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REPORTS OF THE COORDINATORS

Overall coordinator's report

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Since the latest overall coordinator's report in Barley Genetics Newsletter Volume 34, not too many 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. In the meantime a replacement was found for Chromosome 3H, namely Luke Ramsey, Cell and Molecular Genetics Department, Scottish Crop Research Institute, Invergowrie, Dundee, DD2 5DA, United Kingdom. Please observe some address changes have taken place since the last volume of BGN.

The report of the 'Barley Genetic Linkage Workshop' from the 9th International Barley Genetics Symposium in Brno, Czech Republic, 2004, is published in this volume. As it became decided that the current system and trait coordination should continue but with a view towards whole genome coordination, Bill Thomas and Dave Marshall from the Scottish Crop Research Institute, Invergowrie, Dundee, UK, are investigating the potential of modernizing the overall system and integrating all types of current and historic data collections into a single, combined database. More details about this subject are found in the Workshop report in this volume.

Revised and new descriptions of barley genes will be published in this current volume. Also revised lists of BGS descriptions by BGS numbers (Table 2) and by locus symbols in alphabetic order (Table 3) will be republished in this issue. Rules for Nomenclature and Gene Symbolization in Barley with the changed and additional amendments will again be published in this volume.

The AceDB database for 'Barley Genes and Barley Genetic Stocks' is updated continouosly and some more images are added. Also the germplasm part is under revision.

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Grewal *et al.,* (2005) localised a locus for resistance against covered smut caused by *Ustilago hordei* indirectly to the chromosome arm 1HS. Earlier (Ardiel *et al*., 2002), this locus was found to be linked with the RAPD-marker OPJ10$_{450}$ that was converted into a SCAR marker (UhR 450). This SCAR marker was then localized on chromosome 1HS.

Rajasekaran *et al.*, (2004) localised QTLs in a 184 RI line population of a cross between the spring barley varieties 'Tankard' and 'Livet'. They detected one QTL for 'kernel splitting', 'milling energy', 'sieve fraction > 2.5 mm', grain shape, 'gape between lemma and palea' and kernel weight between the loci Bmag504 and HvBDG. This QTL had the highest LOD score within the detected QTLs in for kernel splitting and milling energy.

In a DH population (136 lines) from cross between a winter barley ('Nure') and spring barley variety ('Tremois') winter hardiness and heading date with and without vernalization were determined (Francia *et al.*, 2004). One QTL for heading date with vernalization was found on chromosome 1H nearby the microsatellite marker Bmac0032.

One QTL for kernel weight on the long arm of chromosome 1H and one for kernel number per area on the short arm of chromosome 1H were detected by Verhoeven *et al.*, (2004) in 140 F$_{2:3}$-families from the cross of two *H. vulgare* ssp. *spontaeum* accessions from contrasting habitats. The aim of the study was to determine QTLs for fitness traits leading to adaptation and population differentiation. The linkage map was purely based on AFLP markers. Based on the same population, Elberse *et al.*, (2004) published a further analysis with growth chamber experiments under high and low nutrient level. On chromosome 1H they detected one QTL for leaf length under high nutrient conditions and a large overlapping area with QTLs for seed mass, leaf length under low nutrient conditions and 'leaf mass fraction' and 'leaf mass area' both under high and low nutrient conditions.

Chen *et al.*, (2004) determined the association between SSR marker and kernel weight and kernel colour in wild barley (*H. vulgare* ssp. *spontaneum*) populations in Israel. They found associations between the marker loci BMS90 and HVM43.

Edney and Mather (2004) detected two minor QTL for malt friability on chromosome 1H. One was close to the marker locus ABG452, the other one near the marker locus cMWG706A. They carried out the QTL analysis in the 'Harrington' x 'Morex' population (140 doubled haploid lines).

In order to reveal the relation between grain protein content and malting quality, Emebiri *et al.*, (2004) investigated QTLs for different malting related traits in a double haploid population (180 lines) from a cross between a line with extremely low kernel protein content (VB9524) and a line with poor α-amylase activity (NB11231*1). On chromosome 1H, nearby the marker locus XMXwg912, they detected a QTL for β-glucanase activity.

A QTL for non-parasitic leaf spots was detected on chromosome 1H together with a QTL for heading date by Behn *et al.*, (2004). They performed the analysis in a population of 86 doubled haploid lines from a cross between the spring barley line IPZ24727 and the spring barley variety 'Barke'. IPZ24727 derives from an Israeli wild barley line and possesses good resistance against non-parasitic leaf spots.

Pillen *et al.*, (2004) used the advanced backcross-strategy to localize QTLs for several agronomic traits in a BC_2F_2-population of 164 plants. The wild parent was the *H. vulgare* ssp. *spontaneum*-line ISR101-23. The recurrent parent was the spring barley variety 'Harry'. $BC_2F_{2:5}$-families were used for the phenotyping. The 'Steptoe' × 'Morex' linkage map was used for the marker localization. On chromosome 1H, they detected one QTL for number of spikes per area, heading date, lodging at flowering and grain weight linked to the marker locus HVM20 and one for lodging at flowering and grain weight linked to the marker locus HVM36.

Another advanced backcross-experiment including *H. vulgare* ssp. *spontaneum* was carried out by Talemè *et al.*, (2004). They analysed the QTLs in a DH population from a BC1F2. The wild barley parent was the line HOR11508, the recurrent parent was the variety 'Barke'. They describe two putative QTLs on chromosome 1H: one for heading date, plant height, ear extrusion and grain yield linked to the marker locus Bmac154 and one for growth habit and heading date linked to the marker locus WMCIE8.

By hybridizing DNA probes with DNA from wheat-barley addition lines, Spielmeyer *et al.*, (2004) localized a 2-oxidase (*Hv3ox2*) from the gibberellin metabolic pathway to the long arm of chromosome 1H. In wheat, the probe hybridised with the chromosomes 1A, 1B and 1D. The orthologous rice gene (*Os3ox2*) is located on chromosome 1S of rice.

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Coordinator's report: Chromosome 2H (2)

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Turuspekov *et al*., (2004) described and mapped to genes associated with closed flowering in barley. The cleistogamy 1 (*cly1*) and cleistogamy 2 (*Cly2*) genes were mapped to loci in the same region of chromosome 2HL near molecular marker MSU21. Plants classified as closed flowering or cleistogamy did not extrude anthers during or after anthesis.

Reinheimer *et al*., (2004) identified QTL for resistance to frost induced floret sterility in chromosomes 2HL and 5HL. The 2HL QTL maps in the same region as the *cly1* gene (Turuspekov *et al*., 2004). The 5HL QTL is near the *Vrn-H1* or *Srh2* (spring growth habit 2) locus. A second QTL in 2H, probably the *Ppd-H1* or *Eam1* gene, was associated with early heading date and escape from frost damage.

Korff *et al*., (2004) reported that introgression of the *Ppd-H1* or *Eam1* segment of chromosome 2HS from *H. vulgare* ssp. *spontaneum* into European barley cultivars had more effect on heading date and other agronomic traits than other introgressed segments. Daib *et al*., (2004) reported then this same region of chromosome 2H was associated with QTL for several physiological measurements of drought stress tolerance. Li *et al*., (2005) reported similar results using backcross-derived lines. Chromosome 2HS was associated with heading date, plant height, yield, lodging, ear length, grain per spike, 1000-kernel weight, and grain protein.

Karsai *et al*., (2004) reported on heading date variations of *Hordeum vulgare* ssp. *spontaneum* accessions caused by photoperiod differences. Vernalized and non-vernalized plants were grown in grown chambers and exposed to various constant day lengths under a constant temperature condition. Early heading under long photoperiods was attributed primarily to the effects of a factor on chromosome 2H, presumably the *PpdH1* or *Eam1* locus. However, a large number of other genetic factors contributed to the range of responses observed.

Spielmeyer *et al*., (2004) reported on the barley genes in the metabolic pathway for gibberellic acid (GA) in barley. Characterization of genes involved in GA biosynthesis and its stimulation of cell elongation in barley, wheat and rice is considered the first in determining whether dwarfing genes in barley involve defective GA metabolism. Eleven genes potentially account for the six enzymes in the core GA biosynthetic pathway. Three (*HvKSL1*, *HvKSL2*, and *Hv3ox1*) of those loci were mapped in chromosome 2H.

He *et al*., (2004) examined molecular markers closely linked to the *vrs1* (six-rowed spike 1) locus in chromosome 2HL and reported on progress in positional cloning of alleles at the *vrs1* locus using amplified fragment length polymorphism (AFLP) markers and their converted sequence tagged sites (STSs) to screen a bacterial artificial chromosome (BAC library.

Tanno and Takeda, 2004 and Casas *et al*., (2005) studied the evolution of barley using markers near the *vrs1* locus. Tanno and Takeda, 2004, analyzed genetic diversity at the MWG699 marker locus in 10 *H. vulgare* ssp. *spontaneum* accessions, 42 six-rowed brittle barley accessions, and 14 six-rowed cultivars. Nine sequence types were found among the *H. vulgare* ssp. *spontaneum* accessions, three in brittle barleys, and three in the cultivars. Since the same three sequences were found in the brittle and cultivated barleys, Tanno and Takeda, 2004 concluded that *H. vulgare* ssp. *vulgare* f. *agriocrithon* from the Central Asia is not wild barley, but a weedy outcross from cultivated six-rowed barley. Casas *et al*., 2005 studied 257 cultivated barleys from the western Mediterranean region using the STS marker MWG699/*Taq*1. Most two-rowed cultivars had the type K allele. The type D allele was wide spread among winter six-rowed landraces from Spain and cultivars from central Europe. The type A allele was found in both spring and winter six-rowed cultivars. These conclusions agree with information reported by Tanno and Takeda, 2005.

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Coordinator's Report: Barley Chromosome 3H.

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Since the last co-ordinator's report in BGN 33 there have been a number of publications reporting the mapping of genes and in particular QTL on barley chromosome 3H. Of particular note is the reporting by Chono *et al*., (2003) of the cloning and functional characterisation of the semi-dwarfing gene *uzu* on 3HL in Bin6. The authors report that the semi-dwarf phenotype arises from a mutation in a gene encoding a putative brassinosteroid receptor that is possibly homologous to a known rice mutant *d61* (Chono *et al*., 2003).

In contrast synteny with rice did not prove so informative for the detailed molecular mapping of leaf rust resistance gene *Rph7* on the distal end of 3HS close to the RFLP marker MWG848 in Bin1 (Brunner *et al*., 2003). The region genetically delineated as containing the *Rph7* locus contained six genes in barley in the cultivar Morex that were not present on the homologous region on rice chromosome 1. Interestingly the characterisation of the same region in the resistance variety Cepada Capa indicated that the colinearity between the barley varieties was restricted to only five genic and two intergenic regions representing less than 35% of the two sequences. The differences were mainly due to the presence of different transposable elements in the intergenic regions but also included the loss of a gene in Cepada Capa (Scherrer *et al*., 2005).

Two other leaf rust resistance genes *Rph5* and *Rph6* were also mapped to the distal end of 3HS (Mammadov *et al*., 2003, Zhong *et al*., 2003). Detailed mapping work indicated that *Rph5* was positioned in the extreme telomeric region of 3HS distal to *Rph7* (Mammadov *et al*., 2003) and that *Rph6*, maps to a similar location. Indeed segregation analyses indicated that *Rph6* is allelic to *Rph5* (Zhong *et al*., 2003). Pellio *et al.* (2005) report the high-resolution mapping of the *Rym4/Rym5* locus conferring resistance to the barley yellow mosaic virus complex (BaMMV, BaYMV, BaYMV-2) on the distal end of the long arm of 3H that has allowed the identification of a candidate gene that has since been confirmed to be involved in the bymovirus resistance (Stein *et al*., 2005).

Several studies reported QTL for disease resistances on 3H including to scald (Patil *et al*., 2002, Genger *et al*., 2003a, 2003b, Bjørnstad *et al*., 2004, Sayed *et al*., 2004), net blotch (Cakir *et al*., 2003a, Raman *et al*., 2003), leaf stripe (Arru *et al*., 2003) and powdery mildew (Backes *et al*., 2003). A new scald resistance gene *Rrs4*$_{\text{CI11549}}$ was mapped on 3H located 22cM distally on the long arm corresponding to the region Bin 8-9 (Patil *et al*., 2003) and the crown rust resistance gene *Rpc1* was mapped 6cM distal to the SSR marker Bmag0006 to the long arm of 3H in the Bin 6 region (Agrama *et al*., 2004).

Quantitative Trait Loci that mapped to chromosome 3H were also reported for hull cracked grain (Kai *et al.,* 2003), kernel discolouration (Li *et al*., 2003), malt friability (Edney and Mather, 2004) grain shape and damage (Rajasekaran, 2004) as well a range of other agronomic and quality traits (Baum *et al*., 2003, Cakir *et al*., 2003b, Collins *et al*., 2003, Read *et al*., 2003, Talame *et al*., 2004). Komatsuda *et al*., (2004) reported high density mapping of the non-brittle rachis 1 (*btr1*) and 2 (*btr2*) genes on 3HS in Bin5. The report confirms the tight linkage of the two loci and a phylogenetic tree based on AFLP markers linked to the genes showed clear separation of occidental and oriental barley lines.

The publications referred to above are in no way an exhaustive list of recently mapped 3H loci which is a reflection of the breadth and vitality of the barley genetics community. Two presentations at the IX. International Barley Genetics Symposium on large scale mapping of barley ESTs highlight the difficulty now in reviewing the mapping of barley genes. Sato *et al*., (2004) presented results of their EST mapping work that included the novel mapping of 163 genes to 3H and Graner *et al*., (2004) presented the relationship they had found between high density gene maps of barley 3H and rice chromosome 1 extending the work of Smilde *et al.,* (2001). However neither sets of genetic maps are as yet in the public domain unfortunately but the reports are indicative of the scale of mapping now possible and the increasing importance of barley's syntenic relationship with the sequenced genome of rice.

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Coordinator’s Report: Barley Chromosome 5H(7)

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Seed dormancy and it’s release during after-ripening are important traits in barley harvesting and the malting industry. The traits are quantitatively inherited and under environmental influence.

In yet another study, a DH mapping population was made from two cultivars with elite malting quality; Triumph (European two row, prone to dormancy) and Morex (North America 6 row, non dormant) (Prada *et al*., 2004).

The QTL for GP3 (7) (germination percentage at 3 days of incubation at 7 days post harvest) obtained from Triumph was located near the centromere of chromosome 7(5H) and explained 52% of the phenotypic variance. The QTL for GP7 (7) (germination percentage at 7 days of incubation at 7 days post harvest) obtained from Triumph was located in the centromere region of chromosome 7(5H) and explained 33% of the phenotypic variance; a second GP7 (7) QTL from the variety Morex was located at the long arm telomere of chromosomes 3(3H) and explained 13% of phenotypic variation. It is not yet known if the common position of GP3 (7) and GP7 (7) is due to linkage or pleiotropy.

In the same population a DR QTL (dormancy release through after-ripening) obtained from Morex, was located on the long arm telomere of chromosome 7(5H) and another on chromosome 2(2H) and explained 19 & 9% of phenotypic variability respectively. It is assumed that a moderate level of dormancy could be maintained by manipulating the balance between the GP and DR loci.

It is interesting to note that in previous studies major dormancy QTL, SD1 and SD2 in a Steptoe/Morex cross were located in the centromeric and long arm telomeric regions respectively of chromosome 7(5H) (Han *et al*., 1996). In addition a major dormancy QTL in the Harrington/TR306 mapping population (Ullrich *et. al*., 2002) and one in the Chebec/Harrington population (Karakousis *et al.* 1996) have been mapped to the long arm telomere of chromosome 7(5H). It is suggested that the QTL located in the Triumph/Morex population could be allelic with those detected in the Steptoe/Morex cross and those detected in the Harrington / TR306 and the Chebec/Harrington populations.

Dormancy was also tested in an F_2 population derived from a cross between Triumph and Steptoe, both cultivars with some degree of dormancy. The distribution of the F_2 population was continuous but a large number of transgressive segregants were obtained, indicating that although the two parents come from distinct gene pools, there is probably some difference in the genetic control of dormancy. Minor genes could be affecting the expression of dormancy in both cultivars.

Winter hardiness is a complex trait involving aspects of low temperature tolerance, vernalization requirement and photoperiod sensitivity. To map the QTL controlling some of those traits a DH mapping population consisting of 136 lines was developed from a hybrid between the cultivars Nure (winter two rowed feed barley) x Tremois (spring two rowed malting barley), (Francia *et al*., 2004).

A total of nine QTL for the various cold-hardiness-related traits were mapped on the long arm of chromosome 5H. These included 2 QTL for winter-field survival, 2 QTL for a controlled field test plus two for functionality of photosystem II. In addition, for COR genes (cold regulated genes) QTL were located on chromosome 5H and 6H, heading date QTL were located on chromosomes 5H, 1H, 2H and 6H and a vernalization QTL was also located on chromosome 5H (long arm).

The vernalization QTL coincided with previously described vernalization loci in the Triticeae and other QTL for all measures of cold hardiness coincided with this locus. In summary all of the QTL reported above coincided with the two major loci on the long arm of chromosome 5H.

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Coordinator's Report: Chromosome 7H.

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As usual, progress in gene and QTL mapping covered numerous traits. In addition to the peer-reviewed papers described here, many reports were presented at the International Barley Genetics Symposium in Brno, Czech Republic in June 2004, available in the Proceedings and the book of abstracts published in the Czech Journal of Genetics and Plant Breeding.

New microarray technology has been applied to mapping. (Potokina *et al.*, 2004) used a 1,400 EST array to identify genes for malting quality traits. Functional associations in ten genotypes identified two ESTs on chromosome 7H. HY05O13 for sucrose synthase1 was associated with malt extract and β-amylase activity. HY03C01 for catalase (*cat1*) was associated with extract, β-amylase, Kolbach index and final attenuation. QTL mapping in the Steptoe x Morex population identified QTLs for extract and α-amylase at HY05O13 but no QTLs at HY03C01.

Rajasekaran *et al*., (2004) mapped QTLs for grain damage traits in a Tankard x Livet population. Nine QTLs were located in chromosome 7H in 3-4 locations. Traits included sieve fraction greater than 2.5 mm (2 QTLs), skinning less than 25% (2 QTLs), grain width by image analysis, ratio of grain width to length, height and grain milling energy (2 QTLs). The major region on chromosome 7H was at the SSR marker Bmag507.

QTLs affecting germination and malt friability were located by Edney and Mather, (2004), using the Harrington x Morex mapping population. A QTL for germination of 100 seeds in 4 ml of water was found in chromosome 7H by composite interval mapping. Morex provided the favorable allele.

Han *et al*., (2004) developed 39 isolines from a Steptoe x Morex cross differing for marker genotype in a 28 cM malting quality QTL region in chromosome 7H. QTL analysis after micromalting identified one QTL for malt extract, and two QTLs each for α-amylase activity, diastatic power and malt β-glucan. Resolutions of 2.0 cM or less were achieved, providing good markers for breeding.

Validation of the many QTL regions identified for Fusarium head blight resistance, kernel discoloration and deoxynivalenol concentration has begun with two populations derived from Chevron (Canci *et al*., 2004). Of the fifteen QTLs identified in the original mapping population, only five were validated in the new populations. None of the QTLs on chromosome 7H were detected in either new population.

Nonbrittle rachis has been a key locus in domestication of barley. Komatsuda *et al*., (2004) compared nonbrittle rachis loci in occidental and oriental barley lines. In addition to the major gene *btr2*, the oriental barley contained two QTLs, one of which was located in chromosome 7H.

Diab *et al*. (2004) mapped 68 QTLs involved in drought tolerance traits using the cross Tadmor x Er/Apm. Ten were located in chromosome 7H, including three for relative water content in stressed and irrigated plots and seven for water soluble carbohydrate concentration traits. Two genes were located in these QTLs, acyl carrier protein III (*Acl3*) and sucrose synthase (*bSS1B*), and an EST for a copper binding protein (BM816463).

The new tetra-primer ARMS-PCR technique was used to validate previously identified single nucleotide polymorphisms (SNPs) in five of nine RFLP clones (Chiapparino *et al*., 2004). Two of these five were located in chromosome 7H, MWG2062 and ABC465. They then screened 132 varieties and determined the frequency of each nucleotide at the polymorphic site. This technique has potential in low to medium throughput laboratories.

Varshney *et al*., 2004 tested transferability of 165 barley EST-SSR markers to wheat, rye and rice, to expand our knowledge of cereal synteny. Four of the barley chromosome 7H EST-SSR markers tested were homologous to group 7 chromosome wheat ESTs. The barley electronic comparisons to rice showed synteny between eleven of the 21 barley 7H EST-SSRs examined and rice chromosomes 2, 5, 6, 8, 9, and 12. The two chromosome 7H barley EST-SSRs mapped in rye were located on rye chromosome 4RL.

Comparisons of sequence-based polymorphisms in barley EST-derived markers were examined by Russell *et al*., 2004. The one sequence evaluated in chromosome 7H was Best 1239, with homology to sucrose synthase. Two polymorphic sites were located in landraces, producing two haplotypes. Spring barley cultivars and *H. spontaneum* both showed no diversity, producing a single haplotype. Markers for other ESTs had as many as nine different haplotypes. In general, cultivated barley showed less diversity than the landraces and *H. spontaneum*.

Wenzl *et al*., (2004) developed and tested diversity arrays technology (DarT) using polymorphism-enriched microarray hybridization. They then applied DarT to the Steptoe x Morex mapping population and mapped 42 markers to chromosome 7H. With this technique, it is possible to create a medium density linkage map in a few days.

Fluorescent in situ hybridization with RFLP clones was used for comparing physical and genetic maps by Stephens *et al*., 2004. One landmark plasmid, p18S5Shor, was used to identify and orient all seven chromosome pairs. Six of the fourteen cDNA clones used mapped to chromosome 7H, Amy2, Brz, Chi, Glx, His3, and Ubi. Physical mapping showed that barley genetic maps do not cover large areas of the genome.

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Integrating Molecular and Morphological/Physiological Marker Maps

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Barley gene mapping and cloning is progressing, albeit slowly. The *Uzu* and *Nec1* genes were identified by homology to Arabidopsis and rice genes (Chono *et al*., Plant Phys. 133:1209, '03; Rostoks *et al*., in press). The *Uzu* gene encodes a brassinosteroid receptor and maps to chromosome 3H Bin6. The *Nec1* gene encodes a cyclic nucleotide-gated ion channel 4 protein and maps to chromosome 5(1H) Bin9. There should be ample opportunities for the identification of other barley genes by homology to the model dicot and monocot plants, Arabidopsis and rice. For example the *rym4,5,6* gene (resistance to yellow mosaic virus) was identified as translation initiation factor eIF4E by recognition of a similar virus resistance pathway in dicotyledonous species (Kanyuka *et al*., in press). The location of rym4 on chromosome 3H Bin016 was previously known (Graner *et al*., TAG 86:689 ´93). The locus is now marked by the CAPS marker BGK105 derived from the *eIF4E* sequence identified as the *Rym4* gene. The Vrs1 gene was mapped at high resolution and shown to co-segregate with markers e40m36-1110 and e34m13-260 (He *et al*., Genome 47:1122, '04). The previously closest marker MWG699 is located 0.1 cM proximal from Vrs1.

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, '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
	fch12	BCD130	Schmierer *et al*., BGN 31:12, '01
	*wax	Wax	Kleinhofs BGN 32:152, '02
	gsh3	His3A	Kleinhofs BGN 32:152, '02
BIN3	fch5	ABC167A	Kleinhofs BGN 32:152, '02
	Rcs5	KAJ185	Johnson & Kleinhofs, unpublished
	yvs2		
	cer-ze	ABG380	Kleinhofs BGN 27:105, '96
BIN4	wnd		
	Lga	BE193581	Johnson & Kleinhofs, unpublished

	abo7		
BIN5	ant1		
	nar3	MWG836	Kleinhofs BGN 32:152, ‘02
	ert-m		
	ert-a		
BIN6	ert-d		
	fch8		
	fst3		
	cer-f		
	dsp1		
	msg14		
BIN7	msg10		
	rsm1	ABC455	Edwards & Steffenson, Phytopath. 86:184,’96 sex6
	seg5		
	seg2		
	pmr	ABC308	Kleinhofs BGN 27:105, ‘96
	mo6b	Hsp17	Soule *et al*., J Her. 91:483, ‘00
	nud	CDO673	Heun *et al*., Genome 34:437, ‘91
	fch4	MWG003	Kleinhofs BGN 27:105, ‘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
	xnt-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	Rph19	Rlch4(Nc)	Park & Karakousis Plt. Breed. 121:232. ‘02
BIN14	none		

Chr.2(2H)

BIN1	sbk		
BIN2	none		
BIN3	gsh6	MWG878A	Kleinhofs BGN 32:152, ‘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		
	Rph15	P13M40	Weerasena *et al.*, TAG 108:712 ‘04
	rph16	MWG874	Drescher et al., 8thIBGS II:95, ‘00
BIN7	yst4	CDO537	Kleinhofs BGN 32:152, ‘02
	Az94	CDO537	Kleinhofs BGN 32:152, ‘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 BGN 27:105, ‘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
	fol-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 BGN 27:105, ‘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 BGN 27:105, '96
	wst7	MWG949A	Costa *et al*., TAG 103:415, '01
	MlLa	Ris16	Giese *et al*., TAG 85:897, '93
	trp		

Chr. 3(3H)

BIN1		BE216031; BF264341; BF623053	
	Rph5		
	Rph6	BCD907	Zhong *et al*., Phytopath. 93:604, '03
	Rph7	MWG848	Brunner *et al*., TAG 101:783, '00
BIN2		BI958652; BF631357; BG369659	
	ant17		
	sld5		
	mo7a	ABC171A	Soule *et al*., J. Hered. 91:483, '00
	brh8		
BIN3		ARD1769.1	Druka *et al*., PNAS 99:850, '02
	xnt6		
BIN4	btr1		
	btr2		
	lzd		
BIN5	alm	ABG471	Kleinhofs BGN 27:105, '96
	abo9		
	sca		
	yst2		
	dsp10		
BIN6		BI956389; BE456118B	
	Rrs1		Graner *et al*., TAG 93: 421 ´96
		BG418711	
	Rh/Pt	ABG396	Smilde *et al*., 8th IBGS 2:178, '00
		BE455901	
	Rrs.B87	BCD828	Williams *et al*., Plant Breed. 120:301, '01
		AtpbB	
	abo6		
	xnt3		
	msg5		
	ari-a		
	yst1		
	zeb1		
	ert-c		

	ert-ii		
	cer-zd		
	Ryd2	WG889B	Collins *et al*., TAG 92:858, ‘96
	*uzu	AB088206	Saisho *et al*., Breeding Sci. 54:409, ‘04
BIN7	cer-r		
BIN8	wst6		
	cer-zn		
	sld1		
BIN9	wst1		
BIN10	vrs4		
	Int1		
	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	*eIF4E*	Kanyuka *et al*., in press ‘05
	*rym5	*eIF4E*	Kanyuka *et al*., in press ’05
			Stein *et al*., Plt.J. 42:912, ‘05
	Est4		
	ant28		

Chr.4(4H)

BIN1	none		
BIN2	fch9		
	sln		
BIN3	int-c	MWG2033	Komatsuda, TAG 105:85, ‘02
	Zeo3		
	Dwf2	Ole1	Ivandic *et al*., TAG 98:728, ‘99
	Ynd		
	glo-a		
	rym1	MWG2134	Okada *et al*., Breeding Sci. 54:319, ‘04
BIN4	*Kap	X83518	Muller *et al*., Nature 374:727, ‘95
	lbi2		
	zeb2		
	lgn3		
BIN5	lgn4		
	lks5		
	eam9		
	msg24		

BIN6	glf1		
	rym11	MWG2134	Bauer *et al*., TAG 95:1263, ‘97
	Mlg	MWG032	Kurth *et al*., TAG 102:53, ‘01
	cer-zg		
	brh2		
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	HVM067	Costa *et al*., TAG 103:415, ‘01
	Hln		
	sgh1		
	yhd1		
BIN13	*Bmy1	pcbC51	Kleinhofs *et al*., TAG 86:705, ‘93
	rym8	MWG2307	Bauer *et al*., TAG 95:1263, ‘97
	rym9	MWG517	Bauer *et al*., TAG 95:1263, ‘97
	Wsp3		

Chr. 5(1H)

BIN1	Rph4		
	Mlra		
	Cer-yy		
	Sex76	Hor2	Netsvetaev BGN 27:51, ‘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	amo1		
BIN7	clh		
	vrs3		
	Ror1	ABG452	Collins *et al*., Plt. Phys. 125:1236, ‘01
BIN8	fst2		
	cer-zi		
	cer-e		
	ert-b		

		MlGa			
		msg1			
		xnt7			
	BIN9	*nec1	BF630384	Rostoks *et al.*, BGNL 35:?, ‘05	
	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	X57845	Kleinhofs *et al.*, TAG 86:705, ‘93	
		abo15			
	BIN2	nar8	ABG378B	Kleinhofs BGN 27:105, ‘96	
		nec3			
		Rrs13			
	BIN3	none			
	BIN4	msg36			
	BIN5	nec2			
		ant21			
		msg6			
		eam7			
	BIN6	rob	HVM031	Costa *et al.*, TAG 103:415, ‘01	sex1
		gsh4			
		ant13			
		cul2	Crg4(KFP128)	Babb & Muehlbauer BGN 31:28, ‘01	
		fch11			
		mtt5			
		abo14			
	BIN7	none			
	BIN8	none			
	BIN9	*Amy1	JR115	Kleinhofs *et al.*, TAG 86:705, ‘93	
		*Nar7	X60173	Warner *et al.*, Genome 38:743, ‘95	
		*Nir	pCIB808	Kleinhofs *et al.*, TAG 86:705, ‘93	
		mul2			
		cur3			
	BIN10	lax-b			
		raw5			
		cur1			
	BIN11	none			

BIN12	xnt5		
	Aat2		
BIN13	Rph11	Acp3	Feuerstein *et al*., Plant breed. 104:318, '90
	lax-c		
BIN14	dsp9		

Chr. 7(5H)

BIN1	abo12		
	msg16		
	ddt		
BIN2	dex1		
	msg19		
	nld		
	fch6		
	glo-b		
BIN3	cud1	ABG705A	
	lys3		
	fst1		
	blf1		
	vrs2		
BIN4	cer-zj		
	cer-zp		
	msg18		
	wst2		
	Rph2	ITS1	Borovkova *et al*., Genome 40:236, '97
	lax-a	PSR118	Laurie *et al*., TAG 93:81, '96
	com1		
	ari-e		
	ert-g		
	ert-n		
BIN5	rym3	MWG028	Saeki *et al*., TAG 99:727, '99
BIN6	none		
BIN7	none		
BIN8	none		
BIN9	srh	ksuA1B	Kleinhofs *et al*., TAG 86:705, '93
	cer-i		
	mtt2		
	lys1		
	cer-t		
	dsk		
	var1		
	cer-w		
	Eam5		
BIN10	raw1		

	msg7		
BIN11	Rph9/12	ABG712	Borokova *et al*., Phytopath. 88:76, '98
	Sgh2		
	*Ror2	AY246906	Collins *et al*., Nature 425:973, '03
	lbi1		
	Rha4		
	raw2		
BIN12	none		
BIN13	rpg4	ARD5303	Druka *et al*., unpublished
	RpgQ	ARD5304	Druka *et al*., unpublished
BIN14	var3		

* - indicates the gene has been cloned

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Coordinator's report: Barley Genetics Stock Collection.

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In 2004, over 560 barley genetic stocks were planted at Aberdeen for evaluation. In collaboration with Dr. Jerry Franckowiak, 393 barley genetic stocks were planted in the field for seed increase. One hundred genetic stocks were increased in the greenhouse.

Over 450 collections of barley genetic male sterile, 626 collections of barley translocation stocks and 94 Oregon Wolfe Barley stocks were increased in the last three years.

One hundred fifty-nine samples were shipped to researchers in 2004.

A new chlorina seedling mutation derived from six-rowed cultivar "Russell" was again crossed with various chlorina stocks including GSHO 18, GSHO 26, GSHO 33, GSHO 119 and GSHO 174. All of F1 seedlings are green. This indicates that the Russell mutant is not allelic to the above GSHO stocks.

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: Translocations and balanced tertiary trisomics

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One consequence of the structural rearrangement of chromosomes is the change of the gene expression, which can alter the gene expression (position effect). Knowledge of the mechanism underlying the position-dependent activity of genes is of interest for manipulation gene expression by alteration in the gene position. The Bulgarian scientist N. Papazova and K. Gecheff reported on the position-dependent gene activity of ribosomal RNA genes based on data using cytologically reconstructed barley karyotypes (Papazova and Gecheff, 2003).

The data provide evidence that the intraspecific nucleolar dominance results from interchromosomal interactions, probably of cis-acting regulatory factors. In addition, the degree of repression varies in every translocation line and depends on the distance of the translocated NOR from the centromere.

One barley translocation line has been sent to Prof. Sevdalin Georgiev (Sofia University, Bulgaria). 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.

Reference:

Papazova, N. and K. Gecheff. 2003. Position-dependent gene activity in cytologically reconstructed barley karyotypes. Cell Biol. Int. 27.247-248.

Coordinator's report: *Eceriferum* Genes

Udda Lundqvist

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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 database of the Swedish collection has been updated during the last months and will soon be searchable within International European databases. All Swedish *Eceriferum* alleles can be seen in the SESTO database of thr Nordic Gene Bank. 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 coordinator udda@ngb.se or to the Nordic Gene Bank, nordgen@ngb.se, all others to the Small Grain Germplasm Research Facility (USDA-ARS), Aberdeen, ID 83210, USA, anhang@uida.edu or to the coordinator at any time.

Coordinator’s report: Nuclear genes affecting the chloroplast

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Eight induced barley *xantha-f* mutants have been characterized at the DNA level (Olsson *et al*., 2004). All the *xantha-f* mutations affect chlorophyll biosynthesis, as they are defective in magnesium chelatase that is the first unique enzyme of the chlorophyll biosynthetic pathway. The barley *xantha-f* gene encodes the largest of the three magnesium chelatase subunits. The phenotype of the studied mutants can in a satisfactory way be explained by the characterized mutations. The mutant octet showed a rich variation of mutations including deletions and missense mutations, which will be helpful tools in future studies concerning structural, mechanistic and regulatory aspects of the magnesium chelatase.

Three of the *xantha-f* mutants, *xantha-f*.26, -*f*.27 and -*f*.40, were also used to study the stability of mRNA affected by non-sense mutations (Gadjieva *et al*., 2004). Mutations *xantha-f*.27 and -*f*.40 are non-sense mutations in exon 4 and 3, respectively. Mutant *xantha-f*.26 has a miss-sense mutation and was included as a control in the experiment. It was found that both *xantha-f*.27 and *xantha-f*.40 had a reduced amount of *xantha-f* mRNA, whereas wild type level of mRNA was found in *xantha-f*.26. It is well known that non-sense mutations cause instability of mRNA in mammalian cells. The phenomenon is called non-sense mediated mRNA decay′, but the mechanism behind it is not understood. A very few studies have been performed in plants. Our study demonstrates that non-sense mediated mRNA decay exists in monocotyledonous plants like barley. The study explains how mutants with reduced levels of mRNA will be explored for cloning of the mutated gene by a microarray approach.

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

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New references:

Gadjieva, R., E. Axelsson, U. Olsson, J. Vallon-Christersson, and M. Hansson. 2004. Nonsense-mediated mRNA decay in barley mutants allows the cloning of mutated genes by a microarray approach. Plant Physiol. Biochem. 42:681-685.

Olsson, U., N. Sirijovski, and M. Hansson. 2004. Characterization of eight barley *xantha-f* mutants deficient in magnesium chelatase. Plant Physiol. Biochem. 42:557-564.

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: 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. All different types and characters with its many alleles of the Swedish ear morphology genes are found in the SESTO database of the Nordic Gene Bank. 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 coordinator udda@ngb.se or to the Nordic Gene Bank, nordgen@ngb.se , all others to the Small Grain Germplasm Research Facility (USDA-ARS), Aberdeen, ID 83210, USA, anhang@uida.edu or to the coordinator at any time.

Coordinator's report: Wheat-barley genetic stocks

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Following last year's report on the selection of six monosomic additions of *Hordeum marinum* chromosomes to common wheat, presumptive disomic addition lines of *H. marinum* chromosomes 1Hm, 2Hm, 4Hm, 5Hm and 7Hm have been produced. Four ditelosomic addition lines obtained as well are yet to be characterised. Apart from *H. marinum*, it has also been possible to produce an amphiploid of *H. intercedens* with common wheat (Islam and Colmer, unpublished).

Coordinator's report: Semidwarf genes

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Spielmeyer *et al*., (2004) reported on the barley genes in the metabolic pathway for gibberellic acid (GA) in barley. The characterization of genes involved in GA biosynthesis and its stimulation of cell elongation in barley, wheat, and rice is considered the first step in determining whether specific dwarfing genes in barley involve defective GA metabolism. Eleven genes potentially account for the six enzymes in the core GA biosynthetic pathway. The *HvKAO1* (*ent*-Kaurenoic acid oxidase 1) gene was associated with mutants at the *grd5* (GA responsive dwarf 5) locus in Himalaya barley (Helliwell *et al*., 2001). The *HvKO1* (*ent*-Kaurene oxidase 1) gene was associated with mutants at the *grd3* locus (Spielmeyer *et al*., 2004). Both loci were mapped to chromosome 7H. Other pathway genes were mapped, but not associated with specific mutant phenotypes.

MlČochová *et al*., (2004) conducted a molecular marker study of the semidwarf mutant Diamant and its parental cultivar Valticky. Using14 European cultivars, MlČochová *et al*., (2004) analyzed AFLP (amplified fragment length polymorphism) bands and SRRs (simple sequence repeats). For the 1591AFLP bands, 42.1% were polymorphic among cultivars and 11.4% were polymorphic between Valticky and Diamant. Of the 122 SSRs, 72.7% were polymorphic among cultivar and 42.8% between Valticky and Diamant. Thus, it is unlikely that Diamant was derived directly as a Valticky mutant.

MlČochová *et al*., (2004) summarized information showing that the *denso* or *sdw1.d* gene from Diamant is one of the most successful induced mutants in barley. Over 120 European spring barley cultivars have Diamant in their parentage and probably have the denso dwarf. In contrast, the Jotun mutant, *sdw1.a*, has been used to a very limited extent in North America. This difference in utilization can be partially explained by the lower vigor of cultivars with the Jotun gene, which is expressed in 'Bowman' backcross-derived near-isogenic lines for the two mutants. (Franckowiak, unpublished). Both mutants are associated with delayed heading, especially in short-day environments. Since heading date is more critical in continental environments, the delayed heading associated with *sdw1* mutants may influence their utilization in North America.

References:

Helliwell, C.A., P.M. Chandler, A. Poole, E.S. Dennis, and W.J. Peacock. 2001. The CYP88A cytochrome P450, *ent*-kaurenoic acid oxidase, catalzes three steps of the gibberellin biosynthesis pathway. Proc. Natl. Acad. Sci. USA 98:2065-2070.

MlČochová, L., O. Chloupek, R. Uptmoor, F. Ordon, and W. Friedt. 2004. Molecular analysis of the barley cv. 'Valticky' and its X-ray-derived semidwarf-mutant 'Diamant'. Plant Breed. 123:421-427.

Spielmeyer, W., M. Ellis, M. Robertson, S. Ali, J.R. Lenton, and P.M. Chandler. 2004. Isolation of gibberellin metabolic pathway genes from barley and comparative mapping in barley, wheat and rice. Theor. Appl. Genet. 109:847-855.

Coordinator's report: Early maturity genes

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Franckowiak *et al*. (2004) reported at the International Barley Genetics Symposium in Brno, Czech Republic, regarding identifying genes that controlls heading date and reviewed some principles of the existing genes. Photoperiod sensitive genes are commonly called early maturity (*eam*) or praematurum (*mat*) genes. The *Eam1* gene is frequently present in wild barley, winter and spring cultivars. It is expressed only under long day conditions. The *Eam5* and *eam9* genes confer earliness under short-day conditions. The *Eam6* gene confers early heading under both long- and short-day conditions. It exhibits additive interactions with *Eam1*, *Eam5* and *eam9*. The *eam8* gene acts as day-length neutral. The *Eam11* gene, a long-day gene, is present in most two-row breeding cultivars. The *eam10, mat-f* and *mat-i* genes are early under most conditions. The long-day genes *Eam1*, *Eam6* and *Eam11* genes are located in chromosome 2H near QTLs for resistance Fusarium head blight. The last two ones are near the six-row typed 1 (*vrs1*) locus.

All detailed descriptiions made in the different volumes of Barley Genetics Newsletter (26, 28, 29 and 32) are still up-to-date and valid. They are also available in the AceDB database for Barley Genes and Barley Genetic Stocks and found under address: www.untamo.net/bgs.

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

Reference:

Franckowiak, J.D., N.N. Krasheninnik, and G.T. Yu. 2004. Identifying Genes Controlling Heading Date in Spring Barley. *In*: J. Spunar and. J. Janikova (eds,), Barley Genetics IX. Book of Abstracts, Proc. Ninth Int. Barley Genet. Symp., Brno, Czech Republic, June 20-26, 2004. Czech Journal of Genetics and Plant Breeding 40:44.