

IV. CULTIVARS AND GERM PLASM

USDA-ARS NATIONAL SMALL GRAINS GERMPLASM RESEARCH FACILITY
P.O. Box 307, Aberdeen, ID 83210, USA.
www.ars-grin.gov/npgs

National Small Grains Collection wheat germ plasm evaluations.

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The USDA-ARS National Small Grains Collection (NSGC) is one of the several components of the National Plant Germplasm System. The NSGC is a working collection in contrast to the base collection at the National Seed Storage Laboratory (NSSL) at Fort Collins, CO. The numbers of accessions in the NSGC are summarized Table 1.

Taxonomy	NSGC Accessions
<i>Triticum</i>	54,455
<i>Aegilops</i>	2,204
<i>Secale</i>	2,105
<i>X Triticosecale</i>	1,998
Intergeneric hybrids	538

The systematic evaluation of wheat accessions in the NSGC and other elite germ plasm continued to be coördinated or conducted by National Small Grains Germplasm Research Facility (NSGGRF) staff at Aberdeen during 2001.

Descriptors appropriate for wheat have been established in collaboration with the Wheat Crop Germplasm Committee. Field evaluation data are recorded on such descriptors as growth habit, number of days from planting to anthesis (heading), plant height, spike or panicle density, lodging, straw breakage, shattering, and awn and glume characteristics, including color. Special nurseries are grown for that purpose at Aberdeen, Idaho, and

Maricopa, AZ. Disease and insect evaluations are conducted in collaboration and coöperation with ARS and state experiments station specialists.

Data obtained from evaluations of NSGC germ plasm are entered in the Germplasm Resources Information Network (GRIN) system by the NSGGRF staff in coöperation with the ARS National Germplasm Resources Laboratory, Beltsville, MD. GRIN is a database containing the characteristics and availability of all genetic resources included in the National Plant Germplasm System. The Database Manager is J.D. Mowder, Beltsville, Maryland. The NSGGRF staff interacts with the GRIN system in recording NSGC orders (seed requests), entering a variety of data, and conducting information searches. No evaluations have been conducted to date for descriptors such as drought tolerance; salt tolerance; winterhardiness; resistance to *Cephalosporium* stripe, flag smut, leaf blight, loose smut, snow mold, take-all, tan spot, and WSMV; and protein.

Triticum descriptors with data currently on the GRIN system are summarized in Table 2, p. 280-281.

The authors wish to acknowledge the important contributions of the NSGGRF staff in this effort, with special thanks to Glenda B. Rutger, Scott McNeil, Carol S. Truman, Kay B. Calzada, and Judy Bradley. Mr. Greg Laine is coöordinating the wheat evaluations efforts at Maricopa, AZ.

National Small Grains Collection activities.

H.E. Bockelman.

Cultivar name clearance. Breeders in the United States are encouraged to have proposed names for new cultivars checked for duplication. The National Small Grains Collection will be glad to assist you. Send the proposed name to: Harold E. Bockelman, USDA-ARS-NSGC, P.O. Box 307, Aberdeen, ID 83210, Fax 208-397-4165, E-mail to

nsgchb@ars-grin.gov. If desired, more than one name may be submitted, listed in order of preference. This will save considerable time if a conflict is found with the first name. Available records (GRIN, CI/PI cards, variety files, etc.) here at Aberdeen are checked for conflicts with the proposed name. If a conflict is found (previous use of the name for that crop), the breeder is requested to submit a different name. If no conflicts are found, the requested name is forwarded to the Federal Seed Lab, Agricultural Marketing Service where the proposed name is checked against the databases they maintain. The Agricultural Marketing Service does not guarantee that its findings are the final word since there is no single, complete name database. This clearance procedure generally requires about four weeks. Trademark searches should be done by the breeder online at <http://www.uspto.gov>.

Elite germ plasm requested. Breeders are encouraged to consider submitting their elite lines for inclusion in the NSGC. Of special interest are lines that have been in uniform nurseries, but are not to be released as cultivars. Histori-

Table 2. National Small Grains Collection evaluation of disease; insect; and agronomic, taxonomic, and quality data for wheat on the GRIN system, updated May, 2004.

Character	Years	Location	Accessions
DISEASE EVALUATIONS.			
Barley Yellow Dwarf Virus	1985–92	Davis, CA	2,287
Barley Yellow Dwarf Virus	1988–94	Urbana, IL	17,517
Soilborne Mosaic Virus	1985–89	Urbana, IL	6,587
Soilborne Mosaic Virus	2000	Manhattan, KS	4,998
Leaf Rust	1983–89, 91–95	Manhattan, KS	38,751
Leaf Rust – Adult	2000	Manhattan, KS	5,000
Stripe Rust – Adult	1984–2003	Mt. Vernon, WA	41,719
Stripe Rust – Adult	1984–2003	Pullman, WA	32,222
Stripe Rust – PST 17	1984–2001	Pullman, WA	18,832
Stripe Rust – PST 20	1984–95	Pullman, WA	12,508
Stripe Rust – PST 25	1984–95	Pullman, WA	1,682
Stripe Rust – PST 27	1984–95	Pullman, WA	14,511
Stripe Rust – PST 29	1984–95	Pullman, WA	14,259
Stripe Rust – PST 37	1984–2001	Pullman, WA	6,146
Stripe Rust – PST 43	1984–2001	Pullman, WA	5,137
Stripe Rust – PST 45	1984–2001	Pullman, WA	6,138
Stripe Rust – PST 78	2000–01	Pullman, WA	1,835
Stem Rust – Adult	1987–94	Rosemount, MN	8,078
Stem Rust – Adult	1987–94	St. Paul, MN	19,141
Stem Rust – HJCS	1987–92	St. Paul, MN	4,342
Stem Rust – QFBS	1987–92	St. Paul, MN	8,639
Stem Rust – QSHS	1987–92	St. Paul, MN	4,455
Stem Rust – RHRS	1987–92	St. Paul, MN	4,312
Stem Rust – RTQQ	1987–92	St. Paul, MN	8,973
Stem Rust – TNMH	1987–92	St. Paul, MN	4,402
Stem Rust – TNMK	1987–92	St. Paul, MN	8,938
Stem Rust – HNLQ	1987–92	St. Paul, MN	4,705
Stem Rust – RKQS	1987–92	St. Paul, MN	4,682
Stem Rust – Genes	1987–92	St. Paul, MN	1,018
Common Bunt	1981–2003	Aberdeen, ID ¹	24,948
Dwarf Bunt	1978–2003	Aberdeen, ID ²	15,892
<i>Septoria nodorum</i>	1970–78	Bozeman, MT	8,095
Powdery Mildew	1996–2003	Kinston, NC	12,973
Fusarium Head Blight/Scab	1998–2002	Brookings, SD	4,084

Table 2 (continued). National Small Grains Collection evaluation of disease; insect; and agronomic, taxonomic, and quality data for wheat on the GRIN system, updated May, 2004.

Character	Years	Location	Accessions
INSECT EVALUATIONS.			
Hessian Fly – B	1983–94	W. Lafayette, IN	449
Hessian Fly – C	1983–94	W. Lafayette, IN & Manhattan, KS	24,165
Hessian Fly – E	1983–94	W. Lafayette, IN & Manhattan, KS	24,149
Hessian Fly – GP	1983–94	W. Lafayette, IN & Manhattan, KS	14,441
Hessian Fly – L	1983–97	W. Lafayette, IN & Manhattan, KS	8,315
Russian Wheat Aphid (RWA)	1988–95	Stillwater, OK	40,842
Cereal Leaf Beetle	1963–70	Indiana, Michigan	16,347
AGRONOMIC, TAXONOMIC, AND QUALITY EVALUATIONS.			
Growth Habit	1987–02	Aberdeen, ID	53,385
Lysine Content	1966–69	Lincoln, NE	10,367
Awn Color	1983–97	Aberdeen, ID & Maricopa, AZ	22,650
Awn Type	1983–97	Aberdeen, ID & Maricopa, AZ	26,561
Glume Color	1983–97	Aberdeen, ID & Maricopa, AZ	22,812
Glume Pubescence	1983–97	Aberdeen, ID & Maricopa, AZ	24,312
Heading Date	1983–94	Aberdeen, ID & Maricopa, AZ	18,365
Heading Date – related to check	1999–2001	Maricopa, AZ	24,968
Kernel Color	1983–94	Aberdeen, ID & Maricopa, AZ	21,319
Kernels/Spike	1983–94	Aberdeen, ID & Maricopa, AZ	3,666
Kernel Weight	1983–94	Aberdeen, ID & Maricopa, AZ	3,669
Leaf Pubescence	1983–94	Aberdeen, ID & Maricopa, AZ	20,888
Plant Height	1983–97	Aberdeen, ID & Maricopa, AZ	21,841
Plant Height – related to check	1999–2001	Maricopa, AZ	24,958
Rachis Length	1995	Maricopa, AZ	2,512
Shattering	1983–94	Aberdeen, ID & Maricopa, AZ	10,637
Spike Density	1983–98	Aberdeen, ID & Maricopa, AZ	15,823
Spikelets/Spike	1995	Maricopa, AZ	2,502
Spike Type	1983–97	Aberdeen, ID & Maricopa, AZ	15,551
Straw Breakage	1983–94	Aberdeen, ID & Maricopa, AZ	16,829
Straw Color	1983–97	Aberdeen, ID & Maricopa, AZ	24,142
Straw Lodging	1983–94	Aberdeen, ID & Maricopa, AZ	23,075

¹ 1985–86 Pendleton, OR.² Field tests are conducted at Logan, UT, by Aberdeen ARS staff.

cally, uniform nurseries been the testing grounds for the most advanced, elite germ plasm from the various public and private breeding programs. Entries in uniform nurseries and other breeding materials that are never released as cultivars are still of potential value to breeders, pathologists, entomologists, and other researchers. Breeders should submit 200–500 g of *untreated* seed to the NSGC (address: P.O. Box 307, Aberdeen, ID 83210). Seed from outside of the United States should be sent to the USDA Plant Germplasm Quarantine Center (address: Bldg. 580, BARC-East, Beltsville, MD 20705) with enclosed forwarding directions. Provide a description of the germ plasm, including donor (breeder, institution); botanical and common name; cultivar name and/or other identifiers (breeder line or selection number, etc.); pedigree; descriptive information (of important traits and special characteristics); and growth habit. Assignment of a PI number and inclusion in the NSGC makes the germ plasm available for research purposes to bona fide scientists in the U.S. and worldwide. Please note that a different procedure applies if you are obtaining *Crop Science* registration. Follow directions provided by the crop registration committee.

Guidelines for exporting seed. All seed sent to a foreign country should be inspected and receive a phytosanitary certificate. In most cases, a fee payable to APHIS (Animal & Plant Health Inspection Service) is required to cover the

cost of the phytosanitary certificate. You may wish to work with APHIS personnel in your state or your State Department of Agriculture to obtain a phytosanitary certificate. Also, please be aware of any import permits and additional declarations that certain importing countries may require to accompany the shipment.

Guidelines for importing seed. Any scientist importing seed should be aware of any restrictions that apply. APHIS personnel can provide current information on applicable restrictions. Of particular importance to wheat researchers are import restrictions related to flag smut and karnal bunt. Presently, some 34 countries have flag smut import restrictions. Six countries currently have karnal bunt import restrictions. *Importation of seed from flag smut and Karnal bunt countries requires a permit from APHIS.* Special handling and grow-out procedures apply to such shipments.

PI Assignments in *Triticum* and *X Triticosecale* from January 2003–February 2004.

PI number	Taxon	Cultivar name or Identification number	Country	State/Province
632635	<i>aestivum</i> subsp. <i>aestivum</i>	Ok102	United States	Oklahoma
632688	<i>aestivum</i>	38206	United States	Virginia
632689	<i>aestivum</i>	Tribute	United States	Virginia
632690	<i>aestivum</i>	Pearl	United States	Virginia
632691	<i>aestivum</i>	McCormick	United States	Virginia
632710	<i>aestivum</i> subsp. <i>aestivum</i>	IDO545	United States	Idaho
632711	<i>aestivum</i> subsp. <i>aestivum</i>	IDO562	United States	Idaho
632712	<i>aestivum</i> subsp. <i>aestivum</i>	IDO566	United States	Idaho
632713	<i>aestivum</i> subsp. <i>aestivum</i>	IDO586	United States	Idaho
632857	<i>aestivum</i> subsp. <i>aestivum</i>	Hollis	United States	Washington
632906	<i>aestivum</i> subsp. <i>aestivum</i>	AC Meena	Canada	Alberta
632907	<i>aestivum</i> subsp. <i>aestivum</i>	AC Andrew	Canada	Alberta
632970	<i>aestivum</i>	Briggs	United States	South Dakota
632989	<i>aestivum</i>	Coker 9295	United States	
633020	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 95 711	United States	Washington
633021	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 95 712	United States	Washington
633022	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 95 713	United States	Washington
633023	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 95 714	United States	Washington
633024	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 95 716	United States	Washington
633025	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 95 726	United States	Washington
633026	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 96 659	United States	Washington
633027	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 96 660	United States	Washington
633028	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 96 662	United States	Washington
633029	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 96 663	United States	Washington
633030	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 96 665	United States	Washington
633031	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 96 666	United States	Washington
633032	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 96 667	United States	Washington
633033	<i>aestivum</i> subsp. <i>aestivum</i>	ARS 96 668	United States	Washington
633037	<i>aestivum</i> subsp. <i>aestivum</i>	NC-Neuse	United States	North Carolina
633571	<i>aestivum</i>	Benton	United States	
633572	<i>aestivum</i>	Douglas	United States	
633575	<i>aestivum</i>	MSU D6234	United States	Michigan
633597	<i>aestivum</i> subsp. <i>aestivum</i>	PA8769-158	United States	Pennsylvania
633737	<i>aestivum</i> subsp. <i>aestivum</i>	G9608B1-L12J11BF02	Canada	Saskatchewan
633738	<i>aestivum</i> subsp. <i>aestivum</i>	G9608B1-L12J13AU01	Canada	Saskatchewan
633765	<i>aestivum</i>	OCRF-101	United States	Oregon
633772	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y4514	United States	Nebraska
633773	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y4518	United States	Nebraska
633774	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y4529	United States	Nebraska
633775	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y4530	United States	Nebraska

PI Assignments in *Triticum* and *X Triticosecale* from January 2003–February 2004.

PI number	Taxon	Cultivar name or Identification number	Country	State/Province
633776	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y4532	United States	Nebraska
633777	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y4648	United States	Nebraska
633778	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y4663	United States	Nebraska
633834	<i>aestivum</i> subsp. <i>aestivum</i>	UC66049	United States	California
633857	<i>aestivum</i>	Cebeco 1404	Netherlands	
633862	<i>aestivum</i>	Dapps	United States	North Dakota
633863	<i>aestivum</i>	Burchett	United States	
633864	<i>aestivum</i>	Prairie White	United States	
633865	<i>aestivum</i>	Baker's White	United States	
633871	<i>aestivum</i>	25W41	United States	
633872	<i>aestivum</i>	25R54	United States	
633873	<i>aestivum</i>	25R35	United States	
633874	<i>aestivum</i>	26R15	United States	
633876	<i>aestivum</i> subsp. <i>aestivum</i>	P921696	United States	Indiana
633877	<i>aestivum</i> subsp. <i>aestivum</i>	N98L20013-1	United States	Nebraska
633878	<i>aestivum</i> subsp. <i>aestivum</i>	N98L20120-17	United States	Nebraska
633879	<i>aestivum</i> subsp. <i>aestivum</i>	N98L20040-44	United States	Nebraska
633880	<i>aestivum</i> subsp. <i>aestivum</i>	N98L20101-49	United States	Nebraska
633881	<i>aestivum</i> subsp. <i>aestivum</i>	N98L20109-50	United States	Nebraska
633882	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5003	United States	Nebraska
633883	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5038	United States	Nebraska
633884	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5047	United States	Nebraska
633885	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5057	United States	Nebraska
633886	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5059	United States	Nebraska
633887	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5062	United States	Nebraska
633888	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5070	United States	Nebraska
633889	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5071	United States	Nebraska
633890	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5076	United States	Nebraska
633891	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5097	United States	Nebraska
633892	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5109	United States	Nebraska
633893	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5110	United States	Nebraska
633894	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5114	United States	Nebraska
633895	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5118	United States	Nebraska
633896	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5154	United States	Nebraska
633897	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5162	United States	Nebraska
633898	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5163	United States	Nebraska
633899	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5173	United States	Nebraska
633900	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5187	United States	Nebraska
633901	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5191	United States	Nebraska
633902	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5195	United States	Nebraska
633903	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5202	United States	Nebraska
633904	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5205	United States	Nebraska
633905	<i>aestivum</i> subsp. <i>aestivum</i>	N02Y5213	United States	Nebraska
633906	<i>aestivum</i> subsp. <i>aestivum</i>	NW97S142-1	United States	Nebraska
633907	<i>aestivum</i> subsp. <i>aestivum</i>	NW97S139-2	United States	Nebraska
633908	<i>aestivum</i> subsp. <i>aestivum</i>	NW99L7171	United States	Nebraska
633909	<i>aestivum</i> subsp. <i>aestivum</i>	NW99L7083	United States	Nebraska
633910	<i>aestivum</i> subsp. <i>aestivum</i>	Antelope	United States	Nebraska
633911	<i>aestivum</i> subsp. <i>aestivum</i>	Arrowsmith	United States	Nebraska
633916	<i>aestivum</i>	NUHILLS	United States	Nebraska
633917	<i>X Triticosecale</i> sp.	1029S	United States	

PI Assignments in *Triticum* and *X Triticosecale* from January 2003–February 2004.

PI number	Taxon	Cultivar name or Identification number	Country	State/Province
633974 <i>aestivum</i> subsp. <i>aestivum</i>		Chotrau	United States	Montana
633975 <i>X Triticosecale</i> sp.		346	United States	
633976 <i>aestivum</i> subsp. <i>aestivum</i>		ND 2710	United States	North Dakota
633996 <i>X Triticosecale</i> sp.		314	United States	
634010 <i>X Triticosecale</i> sp.		96	United States	
634011 <i>aestivum</i>		Stellar	United States	
634012 <i>aestivum</i>		AR 839	United States	
634020 <i>aestivum</i>		JINMAI 50	China	Shanxi
634021 <i>aestivum</i>		JINMAI 61	China	Shanxi
634194 <i>X Triticosecale</i> sp.		Mammoth	United States	Oregon
634195 <i>X Triticosecale</i> sp.		Mammoth II	United States	Oregon
634196 <i>X Aegilopiticum</i> sp.		01NDSWG-2	United States	North Dakota
634197 <i>X Aegilopiticum</i> sp.		01NDSWG-5	United States	North Dakota
634198 <i>X Aegilopiticum</i> sp.		01NDSWG-4-1	United States	North Dakota
634199 <i>X Aegilopiticum</i> sp.		01NDSWG-4-2	United States	North Dakota
634314 <i>aestivum</i> subsp. <i>aestivum</i>		Star	Mexico	Federal District
634315 <i>turgidum</i> subsp. <i>durum</i>		Canelo	Mexico	Federal District
634316 <i>turgidum</i> subsp. <i>durum</i>		Spot 2	Mexico	Federal District
634317 <i>turgidum</i> subsp. <i>durum</i>		Porron	Mexico	Federal District
634318 <i>turgidum</i> subsp. <i>durum</i>		Afuwan	Mexico	Federal District
634537 <i>X Triticosecale</i> sp.		NE426GT	United States	Nebraska
634538 <i>aestivum</i> subsp. <i>aestivum</i>		Sebesta Blue-1	United States	Oregon
634539 <i>aestivum</i> subsp. <i>aestivum</i>		Sebesta Blue-2	United States	Oregon
634540 <i>aestivum</i> subsp. <i>aestivum</i>		Sebesta Blue-3	United States	Oregon
634550 <i>aestivum</i>		Snowbird	Canada	
634553 <i>aestivum</i>		Oklee	United States	Minnesota
634564 <i>aestivum</i>		Pryor	United States	
634567 <i>aestivum</i>		Idaho 587	United States	Idaho
634568 <i>aestivum</i>		Jerome	United States	Idaho

V. WHEAT CULTIVAR ABBREVIATIONS FOR 2001–2003.

Bent Skovmand, CIMMYT, Mexico.

The last update to the list of wheat cultivar abbreviations was published in volume 46 of the Annual Wheat Newsletter. This list includes abbreviations assigned since that date.

Cultivar	Abbreviation	Country	Year	Type
Adana 99	ADA99	TUR	2001	Bread wheat
WAFAQ2000	WAFAQ	PAK	2001	Bread wheat
Olvera	OLVERA	ESP	2001	Bread wheat
THA25	THA25	ESP	2001	Bread wheat
San Dionisio	SDION	ESP	2001	Bread wheat
TH30	TH30	ESP	2001	Bread wheat
Ecija, BW	EJIC	ESP	2001	Bread wheat
THA36	THA36	ESP	2001	Bread wheat
Don Sebastian	DSIAN	ESP	2001	Durum wheat
TDA27	TDA27	ESP	2001	Durum wheat
Rio Colorado	RCOL	MEX	2001	Durum wheat
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Vorobey	VORB	MEX	2002	Bread wheat
Soroca	SOROCA	MEX	2002	Bread wheat
Astreb	ASTREB	MEX	2002	Bread wheat
Berkut	BERKUT	MEX	2002	Bread wheat
Sokoll	SOKOLL	MEX	2002	Bread wheat
Wheatear	WHEAR	MEX	2002	Bread wheat
<hr/>				
Circus	CIRCUS	MEX	2003	Bread wheat
Chibia	CHIBIA	MEX	2003	Bread wheat
Shatabdi	SHTB	BGD	2003	Bread wheat
Dulus	DULUS	MEX	2003	Bread wheat
Metso	METSO	MEX	2003	Bread wheat
Sunsu	SUNSU	MEX	2003	Bread wheat
Tilhi	TILHI	MEX	2003	Bread wheat
Ketupa	TUPA	MEX	2003	Bread wheat
Otus	OTUS	MEX	2003	Bread wheat
Sirkku	SIRKKU	MEX	2003	Bread wheat
Tikka	TIKKA	MEX	2003	Bread wheat
Trost	TROST	MEX	2003	Bread wheat
Sova	SOVA	MEX	2003	Bread wheat
Barsa	BARSA	MEX	2003	Bread wheat
Lerke	LERKE	MEX	2003	Bread wheat
Timba	TIMBA	MEX	2003	Bread wheat
Heilo	HEILO	MEX	2003	Bread wheat
Don Rafael	DRAF	ESP	2003	Durum wheat
Murga	MURGA	MEX	2003	Bread wheat
Don Manuel	DMAN	ESP	2003	Durum wheat
Pandion		MEX	2003	Bread wheat
Escacena	ESCA	MEX	2003	Bread wheat
Fiscal	FISCAL	MEX	2003	Bread wheat
Mesia	MESIA	MEX	2003	Bread wheat
Elvira	ELVIRA	MEX	2003	Bread wheat
BAW 1006		BGD	2003	Bread wheat

VI. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2004 SUPPLEMENT

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The most recent edition of the Catalogue, produced and presented at the 10th International Wheat Genetics Symposium is available on CD. MacGene was produced by Y. Yamazaki in collaboration with R.A. McIntosh. The Catalogue also is displayed on the GrainGenes Website: <http://wheat.pw.usda.gov>.

Revisions.**INTRODUCTION****1. Recommended Rules for Gene Symbolisation in Wheat**

- 2.2. Add: 'Where a molecule is composed of sub-units produced by different genes, a further capital letter may be added to the basic symbol to describe a particular sub-unit; for example, *AhasL* refers to a large sub-unit of the complex enzyme acetohydroxyacid synthase.'
- 6.2.2. Add to end of existing entry: 'R² values, where given, indicate the proportion of variation explained by a QTL.'
12. Add to this rule: 'The entire sequence (134.540 bp) and a genetic map of the circular wheat chloroplast genome is provided in {10036}. A total of 30 tRNA genes and 75 protein-encoding genes were identified.'

9. Laboratory Designators for DNA markers

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10. Organisation of the Catalogue

4. Stock listings:

After **tv2**: add new group: **sutv**: = Chromosome substitutions into tetraploid wheat.

DNA Markers

Group 1S

Add:

<i>XBmac0213-1R</i> {10081}.	Barley SSR.
<i>Xcf61-1A</i> {10071}.	CFD 61 F/CFD 61 R.
<i>Xeco406-1A,B,D</i> {10047}.	Ta01_04b06.
<i>Xiag95-1R</i> {10081,10074}.	STS marker.
<i>Xksu946(NBS-LRR)-1A,B,D</i> {10052}.	KSU946. (2B, 3A).
<i>Xsuk951(Kin)-1D</i> {10052}.	KSUK951. (1A, 1BL, 3D, 6D, 7B).
<i>Xpsr960-1R</i> {10081}.	PSR960.
<i>XSCM9-1R</i> {10081}.	Rye SSR.

Group 1L

Add:

<i>Xcd346</i> -1A {10071}.	CDO346.
<i>Xeco702</i> -1A,B {10047}.	Ta01_07h02.
<i>Xeco812</i> -1D {10047}.	Ta01_08f12.
<i>Xfbb275</i> -1A {10071}.	FBB275.
<i>Xgwm601</i> -1A {10071}.	WMS 601 F/WMS601 R.
<i>Xksuk951</i> (<i>Kin</i>)-1B {10052}.	KSUK951. (1A, 1DS, 3D, 6D, 7B).

Group 1

Add:

<i>Xbcd1514</i> -1A {10048}.	BCD1514.
<i>Xbcd1562</i> -1A {10048}.	BCD1562.
<i>Xbcd1930</i> -1B {10048}.	BCD1930.
<i>Xcdf92</i> -1D {10071}.	CFD 92 F/CFD 92 R.
<i>Xfba118</i> -1B {10048}.	FBA118.
<i>Xfba165</i> -1B {10048}.	FBA165.
<i>Xfba294</i> -1A {10048}.	FBA294.
<i>Xfba298</i> -1B {10048}.	FBA298.
<i>Xfbb90</i> -1A {10048}.	FBB90.
<i>Xfbb160</i> -1D {10048}.	FBB160.
<i>Xfbb190</i> -1A {10048}.	FBB190.
<i>Xfbb196</i> -1B {10048}.	FBB196.
<i>Xfbb278</i> -1A,B {10048}.	FBB278.
<i>Xksu36</i> -1A,D {10048}.	AFLP-36F/AFLP-36R.
<i>Xksu940</i> (<i>NBS-LRR</i>)-1A,B,D {10052}.	KSU940.
<i>Xksu941</i> (<i>NBS-LRR</i>)-1B,D {10052}.	KSU941.
<i>Xksu942</i> (<i>NBS-LRR</i>)-1B,D {10052}.	KSU942.
<i>Xksu945</i> (<i>NBS-LRR</i>)-1B {10052}.	KSU945. (2D).
<i>Xksuk950</i> (<i>Kin</i>)-1A,B,D {10052}.	KSUK950.
<i>Xksuk951</i> (<i>Kin</i>)-1A {10052}.	KSUK951. (1BL, 1DS, 3D, 6D, 7B).
<i>Xksuk955</i> (<i>Kin</i>)-1D {10052}.	KSUK955. (2B, 5A,D, 6A,B).
<i>Xksuk959</i> (<i>Kin</i>)-1A,B {10052}.	KSUK959. (4B).
<i>Xksuk963</i> (<i>Kin</i>)-1D {10052}.	KSUK963. (2B, 3B,D, 5D).
<i>Xksuk969</i> (<i>Kin</i>)-1D {10052}.	KSUK969.
<i>Xksuk970</i> (<i>Kin</i>)-1A {10052}.	KSUK970. (3B, 5D).
<i>Xksuk971</i> (<i>Kin</i>)-1D {10052}.	KSUK971. (2D, 3A, 7B).
<i>Xnau1</i> (<i>NBS</i>)-1A,B {10084}.	RGA WN20.
<i>Wag</i> -1A, B, D {10078}.	Probe 386-bp of the 3' end of GenBank accession AB084577.

Group 2S

Amendments:

Xgdm5-2A. Change the first column to ‘*Xgdm5*-2A {0173}, 2D {10055}.’.*Xpsr102*(*Sam*)-2A,B,D. Add: ‘The development of locus-specific primers for the A, B and D loci was reported in {0049}.’.*Xpsr112*-2A,B,D. Add: ‘The development of locus-specific primers for the A, B, D and R loci was reported in {0049}.’.

Add:

<i>Xbcd348</i> -2N {10073}.	BCD348.
<i>Xcmwg682</i> -2N {10073}.	CMWG682.
<i>Xeco509</i> -2A,B,D {10047}.	Ta01_05h09. (7A,B,D).
<i>Xfbb67</i> -2B {10071}.	FBB67.
<i>Xgwm400</i> -2A {10071}.	WMS 400 F/WMS 400 R.
<i>Xgwm429</i> -2B {10071}.	WMS 429 F/WMS 429 R.

<i>Xgwm682-2B</i> {10055}.	WMS F682/WMS R682.
<i>Xgwm726-2A</i> {10047}.	WMS F726/WMS R726.
<i>Xgwm830-2A</i> {10055}.	WMS F830/WMS R830.
<i>Xgwm886-2D</i> {10055}.	WMS F886/WMS R886.
<i>Xgwm895-2A</i> {10055}.	WMS F895/WMS R895.
<i>Xgwm1045-2A</i> {10055}.	WMS F1045/WMS R1045.
<i>Xgwm1052-2A</i> {10055}.	WMS F1052/WMS R1052.
<i>Xgwm1115-2A</i> {10055}.	WMS F1115/WMS R1115.
<i>XHak2-2A</i> {9932,10073}.	HvHAK2.
<i>Xgwm1128-2B</i> {10055}.	WMS F1128/WMS R1128.
<i>XksuH9-2N</i> {10073}.	KSUH9.
<i>XksuD18-2N</i> {10073}.	KSUD18.
<i>Xpsr150-2N</i> {10073}.	PSR150.
<i>Xpsr933.1-2N</i> {10073}.	PSR933.
<i>Xvrga1-2N</i> {0213,10073}.	VRGA1.

Group 2L

Add:

<i>Xcsl107-2B</i> {10013}.	G4-5', G035-5', G035-3'.	(2D).
<i>Xcsl107-2D</i> {10013}.	G4-5', G035-5', G035-3'.	(2B).
<i>Xeco203-2A,B,D</i> {10047}.	Ta01_02b03.	
<i>Xeco208(L38)-2D</i> {10047}.	Ta01_02g08.	
<i>Xfba259-2B</i> {10071}.	FBA259.	
<i>Xgwm761-2A</i> {10055}.	WMS F761/WMS R761.	
<i>Xgwm940-2B</i> [{10055}].	[<i>Xgwm940a-2B</i> {0455}].	WMS F940/WMS R940.
<i>Xgwm1027-2B</i> {10055}.	WMS F1027/WMS R1027.	
<i>Xgwm1204-2D</i> {10055}.	WMS F1204/WMS R1204.	
<i>Xgwm1249-2B</i> {10055}.	WMS F1249/WMS R1249.	
<i>Xgwm1256-2A</i> {10055}.	WMS F1256/WMS R1256.	
<i>Xgwm1264-2D</i> {10055}.	WMS F1264/WMS R1264.	
<i>Xksu944(NBS-LRR)-2A</i> {10052}.	KSU944.	(5D).
<i>Xksu946(NBS-LRR)-2B</i> {10052}.	KSU946.	(1A,B,D, 3A).
<i>XksuK965(Kin)-2A,B</i> {10052}.	KSUK965.	

Note: The location of the *XksuK965-2A* locus was ambiguous as the same fragment was missing in both N5B and N2A. It is likely, however, that the absence of the fragment in N5B was caused by rearrangements due to the absence of *Ph1* {10053}.

<i>Xwmc474-2B</i> {10055}.	WMC 474F/WMC 474R.	(2A).
<i>Xwmc477-2B</i> {10055}.	WMC 477F/WMC 477R.	
<i>Xwgp17(Rga)-2B</i> {10117}.	S2/AS3.	
<i>Xwgp18(Rga)-2B</i> {10117}.	S2/AS3.	
<i>Xwgp19(Rga)-2B</i> {10117}.	RLRR Rev/LM638.	
<i>Xwgp20(Rga)-2B</i> {10117}.	RLRR Rev/LM638.	
<i>Xwgp21(Rga)-2B</i> {10117}.	Pto kin11N/Pto kin21N.	
<i>Xwgp22(Rga)-2B</i> {10117}.	Cr33LR-R/Pto kin2.	
<i>Xwgp23(Rga)-2B</i> {10117}.	Cr33LR-R/Pto kin2.	
<i>Xwgp24(Rga)-2B</i> {10117}.	Xa1LR-F/Pto kin4.	
<i>Xwgp25(Rga)-2B</i> {10117}.	XLRR Rev/Pto kin1.	
<i>Xwgp26(Rga)-2B</i> {10117}.	Pto kin2/AS3-INV.	
<i>Xwgp27(Rga)-2B</i> {10117}.	CLRR-INV2/Pto kin1.	
<i>Xwgp28(Rga)-2B</i> {10117}.	RLRR Rev/Pto kin4.	
<i>Xwgp29(Rga)-2B</i> {10117}.	RLK-Rev/Xa1 NBS-F.	
<i>Xwgp30(Rga)-2B</i> {10117}.	LM638/S2.	
<i>Xwgp31(Rga)-2B</i> {10117}.	Pto kin2/RLK-For.	
<i>Xwgp32(Rga)-2B</i> {10117}.	Pto kin2/NLRR-INV1.	

Group 2

Add:

<i>Xfbb255-2B</i> {10069}.	FBB255.
<i>Xgwm448-2D</i> {10071}.	WMS 448 F/ WMS 448 R.
<i>Xgwm496-2D</i> {10085}.	WMS 496 F/ WMS 496 R.
<i>Xgwm817-2A</i> {10031}.	WMS F817/WMS R817.
<i>Xksu945(NBS-LRR)-2D</i> {10052}.	KSU945. (1B).
<i>XksuK948(Kin)-2A,B,D</i> {10052}.	KSUK948.

Note: The location of the *XksuK948-2A* locus was ambiguous as the same fragment was missing in both N5B and N2A. It is likely, however, that the absence of the fragment in N5B was caused by rearrangements due to the absence of *Ph1* {10053}.

<i>Xksuk955(Kin)-2B</i> {10052}.	KSUK955. (1D, 5A,D, 6A,B).
<i>Xksuk963(Kin)-2B</i> {10052}.	KSUK963. (1D, 3B,D, 5D).
<i>Xksuk971(Kin)-2D</i> {10052}.	KSUK971. (1D, 3A, 7B).
<i>Xnau2(NBS)-2A,D</i> {10084}.	RGA N9.
<i>Xwmc474-2B</i> {10067}.	WMC474F/WMC474R.
<i>Xwmc499-2B</i> {10067}.	WMC499F/WMC499R.

Group 3S

Add:

<i>Xbarc12-3A</i> {10044}.	BARC 12F/BARC 12R.
<i>Xbarc57-3A</i> {10044}.	BARC 57F/BARC 57R.
<i>Xbarc86-3A</i> {10044}.	BARC 86F/BARC 86R.
<i>Xcf79-3A</i> {10071}.	CFD 79 F/CFD 79 R.
<i>Xcmwg680-3A</i> {10044}.	cMWG680.
<i>Xgwm892-3D</i> {10055}.	WMS F892/WMS R892.
<i>Xgwm1034-3B</i> {10076}.	WMS 1034 F/WMS 1034 R.
<i>Xwmc505-3A</i> {10067}.	WMC505F/WMC505R.

Group 3L

Add:

<i>Xfwm-3B</i> {10080}.	FWM 4 F / FWM 4 R.
<i>Xeco604(Glb3)-3A,B,D</i> {10047}.	Ta01_06f04.
<i>Xgwm234-3B</i> {10071}.	WMS 234 F / WMS 234 R.
<i>Xgwm344-4A</i> {10071}.	WMS 344 F / WMS 344 R.
<i>Xgwm1088-3D</i> {10055}.	WMS F1088/WMS R1088.
<i>Xksu946(NBS-LRR)-3A</i> {10052}.	KSUK946. (1A,B,D, 2B).
<i>Xwmc322-3A</i> {10067}.	WMC322F/WMC322R.
<i>Xwmc56-3B</i> {10067}.	WMC56F/WMC56R.

Group 3

Add:

<i>Xksuk951(Kin)-3D</i> {10052}.	KSUK951. (1A,B,D, 6D, 7B).
<i>Xksuk953(Kin)-3B</i> {10052}.	KSUK953. (6A,B,D).
<i>Xksuk954(Kin)-3A,B,D</i> {10052}.	KSUK954.
<i>Xksuk963(Kin)-3B,D</i> {10052}.	KSUK963. (1D, 2B, 5D).
<i>Xksuk967(Kin)-3D</i> {10052}.	KSUK967. (5B).
<i>Xksuk970(Kin)-3B</i> {10052}.	KSUK970. (1A, 5D).
<i>Xksuk971(Kin)-3A</i> {10052}.	KSUK971. (1D, 2D, 7B).

Group 4S (4AL:4BS:4DS)

Add:

Xeco903(a-Tub)-4A,B,D {10047}.

Ta01_09a03.

(6A)

Note: {10047} states that marker Ta01_09a03 detects loci on 4AS, 4BS, 4DS. Most likely, this should read 4AL, 4BS, 4DS.

Xeco901(L2)-4A,B,D {10047}.

Ta01_09f01.

(5A,B,D).

Note: {10047} states that marker Ta01_09a03 detects loci on 4AS, 4BS, 4DS. Most likely, this should read 4AL, 4BS, 4DS.

Xgwm742-4A {10055}.

WMS F742/WMS R742.

Xgwm832-4A {10055}.

WMS F832/WMS R832.

Xgwm894-4A {10055}.

WMS F894/WMS R894.

Xgwm959-4A {10055}.

WMS F959/WMS R959.

Group 4L (4AS:4BL:4DL)

Add:

XBx1-4A,B,D [{10103}]. [TaBx1-4A,B,D {10103}].Primers based on maize *Bx1*.*XBx2-4A,B,D* [{10103}]. [TaBx2-4A,B,D {10103}].Primers based on maize *Bx1*.*Xgwm929-4A* {10055}.

WMS F929/WMS R929.

Xpsr103-4AL {10080}.

PSR103.

XksuG30-4BL {10080}.

KSUG30.

Xgwm1093-4A {10055}.

WMS F1093/WMS R1093.

Group 4

Add:

Xksu943(NBS-LRR)-4B {10052}.

KSU943.

Xksuk958(Kin)-4A {10052}.

(5B, 6B).

Xksuk959(Kin)-4B {10052}.

(1A,B).

Group 5S

Add:

Xbarc56-5A {10076}.

BARC 56 F/BARC 56 R.

XBx3-5A,B,I,D [{10103}]. [TaBx3-5A,B,D {10103}].Primers based on maize *Bx3*. (5BL).*XBx4-5A,B,D* [{10103}]. [TaBx4-5A,B,D {10103}].Primers based on maize *Bx4*.*XBx5-5A,B,I,D* [{10103}]. [TaBx5-5A,B,D {10103}].Primers based on maize *Bx5*. (5BS).*XBx5-5B.2* [{10103}]. [TaBx5-5B {10103}].

(5BS).

Xeco608-5A {10047}.

Ta01_06h08.

(6B, 7B).

Xeco901(L2)-5A,B,D {10047}.

Ta01_09f01.

(4A,B,D).

Xgwm1057-5A {10076}.

WMS 1057 F/WMS 1057 R.

Xksuk960(Kin)-5B {10052}.

KSUK960. (6B, 7A,B,D).

Group 5L

Add:

XBx3-5B.2 [{10103}]. [TaBX3-5B {10103}].Primers based on maize *Bx1*. (5AS,BS,DS).*Xcfa255-5A* {10071}.

CFA 255 F/ CFA 255 R.

Xcfa2155-5A {10080}.

CFA 2155 F/CFA 2155 R.

Xcfa2163-5A {10080}.

CFA 2163 F/CFA 2163 R.

Xfb166-5A {10080}.

FBB166.

Xgwm271-5A {10071}.

WMS 271 F/WMS 271 R.

Xgwm810-5B {10007}.

WMS F810/WMS R810.

Xksu944(NBS-LRR)-5D {10052}.

KSU944. (2A).

Xksuk952(Kin)-5A {10052}.

(5B,D, 6A,B).

XksuP16-5A {0048}.

pTtksuP16.

<i>Xgwm843-5B</i> {10056}.	WMS F843/WMS R843.
<i>Xgwm1016-5B</i> {10007}.	WMS F1016/WMS R1016.
<i>Xgwm1043-5B</i> {10007}.	WMS F1043/WMS R1043.
<i>Xmwg2062-5A</i> {10079}.	MWG2062.
<i>Xgwm1180-5B</i> {10007}.	WMS F1180/WMS R1180.
<i>XSnf2P-5A</i> {10098}.	Complete sequence from BAC AY485644.
<i>Xucw1(Nuc)-5A</i> {10098}.	UCW1 (Barley Nucellin gene).
<i>Xucw2-5A</i> {10098}.	UCW2.
<i>Xucw26-5A</i> {10109}.	UCW26.
<i>Xucw90(Cbf3)-5A</i> {10079}. [<i>XCb3</i> {10079}].	Barley CBF3.

Group 5

Add:

<i>Xgwm271-5A</i> {10069}.	WMS271F/WMS271R.
<i>Xksuk952(Kin)-5A,B,D</i> {10052}.	KSUK952. (6A,B).
<i>Xksuk955(Kin)-5A,D</i> {10052}.	KSUK955. (1D, 2B, 6A,B).
<i>Xksuk956(Kin)-5A,B</i> {10052}.	KSUK956.
<i>Xksuk957(Kin)-5A,B,D</i> {10052}.	KSUK957.
<i>Xksuk958(Kin)-5B</i> {10052}.	KSUK958. (4A, 6B).
<i>Xksuk963(Kin)-5D</i> {10052}.	KSUK963. (1D, 2B, 3B,D).
<i>Xksuk967(Kin)-5B</i> {10052}.	KSUK967. (3D).
<i>Xksuk968(Kin)-5B</i> {10052}.	KSUK968. (6B).
<i>Xksuk970(Kin)-5D</i> {10052}.	KSUK970. (1A, 3B).
<i>Xksuk972(Kin)-5B,D</i> {10052}.	KSUK972.
<i>Xksuk973(Kin)-5B</i> {10052}.	KSUK973.
<i>Xmta15-5A</i> {10069}.	MTA15.
<i>Xnau3(NBS)-5B,D</i> {10084}.	RGA N9.
<i>Xnau4(NBS)-5B</i> {10084}.	RGA WN16.

Group 6S

Add:

<i>Xeco608-6B</i> {10047}.	Ta01_06h08. (5A, 7B).
<i>Xeco812-6A,B,D</i> {10047}.	Ta01_08f12. (1D).
<i>Xeco903(a-Tub)-6A</i> {10047}.	Ta01_09a03. (4A,B,D).
<i>Xgwm680-6B</i> {10055}.	WMS F680/WMS R680.
<i>Xgwm771-6B</i> {10055}.	WMS F771/WMS R771.
<i>Xgwm825-6B</i> {10055}.	WMS F825/WMS R825.
<i>Xgwm889-6B</i> {10055}.	WMS F889/WMS R889.
<i>Xgwm935-6B</i> {10060}.	WMS F935/WMS R935. (7B).
<i>Xgwm1255-6B</i> {10055}.	WMS F1255/WMS R1255.
<i>Xksuk953(Kin)-6B</i> {10052}.	KSUK953. (6A,D, 3B).
<i>Xksuk958(Kin)-6B</i> {10052}.	KSUK958. (4A, 5B).
<i>Xksuk960(Kin)-6B</i> {10052}.	KSUK960. (5B, 7A,B,D).

Group 6L

Amendments:

Xcd0347-6B {0220}. CDO347. (7A,7D).

Add:

<i>Xeco501-6A,B,D</i> {10047}.	Ta01_05a01.
<i>Xwmc182-6B</i> {0348}.	WMC 182F/WMC 182R.
<i>Xwmc341-6B</i> {10067}.	WMC341F/WMC341R

Group 6

Add:

Xcd0347-6A,6B,6D {0220}.	CDO347.	(6A,B,D) (7A,D).
Xksuk949(<i>Kin</i>)-6B,D {10052}.	KSUK949.	(7A).
Xksuk951(<i>Kin</i>)-6D. {10052}.	KSUK951.	(1A,B,D, 3D, 7B).
Xksuk952(<i>Kin</i>)-6A,B {10052}.	KSUK952.	(5A,B,D).
Xksuk953(<i>Kin</i>)-6A,B,D {10052}.	KSUK953.	(3B).
Xksuk955(<i>Kin</i>)-6A,B {10052}.	KSUK955.	(1D, 2B, 5A,D).
Xksuk961(<i>Kin</i>)-6A,B {10052}.	KSUK961.	
Xksuk966(<i>Kin</i>)-6A,B,D {10052}.	KSUK966.	
Xksuk968(<i>Kin</i>)-6B {10052}.	KSUK968.	(5B).

Group 7S

Amendments:

Xgwm935-7B. Add '(6B.)' in the last column.

Add:

Xcdf2-7D {10071}.	CFD 2 F/ CFD 2 R.
Xeco509-7A,B,D {10047}.	Ta01_05h09. (2A,B,D).
Xeco608-7B {10047}.	Ta01_06h08. (5A, 6B).
It is not known whether Xeco608-7B belongs to group 7S or to group 7AS:4AL:7DS.	
Xgwm302-7A {10071}.	WMS 302 F / WMS 302 R.
Xgwm1014-7D {10055}.	WMS F1014/WMS R1014.
Xgwm1171-7A {10055}.	WMS F1171/WMS R1171.

7AS:4AL:7DS

Add:

Xksu947(*NBS-LRR*)-7A,4A {10052}. KSU947.

Note: The location of the Xksu947 locus was ambiguous as the same fragment was missing in both N5B and N7A. It is likely, however, that the absence of the fragment in N5B was caused by rearrangements due to the absence of *Ph1* {10053}.

Xksuk962(*Kin*)-7A {10052}. KSUK962.**Group 7L**

Amendments:

Xcd0347-7A. Add: '(6B)' to the last column.

Xcd0347-7B Add: '(6B)' to the last column.

Add:

Xeco811(<i>Gapd2</i>)-7A,B,D {10047}.	Ta01_08d11.
Xgwm783-7B {0258}.	WMS 783 F/WMS 783 R.
Xgwm883-7B{0258}.	WMS 883 F/WMS 883 R.
Xgwm984-7B {0258}.	WMS 984 F/WMS 984 R.
Xgwm1144-7B {0258}.	WMS 1144 F/WMS 1144 R .
Xgwm1175-7B {0258}.	WMS 1175 F/WMS 1175 R.
Xgwm1267-7B {0258}.	WMS 1267 F/WMS 1267 R.
Xgwm1498-7B {0258}.	WMS 1498 F/WMS 1498 R.
Xwmc182-7B {10080}.	WMC182 F/WMC182 R.
Xwmc500-7B {10067}.	WMC500F/WMC500R.

Group 7

Add:

<i>Xbcd1930-7A</i> {10071}.	BCD1930.
<i>Xksu23-7A,D</i> {10050}.	AFLP-23F/AFLP-23R.
<i>Xksuk949(Kin)-7A</i> {10052}.	KSUK949. (6B,D).
<i>Xksuk951(Kin)-7B</i> {10052}.	KSUK951. (1A,B,D, 3D, 6D).
<i>Xksuk960(Kin)-7A,B,D</i> {10052}.	KSUK960. (5B, 6B).
<i>Xksuk964(Kin)-7A,B,D</i> {10052}.	KSUK964.
<i>Xksuk971(Kin)-7B</i> {10052}.	KSUK971. (1D, 2D, 3A).

Morphological and Physiological Traits**1. Gross Morphology : Spike Characteristics****1.2. Club/compact spike**

QTL: Two additional QTLs for spike compactness were detected in Courtot/Chinese Spring {10080} on chromosome arms 5DL (*QCp.icf-5D*) and 6DL (*QCp.icf-6D*). Markers *Xcfd26-5D* and *Xcfd38-6D* explained 13.6 % and 12.2 % of the variance in spike compactness, respectively {10080}.

6. Awnedness**6.1. Dominant Inhibitors****6.1.2. Tipped 1**

Bl. v: WAWHT2046 {10040}. ma: *Xgwm6a-5A* – 13.5 cM – *Bl* – 12.2 cM – *Yr34* {10040}.

9. Brittle Rachis (revised section)

Br-A1 {10061}. [*Br1* {9970}]. 3DS {9970}. v: *T. aestivum* var. *tibetanum* {9970}.
Br-A2 {10061}. [*Br2* {0130}]. 3A {0130}. 3AS {10061}. sutv: LDN(DIC 3A){0130}.
Br-A3 {10061}. [*Br3* {0130}]. 3B {0130}. 3BS {10061}. sutv: LTN(DIC 3B){0130}.

Evidence for an orthologous series extending to many related species is discussed in {0130} and {10061}.

Br4 {10082}. 2A {10082}. tv: *T. dicoccoides* {10082}. ma: 33 cM distal to *Xgwm294-2A* (LOD = 6.3, R^2 = 14.4%) {10082}.

11. Cadmium Uptake**11.1. Low cadmium uptake**

Add the following:

Cdu1. 5BL {10104}. v: Kyle*2/Biodur (10104).
cdu1 v: Kofa {10104}.

18. Ear Emergence

QTLs for ear emergence were detected in the cross Renan/Recital {10069}. LOD scores and percent of variation explained by the QTL (R^2) are averages of three years of field tests.

QEet.inra-2B {10069}. ma: 2B linked to *Xgwm148* (LOD = 5.7, R^2 = 11.9.2%).
QEet.inra-2D {10069}. ma: 2D linked to *XksuE3* (LOD = 2.7, R^2 = 6.5%).
QEet.inra-7D {10069}. ma: 7D linked to *Pch1* (LOD = 3.9, R^2 = 7.3%).

19. Earliness per se

Eps-5BL1 {10075}. 5BL (10074). ma: QTL mapped on chromosome 5BL, linked to *Xwmc73-5B* (this QTL explained 8 % of the variance in flowering time, $P < 0.03$) {10074}.

Eps-5BL2 {10074}. 5BL {10074}. ma: QTL mapped on chromosome 5BL, linked to *Xgwm499-5B* (this QTL explained 6 % of the variance in flowering time) {10074}.

QTLs Two QTL for narrow-sense earliness were detected on chromosome 2B in a CS/*T. spelta* var. *duhamelianum* KT19-1 RI population {10057}. The QTL were associated with markers *Xpsr135-2B* and *Xabc451-2B* {10057}. For both QTL, earliness was conferred by the CS allele.

20. Flowering time

Insert at beginning of section: ‘The isolation of wheat genes orthologous to the Arabidopsis *Co* and rice *Hd1* gene was reported in {10054}. The genomic clones TaHd1-1, TaHd1-2, and TaHd1-3 originate from the long arms of chromosomes 6A, 6B, and 6D, respectively. The orthology of the *TaHd1* genes with *Co/Hd1* has been demonstrated by complementation of a rice line deficient in *Hd1* function with the TaHd1-1 genomic clone. It should be noted that the wheat *TaHd1* and rice *Hd1* genes are located in nonsyntenic locations {10054}. To date, no variation for flowering time has been identified on the wheat group 6 chromosomes.’

23. Frost Resistance

Fr-A2 {10079}. **dv:** *Triticum monococcum*. Frost-tolerant parent G3116, frost-susceptible parent DV92. **ma:** The QTL mapped on chromosome 5AL has a LOD score of 9 and explained 49 % of the variation in frost tolerance. Closest markers: *Xbcd508-5A* and *Xucw90(Cbf3)-5A*. These markers are 30 cM proximal to *Xwg644-5A*, which is closely linked to frost tolerance locus *Fr-1*. QTLs for frost tolerance in the *Fr-2* region have been also identified in wheat chromosome 5B (*Fr-B2* {10079}) and in barley chromosome 5H (*Fr-H2* {10083}).

Fr-B2 [*Fr-B1* {10075}]. **ma:** QTL mapped on chromosome 5BL, linked to *Xgwm639-5B* (this QTL explained 12-31 % of the variance in frost tolerance) {10075}. *Xgwm639-5B* mapped close to *Xmwg914-5B*, and to *Xbcd508-5B*, a marker located at the peak of the *Fr-A2* QTL {10075}. This data suggests that this locus is more likely orthologous to *Fr-2* than to *Fr-1*.

24.1. Gametocidal activity

Gc2-SIIb. **ma:** an EMS-induced *Gc-2* mutant was mapped to a wheat-*Aegilops sharonensis* T4B-4S^{sh}#1 translocation chromosome {10068}.

28. Grain hardness / Endosperm texture

Add at end of section: ‘QTL: Two QTL were detected for grain hardness in RILs of the ITMI population (Synthetic / Opata 85) {10051}. The QTL on the short arm of chromosome 5D is associated with *Xmta10-5D*, and increased hardness is contributed by Opata {10051}. The locus located proximally on the long arm of 5D is associated with *Xbcd450-5D* and increased hardness is contributed by the Synthetic allele {10051}.’.

Add at the end of the section:

‘Using proteomic analysis of 2D-protein gels applied to 101 lines of the Opata/W-7984 (ITMI) RI mapping population, and after a preliminary study of a subgroup of these lines {10086}, 446 amphiphilic protein spots were resolved, 170 specific to either of the two parents and 276 common to both {10087}. An important category of these proteins comprises the puroindolines. Seventy-two loci encoding amphiphilic proteins were conclusively assigned to 15 chromosomes. At least one Protein Quantity Locus (PQL) was associated with each of 96 spots out of the 170 spots segregating; these PQL were distributed throughout the genome. The majority of the amphiphilic proteins were shown to be associated with plant membranes and/or play a role in plant defence against external invasions. Not only the puroindolines were associated with kernel hardness – a number of other amphiphilic proteins were also found to influence this trait.’

31. Grain Weight

Grain weight

QGw1.inra-2B {10071}. **v:** Renan/Recital; favorable allele from Renan {10071}.
 $(R^2 = 10.7 - 19.7 \%)$ {10071}.

ma: *Xgwm374-2B* – *Xgwm388-2B*

QGw1.inra-5B {10071}.

v: Renan/Recital; favourable allele from Recital {10071}. ($R^2 = 4.9 - 10.4\%$) {10071}.

ma: *Xgwm639-5B – Xgwm604-5B*

QGw1.inra-7A {10071}.

v: Renan/Recital; favourable allele from Recital {10071}. ($R^2 = 5.2 - 10.3\%$) {10071}.

ma: *Xcfa2049-7A – Xbcd1930-7A* ($R^2 = 5.2 - 10.3\%$) {10071}.

39.3 Reduced Height: QTL

QTLs for height detected in the cross ‘Renan/Recital’ {10069}. LOD scores and percent of variation explained by the QTL (R^2) are averages of three years of field tests.

QHt.inra-2B {10069}. **ma:** Associated with *Xgwm249-2B* (LOD = 5.8, $R^2 = 15.4\%$).

QHt.inra-4A {10069}. **ma:** Associated with *Xfba243-4A* (LOD = 6.5, $R^2 = 15.0\%$).

QHt.inra-5A {10069}. **ma:** Associated with *Xgwm639b-5A* (LOD = 5.7, $R^2 = 10.8\%$).

QHt.inra-6D {10069}. **ma:** Associated with *Xcf76-6D* (LOD = 3.7, $R^2 = 8.1\%$).

QHt.inra-7A {10069}. **ma:** Associated with *Xcd545-7A* (LOD = 3.2, $R^2 = 7.7\%$).

QHt.riso-3A {10067}. **ma:** Mapped on the centromeric region between SSR markers *Xwmc505-3A* and *Xwmc264-3A* (LOD >6) {10067}.

40. Herbicide Response

40.4. Imidazolinone resistance

Resistance alleles found in mutagenised populations were incompletely dominant and additive in effect {10099}.

Resistance is due to single base pair changes in acetohydroxyacid synthase.

Imi1 {10099}. 6DL {10101}. [AhasL-D1 {10101}, *Fs-4* {10100}].

v: BW755 = Grandin*3/Fidel-FS-4 {10099}; CDS Teal IMI 1A {10099}; CDC Teal IMI 9A {10099}; CDC Teal IMI 10A = Fidel-FS-2 {10099}; Clearfield WHS Janz = Janz*4/Fidel-FS-2; Clearfield WHS Stiletto = Stiletto*3//Spear/Fidel-FS-3; Fidel-FS-2 = ATCC 40997 {10100}.

v2: CDC Teal IMI 15A = PTA 3955 *Imi3* {10099}.

Imi2 {10099}. 6BL {10101}. [AhasL-B1 {10101}].

v: CDC Teal IMI 11A = PTA 3953 {10099}.

Imi3 {10099}. 6AL {10101}. [AhasL-A1 {10101}].

v2: CDC Teal IMI 15A *Imi3* {10099}.

dv: *T. monococcum* mutant EM2 (mutant of susceptible line TM23 {10102}).

Mutant EM2 has a serine to asparagine substitution near the carboxyl end of the enzyme. The same change has led to imidazolinone resistance in hexaploid wheat, rice and *Arabidopsis* {10102}.

57. Red grain Color

Add at beginning of the preamble: Red color is probably due to the polyphenol compounds phlobaphene or proanthocyanidin, synthesised through the flavanoid pathway. Himi & Noda {10107} provided evidence that the D genes were wheat forms of Myb-type transcription factors (*Myb10-3A*, *Myb10-3B*, *Myb-3D*).

61. Response to Vernalization

Add to genotype list following *Vrn-A1a*:

Triple Dirk F: *Vrn-A1b Vrn-B1b Vrn-D1b Vrn-D5a*: Yes

Triple Dirk C: *Vrn-A1b Vrn-B1b Vrn-D1b Vrn-D5b*: Yes Winter type.

Vrn-1. Add to end of first section.

Diploid wheat:

Vrn1 {10014}. Spring type. **v:** G2528 {10014}.

vrn1 {10014}. Winter type. **v:** DV 92 {10014}; G1777 {10014}; G3116 {10014}.

ma: *Vrn1* was completely linked to MADS-box genes *AP1* and *AGLG1*. *AP1* was considered a better candidate than *AGLG1* and differences between winter and spring genotypes appeared to be related to differences in the promoter region of *AP1* {10014}. The involvement of *AP1* in vernalization response conditioned by *Vrn-1* was also reported in {10019}.

Vrn-B1a. Add **v:** *T. spelta* var. *duhamelianum* KT19-1 {10057}. **ma:** *Vrn-B1a* – 1.6 cM – *Xwg644-5B* – 2.5 cM – *Xgwm408-5B* {10004}. Closely linked to *Xgwm408-5B* in ‘Diamant I*/Mironovskaya 808 5A //Bezostaya 1’ {10007}. A close association of *Vrn-B1* with *Xcdol326-5B* was reported in {10057}.

Replace the current *Vrn4* section with the following:

Vrn4. After the second sentence in the comments following germ plasm entries insert: ‘Goncharov {10108} confirmed the existence of *Vrn4* but failed to confirm its location on chromosome 5D.’.

Vrn5 {10004}. To date only *Vrn-D5* has been detected.

Vrn-D5a [{10004}]. [*Vrn-D5* {10004}, *Vrn4* {1172}]. **5D** {10002}, **5DL** {10004}.

i: Triple Dirk F.

v2: Gabo *Vrn-B1a* {1172}; IL47 *Vrn-A1a* {10005}.

ma: *Xgdm3-5D* - 11.5 & 4.5 cM - *Vrn-D5a* {10004}.

Eight land races with only *Vrn-D5a* were detected in {10003}; others combined *Vrn-D5a* with other *Vrn* genes.

Stelmakh {1424} doubted the existence of *Vrn-D5a*. Goncharov {10108} confirmed the existence of *Vrn-D5a* but failed to confirm its location on chromosome 5D. References to additional studies are given in {1424}.

QTL: Add: ‘A QTL on chromosome 5BL was linked to *Xgwm604-5B* (this QTL explained 11 % of the variance in flowering time) {10075}.’.

72. Yield Components

72.1. Grain weight

72.1.2. 1,000-grain weight

QT_{kwt.unl-3A.1} {10044}. **3AS** {10044}.

v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; a higher kernel weight of 0.27 g was contributed by Cheyenne and the QTL explained 12.7 % of the phenotypic variation {10044}. The QTL coincided with QTLs for grain yield, kernel number per square meter and kernels per spike {10044}.

ma: Associated with *Xbarc12-3A* and *Xtam55-3A* {10044}.

72.3. Grain number per spike

QK_{p.unl-3A.1} {10044}. **3AS** {10044}.

v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; a higher kernel number of 0.3 kernels was contributed by Wichita and the QTL explained 15.5 % of the phenotypic variation {10044}. The QTL coincided with QTLs for grain yield, kernel number per square meter and 1,000-kernel weight {10044}.

ma: Associated with *Xbarc12-3A* {10044}.

QK_{p.unl-3A.2} [{10044}]. **3A** {10044}.

v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; a higher kernel number of 0.3 kernels was contributed by Cheyenne and the QTL explained 9.5 % of the phenotypic variation {10044}.

ma: Associated with *Xbcd141-3A* {10044}.

72.9. Grain yield

QGyld.unl-3A.1 {10044}. 3AS {10044}.

v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; a higher grain yield of 32 kg/ha was contributed by Wichita and the QTL explained 6.6 % of the phenotypic variation {10044}. The QTL coincided with QTLs for kernel number per square meter, 1000-kernel weight and kernels per spike {10044}.

QGyld.unl-3A.2 {10044}. 3A {04100}.

v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; a higher grain yield of 82 kg/ha was contributed by Wichita and the QTL explained 28.1 % of the phenotypic variation {10044}. The QTL coincided with a QTL for kernel number per square meter {10044}.

ma: Associated with *Xbarc67-3A* and *Xbcd366-3A* {10044}.

QYld.inra-7D {10071}.

v: Renan/Recital {10071}.

ma: *Xcdf69-7D* ($R^2 = 3.7 - 15.7\%$).

72.10. Kernel number per square meter

QKpsm.unl-3A.1 {10044}. 3AS {10044}.

v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; higher kernel number (170 kernels) was contributed by Wichita and the QTL explained 14.6 % of the phenotypic variation {10044}. The QTL coincided with QTLs for grain yield, 1000-kernel weight and kernels per spike {10044}.

ma: Associated with *Xbarc12-3A* {10044}.

QKpsm.unl-3A.2 {10044}. 3A {10044}.

v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; higher kernel number (195 kernels) was contributed by Wichita and the QTL explained 19.1 % of the phenotypic variation {10044}. The QTL coincided with a QTL for grain yield {10044}.

ma: Associated with *Xbarc67-3A* {10044}.

72.11 Grain volume weight

QGvwt.unl-3A.1 [{10044}]. 3A {10044}.

v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; higher grain volume weight (+23 kg/hL) was contributed by Wichita and the QTL explained 43.1 % of the phenotypic variation {10044}. The QTL coincided with a QTL for spikes per square meter {10044}.

ma: Associated with *Xbcd1380-3A* {10044}.

74.1. Grain protein content

Insert as a note before the first *XGpc.ccsu* entry: ‘Thirteen QTL for grain protein content were identified in a RI population from the cross WL711 (low protein content) and PH132 (high grain protein content) {10055}. The QTLs that were identified using more than one method or in more than one environment are listed below. Also listed is a QTL that was identified in the mean over the four environments and was therefore deemed important {10055}.’.

Replace the existing entry for *XGpccsu-2D*.

QGpc.ccsu-2B.1 {10055}. 2BL {10055}.

v: WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 13.4% of the phenotypic variation {10055}.

ma: Associated with *Xgwm1249-2B* {10055}.

QGpc.ccsu-2D.1 {0015,10055}. 2DL {0015,10055}.

v: WL711/PH132 RI mapping population {0015,10055}; higher protein content was contributed by PH132 and the QTL explained 19 % {0015} and 14 % {10055} of the phenotypic variation.

ma: Associated with *XgwmI264-2D* {10055}.

QGpc.ccsu-3D.1 {10055}. 3DS {10055}.

v: WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 16.3 % of the phenotypic variation {10055}.

ma: Associated with *Xgwm456-3D* {10055}.

QGpc.ccsu-3D.2 {10055}. 3DS {10055}.

v: WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 14 % of the phenotypic variation {10055}.

ma: Associated with *Xgwm892-3D* {10055}.

QGpc.ccsu-7A.1 {10055}. 7AS {10055}.

v: WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 32.4 % of the phenotypic variation {10055}.

ma: Associated with *XgwmI171-7A* {10055}.

QPro.inra-2A {10071}.

2A {10071}.

v: Renan/Recital {10071}.

ma: *XksuD18-2A – Xgwm614-2A* ($R^2 = 4.4 - 8.9\%$) {10071}.

QPro.inra-3A {10071}.

3A {10071}.

v: Renan/Recital {10071}.

ma: *Xcf79-3A – Xfbb250-3A* ($R^2 = 4.1 - 8.3\%$) {10071}.

QPro.inra-4D {10071}.

4D {10071}.

v: Renan/Recital {10071}.

ma: Linked to *Xcf71-4D* ($R^2 = 4.6 - 10.3\%$) {10071}.

QPro.inra-7D {10071}.

7D {10071}.

v: Renan/Recital {10071}.

ma: *Xcf79-7D – Pch1* ($R^2 = 6.4 - 10.4\%$) {10071}.

For QTLs conferring grain protein content detected in the cross Renan/Recital {10071}, only QTLs stable over at least 4 of the 6 locations are presented. Renan contributed the four alleles for high grain protein content.

74.2.22. NADH dehydrogenase

74.2.22.3. Ndh-3

Insert as a note following the *Ndh-D3* entry: ‘A *Ndh* locus, designated *Nadhd2*, was mapped 27 cM from *Est-D10* in an *Ae. tauschii* F₂ population derived from VIR-1954/VIR-1345 {10046}. This locus may be homologous to *Ndh-D3*.’.

74.2.27. Catalase

A catalase locus, designated *Cat2*, was mapped 6 cM proximal to *Aco-D2* in an *Ae. tauschii* F₂ population derived from VIR-1954/VIR-1345 cross {10046}. This locus may be orthologous to *Cat-B1* {10046}.

74.2.30. Benzoxinones

The putative role of benzoinones sets *Bx-1* to *Bx-5* is to catalyse the pathway Indole-3-glycerol phosphate to DIBOA. Primers designed from maize sequences were used to generate RT-PCR products utilised to screen a cDNA library from CS seedlings. Full-length cDNAs were heterologously expressed in yeast and the *Bx* gene products had enzymatic action. The *Bx* genes located by Southern analysis of CS deletion stocks occurred as clustered groups in homoeologous groups 4 (*Bx-1, Bx-2*) and 5 (*Bx-3.1,2, Bx-4, Bx-5*) {10103}.

74.2.31. Acetohydroxyacid synthase (EC 4.1.3.18)

An orthologous series was mapped as the active target sites of imidazolinone herbicides. See section 40.4.

AhasL-A1 [{10101}]. [*Imi3* {10099}]. 6AL {10101}.

v2: CDC Teal IMI 15A *Imi3* {10099}.

dv: *T. monococcum* mutant EM2 (mutant of susceptible line TM23 {10102}).

AhasL-B1 [{10101}]. [Imi2 {10099}]. 6BL {10101}.
 v: CDC Teal IMI 11A = PTA 3953 {10099}.

AhasL-D1 [{10101}]. [Imi1 {10099}]. 6DL {10101}.
 v: BW755 = Grandin*3 / Fidel-FS-4 {10099}.

3. Endosperm Storage Proteins

74.3.1.1 Glu-1

In the preamble, in the sentence that reads ‘No ‘y-type’ protein from the *Glu-A1* locus has been demonstrated in hexaploid wheat {1118}, although they are found in diploid wheats {1535,798}, and sequencing experiments have shown the presence of a terminating sequence inside the transcribed portion of the gene {373}.’, replace the last part of the sentence with ‘and sequencing experiments have shown the presence of two stop codons in the transcribed portion of the gene {10088}.’

Glu-B1

In the text that follows the *Glu-B1* listing, after the sentence that reads ‘Possible low gene expression at *Glu-B1* was noted for *Glu-B1w*, where subunits 6*+8* stain very faintly {1146}.’ (par 2), add the following text: ‘Many of the cultivars carrying the over-expressed subunit 7 encoded by *Glu-B1al* show %UPP values that transcend the normal range observed for cultivars that lack this subunit {10089}, which presumably is associated in some way with its unusually high amount in the grain. The underlying cause of the increased amount may be due to an increased transcriptional rate compared to other alleles, for which a known difference in promoter sequence compared to other alleles expressing normal levels of this subunit {10090} may be responsible.’

Glu-D1

Add:

Glu-D1bo [{10091}]. 5'+12 {10091}. v: W958 {10091}.

Note: this putative new allele encodes two subunits that have very similar electrophoretic mobilities compared to subunits 5+12 encoded by *Glu-D1h*, but analysis using the specific PCR primers for Dx5 described in {10092} and {10093} shows that the x-type subunit of *Glu-D1bo*, provisionally denominated 5' {10091}, does not appear to be the same protein as subunit 5 {10091}. Definitive evidence awaits sequencing information (See note to allele *Glu-D1-1s*). Correction: in the opening words of the paragraph following the *Glu-D1* listing, replace ‘*Glu-D1* {421}’ with ‘*Glu-D1k* {421}’. Also, correct the spelling, from ‘arison’ to ‘arisen’, in the same phrase.

Glu-D1-1

Allele *Glu-D1-r* needs to be placed in the correct order.

Add:

Glu-D1-1s [{10091}]. 5' {10091}. v: W958 {10091}.

Note: this putative new allele encodes a subunit, provisionally denominated 5' {10091}, that has a very similar electrophoretic mobility compared to subunit 5 encoded by *Glu-D1-1d*, but analysis using the specific PCR primers for Dx5 described in {10092} and {10093} shows that it does not appear to be the same protein as subunit 5 {10091}. Definitive evidence awaits sequencing information (see note to allele *Glu-D1bo*).

Glu-R1

Add after the *Glu-R1* listing:

‘Five new x-type subunits (plus the null allele) and four y-type subunits were reported in {10094}. They vary principally through duplications and deletions of the tri-, hexa-, and nona-peptide motifs found in the central repetitive region of the subunits. Orthologous genes were found to be more closely related than paralogous genes, supporting the hypothesis that gene duplication occurred before Triticeae speciation {10095, 10094}.’

Glu-B3 (original bread wheat listing)

Add:

Glu-B3z [{10116}]. 6.1 {10116}. tv: Buck Cristal {10116}.

Note: the designation of this protein (subunit 6.1) as an allele of *Glu-B3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies.

74.3.2. Gliadins

Add in the gliadin preamble (par. 3) at the end of ‘... families of gliadin alleles and some of their relationships were described {9988}.’.

‘Twenty eight gamma-gliadin gene sequences from Genbank were grouped into nine subgroups in {10063}. Primers were developed against some of the subgroups and the chromosomal location of the gamma-gliadin genes was determined {10063}.’.

Add at the end of the preamble:

‘A new family of low-molecular-weight gliadin genes located on groups 4 and 7 were reported in {10117}. They appear to influence rheological properties and seem to be closely related to the 17 kDa ϵ hordein, important in beer foam stability.’

74.5.6 Waxy proteins

Add at end of first par: A multiplex PCR assay for identifying waxy genotypes is described in {10032}.

Wx-A1b. v: California {10032}; Shino {10032}; Sturdy {10032}.

v2: Mochi-Otome *Wx-B1b WxD1b* {10032}; Nebarigoshi {10032}.

Wx-B1b. v: {10032}; Reward {10032}; Yukon {10032}.

v2: Mochi-Otome *Wx-A1b WxD1b* {10032}; Nebarigoshi *Wx-A1b* {10032}.

Wx-D1b. v2: Mochi-Otome *Wx-A1b WxD1b* {10032}.

Correction - in the entry:

Wx-D1d {0118}. v: K107wx1{0118}; EMS mutants{0118}; One Iranian and one Italian accession {03101}.
 ‘K107wx1’ should read ‘K107Wx1’ and ‘EMS mutants’ should read ‘K107Wx2’.

5.8. Puroindolines and Grain Softness Protein

Pina-D1.

Pina-D1d. dv: Change the entry ‘TA2521’ to ‘TA2512’

Add:

Pina-D1g {03105}. dv: *Ae. tauschii* TA1583 (GenBank AY252029) *Pinb-D1a, Gsp-D1b* {03105}.

Pina-D1h {10118}. v: *X. Aegilopriticum* CIGM86.946-1B-0B-0PR-0B (GenBank AY573898) *Pinb-D1o* {10118}.

Pina-D1i {10018}. v: *X. Aegilopriticum* CIGM87.2784-1B-0PR-0B (GenBank AY573899) *Pinb-D1k* {10118}.

Pina-D1j {10118}. v: *X. Aegilopriticum* CIGM88.1363-0B (GenBank AY573900) *Pinb-D1o* {10118}.

Pina-D1j {10118}. v: *X. Aegilopriticum* CIGM88.1363-0B (GenBank AY573900) *Pinb-D1o* {10118}.

Pina-D1k {10077}. s: CS*/Red Egyptian 5D substitution line, *Pinb-D1q, Gsp-D1i* {10077}.

This locus has a large deletion encompassing genes *Pina-D1*, *Pinb-D1*, and *Gsp-D1*. This allelic combination confers a harder kernel texture than *Pina-D1a/Pinb-D1b* {10077}.

Pinb-D1.

Pinb-D1l {10119}. v: GaoCheng 8901 {10119}.

Pinb-D1m {10118}. v: *X. Aegilopriticum* CIGM87.2783-1B-0PR-0B (GenBank AY573901) *Pina-D1c* {10118}.

Pinb-D1n {10118}. v: *X. Aegilopriticum* CIGM92.1708 (GenBank AY573902) *Pina-D1d* {10118}.

Pinb-D1o {10118}. v: *X. Aegilopriticum* CIGM93.247 (GenBank AY573903) *Pina-D1e* {10118}.

Pinb-D1p {10121}. v: Nongda 3213 {10121}; Nongda 3395 {10121}.

Pinb-D1q {10077}. s: CS*/Red Egyptian 5D substitution line, *Pina-D1k, Gsp-D1i* {10077}.

This locus has a large deletion encompassing genes *Pina-D1*, *Pinb-D1*, and *Gsp-D1*. This allelic combination confers a harder kernel texture than *Pina-D1a/Pinb-D1b* {10077}.

Add at end of section: ‘In *T. monococcum* the gene order was reported to be: tel – *Gsp-1* – *Pina* – *Pinb* {0083, 10122} whereas in *Ae. squarrosa* it was: tel – *Gsp-1* – *Pinb* – *Pina* {10037}.’.

74.5.9. Grain softness protein

Gsp-D1i {10120}. v: Yecora Rojo (GenBank AY255771) *Pina-D1b, Pinb-D1a* {10120}.

Gsp-D1j {10077}. s: CS*/Red Egyptian 5D substitution line, *Pina-D1k, Pinb-D1q* {10077}.

This locus has a large deletion encompassing genes *Pina-D1, Pinb-D1* and *Gsp-D1* {10077}.

Pathogenic Disease/Pest Reaction**76. Reaction to *Blumeria tritici*****76.1. Designated genes for resistance**

Pm3b. Add at end of entry: The isolation of *Pm3b* is reported in {10064}. The *Pm3b* gene (Genbank accession number AY325736) is a coiled-coil NBS-LRR type of disease resistance gene {10064}.

Pm24. ma: *Xgwm789-1D/Xgwm603-1D* – 2.4 cM – *Pm24* – 3.6 cM – *Xbarc229-1D* {10109}.

Delete the comment at the end of the section.

Pm32 {10025}. Derived from *Ae. speltoides* {10025}. 1B = T1BL·1SS {10025}.

v: L501 = Rodina*6/ *Aeg. speltoides* {10025}.

MITd1055 {10029}. tv: *T. dicoccoides* 1055 {10029}.

78. Reaction to *Diuraphis noxia*

Dn7. Add: ma: *Xbcd1434-1B* – 1.4 cM – *Dn7* – 7.4 cM – *XksuD14-1B* {10059}.

79. Reaction to *Fusarium spp.*

79.1. Disease: Fusarium head scab, scab.

Type II resistance Insert this heading after the disease name.

QFhs.ndsu.3B. Insert comment after gene entry: ‘Associated mainly with resistance to fungal spread {10073}’.

ma: Add at end of first paragraph: ‘*QFhs.ndsu-3B* from Sumai 3 was associated with microsatellite loci *Xgwm533-3B* and *Xgwm274-3B* in certain Sumai 3 derivatives {10062}. In Ning 894037, the QTL has the same location and similar SSR bands to Sumai 3 {10085}. STS marker SRST.3B1 was mapped between *Xgwm533-3B* and *Xgwm389-3B* and associated with *QFhs.ndsu-3B* {10072}. *QFhs.ndsu.3B* was associated with markers *Xgwm533-3B, Xbarc133-3B, Xbarc147-3B*, and *Xgwm493-3B* {10073}.’.

Qfhs.ifa-5A {10076}. Associated mainly with resistance to fungal penetration {10073}. 5A {0240,10076}. v: Remus/CM-82036 {10076}. ma: Associated with markers *Xgwm293-5A, Xgwm304-5A, Xgwm1057-5A, Xbarc117-5A, Xbarc186-5A, Xbarc100-5A*, and *Xbarc40-5A* {10073}.

QTLs for resistance to *Fusarium graminearum* detected in the cross Renan/Recital {10069}. All resistance alleles, except *QFhs.inra-3A*, were contributed by Renan. LOD scores and percent of variation explained by the QTL (R^2) are averages of three years of field tests.

QFhs.inra-2A {10069}. ma: Associated with *Xgwm382c-2A* (LOD = 6.3, R^2 = 14.4 %).

QFhs.inra-2B {10069}. ma: Associated with *Xgwm374-2B* (LOD = 7.6, R^2 = 12 %).

QFhs.inra-3A {10069}. ma: Associated with *Xbcd372-3A* (LOD = 3.7, R^2 = 6.2 %).

QFhs.inra-3B {10069}. ma: Associated with *Xgwm383b-3B* (LOD = 5.4, R^2 = 10.5 %).

QFhs.inra-5A.1 {10069}. ma: Associated with *Xpsr170a-5A* (LOD = 3.8, R^2 = 5 %).

QFhs.inra-5A.2 {10069}. ma: Associated with *Xgwm639b-5A* (LOD = 6.6, R^2 = 14 %).

QFhs.inra-5A.3 {10069}. ma: Associated with *B1* (LOD = 6.3, R^2 = 8.5 %).

QFhs.inra-5D {10069}. ma: Associated with *Xcfd29-5D* (LOD = 4.4, R^2 = 7 %).

QFhs.inra-6D {10069}. ma: Associated with *Xcfd42-6D* (LOD = 2.7 R^2 = 6.6 %).

QFhs.pur.2D {10085}. v: Alondra {10085}.

ma: Located on 2DS between SSR markers *Xgwm296-2D* and *Xgwm261-2D* {10085}.

In the second paragraph of the discussion following the listing of genes, modify the text to: '.....Remus / CM82036' and add reference {10024} to the 3BS and 5A QTLs.

Insert after the 3rd Paragraph: A marker study found that 14 of 66 wheats with putative FHB resistance shared markers indicative of the 3BS QTL in Ning 7840, Sumai 3, Wangshuibai, and, possibly, Wuhan 3, plus Japanese landraces Shinchunaga and Shirasu No 1 {10115}. The original source may be the landrace 'Taiwan Wheat' rather than Funo{10115}.

Four QTLs on chromosomes 3BS (associated with *Xbarc133-3B*), 3BL (*Xgwm247-3B*), and 3AS (*Xgwm5-3A*) from Huapei 57-2, and 5BL (*Xbarc59-5B*) from Patterson, were reported in the cross 'Huapei 57-2/Patterson' {10026}. Huapei 57-2, Ning 7840 and Sumai 3 carried common alleles in the *Xgwm533-3B*, *Xgwm493-3B*, *XBarc147-3B*, and *Xbarc133-3B* region {10026}.

Wuhan-1/Maringa: Two QTLs were located on chromosomes 2DL and 3BS (distal) {10020}.

Of 54 lines with reported FHB resistance, six, including CM-82036, Ning 7840 and Wuhan 3, had the same 5-marker haplotype as Sumai 3, and four lines possessed four of the markers. Twenty-nine lines, including Frontana, had no marker allele in common with Sumai 3, whereas 13 lines had 1 to 3 alleles in common with it {10113}. *Qfhs.ndsu-3B* and the 5-marker loci were placed in 3BS deletion bin 0.78-0.87 {10144}.

Patterson (mod sus)/Fundulea 201R RILS: QTLs accounting for 19 % and 13 % of phenotypic variation were found on chromosomes 1BL (*Xbarc8-1BS – Xgwm131-1BL* region) and 3AS (*Xgwm674-3a/Xbarc67-3A* region) {10114}. Two weak QTLs were possibly associated with chromosomes 3D (Patterson allele) and 5AS {10114}.

Field resistance: Wuhan-1/Maringa, QTLs were located on chromosomes 2DS, 3BS (proximal), and 4B {10020}.

DON accumulation: Wuhan-1/Maringa, QTLs were located on chromosomes 2DL and 5DS {10020}.

79.2. Disease: Crown rot caused by *Fusarium pseudograminearum*, *F. culmorum*, and other *Fusarium* species

QTL: Simple interval mapping in the region *Pst1 ACG.Mse1 CAC – Xgwm251-4B* accounted for 48 % of the variation in crown rot response in a Kukri (R)/Janz (S) DH population {10034}.

80. Reaction to *Heterodera avenae*

Cre1. **v:** Beulah {10013}; Goldmark {10013}; Goroke {10013}; Kellalac {10013}; Ouyen {10013}; RE8607 {10013}; Silverstar {10013}; VI 252 {10013}; VI 727 {10013}.
ma: Co-segregation with *Xcsl107-2B*. Four of six land varieties possessed *Xcsl107-2B*. A variant haplotype of *Xcsl107-2B* was present in AUS4930 {10013}; *Xcd36-2B – 7.5 cM – Xbcd1231-2B/XAtPPr5/Xcsl107-2B/Cre1* {10013}.

Cre3. **ma:** Co-linearity with 2BL for *Xcd36-2D* and *XAtPPr5/Xbcd1231-2D/G4/G12/Cre3* (see *Cre1*) {10013}.

Cre8. Add L to 6B, ie, 6BL.
ma: Replace current entry with: 'Linked to RFLP loci *Xbcd1-6B* and *Xcd347-6B*. The 6B location of the *Xcd347* probe used in this study was confirmed by nulli-tetrasomic analysis {0220}'.

84. Reaction to *Mayetiola destructor*

H31{0332}. Change *Xupw148-5B* to *Xupw4148-5B*.

84. Reaction to *Mycosphaerella graminicola*

Stb1. 5BL {10123}. **v:** P881072-75-1 {10123}; SO852 {10123}.
ma: Located in FL 5BL-11 - 5BL-14 {10123}. Close linkage with two RAPD makers at >0.68 and 1.4 cM in P881072-75-1 {10123}. Cent....*Xbarc74-5B – 2.8 cM – Stb1* {10123}.

Stb2. 3BS {10105}. **ma:** *Xgwm389-3B/Xgwm533-3B – 1.0 cM – Stb2 – 3.7 cM – Xgwm493-3B* {10105}.

Stb3. 6DS {10105}. **ma:** *Stb3 – 3.0 cM – Xgdm132-6D* {10105}.

Stb4. Update to: 7D {0326}, 7DS {10106}. **v:** Cleo {1410}; Gene {10010}; Tadinia {1410, 10106}, Tadorna {1410}.

- ma:** *XAGG/CAT10* – 4.0 cM – *Stb4* – 0.7 cM – *Xgwm111-7D* – 1.4 cM – *XATCG/CAA5* – Cent {10106}.
- Stb6.** **ma:** A resistance gene from Senat located at or near the *Stb6* locus was mapped 5 cM from microsatellite *Xgwm369-3A* on chromosome arm 3AS {10067}.
- Stb9** {10027}. Information withheld until publication.
- Stb10** {10011}. Information withheld until publication.
- Stb11** {10012}. Information withheld until publication.

QTL: Four QTLs for resistance to *Mycosphaerella graminicola* were identified in replicated field experiments in a double haploid population from ‘Savannah (susceptible)/Senat (resistant)’. Senat contributed all the alleles providing resistance {10067}:

QStb.riso-6B was mapped on the centromeric region between SSR markers *Xwmc494-6B* and *Xwmc341-6B* (LOD > 16, R² > 68 %). Also detected at the seedling stage {10067}.

QStb.riso-3A.2 was mapped on chromosome arm 3AS linked to SSR markers *Xwmc489-3A*, *Xwmc388-3A* and *Xwmc505-3A* (LOD > 4, R² > 18 %). Also detected at the seedling stage {10067}. *Xgwm369-3A* is present on chromosome arm 3AS {0187}. A resistance gene from Senat located at or near the *Stb6* locus was mapped 5 cM from microsatellite *Xgwm369-3A* on chromosome arm 3AS {10067}.

QStb.riso-2B was mapped on chromosome arm 2BL linked to SSR marker *Xwmc175-2B* (LOD > 5, R² > 17 %) {10067}.

QStb.riso-7B was mapped on chromosome 7B close to SSR marker *Xwmc5177B* (LOD > 4, R² > 11 %) {10067}.

86. Reaction to *Phaeophaeeria nodorum*

Disease: Add ‘Stagonospora nodorum blotch’.

86.1. Genes for resistance

Snb1 etc.

QTL: A QTL analysis of SNB response in the ITMI population found significant effects associated with chromosomes 1B (probably *Snn1*) and 4BL, with an interactive effect involving the 1BS region and a marker on chromosome 2B {10009}. An additional QTL on 7BL was effective at a later stage of disease development {10009}.

Four QTLs, on chromosomes 2B (proximal part of long arm), 3B (distal part of short arm), 5B, and 5D, were mapped in a ‘Liwillia/Begra’ DH population. Longer incubation period and lower disease intensity were contributed by Liwillia {10045}.

Two QTLs for glume blotch resistance under natural infection were identified on chromosomes 3BS and 4BL in ‘Arina/Forno’ RILs {10065}. The 3BL QTL, designated *QSng.sfr-3BS*, was associated with marker *Xgwm389-3B* and explained 31.2 % of the variation. The resistance was contributed by Arina {10065}. The 4BL QTL, *QSng.sfr-4BL*, was associated with *Xgwm251-4B* and explained 19.1 % of the variation. Resistance was contributed by Forno {10065}. A QTL on 5BL, *QSng.sfr-5BL*, overlapped with QTLs for plant height and heading time {10065}.

86.2. Sensitivity to SNB toxin

- Snn1** (10008). Sensitivity is dominant {10009}. 1BS {10009}.
- v:** CS {10009}; W-7984 (ITMI Synthetic) {10009}.
- snn1.** **i:** CS*/*T. turgidum* subsp. *dicoccoides* 1B {10008}.
- v:** Opata 85 {10008}.
- tv:** *T. turgidum* subsp. *dicoccoides*. {10008}.

87. Reaction to *Puccinia graminis*

- Sr2.** **ma:** Add to present entry: *Xglk683* (STS *Xsun2-3B*) – 0.5 cM – *Xgwm533-3B* {0358}. These SSR loci were located within FL 0.87–0.75 {0358}. All 27 lines with *Sr2* carried a 120-bp allele at *Xgwm533-3B*. A 120-bp allele in four cultivars lacking *Sr2* differed from the *Sr2*-associated allele at four base positions {0358}.

Sr38. **ma:** The 2NS translocated segment carrying *Sr38* replaced the distal half of chromosome 2A (25–38 cM) from *Xcmwg682* to *XksuH9*. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682* {10073}.

88. Reaction to *Puccinia striiformis*

Yr1. **v:** Ritmo {10038}. **v2:** Kraka *Yr32* {10038}.

Yr5. **ma:** Add: ‘Completely linked to Resistance Gene-Analog Polymorphism (GRAP) markers *Xwgp17-2B*, *Xwgp19-2B*, and *Xwgp26-2B* {10096}. *Xwgp-17-2B* was later converted into a simpler Cleaved Amplified Polymorphic Sequence (CAPS) PCR marker {10097}.

Yr9. 1B = T1BL-1RS.
v: Sleipner {10038}. **v2:** Haven *Yr6* {10038}; Lynx *Yr6 Yr17* {10038}.

Yr15. **ma:** Gene order *Yr15 – Yr24 – Xgwm11-1B* {10112}.

Yr17. Move Lynx from **v** to **v2**. **v:** Lynx *Yr6 Yr9* {0044,10038}.

Add at end of section: The 2NS translocated segment carrying *Yr17* replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682-2A* to *XksuH9-2A*. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682* {10073}.

Yr24. **ma:** Gene order *Yr15 – Yr24 – Xgwm11-1B* {10112}.

Yr25. **v:** Strubes Dickkopf {158,10016}. **v2:** Carstens V *Yr32* {10016}; Spaldings Prolific *YrSP*{10016}.

Yr32 {10016}. **YrCV** {1430}. Delete 2BS and substitute with ‘2AS {10016}’.
i: CRW380 = Carstens V/3*Avocet S {10016}.

v: Consort {10021,10023}; Danis {10023}; Hereward {10021,10022}; Kraka {10021}; Oxbow {10021}; Senat {10016}; Solist {10016}; Stakado {10016}; Tres {10016}; Vivant {10023}; Wasmo {10016}.

v2: Carstens V *Yr25* {10016}; Kraka *Yr1* {10021,10038} (Move Kraka from **v**: to **v2**)

Yr33 {10039}. **YrBat** {10039}. More readily detected in seedling tests at elevated temperatures {10039}.

v: Batavia {10039}.

ma: 18 % linkage with a 7DL marker {10039}.

Yr34 {10040}. 5AL {10040}. This gene confers a weak seedling resistance (IT 2C to 3C) and a strong adult-plant resistance (0 to 10R) {10040} to Australian pathotype 134 E16A+, but is not effective against Australian pathotype 110 E143A+ {10040}.

v: WAWHT2046 {10040}.

ma: *Xgwm6-5A* – 13.5 cM – *Bl* – 12.2 cM – *Yr34* {10040}.

88.2 Temporarily designated genes for resistance to stripe rust

YrSP {10018}. 2BS {10018}.
i: Cx1 = Avocet S*4/Spaldings Prolific {10018}. **v2:** Spaldings Prolific *Yr25* {10018}.

88.3. Stripe rust QTLs

QTL: Seven QTLs were identified for stripe rust severity in a joint analysis of five datasets from a Fukuho-komugi/Oligoculm DH population {10060}. Their location, associated marker, percentage variation explained and variety contributing to enhanced resistance at that locus are listed.

3BS; *Xgwm389-3B*; 0.2–4.9 %; Oligoculm {10060}.

4BL; *Xgwm538-4B*; 1.8–12.3 %; Oligoculm {10060}.

4DL; *Xwmc399-4D*; 2.5–8.0 %; Oligoculm {10060}.

5BL; *Xwmc415-5B*; 2.4–16.1 %; Oligoculm {10060}.

6BS (centromeric); *Xgwm935-6B*; 0.5–3.8 %; Oligoculm {10060}.

7BS; *Xgwm935-7B*; 1–5.2 %; Oligoculm {10060}.

7DS; *Xgwm295-7D*; 10.7–23.7 %; Fukuho {10060}; The 7DS QTL was probably *Yr18* {10060}.

Four QTLs were identified for stripe rust infection in a joint analysis of three datasets from a Fukuho-komugi/Oligoculm doubled haploid population {10060}. Their location, associated marker, percentage variation explained and parent contributing to enhanced resistance at that locus are listed.

2DL; *Xgwm349-2D*; 6.5–9.6 %; Fukuho {10060}.

3BS; *Xgwm389-3B*; 15.1–24.5 %; Oligoculm {10060}. The 3BS QTL is probably due to *Yr30* {10060}.

5BL; *Xwmc415-5B*; 6.4–12.7 %; Oligoculm {10060}.

7BL; *Xwmc166-7B*; 2.5–9 %; Oligoculm {10060}.

89. Reaction to *Puccinia triticina*

- Lr3a.** ma: cDNA marker TaR16 was completely linked to *Lr3* in a population of 109 gametes {10058}.
- Lr10.** c: *Lr10* (*T10rga1*, GenBank acc. no. AY270157) encodes a CC-NBS-LRR protein of 919 a.a. {10033}.
- Lr3a** {10028}. *Lr3*. Details as previously listed.
- Lr3b** {10028}. *Lr3bg*. Details as previously listed.
- Lr3c** {10028}. *Lr3ka*. Details as previously listed.
- Lr34** On the basis of leaf tip necrosis and lack of segregation in a diallele, cv. Saar, Simogh, Homa, Parastoo, and Cocnoos were considered to have *Lr34*, but each also possessed two or three additional adult-plant resistance factors {10110}.
- Lr37** Add at end of section: The 2NS translocated segment carrying *Lr37* replaced the distal half of chromosome 2A (25–38 cM) from *Xcmwg682*-2A to *XksuH*-9-2A. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682* {10073}.
- Lr52** {10035}. *LrW* {309}. 5BS {10035}.
- v: Tc-LrW = RL6107 {10035}.
- v2: Insert list from *Lrw* in earlier catalogues.
- LrTt1** [{10031}]. *lrtt1* {10031}. Recessive allele {10031}. 2A {10031}.
- v: Line 842 = Saratovskaya*2/T. *timopheevii* subsp. *viticulosum* {10031}.
- ma: *Xgwm812*-2A – 1.5 cM – *Lrtt1* {10031}.
- LrW.** Delete this entry from the list of temporary symbols.
- In the last paragraph add reference {10111} to those references listed after U.S.A. cultivars, that is {0334, 10111}.

89.3. QTLs for reaction to *P. triticina*

QTLs Two QTLs, located distally on chromosome arm 1BL and on chromosome 7DS, were mapped for leaf rust severity in a ‘Fukuho-komugi/Oligoculm’ DH population {10060}. The resistance on 1BL was contributed by Oligoculm and explained 15 % of the variation. The 1BL QTL may correspond to *Lr46* and was associated with marker *Xwmc44*-1B {0460}. The resistance on 7DS was contributed by Fukuho-komugi and explained 41 % of the variation. The 7DS QTL corresponds to *Lr34* and was associated with marker *Xgwm295*-7D {10060}. Two major QTL, located on chromosomes 7D and 1BS, for leaf rust resistance were mapped in an ‘Arina/Forno’ RIL population {10066}. The resistance on 7D was contributed by Forno and explained 32 % of the variation. This QTL most likely corresponds to *Lr34* {10066}. The resistance on 1BS (*QLr.sfr*-IBS) was associated with *Xgwm604*-1B and was contributed by Forno {10066}. Additional minor QTLs were identified on chromosome arms 2DL, 3DL, 4BS, and 5AL {10066}.

90. Reaction to *Pyrenophora tritici repens***90.1. Insensitivity to tan spot toxin**

tsn1. Add reference {10030} after Erik, that is {0007, 10030}.

Tsn1. Add reference {10030} after Kulm.

Add final comment to section: ‘In Kulm/Erik, toxin response accounted for 24 % of the variation in disease response, which was affected by 4–5 genes {10030}.’

90.2. Insensitivity to chlorosis induction

tsc1. Insensitivity allele {10015}.

v: Opata 85 {0315, 10015}.

Tsc2 Sensitivity allele, sensitivity to Ptr ToxB is dominant {10015}. 2BS {10015}.

v: W-7984 {10015}.

QTL. QTLs affecting response to Ptr ToxB were identified on chromosomes 2AS, 4AL, and 2B (10015).

93. Reaction to *Tapesia yellundae*

Add to *Pchl*: **ma:** *Pchl* was linked to *Ep-D1* and mapped 2 cM from microsatellite marker *XustSSR2001*-7D {10070}.

100. Reaction to Colonization by *Eriophyes tulipae*

- Cmc3*. ma: Wheat lines with the 1RS segment and hence *Cmc3* can be selected with the rye-specific SSR *Xscm09-1R* {0222}.
- Cmc4*. ma: *XksuG8-6D* – 6.4 cM – *Cmc4* – 4.1 cM – *Xgdm141-6D* {0222}.

III. SUMMARY TABLES**Summary Table 1**

Add:

<i>a-Tub</i>		Alpha-tubulin
<i>Ada2</i>		Transcriptional adaptor (AY244515)
<i>Aglg1^o</i>		Agamous-like from grasses MADS-box gene (AAO86522.1)
<i>AhasL</i>	Set	Acetohydroxyacid synthase large subunit
<i>Ap1</i>		<i>Apetala-1</i> . Candidate gene for <i>Vrn1</i> (AAO72630.1)
<i>Bx</i>	Sets	Benxoaxazinone
<i>Cp</i>		Compact spike
<i>Cyb5</i>		Cytochrome b5 (AAO86521.1)
<i>Cys</i>		Cysteine proteinase (AY244510 and AY244511)
<i>Imi</i>		Resistance to Imidazolinone herbicides
<i>Kin</i>		Kinase
<i>L2</i>		Ribosomal protein L2
<i>L38</i>		Ribosomal protein L38
<i>Mtk4</i>		Tousled-like kinase (AY244512 and AY244513)
NBS-LRR		Protein that contains a nucleotide binding site and leucine-rich repeat
<i>Nuc</i>		Nucellin
<i>Pcs</i>		Phytochelatin synthetase (AAO86520.1)
<i>PhyC</i>		Phytochrome C (AY244514)
<i>Rga</i>		Resistance-gene analog
<i>Snf2P</i>		Global transcriptional regulator (AAS58484.1)
<i>Wag</i>	Set	Wheat <i>AGAMOUS</i> homologue (AB084577)

IV. GENETIC LINKAGES**Chromosome 1BS**

<i>Yr10</i> – <i>Yr15</i>	23.6 ± 5.5 cM	{10112}
<i>Yr10</i> – <i>Yr24</i>	37.6 ± 10.7 cM	{10112}
<i>Yr15</i> – <i>Yr24</i>	3.7 ± 1.6 cM	{10112}

Chromosome 2AS

<i>Yr1</i> – <i>Yr32</i>	I	{10016}
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Chromosome 3AS

<i>Br2</i> – cent	21.1 ± 0.2 cM	{10061}
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Chromosome 3BS

<i>Br3</i> – cent	20.1 ± 0.6 cM	{10061}
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Chromosome 3DS

<i>Br1</i> – cent	20.6 ± 0.3 cM	{10061}
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Chromosome 5DL

<i>Vrn-D5</i> – <i>Vrn-D1</i>	I	{10004}
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Chromosome 6DS

<i>Cmc4</i> – <i>Cmc1</i>	I	{0222}
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VII. ABBREVIATIONS USED IN THIS VOLUME.**PLANT DISEASES, PESTS, AND PATHOGENS:**

BYDV = barley yellow dwarf virus
BMV = barley mosaic virus
CCN = cereal cyst nematode, *Heterodera avenae*
FHB = Fusarium head blight
RWA = Russian wheat aphid
SBMV = soilborne mosaic virus
SLB = Septoria leaf blotch
WDF = wheat dwarf mosaic
WSBMV = wheat soilborne mosaic virus
WSMV = wheat streak mosaic virus
WSSMV = wheat spindle streak mosaic virus
E. graminis* f.sp. *tritici = *Erysiphe graminis* f.sp. *tritici* = the powdery mildew fungus
F. graminearum = *Fusarium graminearum* = head scab fungus
F. nivale = *Fusarium nivale* = snow mold fungus
H. avenae = *Heterodera avenae* = cereal cyst nematode
P. recondita* f.sp. *tritici = *Puccinia recondita* f.sp. *tritici* = leaf rust fungus
P. striiformis* f.sp. *tritici = *Puccinia striiformis* f.sp. *tritici* = strip rust fungus
P. graminis = *Polymyxa graminis* = wheat soilborne mosaic virus vector
R. cerealis = *Rhizoctonia cerealis* = sharp eyespot
R. solani = *Rhizoctonia solani* = Rhizoctonia root rot
R. padi = *Rhonopalosiphum padi* = bird cherry-oat aphid
S. tritici = *Septoria tritici* = Septoria leaf spot fungus
S. graminearum = *Schizaphus graminearum* = greenbug
St. nodorum = *Stagonospora nodorum* = Stagonospora glume blotch
T. indica = *Tilletia indica* = Karnal bunt fungus

SCIENTIFIC NAMES AND SYNONYMS OF GRASS SPECIES (NOTE: CLASSIFICATION ACCORDING TO VAN SLAGEREN, 1994):

A. strigosa = *Avena strigosa*
Ae. cylindrica = *Aegilops cylindrica* = *Triticum cylindricum*
Ae. geniculata = *Aegilops geniculata* = *Aegilops ovata* = *Triticum ovatum*
Ae. speltoides = *Aegilops speltoides* = *Triticum speltoides*
Ae. tauschii = *Aegilops tauschii* = *Aegilops squarrosa* = *Triticum tauschii*
Ae. triuncialis = *Aegilops triuncialis* = *Triticum triunciale*
Ae. umbellulata = *Aegilops umbellulata* = *Triticum umbellulatum*
Ae. peregrina = *Aegilops peregrina* = *Aegilops variabilis* = *Triticum peregrinum*
Ae. ventricosa = *Aegilops ventricosa* = *Triticum ventricosum*
S. cereale = *Secale cereale* = rye
T. aestivum = *Triticum aestivum* = hexaploid, bread, or common wheat
T. monococcum subsp. **aegilopoides** = *Triticum boeoticum*
T. dicoccon = *Triticum dicoccon* = *T. dicoccum*
T. durum = *Triticum durum* = durum, pasta, or macaroni wheat
T. macha = *Triticum macha*
T. militinae = *Triticum militinae*
T. spelta = *Triticum spelta*
T. timopheevii subsp. **timopheevii** = *Triticum timopheevii*
T. timopheevii subsp. **armeniacum** = *Triticum araraticum* = *T. araraticum*
T. turgidum subsp. **dicoccoides** = *Triticum dicoccoides* = wild emmer wheat
T. turgidum subsp. **dicoccum** = *Triticum dicoccum*
T. urartu = *Triticum urartu*
Th. bessarabicum = *Thinopyrum bessarabicum*

SCIENTIFIC JOURNALS AND PUBLICATIONS:

Agron Abstr = Agronomy Abstracts
Ann Wheat Newslet = Annual Wheat Newsletter
Cereal Res Commun = Cereal Research Communications
Curr Biol = Current Biology
Eur J Plant Path = European Journal of Plant Pathology
Int J Plant Sci = International Journal of Plant Science
J Cereal Sci = Journal of Cereal Science
J Hered = Journal of Heredity
J Phytopath = Journal of Phytopathology
J Plant Phys = Journal of Plant Physiology
Mol Gen Genet = Molecular and General Genetics
PAG = Plant and Animal Genome (abstracts from meetings)
Plant Breed = Plant Breeding
Plant, Cell and Envir = Plant, Cell and Environment
Plant Cell Rep = Plant Cell Reporter
Plant Physiol = Plant Physiology
Sci Agric Sinica = Scientia Agricultura Sinica
Theor Appl Genet = Theoretical and Applied Genetics
Wheat Inf Serv = Wheat Information Service

UNITS OF MEASUREMENT:

bp = base pairs
bu = bushels
cM = centimorgan
ha = hectares
T = tons
m³ = cubic meters
μ = micron
me = milli-equivalents
mmt = million metric tons
mt = metric tons
Q = quintals

MISCELLANEOUS TERMS:

Al = aluminum
AFLP = amplified fragment length polymorphism
ANOVA = analysis of variance
A-PAGE = acid polyacrylamide gel electrophoresis
AUDPC = area under the disease progress curve
BW = bread wheat
CHA = chemical hybridizing agent
CMS = cytoplasmic male sterile
CPS = Canadian Prairie spring wheat
DH = doubled haploid
DON = deoxynivalenol
ELISA = enzyme-linked immunosorbent assay
EMS = ethyl methanesulfonate
EST = expressed sequence tag
FAWWON = Facultative and Winter Wheat Observation Nursery
GA = gibberellic acid
GIS = geographic-information system
GM = genetically modified
HPLC = high pressure liquid chromatography

HMW = high-molecular weight (glutenins)

HRSW = hard red spring wheat

HRRW = hard red winter wheat

HWSW = hard white spring wheat

HWWW = hard white winter wheat

ISSR = inter-simple sequence repeat

kD = kilodalton

LMW = low molecular weight (glutenins)

MAS = marker-assisted selection

NSF = National Science Foundation

NILs = near-isogenic lines

NIR = near infrared

NSW = New South Wales, region of Australia

PAGE = polyacrylamide gel electrophoresis

PCR = polymerase chain reaction

PFGE = pulsed-field gel electrophoresis

PMCs = pollen mother cells

PNW = Pacific Northwest (a region of North America including the states of Oregon and Washington in the U.S. and the province of Vancouver in Canada)

PPO = polyphenol oxidase

QTL = quantitative trait loci

RAPD = random amplified polymorphic DNA

RCB = randomized-complete block

RFLP = restriction fragment length polymorphism

RILs = recombinant inbred lines

RT-PCR = real-time polymerase-chain reaction

SAMPL = selective amplification of microsatellite polymorphic loci

SAUDPC = standardized area under the disease progress curve

SCAR = sequence-characterized amplified region

SDS-PAGE = sodium dodecyl sulphate polyacrylamide gel electrophoresis

SE-HPLC = size-exclusion high-performance liquid chromatography

SH = synthetic hexaploid

SNP = single nucleotide polymorphism

SRPN = Southern Regional Performance Nursery

SRWW = soft red winter wheat

SRSW = soft red spring wheat

STMA = sequence taggess microsatellite site

SWWW = soft white winter wheat

SSD = single-seed descent

SSR = simple-sequence repeat

STS = sequence-tagged site

TKW = 1,000-kernel weight

UESRWWN = Uniform Experimental Soft Red Winter Wheat Nursery

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XI. VOLUME 51 MANUSCRIPT GUIDELINES.

Manuscript guidelines for the *Annual Wheat Newsletter*, volume 51. The required format for Volume 51 of the *Annual Wheat Newsletter* will be similar to Volume 50 and previous editions.

CONTRIBUTIONS MAY INCLUDE:

- Current activities on your projects.
- New cultivars and germ plasm released.
- Special reports of particular interest, new ideas, etc., normally not acceptable for scientific journals.
- A list of recent publications.
- News: new positions, advancements, retirements, necrology.
- Wheat stocks; lines for distribution, special equipment, computer software, breeding procedures, techniques, etc.

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Follow the format in volume 44–50 of the *Newsletter* in coördinating and preparing your contribution, particularly for state, station, contributor names, and headings. Limited editing is done. Use the WordPerfect or Word programs, or send an RTF file that can be converted. Use Times 12 CPI and 1.0" (2.5 cm) margins. DO NOT use the table settings or column setting functions, create tables with tabs and spaces. Double-space the text of your contribution if you must use a typewriter.

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In the interest of remaining solvent, the NWIC has approved future distribution primarily by computer diskette. We are asking that you renew your contribution or, if you have not contributed in the past, to join the growing list of contributors. Contributions from individuals in the range of \$25 to \$50 play a significant role in financing the Newsletter. An increase in the number of individual contributors is very important, and we are confident that, with continued corporate support, we will be able to meet our financial obligations in 2005. The address for contributions is Dr. Brett Carver, Department of Agronomy, Oklahoma State University, Stillwater, OK 74078, U.S.A.