Barley Genetics newsletter 43 (2013): 224-249

REPORTS OF THE COORDINATORS

Overall coordinator's report

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Since the latest overall coordinator's report not too many news have happened. Unhappily no research reports were received the last year for including in this volume. Therefore I want again to stress the importance of publishing short research notes after having been published in high level journals. The barley community should gain of an overwiev what different barley research groups are working on and receiving new results to investigate the whole barley genome.

As the workshop of the 'Barley Linkage Groups and Collections' has decided at the 11th International Barley Genetics Symposium in Hangzhou, China, 2012 to continue with Barley Genetics Newsletter and also suggested that it is the best forum and is the most important part for barley genetic stocks descriptions. An updated complete version of the genetic stocks descriptions in one volume was published in Volume 42:36-792. Many new stocks are described in this volume, BGN43, but also several ones are updated with the latest research results and literature citied. Additional two tables with the alphabetic order of the recommended locus names and symbols and the BGS number order are again published to make it easy for barley researchers to find gene descriptions.

Unhappily I have to inform the barley community that the 'International Database for Barley Genes and Barley Genetic Stocks', Untamo, is closed down and not available for some months. Morten Huldén who had constructed and developed the format according to GrainGenes and it was on his private server passed away about one year ago. The server had to be cancelled. All text of information is saved at the Nordic Genetic Resource Center (NordGen), Sweden, all images are also saved but on separate files. As the AceDB format which was used originally do not exist any more, we will develop a complete new database together with the IT department at NordGen and include it in their dataset programme. The idea is to make it possible for updating descriptions directly in the electronic version. Hopefully, it will be constructed by the end of the year 2014.



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Barley Genetic Stocks (GSHO – *Genetic Stocks Hordeum*) in the USDA-ARS National Small Grains Collection

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Dr. Andris Kleinhofs, Washington State University, Pullman, USA, donated 69 of his mutant stocks and GSHO numbers have been assigned as shown in table 1.

Table1: Barley mutant stocks from Andris Kleinhofs, Washington State University, Pullman, with assigned GSHO numbers for the Barley Genetic Stock Collection held by USDA-ARS National Small Grains Germplasm Research Facility at Aberdeen, Idaho, including mutant names, locus and allele symbols, and BGS description numbers.

GSHO Nr	Origin Stock Nr	Mutant name	Gene symbol	BGS descr.	BGN vol
3602	FN 338	Necrotic leaf spot 1	nec1.i	222	43
3603	FN 085	Necrotic leaf spot 1	nec1.j	222	43
3604	FN 370	Necrotic leaf spot 1	nec1.y	222	43
3605	FN 362	Necrotic leaf spot 3	nec3.l	265	43
3606	FN 363	Necrotic leaf spot 3	nec3.m	265	43
3607	FN 044	Necroticans 10	nec10.o	681	43
3608	FN 211	Necroticans 10	nec10.ab	681	43
3609	FN 303	Necroticans 10	nec10.ac	681	43
3610	FN 227	Necroticans 11	nec11.ad	682	43
3611	FN 364	Necroticans 11	nec11.ae	682	43
3612	FN 450	Necroticans 11	nec11.af	682	43
3613	FN 225	Necroticans 12	nec12.ag	683	43
3614	FN 248	Necroticans 12	nec12.ah	683	43
3615	FN 250	Necroticans 12	nec12.ai	683	43
3616	FN 360	Necroticans 13	nec13.aj	684	43
3617	FN 361	Necroticans 13	nec13.ak	684	43
3618	FN 365	Necroticans 13	nec13.al	684	43
3619	FN 065	Necroticans 14	ned14.am	685	43
3620	FN 093	Necroticans 15	nec15.an	686	43
3621	FN 201	Necroticans 16	nec16.ao	687	43
3622	FN 242	Necroticans 17	nec17.ap	688	43

Table 1 contin.

GSHO Nr	Origin Stock Nr	Mutant name	Gene symbol	BGS descr.	BGN vol
3623	FN 275	Necroticans 18	nec18.aq	689	43
3624	FN 327	Necroticans 19	nec19.ar	690	43
3625	FN 366	Necroticans 20	nec20.as	691	43
3626	FN 367	Necroticans 21	nec21.at	692	43
3627	FN 368	Necroticans 22	Nec22.au	693	43
3628	FN 369	Necroticans 23	nec23.av.	694	43
3629	FN 371	Necroticans 24	Nec24.aw	695	43
3630	FN 396	Necroticans 25	nec25.ax	696	43
3631	FN 451	Necroticans 26	Nec26.ay	697	43
3632	FN 452	Necroticans 15	Nec15.az	686	43
3633	γ06-005	Necroticans 27	nec27.ba	698	43
3634	γ08-125	Necroticans 27	nec27.bb	698	43
3635	γ08-126	Necroticans 28	nec28.bc	699	43
3636	γ08-127	Necroticans 29	nec29.bd	700	43
3637	γ08-128	Necroticans 30	nec30.be	701	43
3638	γ08-129	Necroticans 31	nec31.bf	702	43
3639	γ08-130	Necroticans 32	nec32.bg	703	43
3640	γ07-93	Necroticans 33	nec33.bh	704	43
3641	FN 01	Multiovary 1	mov1.f	43	43
3642	FN 243	Multiovary 2	mov2.g	147	43
3643	FN 315	Multiovary 4	mov4.k	648	43
3644	FN 43	Tip sterile 1	tst1.c	647	43
3645	FN 47	Narrow leafed dwarf 2	nld2.b	660	43
3646	FN 53	Brachytic 1	brh1.ae	1	43
3647	FN 216	Eligulum-a	eli-a.216	623	43
3648	FN 237	Uniculm 2	cul2.1	253	43
3649	FN 16	Waxy spike 1	wxs1.a	615	43
3650	FN 395	Sensitivity to *Ustilago nuda*1	sun1.a	650	43
3651	γ07-014	Six-rowed spike 1	vrs1.u	6	42
3652	FN 346	Bushy spike 1	bsp1.a	645	43
3653	FN 2	Late maturirty 1	lam1.a	651	43
3654	FN 222	Aborted spike 1	asp1.a	649	43
3655	FN 347	Ovaryless 2	ovl2.b	646	43
3656	FN 05	Elongated outer glume 1	eog1.d	57	43
3657	FN 284	Elongated outer glume 1	eog1.f	57	43
3658	FN 96	Elongated outer glume 1	eog1.g	57	43
3659	FN 297	Elongated outer glume 1	eog1.h	57	43
3660	FN 298	Elongated outer glume 1	eog1.i	57	43
3661	FN 325	Elongated outer glume 1	eog1.j	57	43
3662	FN 34	Elongated outer glume 1	eog1.k	57	43
3663	FN 421	Elongated outer glume 1	eog1.l	57	43

Table 1 contin.

GSHO Nr	Origin Stock Nr	Mutant name	Gene Symbol	BGS Nr.	BGN vol
3664	FN 428	Elongated outer glume 1	eog1.m	57	43
3665	FN 463	Elongated outer glume 1	eog1.n	57	43
3666	FN 464	Elongated outer glume 1	eog1.o	57	43
3667	FN 465	Elongated outer glume 1	eog1.p	57	43
3668	FN 466	Elongated outer glume 1	eog1.q	57	43
3669	FN 491	Elongated outer glume 1	eog1.r	57	43
3670	FN 503	Elongated outer glume 1	eog1.s	57	43

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Coordinator's report: Translocations and balanced tertiary trisomics

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Georgieva and Gecheff (2013) applied multicolor fluorescence *in situ* hybridization to mitotic metaphase chromosomes of the standard barley cultivar Freya and a new reconstructed karyotype, PK 88-19, with complete cytological marking of the chromosome complement in order to map physically the rearrangement breakpoints induced by gamma-irradiation. Three repetitive DNA sequences, namely, GAA satellite sequence, Afa-family subclone pAs1, and rDNA clone pTa71, were used as FISH probes. The comparative analysis of the distribution patterns of FISH signals in the reconstructed chromosomes resulting from three reciprocal translocations (1H-5H, 2H-7H and 3H-4H) and two pericentric inversions (4H(3H) and 6H) on the one hand, and the respective standard chromosomes, on the other, allowed a precise identification of the putative regions where the rearrangement breakpoints have occurred. In addition, three new minor rDNA sites located in the long arms of chromosomes 2H, 5H and 6H were identified. Due to the clear morphological distinctions of the different chromosome types and the available detailed positions of their rearrangement breakpoints, PK-88-19 may offer an essential gain in the resolution power over other reconstructed karyotypes in various research areas of barley cytogenetics

Stoilov and colleagues (2013) addressed the potential of cytologically reconstructed barley line D-2946 to cope with the major lesions that hamper genome integrity, namely DNA single- and double-strand breaks. Strand breaks induced by irradiation and Li ions were assessed by neutral and alkaline comet assay. Results indicate that radiation-mediated constitutive rearrangement of the chromosome complement has led to a substantial modulation of the sensitivity of barley genome towards DNA strand breaks, produced by ionising radiation, Li ion implantation and bleomycin in an agent-specific manner, as well as of the clastogenic response to irradiation. Based on these findings, reconstructed barley karyotype D-2946 can be considered a candidate radio-sensitive line with reduced ability to maintain genome integrity with respect to both DNA and chromosomal damage.

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.

References:

Georgieva, M., and K.Gecheff. 2013. Molecular cytogenetic characterization of a new reconstructed barley karyotype. Biotechnol Biotec Eq *27*, 3577-3582.

Stoilov, L., M.Georgieva, V.Manova, L.X. Liu, and K.Gecheff. **2013**. Karyotype reconstruction modulates the sensitivity of barley genome to radiation-induced DNA and chromosomal damage. Mutagenesis *28*, 153-160.

Coordinator's Report: Desynaptic Genes

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The status of this genetic stock collection described in Barley Genetics Newsletter Vol. 42 did not change.

No work was published describing the application of one of the desynaptic mutants. However in rye the recessive spontaneous sy18 mutation with nonhomologous synapsis was mapped. The sy18 gene was located in the centromeric region of chromosome 2R in relation to three rye SSR (simple sequence repeats) loci. The possible evolutionary relationships of the mapped gene with homologous loci of the related species are discussed. (Dolmatovich *et al*., 2013).

Reference:

Dolmatovich, T.V., Malyshev, S.V., Sosnikhina, S.P., Tsvetkova, N.V., Kartel, N.A., and Voilokov, A.V. 2013. [Mapping of meiotic genes in rye (Secale cereale L.): localization of sy18 mutation with impaired homologous synapsis using microsatellite markers]. Genetika *49*, 472-478.

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Coordinator's report: Autotetraploids

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A collection of autotetraploid barley accessions, exclusively containing spring types, is maintained at our institute. Details on the characteristics of the barley stocks have been described in previous issues of BGN. The following table contains a list of the currently available tetraploid samples.

Table 1.

Id. No.: HOR	Taxon, Author(s)	Name or Number (Originator)	Germination (%)
21652 / 2000	H. vulgare L.	2-1 (Ahokas) 4x'	18
21664 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	224/1328 (Friedt) 4x'	83
21709 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	297/1347 (Friedt) 4x'	17
21651 / orig A	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	302/1807-12 (Friedt) 4x'	44
21703 / 2000	H. vulgare L.	302/1807-223 (Friedt) 4x'	33
21673 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	302/1807-F (Friedt) 4x'	70
20927 / 1987	H. sp.	478/1370 (Friedt) 4x'	70
20933 / 1999	H. sp.	48/711-D (Friedt) 4x'	88
21616 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	50/721-C (Friedt) 4x'	57
21788 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	548/1812 (Friedt) 4x'	55
21776 / 2000	H. vulgare L.	57-Ab-5002 (Wiebe) 4x'	36
21727 / 2000	H.vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	592/1939 (Friedt) 4x'	66
21611 / 2000	H. vulgare L.	681/1682-4 (Friedt) 4x'	83
21732 / 2000	H. vulgare L. convar. distichon (L.) Alef.	744/1277 (Friedt) 4x'	62
21714 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	744/1277-Locker (Friedt) 4x'	74

Id. No.: HOR	Taxon, Author(s)	Name or Number (Originator)	Germination (%)
20911 / 1987	H. sp.	744/1277-Steril (Friedt) 4x'	68
21646 / orig A	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	79/755-15 (Friedt) 4x'	21
21787 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	79/756-12 (Friedt) 4x'	51
20920 / 1987	H. sp.	90/771-21 (Friedt) 4x'	59
20931 / 1987	H.sp.	90/772-1 (Friedt) 4x'	61
20662 / 1999	H. sp.	Alma (Frimmel) 4x'	80
21744 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Ammer (Frimmel) 4x'	69
21721 / 2000	H. vulgare L.	Amsel (Bender) 4x'	45
21653 / 2000	H.vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Aramir (Friedt) 4x'	60
21700 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Balder (Hoffmann) 4x'	66
21718 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Balder (Lange) 4x'	53
20728 / 1999	H. sp.	Balder (Müntzing) 4x'	62
15189 / 1987	H. sp.	Barbless (Wiebe) 4x'	74
21742 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Bella (Frimmel) 4x'	64
21764 / 2005	H. vulgare L. convar. vulgare	Big Boy (Wiebe) 4x'	89
20364 / 1987	H. sp.	Bohemian (Wiebe) 4x'	56
20669 / 1999	H. sp.	Brage (Ellerström) 4x'	80
20857 / 1999	H. sp.	Brage (Müntzing) 4x'	72
21728 / 2000	H. vulgare L.	Brant (Jenkins) 4x'	71
20815 / 1987	H. sp.	Brant 387 X Brant 732 (Reinbergs) Mz 4x'	81
21757 / 2000	H. vulgare L.	Brant 387 X Brant 732 (Reinbergs) Mz 4x'	75
15208 / 1987	H. sp.	Brant 57-754 (Reinbergs) 4x'	82
21625 / 2000	H. vulgare L.	Brant 57-754 X Gb 96 4x'	68
21741 / 2000	H. vulgare L.	Brant X Oac 21 (Reinbergs) 4x'	69
21777 / 2000	H. vulgare L.	Brio (Müntzing) 4x'	31
20349 / 1999	H. sp.	Busser (Bender) 4x'	83
21621 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Carina (Friedt) 4x'	34
20671 / 1999	H. sp.	Ceresia (Bender) 4x'	72
21669 / 2000	H. vulgare L. convar. distichon (L.) Alef.	Cowra (Bender) 4x'	26
21626 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	D 8/55 (Gaul) 4x'	58

Id. No.: HOR	Taxon, Author(s)	Name or Number (Originator)	Germination (%)
21740 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	D 9/55 (Gaul) 4x'	70
21680 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Dioseger 4x'	58
21619 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Doppelhaploide Aus (Trumpf X Vm 260)(Foroughi-Wehr) 4x'	43
15225 / 1999	H. sp.	Edda (Jenkins) 4x'	55
21638 / 2000	H. vulgare L. convar. vulgare var. hybernum Viborg	Edda (Müntzing) 4x'	28
20665 / 1999	H. sp.	Emir (Frimmel) 4x'	72
20693 / 1999	H. sp.	Ert 23 (Hoffmann) 4x'	47
20688 / 1999	H. sp.	Ert 32 (Ellerström) 4x'	73
20704 / 1999	H. sp.	Ert 32 (Hoffmann) 4x'	59
21635 / 2005	H. vulgare L. convar. vulgare var. hybernum Viborg	Everest (Wiebe) 4x'	67
20907 / 1987	H. sp.	F13 Kreuzung Nr. 74 4x'	76
20936 / 1987	H. sp.	F7-Bulk (Reinbergs) Mz 4x'	65
20914 / 1987	H. sp.	F8-Bulk (Reinbergs) Mz 4x'	71
20937 / 1987	H. sp.	Fg Kreuzung Nr. 138 4x'	79
21683 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Firlbeck (Rommel) 4x'	73
21783 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Frankonia 4x'	68
20369 / 1999	H. sp.	Frederickson (Wiebe) 4x'	50
21701 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Fruehe 12=W7 (Gaul) Hm 4x'	19
21606 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Fruehe 58 (Gaul) Hm 4x'	67
21684 / 2001	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Fuchs Pfaelzer (Bender) 4x'	73
21778 / 2000	H. vulgare L.	Gb 96 (Reinbergs) 4x'	46
21695 / 2000	H.vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Gerda (Frimmel) 4x'	69
20373 / 1987	H. sp.	Gold Foil (Rommel) 4x'	69
20663 / 1987	H. sp.	Haisa Ii (Gaul) 4x'	81
20678 / 1987	H. sp.	Hatvany 4x'	80
20945 / 1987	H. sp.	Hes Type I (Takahashi) 4x'	90
21713 / 2000	H. vulgare L.	Hoffmann 10/634 4x'	65
20697 / 1999	H. sp.	Hoffmann 11/344 4x'	65
21608 / 2000	H. vulgare L. convar. vulgare var. hybernum Viborg	Hoffmann 11/344 4x'	57
14120 / 2003	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Hoffmann 3500 4x'	93

Id. No.: HOR	Taxon, Author(s)	Name or Number (Originator)	Germination (%)
21660 / 2000	H. vulgare L.	Hoffmann 3501 4x'	73
21719 / orig A	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Hoffmann 3502 4x'	47
20377 / 1999	H. sp.	Hoffmann 3505 4x'	71
21702 / 2000	H. vulgare L.	Hoffmann 3506 4x'	41
14122 / 2003	H. vulgare L. Population	Hoffmann 3508 4x'	93
21775 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Hoffmann 3509 4x'	23
21750 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Hoffmann 3511 4x'	
20690 / 1999	H. sp.	Hoffmann 3512 4x'	78
21736 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Hoffmann 3514 4x'	51
14105 / 2003	H. vulgare L. Population	Hoffmann 3515 4x'	93
14102 / 2003	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Hoffmann 3516 4x'	48
20353 / 1987	H. sp.	Hoffmann 3517 4x'	78
21759 / orig A	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Hoffmann 3518 4x'	71
14111 / 2001	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Hoffmann 3519 4x'	38
21720 / 2000	H. vulgare L. convar. vulgare var. hybernum Viborg	Hoffmann 3520 4x'	38
21722 / 2000	H. vulgare L. convar. vulgare var. hybernum Viborg	Hoffmann 3521 4x'	18
20694 / 1999	H. sp.	Hoffmann 3522 4x'	58
21643 / 2000	H. vulgare L. convar. vulgare var. hybernum Viborg	Hoffmann 3524 4x'	25
20355 / 1987	H. sp.	Hosomugi (Takahashi) 4x'	67
20664 / 1987	H. sp.	Impala (Frimmel) 4x'	66
21627 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Ingrid (Frimmel) 4x'	48
20691 / 1987	H. sp.	Johanna (Frimmel) 4x'	41
20822 / 1987	H. sp.	Kenia (Hoffmann) 4x'	38
20350 / 1987	H. sp.	Kenia (Müntzing) 4x'	76
21712 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Kihara Early Golden (Müntzing) 4x'	84
21688 / 2000	H.vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Kihara Hakata (Müntzing) 4x'	54
20388 / 1999	H. sp.	Kihara Hakata 2 (Wiebe) 4x'	84
21648 / 2000	H. vulgare L. convar. vulgare var. hybernum Viborg	Kihara Mochimugi (Müntzing) 4x'	69
21671 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Macrolepis (Gaul) Hm 4x'	40
20668 / 1987	H. sp.	Maja (Hoffmann) 4x'	75

Id. No.: HOR	Taxon, Author(s)	Name or Number (Originator)	Germination (%)
21725 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Maja (Müntzing) 4x'	50
20922 / 1987	H. sp.	Mamie 4x'	58
21762 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Matura (Frimmel) 4x'	75
14125 / 2001	H. sp.	Mgh 1998 (Friedt) 4x'	50
20701 / 1987	H. sp.	Montcalm (Reinbergs) 4x'	56
20929 / 1987	H. sp.	Mrm 52 (Friedt) 4x'	31
21717 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Mutina (Friedt) 4x'	71
20675 / 1987	H. sp.	New Ebis (Wiebe) 4x'	65
20680 / 1999	H. sp.	Nord (Reinbergs) 4x'	72
20836 / 1987	H. sp.	Ns Morgenrot 4x'	59
21628 / 2000	H. vulgare L.	Oac 21 (Jenkins) 4x'	57
21730 / 2000	H. vulgare L. convar. vulgare var. hybernum Viborg	Oac 21 (Reinbergs) 4x'	62
20919 / 1987	H.sp.	Oac 21 X Brant 387 (Reinbergs) Mz 4x'	77
20917 / 1987	H. sp.	Oac 21 X Brant 732 (Reinbergs) Mz 4x'	71
20666 / 1987	H. sp.	Ochsenhauer Ria (Bender) 4x'	84
20824 / 1987	H. sp.	Opal B (Müntzing) 4x'	69
20840 / 1987	H. sp.	Opal B (Wiebe) 4x'	70
20819 / 1987	H. sp.	Palmella Blue (Frimmel) 4x'	56
21748 / 2000	H. vulgare L.	Pgr 8480 (Fedak) 4x'	48
20932 / 1987	H. sp.	Primus Ii (Ellerström) 4x'	55
20696 / 1987	H. sp.	Primus Ii (Müntzing) 4x'	63
20683 / 1987	H. sp.	Shin Ebisu (Takahashi) 4x'	75
21647 / 2000	H. vulgare L. convar. vulgare var. hybernum Viborg	Slender (Wiebe) 4x'	50
20918 / 1987	H. sp.	Stanka'S Frueh (Frimmel) 4x'	81
20853 / 1987	H. sp.	Starnauer Kneifel (Bender) 4x'	70
20841 / 1987	H. sp.	Streng'S Franken Iii (Rommel) 4x'	72
20673 / 1987	H. sp.	Szekacs 4x'	60
21753 / 2000	H. vulgare L.	Traill (Reinbergs) 4x'	48
20835 / 1987	H. sp.	Ulonska'S 41/18 4x'	41
20810 / 1987	H. sp.	Ulonska'S 41/65 4x'	50
21672 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Ulonska'S Nackt 4x'	23

Id. No.: HOR	Taxon, Author(s)	Name or Number (Originator)	Germination (%)
21751 / 2000	H. ordeum vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Union (Bender) 4x'	59
21629 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Villa (Friedt) 4x'	67
21649 / 2000	H. vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Volla (Frimmel) 4x'	26
20803 / 1987	H. sp.	W 1173/472311 (Frimmel) 4x'	64
20923 / 1987	H. sp.	W 1749/31681 (Frimmel) 4x'	57
20674 / 1987	H. sp.	Wasegoru (Takahashi) 4x'	69
14110 / 2001	H. sp.	Wisa (Rommel) 4x'	47
20943 / 1987	H. sp.	Ymer (Ellerström) 4x'	53
20802 / 1987	H. sp.	Ymer (Hoffmann) 4x'	41
21663 / orig A	Hordeum vulgare L. convar. distichon (L.) Alef. var. nutans (Rode) Alef.	Ymer (Müntzing) 4x'	61
21693 / 2000	Hordeum vulgare L. convar. vulgare var. hybernum Viborg	York (Reinbergs) Mz2 4x'	86

The complete set of accessions, i.e. autotetraploids (4x) and corresponding diploid (2x) progenitors (if available), have been incorporated into stocks at:

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
Genebank Department
Corrensstr. 3, Gatersleben
DE-06466 Stadt Seeland, Germany
phone: +49-39482-5229
fax: +49-39482-5155
http://www.ipk-gatersleben.de
Dr. Andreas Börner, Head Management and Evaluation

The whole set of tetraploids and corresponding diploid barleys has been grown this year (2014) in the greenhouse and field at Giessen for seed multiplication. Limited seed samples of the stocks are available for distribution either from the IPK Gene Bank or under the below address:

Institute of Agronomy and Plant Breeding, Justus-Liebig-University
Prof. Wolfgang Friedt
Heinrich-Buff-Ring 26-32
DE-35392 Giessen, Germany
wolfgang.friedt@uni-giessen.de
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Coordinator's report: *Eceriferum* genes

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Presence of wax coating and its composition is an important feature of the barley plant. It reduces evaporation of water from the plant and helps protect it against pathogens. The waxless *Eceriferum* and glossy mutants affect the presence and type of epicuticular waxes on the different organs. Many different surface wax mutants have been isolated as induced or spontaneous mutants. All 79 defined loci are published as descriptions in Barley Genetics Newsletter (BGN) 42 and some of the descriptions are updated in this volume. All of them are valid and up-to-date.

All the 79 gene loci have been backcrossed to a common genetic background, the cultivar 'Bowman' by J.D. Franckowiak, USA, to-day Australia. They are available as Near Isogenic Lines (NIL) at the Nordic Genetic Resource Center (NordGen), Sweden, www.nordgen.org and at the Small Grain Germplasm Research Facility (USDA–ARS), Aberdeen, ID 83210, USA, nsgchb@ars-grin.gov. But keep attention that many of them are a higher backcross derived line incorporated at NordGen than those at the Small Grain Research Facility in Aberdeen. The material in Sweden gets regenerated continously.

Since the last publication of Barley Genetics Newsletter no work was published describing the application of the *eceriferum* mutants and genes.

Coordinator´s Report: Disease and Pest Resistance Genes

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In the table below you will find papers published in 2012/2013 extending last year´s list of information available on molecular markers for major resistance genes in barley published in Barley Genetics Newsletter 42.

List of papers published on mapped major resistance genes in barley updated until November 30, 2013.

Resistance gene	**Chromsomal location**	**Reference**
Puccinia hordei		
Rph22	2HL	Johnston et al. 2013
Puccinia striiformis		
rpsSa3771	7HL	Golegaonkar et al. 2013
Pyrenophora graminea		
Rdg2a	7HS	Biselli et al. 2013
Barley yellow mosaic virus (BaYMV), Barley mild mosaic virus (BaMMV)		
rym7 *rym11*	1H 4HL	Yang et al. 2013 Lüpken et al. 2013

References:

Biselli, C, S.Urso, G.Tacconi, B.Steuernagel, D.Schulte, A.Gianinetti, P.Bagnaresi, N. Stein, L.Cattivelli, G.Valè. 2013. Haplotype variability and identification of new functional alleles at the *Rdg2a* leaf stripe resistance gene locus. Theor Appl Genet 126:1575-1586.

Golegaonkar, P.G., C.R.Wellings, D.Singh, R.F.Park. 2013. Genetic and molecular analyses of resistance to a variant of *Puccinia striiformis* in barley. J Appl Genet 54(1):1-9.

Johnston, P.A., R.F.Niks, V.Meiyalaghan, E.Blanchet, R.Pickering. 2012. *Rph22*: mapping of a novel leaf rust resistance gene introgressed from the non-host *Hordeum bulbosum vulgare* L.). Theor Appl Genet 126:1613-1625.

Lüpken, T, N.Stein, D.Perovic, A.Habekuß, I.Krämer, U.Hähnel, B.Steuernagel, U.Scholz, R.Zhou, R.Ariyadasa, S.Taudien, M.Platzer, M.MartisM, K.Mayer, W.Friedt, F.Ordon. 2013. Genomics-based high-resolution mapping of the BaMMV/BaYMV resistance gene *rym11* in barley (*Hordeum vulgare* L.). Theor Appl Genet 126:1201-1212.

Yang, P, D.Perovic, A.Habekuß, R.Zhou, A.Graner, F.Ordon, N.Stein. 2013. Gene-based high-density mapping of the gene *rym7* conferring resistance to *Barley mild mosaic virus* (BaMMV). Mol Breeding 32:27-37.

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Coordinator's report: Early maturity and Praematurum genes

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The demand for early maturity in barley has become an important goal for plant breeding during the last century. Time of flowering has an important impact on yield and has been a key trait in the domestication of crop plants worldwide. Early maturity material has been collected in different geographic regions and climate conditions, today a critical issue in times of global warming. Many different *early maturity* and *Praematurum* mutants are isolated in many different cultivars and they are incorporated in Genebanks in several parts of the world. Only in Scandinavia more than 1000 such mutants have been isolated, their phenotypes described, analysed genetically and used in plant breeding worldwide. 10 early maturity (*eam*) and 9 Praematurum (*mat*) loci have been identified among them also day-length neutral ones. All of them are incorporated into a common background, the cultivar 'Bowman' by J.D. Franckowiak, USA, today Australia, and he established Bowman backcross derived lines (Near Isogenic Lines, 'NIL'). They are very important and useful for intensive molecular studies, cloning genes and understanding the barley genome.

Recently it became reported by Zakhrabekova, S. *et al.* (2012) that the famous early maturity *mat-a* (*eam8*) gene with its photoperiod insensitivity got identified as a homolog of the *Arabidopsis thaliana* circadian clock regulator *Early flowering 3* (*Elf3*) by characterizing 87 induced *mat-a* mutant lines. Only some months later Faure *et al*. (2012) showed that commercial barley cultivars bred for short growing seasons by use of *early maturity 8* (*eam8*) mutations also termed *mat-a* are severely compromised in clock gene expression and clock outputs. They also identified *EAM8* at a barley ortholog of the *Arabidopsis thaliana* circadian clock regulator *EARLY FLOWERING 3* (*ELF3*). They further showed that *eam8* mutants have increased expression of the floral activator *HvFT1* which is independent of allelic variation at *Ppd-H1*.

Campoli, Ch. *et al*. (2013) reported a second *early maturity* (*eam10*) gene that also responses to photoperiod insensitivity. Flowering under long-day conditions is controlled by the major photoperiod response *PHOTOPERIOD 1* gene (*Ppd-H1*). This gene is homologous to *PSEUDO_RESPONSE REGULATOR* (*PPR*) genes implicated in the circadian clock of the model species *Arabidopsis thaliana*. Photoperiodic flowering is a major factor determining crop performance and is controlled by interactions between environmental signals and the circadian clock. They proposed *Hvlux1* an ortholog of the *Arabidopsis* circadian gene *LUX ARRHYTHMO*, as a candidate underlying the *early maturity 10* (*eam10*) locus in barley. They could demonstrate that the *eam10* gene in the cultivar Super Precoz 2H from Russia causes circadian defects and interacts with the photoperiod response gene *Ppd-H1* to accelerate under long-day and short-day conditions. They conducted functional, phylogenetic and diversity studies of *eam10* and *HvLUX1* to understand the genetic control of photoperiod response and

to characterize the evolution of *LUX*-like genes within barley and across monocots and eudicots.

Reference:

Campeli, Ch., A. Pankin, B. Drosse, Ch.M. Casao, S.J. Davis, and M. von Korff. 2013. *HvLUX1* is a candidate gene underlying the *early maturity 10* locus in barley: phylogeny, diversity, and interaction with the circadian clock and photoperiodic pathways. New Phytologist 199:1045-1059.

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Coordinator's report: Nuclear genes affecting the chloroplast

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Lundqvist et al. (2013) explored semi-dominant mutants in the *Xantha-h* locus for a biochemical analysis of the enzyme magnesium chelatase. This enzyme is the first committed enzyme of the chlorophyll biosynthetic pathway. Three genes, *Xantha-f*, *Xantha-g* and *Xantha-h*, encode three proteins which build up the heterotrimeric enzyme complex. From structural studies with X-ray crystallography and cryo-electron microscopy, it is known that the XanH and XanG subunits belong to the conserved family of AAA+ proteins and form a two-ring structure with six XanH in one layer and six XanG in the other layer. The XanH-XanG-complex is the molecular motor of the magnesium chelatase that upon ATP hydrolysis uses XanF as a substrate and promote XanF to insert Mg^{2+} into protoporphyrin IX. The semi-dominant mutations changes amino-acid residues in the ATP-binding site. In the study, different combinations of subunits were used. It was found that addition of XanH, modified according to the semi-dominant mutations, stopped a running magnesium chelatase reaction. It was concluded that there is an exchange of XanH subunits in magnesium chelatase during the catalytic cycle, which indicates that dissociation of the complex may be part of the reaction mechanism related to product release.

The stock list of barley mutants defective in chlorophyll biosynthesis and chloroplast development is found in Barley Genetics Newsletter issue 37 (2007): 37-43 and is also linked from
http://www.carlsberglab.dk/professors/Hansson/Pages/default.aspx

Barley chlorophyll mutants have been named *albina*, *xantha*, *viridis*, *chlorina*, *tigrina* and *striata* depending on their colour and colour pattern. In the *albina* mutants the leaves are completely white due to lack of both chlorophyll and carotene pigments. The *xantha* mutants are yellow and produce carotene, but no chlorophyll. The *chlorina* and *viridis* mutants are both pale green, but differ in *chlorina* being viable. The *tigrina* and *striata* mutants are stripped transverse and along the leaves, respectively.

New references:

Lundqvist, J., I. Braumann, M. Kurowska, A. H. Müller, and M. Hansson. 2013. Catalytic turnover triggers exchange of subunits of the magnesium chelatase AAA+ motor unit. J. Biol. Chem. 288: 24012-24019.

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Coordinator's report: ear morphology genes.

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Historically, barley genetic studies have their foundations in Mendelian mutants, characterized by altered physiology and/or morphology and still preserved as Barley Genetic Stocks. In this regard there are examples of morphological mutations described in the past for which the gene/ genes responsible have been recently cloned and characterized. Several morphological-physiological forms have evolved, including winter, spring, two row, six row, awned, awnless, hooded, naked and covered grain, malting, feed (grain and forage), and food types. Structural and functional genomics that merged in the integrative genomics is supporting a knowledge-oriented breeding to design the "Barley for the Future", in which good alleles will be operating all together in a superior genotype. Barley structural genomics has developed EST sequences databases and genotyping platforms based on different types of molecular markers. The new genomic platforms based on NGS technologies are providing opportunities to advance radically in the discovery of beneficial genes and alleles for barley breeding. Functional genomics use transcriptional analysis –i.e. comprehensive and high-throughput analysis of gene expression for screening candidate genes, predicting gene function, discovering cis-regulatory motifs and characterizing transcriptional regulatory networks- models and reverse genetics. Genome-wide reverse genetics have been developed in barley to understand the gene-function relationships, including both transgenic strategies, like insertional mutagenesis or activation tagging and non-transgenic ones, like TILLING (Targeting Induced Local lesions IN Genomes). Even metabolomics –i.e. the characterization of metabolites present in a tissue in a specific environment condition- can be very informative. Epigenetic effects have been shown to be strongly involved in developmental and physiological processes in model plants. Recently it has been demonstrated that in barley evidences exist on the impact of epigenetic factors on seed development and response to hormones.

As reported in BGN 42 attention is mainly focused on the morphological mutants of barley spike, which affect the phytomeric structure of the rachis, spikelets, lemma glumes, awns, grains, timing of flowering. A new Hooded mutant has been observed in rare out crosses of the extra flower in the Hood, named "Seeded in Hood", in which small seed in some Hood is developed. This mutant generated a complex segregant population from which several Hooded double mutants have been isolated. Genetic studies are in progress to define the segregation of the F2 derived by the cross "Seeded in Hood" x Cometa (two-rowed

commercial cultivar) and to find morphological differences in plants generated by the true seed and "seeded in hood "of the same floret.

The molecular structure and function of several mutants have been studied and genetic analysis performed (Houston et al., 2013). The characteristic variation in the density of grains along the inflorescence, or spike, of modern cultivated barley is largely the consequence of a perturbed interaction between microRNA172 and its corresponding binding site in the mRNA of an APELATA2 (AP2) like transcription factor, HvAP2. Genome-wide association and biparental mapping has been used to identify HvAP2. By comparing inflorescence development and HvAP2 transcript abundance in an extreme dense-spike mutant and its nearly isogenic WT line, the authors showed that HvAP2 turnover driven by microRNA 172 regulates the length of a critical developmental window that is required for elongation of the inflorescence internodes. The data indicate that this heterochronic change, an altered timing of developmental events caused by specific temporal variation in the efficiency of HvAP2 turnover, leads to the striking differences in the size and shape of the barley spike (Houston et al. 2013). It is well known that the inflorescence architecture of barley is common among the Triticeae species, which bear one to three single flowered spikelets at each rachis internode. Triple spikelet meristem is one of the unique features of barley spikes, in which three spikelets (one central and two lateral spikelets) are produced at each rachis internode. Fertility of the lateral spikelets at triple spikelet meristem gives row-type identity to barley spikes. Six-rowed spikes show fertile lateral spikelets and produce increased grain yield per spike, compared with two-rowed spikes with sterile lateral spikelets. Thus, far, two loci governing the row-type phenotype were isolated in barley that include Six-rowed spike1 (*vrs1*) and Intermedium spike-c (*int-c*). Six-rowed has also been isolated as Six-rowed spike 4 (*vrs4*), a barley ortholog of the maize inflorescence architecture gene RAMOSA2 (RA2). Eighteen coding mutations in barley RA2 (HvRA2) were specifically associated with lateral spikelet fertility and loss of spikelet determinacy. Expression analyses through mRNA in situ hybridization and microarray showed that Vrs4 (HvRA2) controls the row-type pathway through Vrs1 (HvHox1), a negative regulator of lateral spikelet fertility in barley. Moreover, Vrs4 may also regulate transcripts of barley SISTER OF RAMOSA3 (HvSRA), a putative trehalose-6-phosphate phosphatase involved in trehalose-6-phosphate homeostasis implicated to control spikelet determinacy. The expression data illustrated that, although RA2 is conserved among different grass species, its down-stream target genes appear to be modified in barley and possibly other species of tribe Triticeae (Koppolu et al 2013).

The transitions from juvenile to adult and adult to reproductive phases of growth are important stages in the life cycle of plants. The regulators of these transitions include miRNAs, in particular miR156 and miR172 which are part of a regulatory module conserved across the angiosperms.

Curaba et al (2013) suggest roles for miR171 and its targets in regulating shoot development in barley. Over-expression of miR171 results in an extended vegetative phase characterized by an increased number of leaves and the initiation of indeterminate axillary meristems instead of spikelet meristems. Additionally, OE171 plants have a reduced number of tillers emerging from the axillary meristems of the crown (under SD conditions) and a delay in the differentiation of spikelet meristems into floral organs. A model is proposed in which miR171 is an upstream regulator that coordinates the timing of shoot development in barley through three independent pathways. First, the results, together with current knowledge from Arabidopsis, suggest that miR171 affects meristem maintenance and axillary meristem differentiation in barley through the down-regulation of HvSCL, and consequently affects the

expression of meristem specific genes such as the homologs of WUS and KN1 analyzed in this study. Secondly, miR171 could repress vegetative phase transitions in barley through the upregulation of miR156, a known regulator of the transition from juvenile to adult phases across the angiosperms. Interestingly, OE171 and OE156 in Arabidopsis show opposite effects on leaf initiation, suggesting that the possible connection between the miR171 and miR156 pathways may be monocotyledon specific. Thirdly, miR171 promotes vegetative traits in barley through a secondary pathway, independent from miR156 that involves TRD and HvPLA1. These apparent additional roles for miR171 and its targets in barley shoot development may represent an important evolutionary difference between monocot and dicot plants.

Most of these mutants, behind the morphological, molecular and genetic studies, will provide breeders with original materials for pre-breeding work.

References

Curaba, Julien, et al. Over-expression of microRNA171 affects phase transitions and floral meristem determinancy in barley. 2013. BMC plant biology 13.1: 6.

Houston, K., S.M. McKim, J. Comadran, N. Bonar, I. Druka, N. Uzrek, E. Cirillo, J. Guzy-Wrobelska, N.C. Collins, C. Halpin, M. Hansson, C. Dockter, A. Druka, and R. Waugh. 2013. Variation in the interaction between alleles of HvAPETALA2 and microRNA172 determines the density of grains on the barley inflorescence. Proceedings of the National Academy of Sciences 110.41:16675-16680.

Koppolu, R., N. Anwar, S. Sakuma, A. Tagiri, U. Lundqvist, M. Pourkheirandish, T. Rutten, Ch. Seiler, A. Himmelbach, R. Ariyadasa, H. M. Youssef, N. Stein, N. Sreenivasulu, T. Komatsuda, and T. Schnurbusch. 2013. Six-rowed spike4 (*Vrs4*) controls spikelet determinacy and row-type in barley. Proceedings of the National Academy of Sciences110.32: 13198-13203.

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Coordinator's report: Semidwarf genes

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Nine QTL for reduced plant height were found by Wang *et al*. (2014), but the one with largest effect is from the Japanese malting barley cultivar Naso Nijo. This QTL explained 23.2% of the height variation observed in a doubled-haploid population and was located in the short arm of chromosome 7H. The nearest molecular marker was DArT marker bPb-9269, which is positioned at 53.1 cM on the DArT. No pleiotropic effects of this semi-dwarfing gene on other agronomic traits including yield and grain size were observed (Wang *et al*., 2014). The DArT marker can serve as a molecular marker for the semidwarf (*sdw*) gene in Naso Nijo and is likely located in bin 04 of the short arm of 7H.

Chen *et al*. (2013) reported that a QTL for reduced plant height is present in chromosome 6HS of Australian cultivar Baudin (Stirling/Franklin). This QTL accounted for about 20 to 25% of the variation in plant height while the uzu 1 or semibrachytic 1 (*uzu1*) gene in 3HL accounted for 30 to 40% of the height variation in the same progeny. The donor of the reduced height QTL was likely Stirling (Dampier//A14 Prior/Ymer/3/Piroline). A QTL for reduced plant height in this region of 6HS was previously reported by Negeri (2009). This QTL originated from the Chinese cultivar Shenmai 3 (Gobernadora/Humai 10). The donor of the reduced plant height QTL was likely the CIMMYT/ICARDA line Gobernadora (OC640/Mari//Pioneer/3/Maris Concord). The DArT marker bPb-6002 in bin 05 of 6HS is closely associated with the plant height (Negeri, 2009).

The origin of this 6H QTL for plant height may trace to the early history of barley breeding. Based DArT markers of cultivars and breeding lines, the DArT marker bPb-6002, and the closely linked markers bPb-0597 and bPb-3927, produce a unique haplotype in a small subset of cultivars originating from Australia, Europe, and North America. One or more parents of these cultivars originated from European barley breeding programs. The parentage Gobernadora and Stirling can be traced back via Kenia and Ymer to Abed Binder, a reselection from Hanna released by the Abed Plant Breeding Station in Denmark in 1916.

Kuczyńska *et al*. (2013) reviewed and summarized published information on barley semi-dwarfing genes. The most commonly used semidwarf gene in barley cultivars worldwide is *sdw1*, but only the Abed Denso (*sdw1.c, denso*) and the Diamant mutants (*sdw1.d*) are widely used to increase tillering and grain yield and reduce lodging (Kuczyńska *et al*., 2013).

Liu *et al*. (2014) applied genotyping by sequence (GBS) procedures to recombinant inbred lines from a Golden Promise by Morex cross to position the breviaristatum-e (*ari-e*) locus. The *ari-e.GP* allele from Golden Promise was mapped in chromosome 5HL proximal from the short rachilla hair 1 (*srh1*) locus. Other plant height QTL were located in 3HS and in 2HL

at the same position as the six-rowed spike 1 (*vrs1*) locus. The three QTL explained about 75% of the observed variation in plant height (Liu *et al*., 2014).

Chen *et al*. (2014) studied the interaction of the uzu 1 (*uzu1*) or semi-brachytic gene for reduced plant height and resistance to crown rot, *Fusarium pseudograminearum*, in near-isogenic lines from crosses between a Chinese accession and two Australian cultivars. The uzu component of the near-isogenic pairs showed a 35% reduction in plant height under cool conditions, 22°/16°C day/night temperatures, and nearly 70% reduction in plant height under warm conditions, 28°/20°C day/night temperatures. The crown rot disease index for the short near-isogenic lines averaged 30% less than that for tall ones under lower temperatures and 35% less under higher temperatures (Chen *et al*., 2014).

Chandler and Harding (2013) induced and studied 'overgrowth' mutants in barley lines with extreme dwarf mutants. The mutant genes in lines treated were at the slender 1 (*Sln1.d*) locus (Chandler *et al*., 2002), the GA-responsive dwarf 2 (*grd2*) locus (Wolbang *et al*., 2004), and the GA sensitivity 1 (*gse1*) locus (Chandler *et al*., 2008). Eleven of 13 new mutants were positioned in the *Sln1* locus, which encodes the *DELLA* protein central to gibberellin (GA) signalling.

Hoffman *et al*. (2012) grew introgression lines from backcrosses of Scarlett to the wild barley accession 'ISR42-8' under hydroponic conditions and examined the variation for many agronomic traits. QTL for plant height were detected in all seven barley chromosomes.

Houston *et al*. (2013) studied mutants and naturally occurring variants associated with dense spikes expressed as reduced rachis internode lengths. Many of these variants were identified as zeocriton (*Zeo*) mutants and mapped in 2HL. The *Zeo* mutants produced a wide range of dominant and incomplete dominant phenotypes affecting both spike density and plant height. Most *Zeo* accessions were found to mutant in the barley ortholog of an APELATA2 transcription factor (*HvAP2*) locus. All the *Zeo* mutants were found to express the small lodicules trait associated with cleistogamous 1 (*cly1*) gene, closed flowering (Houston *et al*., 2013), which was previously associated with *HvAP2* (Nair et al., 2010).

Hussien *et al*. (2014) reviewed information on tillering mutants in barley and the pleiotropic effects of some tillering mutants on plant height. A balance between tiller number and tiller size must be achieved because the number tillers produced affects the size of each tiller and the number of tillers surviving to produce grain.

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