiotic transmission was not impaired because of the larger spindle dimensions in meiocytes as compared to those in mitotic cells.

PCR with the DNA of translocation chromosomes and marker-specific primers has been used to merge genetically mapped microsatellite (MS) markers into the physically integrated restriction fragment length polymorphism (RFLP) map of barley chromosome 3H. It was shown that the pronounced clustering of MS markers around the centromeric region within the genetic map of this chromosome results from suppressed recombination. This yielded a refinement of the physically integrated RFLP map of chromosome 3H by subdivision of translocation breakpoints (TBs) that were previously not separated by markers. The physical distribution of MS markers within most of the subchromosomal regions corresponded well with that of the RFLP markers, indicating that both types of markers are similarly valuable for a wide range of applications in barley genetics (Künzel and Waugh, 2002).

Ten barley translocation stocks have been sent to An Hang (USDA, Aberdeen, USA). There were no requests for samples of balanced tertiary trisomics stock collection.

The collection is being maintained in cold storage. To the best knowledge of the coordinator, there are no new publications dealing with balanced tertiary trisomics in barley. Limited seed samples are available any time, and requests can be made to the coordinator.

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- Hudakova S, Kunzel G, Endo TR, Schubert I, 2002: Barley chromosome arms longer than half of the spindle axis interfere with nuclear divisions. *Cytogenetic and Genome Research* 98: 101-107.
- Künzel G, Waugh R, 2002: Integration of microsatellite markers into the translocation-based physical RFLP map of barley chromosome 3H. *Theor. Appl. Genet.* 105:660-66

Coordinator's report: *Eceriferum* Genes

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No research work on gene localization has been reported on the collections of *Eceriferum* and *Glossy* genes since the latest reports in Barley Genetics Newsletter (BGN). All information and descriptions done in Barley Genetics Newsletter (BGN) Volume 26 are valid and still up-to-date. The databases of the Swedish collection has been updated during the last months and will soon be searchable within International European databases. As my possibilities in searching literature are very limited, I apologize if I am missing any important papers. Please send me notes of publications and reports to include in next year's reports. Descriptions, images and graphic chromosome maps displays of the *Eceriferum* and *Glossy* genes are available in the AceDB database for Barley Genes and Barley Genetic Stocks, and they get currently updated. Its address is found by: www.untamo.net/bgs

Every research of interest in the field of *Eceriferum* genes, 'Glossy sheath' and 'Glossy leaf' genes can be reported to the coordinator as well. Seed requests regarding the Swedish mutants can be forwarded to the Nordic Gene Bank, nordgen@ngb.se, all others to the Small Grain Germplasm Research Facility (USDA-ARS), Aberdeen, ID 83210, USA, anhang@uidaho.edu or to the coordinator at any time.

Coordinator's report: Nuclear genes affecting the chloroplast

Diter von Wettstein

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The stock list and genetic information presented in the Barley Genetics Newsletter 21: 102-108 is valid and up-to-date. The stocks have been transferred to the Nordic Gene Bank. Requests for stocks available for distribution are to be either sent to:

Dr. Mats Hansson
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Center for Chemistry and Chemical Engineering
Lund University
P.O.Box 124
SE-221 00 Lund, SWEDEN
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E-mail: Mats.Hansson@biokem.lu.se

or to

Nordic Gene Bank
P.O. Box 41
SE-230 53 Alnarp
Sweden
Phone: +46 40 536640
FAX: +46 40 536650
e-mail: nordgen@ngb.se

References:

- A. Hansson, R.D. Willows, T.H. Roberts and M. Hansson 2002. Three semidominant barley mutants with single amino acid substitutions in the smallest magnesium chelatase subunit form defective AAA⁺ hexamers. *Proc. Natl. Acad. Sci. USA* 99: 13944-13949.
- U. Olsson, N. Sirijovski and M. Hansson 2003. Characterization of eight barley *xantha-f* mutants, deficient in magnesium chelatase. *In*: U. Olsson: Ferrochelatase and Magnesium chelatase: Metal chelation studies with mutants. pp.146. Doctoral Dissertation, Department of Biochemistry, Lund University. (4: 1-13). ISBN 91-7422-031-4. E-mail: Mats.Hansson@biokem.lu.se

Coordinator's report: Semidwarf genes

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Zhang 2003 traced the pedigree history of more than 350 dwarf and semidwarf barley cultivars released in China since 1950. The results showed that 68.4% of the cultivars were derived from six semidwarf accessions. 'Chibadamai', 'Xiaoshanlixiahuang', and 'Changzhouluodamai' are landraces and are in the pedigrees of many semidwarf cultivars released between 1950 and 1980. They have the same temperature sensitive dwarfing gene, *uzu* (uzu dwarf), which is located in chromosome 3HL (Zhang 2000). The other three sources are in released cultivars since 1980. 'Aiganqi' contains the *uzu* dwarfing gene. The dwarfing genes in 'Zhepi 1' and 'Yanfu Aizao 3' were not identified. Zhepi 3 was selected from a cross to Zhaori 19 and released by the Zhejiang Academy of Agricultural Sciences in 1978. Yanfu Aizao 3, which was released in Jiangsu Province in 1980, is a gamma-ray induced mutant of the Japanese barley 'Zaoshu 3'.

In another paper, Zhang and Zhang 2003 reported their results from inheritance and allelism tests of reduced plant height using 25 Chinese accessions. Twenty of the accessions showed monogenic recessive inheritance patterns and four had digenic recessive patterns. Eleven of the monogenic accessions and two of the digenic accessions contained alleles at the *uzu* locus. Accession '1974E' had the *uzu* gene plus a dominant dwarfing gene. Two of monogenic accessions and one digenic accession had alleles to the mutant in India Dwarf. Based on the crosses the *uzu* stock and India Dwarf, eight potential new dwarfing genes were identified.

Zhang and Zhang 2003 demonstrated that the dwarfing gene in India Dwarf is not *sdw1* (semidwarf 1). Studies on the dwarfing gene in India Dwarf are not complete. Thus, its relationship to the *sld5.e* (slender dwarf 5) gene, which was reported to have been derived from Indian Dwarf (CIho 13994) (Franckowiak 2002), is unknown. Because the *sld5.e* gene backcrossed into Bowman produces relatively weak plants that have little agronomic potential, different genes may be present in the dwarf accessions from India. Zhang (personal communications) reported that the dwarfing gene in Zhepi 1 is allelic to the one present in the Chinese India Dwarf accession.

The dwarfing gene in Zhepi 1 may be of agronomic interest because it does not seem to delay maturity like the *sdw1* gene. The *sdw1* gene delays maturity about three days in the Upper Midwest of the USA and has not been incorporated into cultivars recommended for malting and brewing (Hellewell *et al.*, 2000). The alleles *sdw1.a* (Jotun) and *sdw1.c* (denso) at the *sdw1* locus are used to reduce plant height in many semidwarf cultivars in North America and Europe, respectively (Hellewell *et al.*, 2000).

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- Zhang, J., and W. Zhang. 2003. Tracing sources of dwarfing genes in barley breeding in China. *Euphytica* 131:285-293.

Coordinator's report: Ear morphology genes

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No new research on gene localization or descriptions on different morphological genes have been reported since the latest reports in Barley Genetics Newsletter (BGN). All descriptions made in the volumes 26, 28, 29 and 32 are still up-to-date and valid. The databases of the Swedish Ear morphology genes have been updated during the last months and will soon be searchable within International European databases. As my possibilities in searching literature are very limited, I apologize if I am missing any important papers. Please send me notes of publications or reports to include in next year's reports. Descriptions, images and graphic chromosome maps displays of the Ear morphology genes are also available in the AceDB database for Barley Genes and Barley Genetic Stocks, and they get currently updated. Its address is found by : www.untamo.net/bgs

Every research of interest in the field of Ear morphology genes can be reported32 are still up-to-date and valid. The databases of the Swedish Ear morphology genes have been updated during the last months and will soon be searchable within International European databases. As my possibilities in searching literature are very limited, I apologize if I am missing any important papers. Please send me notes of publications or reports to include in next year's reports. Descriptions, images and graphic chromosome maps displays of the Ear morphology genes are also available in the AceDB database for Barley Genes and Barley Genetic Stocks, and they get currently updated. Its address is found by : www.untamo.net/bgs

Every research of interest in the field of Ear morphology genes can be reported to the coordinator as well. Seed requests regarding the Swedish mutants can be forwarded to the Nordic Gene Bank, nordgen@ngb.se, all others to the Small Grain Germplasm Research Facility (USDA-ARS), Aberdeen, ID 83210, USA, anhang@uidaho.edu or to the coordinator at any time.

Coordinator's report: Early maturity genes

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No new research work on gene localization has been reported on the Early maturity or Praematurum genes since the latest reports in Barley Genetic Newsletter (BGN). All information and descriptions made in Barley Genetics Newsletter (BGN) Volumes 26 and 32 are valid and up-to-date. The database of the Swedish Praematurum genes has been updated during the last months and will soon be searchable within International European databases. As my possibilities in searching literature are very limited, I apologize if I am missing any important papers. Please send me notes of publications or reports to include in next year's reports. Descriptions, images and graphic chromosome maps displays of the Early maturity or Praematurum genes are available in the AceDB database for Barley Genes and Barley Genetic Stocks, and they get currently updated. Its address is found by: www.untamo.net/bgs

Every research of interest in the field of Early maturity or Preamaturum genes can be reported to the coordinator as well. Seed requests regarding the Swedish mutants can be forwarded to the Nordic Gene Bank, nordgen@ngb.se, all others to the Small Grain Germplasm Research Facility (USDA-ARS), Aberdeen, ID 83210, USA, anhang@uidaho.edu or to the coordinator at any time.

Coordinator's report:Wheat-barley genetic stocks

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The production of amphiploid of *Hordeum marinum* with both durum and common wheat has been reported earlier. The amphiploid with common wheat has been backcrossed onto the wheat parent to change the cytoplasmic background to wheat. It has recently been possible to select six different monosomic addition lines (1Hm, 2Hm, 4Hm, 5Hm, 7Hm and possibly 6Hm) from among the second backcross progeny (Islam and Colmer, unpublished).

Disease and pest resistance genes

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(in preparation)