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.

H.E. Bockelman, C.A. Erickson, and B.J. Goates.

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.

Table 1. USDA–ARS National Small Grains Collection, April, 2002, relative to wheat.

Taxonomy	NSGC Accessions
Triticum	54,262
Aegilops	2,204
Secale	2,105
X Triticosecale	1,987
Intergeneric hybrids	534

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. 240-241.

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 coördinating 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 their 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, 2003.

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	1984–2002	Mt. Vernon, WA	38,719
Stripe Rust – Adult	1984–2002	Pullman, WA	29,227
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	1981–2002	Aberdeen, ID [1]	23,374
Dwarf Bunt	1978–2002	Aberdeen, ID [2]	15,120
Septoria nodorum	1970-78	Bozeman, MT	8,095
Powdery Mildew	1996–2002	Kinston, NC	11,473
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, 2002.

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	19,142
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* from January 2002–February 2003.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
615227	*aestivum* subsp. *aestivum*	Nagyatadi TF	Hungary	
628640	*aestivum* subsp. *aestivum*	Finch	United States	Washington
628641	*aestivum* subsp. *aestivum*	Chukar	United States	Washington
628644	*aestivum* subsp. *aestivum*	UCRBW01-1	United States	California
628645	*aestivum* subsp. *aestivum*	UCRBW01-2	United States	California
628646	*aestivum* subsp. *aestivum*	UCRBW01-3	United States	California
628647	*aestivum* subsp. *aestivum*	UCRBW01-4	United States	California
628648	*aestivum* subsp. *aestivum*	UCRBW01-5	United States	California
628649	*aestivum* subsp. *aestivum*	UCRBW01-6	United States	California
628650	*turgidum* subsp. *durum*	UCRD01-1	United States	California
628651	*turgidum* subsp. *durum*	UCRD01-2	United States	California
628652	*turgidum* subsp. *durum*	UCRD01-3	United States	California
628653	*turgidum* subsp. *durum*	UCRD01-4	United States	California
628654	*turgidum* subsp. *durum*	UCRD01-5	United States	California
628655	*turgidum* subsp. *durum*	UCRD01-6	United States	California
628987	*aestivum*	Residence	Netherlands	
628988	*aestivum*	Semper	Netherlands	
629114	*aestivum* subsp. *aestivum*	Tubbs	United States	Oregon
629117	*aestivum* subsp. *aestivum*	W-444	United States	
629118	*aestivum* subsp. *aestivum*	Pinnacle	United States	Idaho
629119	*turgidum* subsp. *polonicum*	RF-75	United States	Oregon
629120	*aestivum* subsp. *aestivum*	Krichauff	Australia	South Australia
629277	*aestivum* subsp. *aestivum*	KW943683	United States	Oregon
629278	*aestivum* subsp. *aestivum*	KW940568H	United States	Oregon
629279	*aestivum* subsp. *aestivum*	KW940568F	United States	Oregon
629280	*aestivum* subsp. *aestivum*	KW940426pa	United States	Oregon
629281	*aestivum* subsp. *aestivum*	KW940426pb	United States	Oregon
630935	*aestivum*	Challis	United States	
630938	*aestivum*	Walworth	United States	South Dakota
630978	*aestivum* subsp. *aestivum*	93-11-14-2-1	Canada	Ontario
630979	*aestivum* subsp. *aestivum*	93-11-14-2-2	Canada	Ontario
630980	*aestivum* subsp. *aestivum*	93-11-14-4-5	Canada	Ontario
630981	*aestivum* subsp. *aestivum*	93-11-2-3-1	Canada	Ontario
630982	*aestivum* subsp. *aestivum*	93-11-2-3-2	Canada	Ontario
630983	*aestivum* subsp. *aestivum*	Edem	United States	Washington
631087	*aestivum*	2145	United States	
631088	*aestivum*	COKER 9152	United States	
631089	*aestivum*	COKER 9184	United States	
631090	*aestivum* subsp. *aestivum*	ARS92 302	United States	Washington
631091	*aestivum* subsp. *aestivum*	ARS92 303	United States	Washington

PI Assignments in *Triticum* from January 2002–February 2003.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
631092	*aestivum* subsp. *aestivum*	ARS92 304	United States	Washington
631093	*aestivum* subsp. *aestivum*	ARS92 305	United States	Washington
631094	*aestivum* subsp. *aestivum*	ARS92 306	United States	Washington
631095	*aestivum* subsp. *aestivum*	ARS92 307	United States	Washington
631096	*aestivum* subsp. *aestivum*	ARS92 309	United States	Washington
631097	*aestivum* subsp. *aestivum*	ARS92 311	United States	Washington
631098	*aestivum* subsp. *aestivum*	ARS92 312	United States	Washington
631099	*aestivum* subsp. *aestivum*	ARS92 313	United States	Washington
631100	*aestivum* subsp. *aestivum*	ARS92 314	United States	Washington
631101	*aestivum* subsp. *aestivum*	ARS92 315	United States	Washington
631102	*aestivum* subsp. *aestivum*	ARS92 319	United States	Washington
631103	*aestivum* subsp. *aestivum*	ARS92 320	United States	Washington
631104	*aestivum* subsp. *aestivum*	ARS92 321	United States	Washington
631105	*aestivum* subsp. *aestivum*	ARS92 322	United States	Washington
631106	*aestivum* subsp. *aestivum*	ARS92 328	United States	Washington
631107	*aestivum* subsp. *aestivum*	ARS92 334	United States	Washington
631108	*aestivum* subsp. *aestivum*	ARS92 345	United States	Washington
631109	*aestivum* subsp. *aestivum*	ARS92 347	United States	Washington
631110	*aestivum* subsp. *aestivum*	ARS92 352	United States	Washington
631111	*aestivum* subsp. *aestivum*	ARS92 355	United States	Washington
631112	*aestivum* subsp. *aestivum*	ARS92 362	United States	Washington
631113	*aestivum* subsp. *aestivum*	ARS92 364	United States	Washington
631158	*turgidum* subsp. *durum*	90	Iran	Lorestan
631159	*aestivum* subsp. *aestivum*	VII/16-X14	Macedonia	
631160	*turgidum* subsp. *durum*	1782	Afghanistan	
631161	*aestivum subsp. spelta*	1803	Afghanistan	
631164	*aestivum* subsp. *aestivum*	W4909	United States	Utah
631165	*aestivum* subsp. *aestivum*	W4910	United States	Utah
631352	*aestivum* subsp. *aestivum*	TAM 111	United States	Texas
631376	*aestivum*	Jagalene	United States	
631389	*aestivum*	Cutter	United States	
631402	*aestivum* subsp. *aestivum*	Intrada	United States	Oklahoma
631403	*aestivum* subsp. *aestivum*	ARS95 715	United States	Washington
631404	*aestivum* subsp. *aestivum*	ARS95 717	United States	Washington
631405	*aestivum* subsp. *aestivum*	ARS95 719	United States	Washington
631406	*aestivum* subsp. *aestivum*	ARS95 720	United States	Washington
631407	*aestivum* subsp. *aestivum*	ARS95 725	United States	Washington
631408	*aestivum* subsp. *aestivum*	ARS95 730	United States	Washington
631409	*aestivum* subsp. *aestivum*	ARS96 651	United States	Washington
631410	*aestivum* subsp. *aestivum*	ARS96 652	United States	Washington
631411	*aestivum* subsp. *aestivum*	ARS96 661	United States	Washington
631412	*aestivum* subsp. *aestivum*	ARS96 673	United States	Washington
631413	*aestivum* subsp. *aestivum*	ARS96 674	United States	Washington
631414	*aestivum* subsp. *aestivum*	ARS96 678	United States	Washington
631445	*aestivum* subsp. *aestivum*	Kanto 107	Japan	
631446	*aestivum* subsp. *aestivum*	Pat	United States	Arkansas
631447	*aestivum* subsp. *aestivum*	Deloris	United States	Utah
631449	*aestivum*	Above	United States	Colorado
631450	*aestivum*	Savage	United States	
631473	*aestivum*	25R47	United States	
631474	*aestivum*	26R58	United States	

PI Assignments in *Triticum* from January 2002–February 2003.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
631475	*aestivum*	26R12	United States	
631480	*aestivum*	Summit	United States	
631481	*aestivum*	Blanca Grande	United States	
631482	*aestivum*	Plata	United States	
631486	*aestivum* subsp. *aestivum*	Brundage 96	United States	Idaho
631493	*aestivum* subsp. *aestivum*	OK101	United States	Oklahoma
631514	*aestivum* subsp. *aestivum*	ARS95 451	United States	Washington
631515	*aestivum* subsp. *aestivum*	ARS95 452	United States	Washington
631516	*aestivum* subsp. *aestivum*	ARS95 453	United States	Washington
631517	*aestivum* subsp. *aestivum*	ARS95 454	United States	Washington
631518	*aestivum* subsp. *aestivum*	ARS95 456	United States	Washington
631519	*aestivum* subsp. *aestivum*	ARS95 457	United States	Washington
631520	*aestivum* subsp. *aestivum*	ARS95 458	United States	Washington
631521	*aestivum* subsp. *aestivum*	ARS95 460	United States	Washington
631522	*aestivum* subsp. *aestivum*	ARS95 461	United States	Washington
631523	*aestivum* subsp. *aestivum*	ARS95 462	United States	Washington
631524	*aestivum* subsp. *aestivum*	ARS95 463	United States	Washington
631525	*aestivum* subsp. *aestivum*	ARS95 464	United States	Washington
631526	*aestivum* subsp. *aestivum*	ARS95 465	United States	Washington
631527	*aestivum* subsp. *aestivum*	ARS95 468	United States	Washington
631528	*aestivum* subsp. *aestivum*	ARS95 469	United States	Washington
631529	*aestivum* subsp. *aestivum*	ARS95 470	United States	Washington
631530	*aestivum* subsp. *aestivum*	ARS95 471	United States	Washington
631531	*aestivum* subsp. *aestivum*	ARS95 472	United States	Washington
631532	*aestivum* subsp. *aestivum*	ARS95 473	United States	Washington
631533	aestivum subsp. aestivum	ARS95 474	United States	Washington
631534	*aestivum* subsp. *aestivum*	ARS95 475	United States	Washington
631535	*aestivum* subsp. *aestivum*	ARS95 477	United States	Washington
631536	*aestivum* subsp. *aestivum*	ARS95 478	United States	Washington
631537	*aestivum* subsp. *aestivum*	ARS95 479	United States	Washington
631538	*aestivum* subsp. *aestivum*	ARS95 480	United States	Washington
632252	*aestivum* subsp. *aestivum*	Outlook	United States	Montana
632260	*aestivum*	Alturas	United States	Idaho
632261	*aestivum*	Moreland	United States	Idaho
632272	*aestivum*	AGS485	United States	Georgia
632272	*aestivum* subsp. *aestivum*	Hubbard	United States	Idaho
632275	*aestivum* subsp. *aestivum*	Ankor	United States	Colorado
632343	*aestivum*	KS00WGRC44	United States	Kansas
632345	*aestivum* subsp. *aestivum*	NW97S277	United States	Nebraska
632346	*aestivum* subsp. *aestivum*	NW98S078	United States	Nebraska
632347	*aestivum* subsp. *aestivum*	NW99L7042	United States	Nebraska
632366	*turgidum* subsp. *durum*	Pierce	United States	North Dakota
632367	*turgidum* subsp. *durum*	Dilse	United States	North Dakota
632374	*aestivum*	AP502 CL	United States	
632375	*aestivum*	AP401 CL	United States	
632399	*aestivum* subsp. *aestivum*	Richland	United States	New York
632433	*aestivum* subsp. *aestivum*	Jerry	United States	Utah
632434	*aestivum* subsp. *aestivum*	Goodstreak	United States	Nebraska
632435	*aestivum* subsp. *aestivum*	Harry	United States	Nebraska
632635	*aestivum*	OK102	United States	Oklahoma

PI Assignments in *Secale* and *X Triticosecale* from January 2002–February 2003.

PI number	Taxon	Cultivar name or Identifcation number	Country	State/Province
628642	*cereale* subsp. *cereale*	UCRR1-2001	United States	California
628643	*cereale* subsp. *cereale*	UCRR2-2001	United States	California
628656	*X Triticosecale sp.*	UCRTCL1-2001	United States	California
628657	*X Triticosecale sp.*	UCRTCL2-2001	United States	California
628658	*X Triticosecale sp.*	UCRTCL3-2001	United States	California
629011	*X Triticosecale sp.*	Forerunner	United States	Oregon
629028	*X Triticosecale sp.*	NE422T	United States	Nebraska
629282	*X Triticosecale sp.*	KT982230	United States	Oregon
629283	*X Triticosecale sp.*	KTG06-hr-01	United States	Oregon
629284	*X Triticosecale sp.*	KTG06-hr-03	United States	Oregon
629285	*X Triticosecale sp.*	KTG06-hr-04	United States	Oregon
629286	*X Triticosecale sp.*	KTG06-hr-09	United States	Oregon
630955	*Secale strictum*	497	Poland	
630956	*Secale strictum*	17778	Poland	
630957	*Secale strictum*	544	Poland	
630958	*Secale strictum*	I1785/94/INN	Turkey	
630959	*Secale strictum*	805	Poland	
630960	*Secale strictum*	789/95	Italy	
630961	*Secale strictum*	2706	Hungary	
630962	*Secale strictum*	14567	Armenia	
630963	*Secale strictum* subsp. *africanum*	6043	South Africa	
630964	*Secale strictum* subsp. *africanum*	834/96/144	South Africa	
630965	*Secale strictum* subsp. *anatolicum*	14363	Turkey	
630966	*Secale strictum* subsp. *anatolicum*	2702	Armenia	
630967	*Secale strictum* subsp. *ciliatoglume*	24266	Poland	
630968	*Secale strictum* subsp. *kuprijanovii*	2704	Armenia	
630969	*Secale strictum* subsp. *kuprijanovii*	6143	Poland	
630970	*Secale strictum* subsp. *kuprijanovii*	2705	Azerbaijan	
630971	*Secale strictum* subsp. *strictum*	24267	Poland	
630972	*Secale cereale* subsp. *cereale*	32114/70	Turkey	
630973	*Secale cereale* subsp. *cereale*	32635/71	Turkey	
631456	*X Triticosecale sp.*	348	United States	
631457	*X Triticosecale sp.*	336	United States	
632262	*X Triticosecale sp.*	2115	United States	
632263	*X Triticosecale sp.*	308	United States	
632264	*X Triticosecale sp.*	2205	United States	
632593	*Secale cereale* subsp. *cereale*	77 A-48	Portugal	
632594	*Secale cereale* subsp. *cereale*	77 A-69	Portugal	
632595	*Secale cereale* subsp. *cereale*	77 A-81	Portugal	
632596	*Secale cereale* subsp. *cereale*	77 A-85	Portugal	

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2003 SUPPLEMENT

R.A. McIntosh [1], K.M. Devos [2], J. Dubcovsky [3], C.F. Morris [4] and W.J. Rogers [5].

[1] Plant Breeding Institute, The University of Sydney, 107 Cobbitty Road, Cobbitty, N.S.W., Australia, 2570.

[2] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk, NR4 7UH, U.K.

[3] Department of Agronomy and Range Science, University of California, Davis, CA 95616, U.S.A.

[4] Western Wheat Quality Laboratory, USDA-ARS, Washington State University, Pullman, WA 99164-6394, U.S.A.

[5] Catedra de Genetica y Fitotecnia, Universidad Nacional del Centro de la Provincia de Buenos Aires, 7300 Azul, Argentina.

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The 1999, 2000, 2001, and 2002 supplements are included in *Annual Wheat Newsletter* Vols. 44–47 and the *Wheat Information Service* and are listed in the Graingenes Website. The present Supplement will be offered to editors/curators for similar listing.

Revisions.

10. Laboratory Designators for DNA markers

aww	Langridge, P. Department of Plant Science Waite Campus University of Adelaide Glen Osmond South Australia 5064 Australia plangrid@waite.adelaide.edu.au
bfc	Nomura, T. Biofunction Chemistry Division of Applied Life Sciences Graduate School of Agriculture Kyoto University Kyoto 606-8502 Japan thaidi@kais.kyoto-u.ac.jp
DuPw	Wolters, Petra DuPont Company P.O. Box 6104 Newark, DE 19714-6104 U.S.A. petra.wolters@usa.dupont.com

scu Henry, R.J.
Centre for Plant Conservation Genetics
Southern Cross University
P.O. Box 157
Lismore, NSW 2480
Australia

a*cfd* Bernard, M.
UMR Amélioration et Santé des Plantes
INRA–UBP63039 Clermont-Ferrand
Cedex 2
France
michel.Bernard@clermont.inra.fr

iag Wricke, G.
Institut für Angewandte Genetic
Universitat Hannover
Herrenhauser Strasse 23000
Hannover 21
Germany
office@mbox.genetik.uni-hannover.de

whs Mohler, V.
mohler@wzw.tum.de
Lehrstuhl für Pflanzenbau und Pflanzenzüchtung
Wissenschaftszentrum Weihenstephan
Technische Universität München
Am Hogancher
285350 Freising
Germany

Gross Morphology : Spike Characteristics

1. Squarehead/spelt

Q. **ma:** Fine mapping of the 20-cM region possessing *Q* and delimited by deletions 5AL-7 and-23 is reported in {0324}.

5. Elongated glume

According to {0254} the loci of *T. polonicum, T. petropavlovsky,* and *T. isphanicum* are allelic (‘homoeoallelic’), whereas other workers had claimed genes in the first two forms were not allelic. Wang et al. {0254} however concluded that loci bearing alleles for elongated glumes in *T. turanicum* and *T. durum* conv. *falcatum* were not part of the above series.

P1. 7A. **ma:** *Xgwm260-7AS* – 2.3cM - *P1*^{pol} – 5.6cM - *Xgwm1083-7AL* {0254}; *Xgwm890-7AS* – 2.1cM – *P1*^{pet} {0254}.

Awnedness

1. Dominant Inhibitors

1.1. Hooded

Hd. Add at the end of **ma:** ‘*Hd* was mapped as a QTL with a peak on *Xfba78-4A* in {0309}.’.

1.2. Tipped 1

B1. At the end of section add: ‘The postulation of *B1* in both CS and Courtot {0309} based on the phenotype of a CS deletion stock is not supported by genetic observations.’.

1.3. Tipped 2

B2. Add at the end of **ma:** ‘*B1* was mapped as a QTL with a peak on *Xwmc182-6B* {0309}.’.

DNA Markers

Group 1S

Amendments:

XgbxG746-1B. Add ‘(1BL).’ in the last column.

Xutv1518-1A,B. Revise the first column to ‘*Xutv1518-1A,B* {9959}^{2}, *1D* {0360}^{1}.’.

Add:

Xabg53-1A,B,D {0252}.		ABG53.	
Xcsl106(NBS-LRR)1-1D [{0360}].			
	[*rga5.2a* {0360}].	Rga5.2.	(1DS).
Xcsl106(NBS-LRR)2-1D [{0135}].			
	[*rga5.2b* {0135}].	Rga5.2.	(1DS).
Xcsl106(NBS-LRR)3-1D [{0360}].			
	[*rga5.2c* {0360}].	Rga5.2.	(1DS).
Xiag95-1D {0360}.		IAG95.	
Xunl11-1B {0373}.		UNL11.	
Xunl12-1B {0373}.		UNL12.	
Xunl13-1B {0373}.		UNL13.	
Xunl14-1B {0373}.		UNL14.	
Xunl15-1B {0373}.		UNL15.	
Xunl16-1B {0373}.		UNL16.	
Xunl17-1B {0373}.		UNL17.	
Xunl24-1B {0373}.		UNL24.	
Xunl27-1B {0373}.		UNL27.	
Xunl31-1B {0373}.		UNL31.	
Xwhs2001-1D [{0370}].	[*XaAXT/CAA-1D* {0370}].	aACT/CAA-1/aACT/CAA-2.	
Xwmc49-1B {0348}.		WMC 49F/WMC 49R.	
Xwmc51-1B {0348}.		WMC 51F/WMC 51R.	
Xwmc329-1B,D {0348}.		WMC 329F/WMC 329R.	

Group 1L

Amendments:

Xbcd200-1A,B. Add ‘(7A).’ in the last column.

Xbcd454-1A. Revise the first column to ‘*Xbcd454-1A* {1529}^{5}, *1B* {0354}.’.

Xbcd1495-1B. Revise the last column to ‘(6A,B,D).’.

Xgbx3581-1B. Revise the last column to ‘(2A, 4B).’.

XgbxG177-1D. Revise the first column to ‘*XgbxG177-1A,B* {0354}, *1D* {9958}.’.

XgbxG557-1A. Add ‘(4A).’ in the last column.

Xwg180-1A. Revise the first column to ‘*Xwg180-1A* {280}^{5}, *1B* {0354}.’.

Xwg241-1A,B,D. Add ‘(6B, 7D.).’ in the last column.

Add:

Xcdo57-1A [{0354}].	[*Xcdo57a-1A* {9354}].		(2A, 5A,B,D, 7A,B,D).
XgbxG263-1B {0354}.		gbxG263.	
XgbxG542-1A {0354}.		gbxG542.	(2A, 3D, 4A).
XgbxG597-1A {0354}.		gbxG597.	
XgbxG746-1B {0354}.			(1BS).
Xwmc44-1B {0153,0348}.		WMC 44F/WMC 44R.	
Xwmc156-1B {0348}.		WMC 156F/WMC 156R.	
Xwmc216-1D {0348}.		WMC 216F/WMC 216R.	(7B).
Xwmc254-1A {0348}.		WMC 254F/WMC 254R.	(4B).

Group 1

Amendments:

Xgbx3076-1A. Revise the first column to '*Xgbx3076-1A* {9958}, *1B* {0354}.'

Xwmc44-1B. Delete (moved to 1L).

Xwmc120-1A {0153}. Add '(6B).' in the last column.

Add:

TaMlo-A1,B1,D1 {0336}.		Mlo.	

Note: Sequences from each of these genes were identical with those from *T. urartu, Ae. speltoides*, and *Ae. tauschii*, respectively (0336).

Xabc310-1B [{0354}].	[*Xabc310a-1B* {0354}.].	ABC310.	(3B, 4A,5B, 7A,B).
Xcfd15-1A {0349}.		CFD 15F/CFD 15R.	
Xcfd19-1D {0349}.		CFD 19F/CFD 19R.	(5B, 6D).
Xcfd20-1B {0349}.		CFD 20F/CFD 20R.	
Xcfd21-1D {0349}.		CFD 21F/CFD 21R.	(7D).
Xcfd27-1D {0349}.		CFD 27F/CFD 27R.	
Xcfd28-1D {0349}.		CFD 28F/CFD 28R.	
Xcfd32-1D {0349}.		CFD 32F/CFD 32R.	
Xcfd48-1B {0349}.		CFD 48F/CFD 48R.	
Xcfd58-1D {0349}.		CFD 58F/CFD 58R.	
Xcfd59-1B {0349}.		CFD 59F/CFD 59R.	(1D).
Xcfd59-1D {0349}.		CFD 59F/CFD 59R.	(1B).
Xcfd61-1D {0349}.		CFD 61F/CFD 61R.	
Xcfd63-1D {0349}.		CFD 63F/CFD 63R.	
Xcfd65-1B {0349}.		CFD 65F/CFD 65R.	(1D).
Xcfd65-1D {0349}.		CFD 65F/CFD 65R.	(1B).
Xcfd72-1D {0349}.		CFD 72F/CFD 72R.	
Xcfd83-1D {0349}.		CFD 83F/CFD 83R.	
XDuPw38-1A {0366}.		DUPW 38F/DUPW 38R.	
Xgbx3321-1A,B [{0354}].	[*Xgbx3321a-1A*, *Xgbx3321b-1B* {0354}].	gbx3321.	(6A,B).
Xgwm325-1D [{0354}].	[*Xgwm325b-1D* {0354}].	WMS 325F/WMS 325R.	(6D).
Xscu2-1D [{0368}].		SFR002.B09 F/R.	
Xscu4-1A,B,D [{0368}].		HWM004.H07 F/R.	
Xscu7-1B [{0368}].		SFR007.D06 F/R.	
Xscu19-1A,B,D [{0368}].		HWM019cc.05 F/R.	
XscuTAE-1D [{0368}].		TAE F/TAE R.	
Xunl18-1B {0373}.		UNL18.	
Xunl19-1B {0373}.		UNL19.	
Xunl20-1B {0373}.		UNL20.	
Xunl26-1B {0373}.		UNL26.	
Xunl29-1B {0373}.		UNL29.	
Xunl30-1B {0373}.		UNL30.	
Xunl32-1B {0373}.		UNL32.	
Xwmc106-1A {0366}.		WMC 106F/WMC 106R.	

Group 2S

Amendments:

Xbcd102-2D. Revise the last column to '(5B, 6A,B).'.

Xcdo57-2A. Revise the last column to '(1A, 5A,B,D, 7A,B,D).'.

Xgbx3832-2A. Revise the last column to '(2DL, 4A, 5A).'.

XgbxG35-2B. Revise the first column to '*XgbxG35-2B.1* [{9958,0354}].', revise the second column to '[*XgbxG035c-2B* {9958}, *XgbxG035a-2B* {0354}].' and revise the last column to '(2BL, 4A, 7B).'.

XgbxG36-2A. Revise the last column to '(4A, 6A, 7B).'.

Add:

Xbcd438-2D {0354}.		BCD438.	
Xbcd1069-2D {0354}.		BCD1069.	
Xbcd1086-2B [{0074}],{0354}.	[*Xbcd1086b-2B* {0074}].	BCD1086.	
Xfba127-2B [{0354}].	[*Xfba127a-2B* {0354}].	FBA127.	(3A, 5B, 6B, 7A).
Xfbb67-2A {0354}.		FBB67.	(4B, 7AS, 7BL).
Xgbx3581-2A {0354}.		gbx3581.	(1B, 4B).
Xwmc166-2D {0348}.		WMC 166F/WMC 166R.	(7B).
Xwmc177-2A {0348}		WMC 177F/WMC 177R.	
Xwmc213-2B {0348}.		WMC 213F/WMC 213R.	
Xwmc243-2B {0348}.		WMC 243F/WMC 243R.	
Xwmc257-2B {0348}.		WMC 258F/WMC 258R.	
Xwmc265-2B {0348}.		WMC 265F/WMC 265R.	
Xwmc272-2B {0348}.		WMC 272F/WMC 272R.	

Group 2L

Amendments:

Xbcd135-2B,D. Revise the first column to '*Xbcd135-2A* {0354}, *2B* {1060}, *2D* {864}.'.

Xgbx3832-2D. Revise the last column to '(2AS, 4A, 5A).'.

Add:

Xgbx3110-2A [{0354}].	[*Xgbx3110a,b-2A* {0354}].	gbx3110.	(7A,B).
Xgwm82-2A {0354}.		WMS 82F/WMS 82R.	(6A).
Xwmc167-2D {0153,0348}.		WMC 167F/WMC 167R.	
Xwmc175-2B,D {0348}.		WMC 175F/WMC 175R.	
Xwmc181-2A,D {0348}.		WMC 181F/WMC 181R.	
Xwmc261-2A {0348}.		WMC 261F/WMC 261R.	

Group 2

Amendments:

Xbcd1086-2B. Delete (moved to 2S).

XgbxG542-2A. Revise the last column to '(1A, 3D, 4A).'.

XgbxR635-2D. Revise the first column to '*XgbxR635-2A* {0354}, *2D* {9958}.'.

Xwmc25-2D. Delete (moved to 2S).

Xwmc167-2D. Delete (moved to 2L).

Add:

Xcfd2-2A {0349}.	CFD 2F/CFD 2R.	(4A, 5B).
Xcfd11-2B {0349}.	CFD 11F/CFD 11R.	(2D).
Xcfd11-2D {0349}.	CFD 11F/CFD 11R.	(2B).
Xcfd17-2D {0349}.	CFD 17F/CFD 17R.	
Xcfd25-2B {0349}.	CFD 25F/CFD 25R.	
Xcfd36-2D {0349}.	CFD 36F/CFD 36R.	
Xcfd43-2D {0349}.	CFD 43F/CFD 43R.	
Xcfd44-2D {0349}.	CFD 44F/CFD 44R.	
Xcfd50-2D {0349}.	CFD 50F/CFD 50R.	
Xcfd51-2D {0349}.	CFD 51F/CFD 51R.	
Xcfd53-2D {0349}.	CFD 53F/CFD 53R.	
Xcfd56-2D {0349}.	CFD 56F/CFD 56R.	
Xcfd62-2D {0349}.	CFD 62F/CFD 62R.	(7A).
Xcfd73-2B {0349}.	CFD 73F/CFD 73R.	
Xcfd77-2D {0349}.	CFD 77F/CFD 77R.	
XDuPw207-2B {0366}	DUPW 207F/DUPW 207R.	

XDuPw210-2A {0366}.		DUPW 210F/DUPW 210R.	
XgbxG35-2B.2 [{0354}].	[*XgbxG035b-2B* {0354}].	gbxG035.	(2BS, 4A, 7B).
Xscu6-2A,B,D [{0368}].		CSB006.H05 F/R.	

Group 3S

Amendments:

Xbcd15-3A. Revise the last column to '(4A,D, 4B,D).'.

Xfba127-3A. Revise the last column to '(2B, 5B, 6B, 7A).'.

Xwmc43-3B. Revise the first column to '*Xwmc43-3B* [{0242}],{0348}, *3D* {0348}.'.

Add:

Xaww1(Msh7)-3A,B,D [{0345}].	[*TaMSH7-3A,B,D* {0345}].	TaMSH7.	
XgbxGx71-3B [{0354}].	[*XgbxGx71d-3B* {0354}].	gbxGx71.	(2B).

Group 3L

Amendments:

Xfbb283-3B. Revise the last column to '(6A, 6D).'.

Xgbx3864-3D. Revise the first column to '*Xgbx3864-3B* [{0354}], *3D* {9958}.' and revise the second column to '[*Xgbx3864a-3B* {0354}, *Xgbx3864a-3D* {9958}].'.

XgbxG65-3B. Revise the first column to '*XgbxG65-3B* {9958}, *3D* [{0354}].' and add '[*XgbxG065-3D* {0354}].' in the second column.

XgbxG305-3D. Revise the first column to '*XgbxG305-3A* {0354}, *3D* {9958}.'.

XgbxG542-3D. Revise the last column to '(1A, 2A, 4A).'.

XgbxG773-3B. Revise the first column to '*XgbxG773-3A* {0354}, *3B* {9958}.'.

Add:

XgbxG147-3D {0354}.	gbxG147.	(4B).
XgbxG541-3D {0354}.	gbxG541.	(3B, 5B).
Xwmc153-3A {0348}.	WMC 153F/WMC 153R.	
Xwmc264-3A {0348}.	WMC 264F/WMC 264R.	
Xwmc322-3B {0348}.	WMC 322F/WMC 322R.	
Xwmc326-3B {0348}.	WMC 326F/WMC 326R.	

Group 3

Amendments:

Xwg178-3D. Revise the first column to '*Xwg178-3B* {0354}, *3D* {9926}[4].'

Add:

Xabc158-3D {0354}.		ABC158.	(7A,B).
Xabc310-3B {0354}.		ABC310.	(1B, 4A,5B, 7A,B).
Xcfd4-3B {0349}.		CFD 4F/CFD 4R.	
Xcfd9-3D {0349}.		CFD 9F/CFD 9R.	
Xcfd34-3D {0349}.		CFD 34F/CFD 34R.	
Xcfd35-3D {0349}.		CFD 35F/CFD 35R.	
Xcfd55-3D {0349}.		CFD 55F/CFD 55R.	
Xcfd64-3D {0349}.		CFD 64F/CFD 64R.	
Xcfd70-3D {0349}.		CFD 70F/CFD 70R.	
Xcfd79-3B {0349}.		CFD 79F/CFD 79R.	(3D).
Xcfd79-3D {0349}.		CFD 79F/CFD 79R.	(3B).
XDuPw173-3D {0366}.		DUPW 173F/DUPW 173R.	
XDuPw227-3A {0366}.		DUPW 227F/DUPW 227R.	
Xgbx3793-3B {0354}.		gbx3793.	
XgbxG83-3D [{0354}].	[*XgbxG083b-3D* {0354}].	gbxG083.	(4D, 5D, 6B).

XgbxG276-3B [{0354}].	[*XgbxG276a-3B* {0354}].	gbxG276.	(5A,4B).
XgbxG541-3B [{0354}].	[*XgbxG541a-3B* {0354}].	gbxG541.	(3D, 5B).

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

Amendments:
Xcdo1338-4A. Revise the first column to '*Xcdo1338-4A* {1008}, *4B* {0354}.'.
Xcn110(Lpx)-4B. Revise the first column to '*Xcn110(Lpx-1)-4B* [{0269}]^{2}.'.

Add:

XcsME1-4B {0379}.		csME1.	
Xksu919(Lpx-1)-4A [{0091}].			
	[*Lpx-4A* {0091}].	6C02E12 {0094}.	

Note: KSU919 cross-hybridizes to the *Xksu919(Lpx-2)-5A,B* loci.

Xwmc52-4D {0348}.		WMC 52F/WMC 52R.	
Xwmc238-4B {0348}.		WMC 238F/WMC 238R.	

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

Amendments:
XgbxG147-4B. Add '(3D).' in the last column.
XgbxR866-4A. Revise the first column to '*XgbxR866-4A* {9958}, *4B* [{0354}].', add '[*XgbxR866c-4B* {0354}].' in the second column and add '(5A).' in the last column.

Add:

Xbcd15-4A,D [{0354}].	[*Xbcd015c,a-3A,D* {0354}].	BCD15.	(3A, 4B,D).
XgbxG83-4D [{0354}].	[*XgbxG083a-4D* {0354}].	gbxG083.	(3D, 5D, 6B).

It is not known whether *XgbxG83-4D* belongs to Group 4AS:4BL:4DL or 5AL:4BL:4DL.

Xwmc96-4A {0348}.		WMC 96F/WMC 96R.	(5A).
Xwmc173-4A {0348}.		WMC 173F/WMC 173R.	
Xwmc331-4D {0348}.		WMC 331F/WMC 331R.	

Group 5AL:4BL:4DL

Amendments:
Xbcd15-4B,D. Revise the last column to '(3A, 4A,D).'.
Xfbb67-4B. Revise the last column to '(2A, 7AS, 7BL).'.
Xgbx3581-4B. Revise the last column to '(1B, 2A).'.
XgbxG276-4B. Revise the first column to '*XgbxG276-5A* [{0354}], *4B* {9958}.', add '[*XgbxG276a,b-5A* {0354}].' in the second column and add '(3B).' in the last column.
XgbxG367-4D. Revise the last column to '(4B, 6A, 6B, 7A).'.

Group 4

Amendments:
Xwg180-4B. Revise the last columnt to '(1A,B, 7BS,L).'.
Xwmc254-4B. Add '(1A).' in the last column.

Add:

Xbfc9v(cyp71C)-4A, B, D [{0371}].			
	[*Cyp*71C9v-*4A,B,D* {0371}].	CYP71C9v {0371}.	
Xcfd2-4A {0349}.		CFD 2F/CFD 2R.	(2A, 5B).
Xcfd16-4A {0349}.		CFD 16F/CFD 16R.	
Xcfd22-4B {0349}.		CFD 22F/CFD 22R.	
Xcfd23-4D {0349}.		CFD 23F/CFD 23R.	
Xcfd24-4A {0349}.		CFD 24F/CFD 24R.	

Xcfd39-4B {0349}.		CFD 39F/CFD 39R.	
Xcfd54-4B {0349}.		CFD 54F/CFD 54R.	
Xcfd71-4A {0349}.		CFD 71F/CFD 71R.	(4D).
Xcfd71-4D {0349}.		CFD 71F/CFD 71R.	(4A).
Xcfd84-4D {0349}.		CFD 84F/CFD 84R.	
XDuPw4-4A {0366}.		DUPW 4F/DUPW 4R.	
XDuPw23-4B {0366}.		DUPW 23F/DUPW 23R.	
XDuPw43-4B {0366}.		DUPW 43F/DUPW 43R.	
XDuPw108-4A {0366}.		DUPW 108F/DUPW 108R.	
XDuPw238-4D {0366}.		DUPW 238F/DUPW 238R.	
Xfba248-4B [{0354}].	[*Xfba248b-4B* {0354}].	FBA248.	(7A).
XgbxG36-4A [{0354}].	[*XgbxG036-4A* {0354}].	gbxG036.	(2A, 6A, 7B).
XgbxG102-4D {0354}.		gbxG102.	
XgbxG328-4D {0354}.		gbxG328.	
XgbxG367-4B [{0354}].	[*XgbxG367a-4B* {0354}].	gbxG367.	(4D, 6A, 6B, 7A).
XgbxG542-4A {0354}.		gbxG542.	(1A, 2A, 3D).
XgbxG557-4A {0354}.		gbxG557.	(1A).
Xscu6465-4A [{0368}].		PSR6465 F/PSR6465 R.	
XSut1-4A,B,D {0361}.		TaSUT1D	(4A,B,D).

Group 5S

Amendments:

Xcdo1338-5A,B,D . Revise the last column to '(4A,B).'.

XgbxG625-5A. Revise the first column to '*XgbxG625-5A* {9958}, *5B* [{0354}].' and add '[*XgbxG625b-5B* {0354}].' in the second column.

Group 5L

Amendments:

Xbcd454-5A. Revise the last column to '(1A,B).'.

Xcdo57-5A,B,D. Revise the last column to '(1A, 2A, 7A,B,D).'.

Xcdo412-5A,B,D. Add '(7B).' in the last column.

Xcn111(Lpx)-5B. Revise the first column to '*Xcn111(Lpx-2)-5B* [{0269}]^{2}.'.

Xfba127-5B. Revise the last column to '(2B, 3A, 6B, 7A).'.

XgbxG70-5D . Revise the first column to '*XgbxG70-5A* [{0354}], *5D* {9958}.' and the second column to '[*XgbxG070a-5A* {0354}, *XgbxG070-5D* {9958}].'.

XgbxG134-5D. Revise the first column to '*XgbxG134-5B* {0354}, *5D* {9958}.'.

XgbxG541-5B. Add (3B, 3D).' in the last column.

XgbxR33-5A. Revise the first column to '*XgbxR33-5A* [{9958}], *5B* [{0354}].' and revise the second column to '[*XgbxR033-5A* {9958}, *XgbxR033-5B* {0354}].'.

XgbxR678-5D. Revise the first column to '*XgbxR678-5B* {0354}, *5D* {9958}.'.

Xksu919(Lpx)-5A,B. Revise the first column to '*Xksu919(Lpx-2)-5A,B* [{0091}], *5D* [{0148}].', revise the second column to [*Lpx-5A,B* {0091}, *5D* {0148}].', delete '(4A).' from the last column and add 'Note: The probe KSU919 cross-hybridizes to the *Xksu919(Lpx-1)-4A* locus.'.

Add:

Xbcd102-5B {0354}.		BCD102.	(2D, 6A,B).
Xcdo475-5B {0354}.		CDO475.	(4A,7A,D).
Xcfd7-5D [{0354}].	[*Xcfd4A6-5D* {0354}].	CFD 7F/CFD 7R.	
Xfba340-5D [{0354}].	[*Xfba340b-5D* {0354}].	FBA340.	(6B, 7A).

It is not known whether *Xfba340-5D* belongs to group 5L or 4AL:5BL:5DL.

Xgbx3832-5A [{0354}].	[*Xgbx3832c-5A* {0354}].	gbx3832.	(2A, 2D, 4A).
XgbxG83-5D [{0354}].	[*XgbxG083c-5D* {0354}].	gbxG083.	(3D, 4D, 6B).
Xgwm44-5A {0354}.		WMS 44F/WMS 44R.	(7D).
Xocs(CK2a)-5A,B,D [{0369}].		tck2a.	

Xwmc97-5D {0348}.		WMC 97F/WMC 97R.	
Xwmc215-5A {0348}.		WMC 215F/WMC 215R.	
Xwmc327-5A {0348}.		WMC 327F/WMC 327R.	

4AL:5BL:5DL

Amendments:
Xabc310-4A,5B. Revise the last column to '(1B, 3B, 7A,B).'.

Group 5

Amendments:
Xbcd135-5D. Revise the last column to '(2A,B,D, 7A,4A).'.
Xwmc96-5A. Add '(4A).' in the last column.

Add:

Xbfc6(cyp71C)-5A, B, D [{0371}].	[*Cyp*71C6-*5A,B,D* {0371}].	CYP71C6.	
Xbfc7v2(cyp71C)-5A, B, D [{0371}].	[*Cyp*71C7v2-*5A,B,D* {0371}].	CYP71C7v2.	
Xbfc8v2(cyp71C)-5A, B, D [{0371}].	[*Cyp*71C8v2-*5A,B,D* {0371}].	CYP71C8v2	
Xcfd2-2A {0349}.		CFD 2F/CFD 2R.	(4A, 5B).
Xcfd3-5D {0349}.		CFD 3F/CFD 3R.	
Xcfd8-5D {0349}.		CFD 8F/CFD 8R.	
Xcfd10-5D {0349}.		CFD 10F/CFD 10R.	
Xcfd12-5D {0349}.		CFD 12F/CFD 12R.	
Xcfd18-5D {0349}.		CFD 18F/CFD 18R.	
Xcfd19-5B {0349}.		CFD 19F/CFD 19R.	(1D, 6D).
Xcfd26-5D {0349}.		CFD 26F/CFD 26R.	
Xcfd29-5D {0349}.		CFD 29F/CFD 29R.	
Xcfd40-5D {0349}.		CFD 40F/CFD 40R.	
Xcfd52-5D {0349}.		CFD 52F/CFD 52R.	
Xcfd57-5D {0349}.		CFD 57F/CFD 57R.	
Xcfd67-5D {0349}.		CFD 67F/CFD 67R.	
Xcfd78-5D {0349}.		CFD 78F/CFD 78R.	
Xcfd81-5D {0349}.		CFD 81F/CFD 81R.	
XDuPw115-5B {0366}.		DUPW 115F/DUPW 115R.	
XDuPw205-5B {0366}.		DUPW 205F/DUPW 205R.	
XgbxR866-5A [{0354}].	[*XgbxR866-5A* {0354}].	gbxR866.	(4A,B).
Xscu6394-5D [{0368}].		PSR6394 F/PSR6394 R.	
Xwmc27-5B {0348}.		WMC 27F/WMC 27R.	

Group 6S

Amendments:
Xabg466-6A,D. Revise the first column to '*Xabg466-6A* {282}[3], *6B* {0351}[1], *6D* {900}[1].'.
Xbcd1383-6B. Revise the first column to '*Xbcd1383-6B* {900}, *6D* {0351}.'.
Xbcd1495-6B. Revise the first column to '*Xbcd1495-6A,B,D* {0351}, *6B* {865}.'.
Xbcd1882-6B. Revise the first column to '*Xbcd1882-6A,B,D* {0351}, *6B* {865}.'.
Xcdo476-6A,B. Revise the first column to '*Xcdo476-6A,B* {900}, *6D* {0351}.'.
Xcdo524-6B. Revise the first column to '*Xcdo524-6A,B,D* {0351}, *6B* {900}.'.
Xcdo1380-6B. Revise the first column to '*Xcdo1380-6A* {0351}, *6B* {9927}[2],{0351}.' and add '(6BL).' in the last column.
Xfba148-6A,D. Revise the first column to '*Xfba148-6A* {900}, *6B* {0351}, *6D* {0081}.'.
Xfba399-6B. Revise the first column to '*Xfba399-6A,B,D* {0351}, *6B* {900}.'.

Xfbb194-6A. Revise the first column to '*Xfbb194-6A* {900}, *6D* {0351}.'.
Xgbx3165-6B,D. Revise the first column to '*Xgbx3165-6A* [{0354}], *6B,D* [{9958}].' and revise the second column to '[*Xgbx3165a-6A* {0354}, *Xgbx3165a,b-6B,D* {9958}].'.
XgbxG36-6A. Revise the last column to '(2A, 4A, 7B).'.
XgbxG83-6B. Add '(3D, 4D, 5D).' in the last column.
XgbxR593-6A. Revise the first column to '*XgbxR593-6A* {9958}, *6B* {0354}.'.
Xgwm82-6A. Add '(2A).' in the last column.
XksuI28-6B,D. Revise the first column to '*XksuI28-6A* {0351}^{1}, *6B* {444,860}^{1}, *6D* {448}^{4}, {444}^{1}.'.
Xmwg59-6A,B. Revise the first column to '*Xmwg59-6A,B* {9926}^{2},{0351}^{1}, *6D* {0351}^{1}.'.
Xmwg887-6A.1. Revise the first column to '*Xmwg887-6A.1* {9927}^{2},[{0351}]^{1}, *6D* {0351}^{1}.' and the second column to '[*Xmwg887-6A* {0351}].'.
Xmwg916-6A,D. Revise the first column to '*Xmwg916-6A* {9927}^{2},{0351}^{1}, *6B* {0351}^{1}, *6D* {900}^{1}.'.
Xmwg966-6A,B. Revise the first column to '*Xwmg966-6A* {9927}^{2}, *6B* {0081}^{1}, *6D* {0351}^{1}.'.
Xpsr962-6B,D. Revise the first column to '*Xpsr962-6A* {0351}, *6B,D* {598}.'.
Xtam60-6A,B. Revise the first column to '*Xtam60-6A* {187}^{2},{0351}^{1}, *6B* {187}^{2}, {245}^{1}, *6D* {0351}.'.

Add:

Xfba340-6B [{0354}].	[*Xfba340b-6B* {0354}].	FBA340.	(5D, 7A).
Xfbb283-6D {0351}.		FBB283.	(3B, 6AL).
XgbxG367-6B [{0354}].	[*XgbxG367b-6B* {0354}].	gbxG367.	(4B, 4D, 6BL, 7A).
XksuM95-6A,B,D {0351}.		pTtksuM95.	
Xmwg2218-6B,D {0351}.		MWG2218.	
Xwg241-6B [{0354}]].	[*Xwg241d-6B* {0354}].	WG241.	(1A,B,D, 7D).
Xwmc95-6B {0248}.		WMC 95F/WMC 95R.	
Xwmc105-6B {0348}.		WMC 105F/WMC 105R.	

Group 6L

Amendments:
Xbcd102-6A,B. Revise the last column to '(2D, 5A).'.
Xcdo1380-6B. Add '(6AS,BS).' in the last column.
Xfba127-6B. Revise the last column to '(2B, 3A, 5B, 7A).'.
Xfbb283-6B. Revise the last column to '(3B, 6DS).'.
Xgbx3864-6A. Revise the last column to '(3B,D).'.
Xgbx3317-6D. Revise the first column to '*Xgbx3317-6A* {0354}, *6D* {9958}.'.
Xgbx4071-6A. Revise the first column to '*Xgbx4071-6A* {9958}, *6D* [{0354}].' and add '[*Xgbx4071a-6D* {0354}].' in the second column.
Xmwg887-6A.2. Revise the last column to '(6AS,DS).'.

Add:

XgbxG367-6A [{0354}].	[*XgbxG367b-6A* {0354}].	gbxG367.	(4B, 4D, 6BS, 7A).
Xgwm494-6A {9929},[{0354}]..	[*Xgwm494a,b-6A* {0354}].	WMS 494F/WMS 494R.	
Xwmc182-6B {0348}.		WMC 182F/WMC 182R.	

Group 6

Amendments:
Xcdo1380-6B. Add '(6AS,BS, 6BL).' in the last column.
Xgbx3321-6A,B. Add '(1A,B).' in the last column.
XgbxR4-6A. Revise the first column to '*XgbxR4-6A* [{9958}], *6B* [{0354}].' and revise the second column to '[*XgbxR004-6A* {9958}, *XgbxR004-6B* {0354}].'.
Xgwm325-6D. Add '(1D).' in the last column.
Xgwm494-6A. Delete (moved to 6L).

Add:

Xcfd1-6A {0349}.	CFD 1F/CFD 1R.	
Xcfd5-6D {0349}.	CFD 5F/CFD 5R.	
Xcfd13-6B {0349}.	CFD 13F/CFD 13R.	
Xcfd19-6D {0349}.	CFD 19F/CFD 19R.	(1D, 5B).
Xcfd30-6A {0349}.	CFD 30F/CFD 30R.	
Xcfd33-6D {0349}.	CFD 33F/CFD 33R.	
Xcfd37-6D {0349}.	CFD 37F/CFD 37R.	
Xcfd38-6D {0349}.	CFD 38F/CFD 38R.	
Xcfd42-6D {0349}.	CFD 42F/CFD 42R.	
Xcfd45-6D {0349}.	CFD 45F/CFD 45R.	
Xcfd47-6D {0349}.	CFD 47F/CFD 47R.	
Xcfd49-6D {0349}.	CFD 49F/CFD 49R.	
Xcfd60-6D {0349}.	CFD 60F/CFD 60R.	
Xcfd75-6D {0349}.	CFD 75F/CFD 75R.	
Xcfd76-6D {0349}.	CFD 76F/CFD 76R.	
Xcfd80-6D {0349}.	CFD 80F/CFD 80R.	
Xcfd82-6A {0349}.	CFD 82F/CFD 82R.	
XDuPw167-6A {0366}.	DUPW 167F/DUPW 167R.	
XDuPw216-6B {0366}.	DUPW 216F/DUPW 216R.	
XDuPw217-6B {0366}.	DUPW 217F/DUPW 217R.	
Xscu1-6D [{0368}].	HWM001.F10 F/R.	
Xscu4-6D [{0368}].	HWM004.B10 F/R.	

Group 7S

Amendments:

Xabc158-7A,B. Add '(3D}.' in the last column.

Xcdo57-7A,B,D. Revise the last column to '(1A, 2A, 5A,B,D).'.

Xfba248-7A. Add '(4B).' in the last column.

Xfba340-7A. Add '(5D, 6B).' in the last column.

Xgbx3110-7B. Revise the first column to '*Xgbx3110-7A* [{0354}], *7B* {9958}.', add '[*Xgbx3110b-7A* {0354}]' in the second column, and add '(2A).' in the last column.

XgbxG367-7A. Revise the last column to '(4B, 4D, 6A, 6B).'.

Xgwm44-7D. Add '(5A).' in the last column.

Xwg180-7B. Revise the last column to '(1A,B, 4B, 7BL).'.

Add:

Xbcd130-7B {0354}.	BCD130.	(4A,7A,D).

7AS:4AL:7DS

Amendments:

Xbcd130-7A,4A,7D. Add '(7B).' in the last column.

Xbcd135-7A,4A. Revise the last column to '(2A,B,D, 5D).'.

Xcdo475-7A,4A,7D. Add '(5B).' in the last column.

Xfba109-7A. Revise the first column to '*Xfba109-7A* {1059}, *4A* {0354}.'.

Xfbb67-7A. Revise the last column to '(2A, 4B, 7BL).'.

Xfbb194-4A. Revise the last column to '(6A,D).'.

Xgbx3832-4A. Revise the last column to '(2A, 2D, 5A).'.

XgbxG141-4A. Add '(7B).' in the last column.

Xksu919(Lpx)-4A. Delete (modified and moved to 4AL:4BS:4DS).

Xwg834-7A,D. Revise the first column to '*Xwg834-4A* {0354}, *7A,D* {553}.'.

Add:

Xbcd200-7A {0354}.		BCD200.	(1A,B).
Xwmc168-7A {0348}.		WMC 168F/WMC 168R.	
Xwmc232-4A {0348}.		WMC 232F/WMC 232R.	

Group 7L

Amendments:

Xabc310-7A,B. Revise the last column to ‘(1B, 3B, 4A,5B).’.

Xcdo347-7A. Revise the first column to ‘*Xcdo347-7A* {1059}, *7D* [{0354}].’ and revise the second column to ‘[*Xcdo347a-7D* {0354}].’.

Xfba127-7A. Revise the last column to ‘(2B, 3A, 5B, 6B).’.

Xfbb67-7B. Revise the last column to ‘(2A, 4B, 7AS).’.

Xgbx4046-7B. Revise the first column to ‘*Xgbx4046-7A* {0354}, *7B* {9958}.’.

XgbxG218-7A,B. Revise the first column to ‘*XgbxG218-7A,B* [{9958}], *7D* [{0354}].’ and revise the second column to ‘[*XgbxG218c,a-7A,B* {9958}, *XgbxG218b-7D* {0354}].’.

XgbxR35-7A. Revise the first column to ‘*XgbxR35-7A* [{9958}], *7B,D* [{0354}].’ and revise the second column to ‘[*XgbxR035b-7A* {9958}, *XgbxR035b,a-7B,D* {0354}].’.

XgbxR138-7B. Revise the first column to ‘*XgbxR138-7A* {9958}, *7B,D* [{0354}].’ and add ‘[*XgbxR138a,b-7B* {0354}].’ in the second column.

Xutv1518-7A. Revise the last column to ‘(1A,B,D).’.

Xwg180-7B. Revise the last column to ‘(1A,B, 4B, 7BS).’.

Xwg514-7B. Revise the first column to ‘*Xwg514-7A* {0354}, *7B* {1059}.’.

Add:

Xcdo412-7B {0354}.		CDO412.	(5A,B,D).
Xcnl1-7B [{0354}].	[*XPDAC01-7B* {0354}].	CNL 1F/CNL 1R.	
Xcnl2-7B [{0354}].	[*XBDAC14-7B* {0354}].	CNL 2F/CNL 2R.	
XgbxG36-7B [{0354}].	[*XgbxG026a-7B* {0354}].	gbxG036.	(2A, 4A, 6A).
XgbxG141-7B {0354}.		gbxG141.	(4A).
XgbxR570-7D [{0354}].	[*XgbxR570b-7D* {0354}].	gbxR570.	(5B).
Xpur1-7A [{0323}].	[*STS637-7A* {0323}].	STS638-L/STS638-R {570}.	
Xrgc607-7A [{0323}].	[*C607-7A* {0323}].	RGC607.	
Xrgs11239-7A [{0323}].	[S11239-7A {0323}].	RGS11239.	
Xrz884-7A [{0323}].	[*RZ884-7A* {0323}].	RZ884.	
Xsfr325-7A [{0323}].	[325D4L-7A {0323}].	325D4L.	
Xwg241-D [{0354}].	[*Xwg241a-7D* {0354}].	WG241.	(1A,B,D, 6B).
Xwhs178-7A [{0323}].	[*WHS178-7A* {0323}].	WHS178.	
Xwmc94-7D {0242,0348}.	[*Xwmc094-7D* {0242}].	WMC 94F/WMC 94R.	
Xwmc166-7B {0348}.		WMC 166F/WMC 166R.	(2D).
Xwmc273-7A {0348}.		WMC 273F/WMC 273R.	
Xwmc276-7B {0348}.		WMC 276F/WMC 276R.	

Group 7

Amendments:

XgbxG161-7D. Revise the first column to ‘*XgbxG161-7B* {0354}, *7D* {9958}.’ and add ‘{*XgbxG161b-7B* {0354}].’ in the second column.

XgbxG732-7A. Revise the first column to ‘*XgbxG732-7A* {9958}, *7B* {0354}.’.

Xwmc94-7D. Delete (moved to 7L).

Xwmc216-7B. Add ‘(1D).’ to the last column.

Add:

Xcfd6-7A {0349}.		CFD 6F/CFD 6R.	
Xcfd14-7D {0349}.		CFD 14F/CFD 14R.	
Xcfd21-7D {0349}.		CFD 21F/CFD 21R.	(1D).
Xcfd31-7D {0349}.		CFD 31F/CFD 31R.	

Xcfd41-7D {0349}.		CFD 41F/CFD 41R.	
Xcfd46-7D {0349}.		CFD 46F/CFD 46R.	
Xcfd62-7A {0349}.		CFD 62F/CFD 62R.	(2D).
Xcfd66-7D {0349}.		CFD 66F/CFD 66R.	
Xcfd68-7D {0349}.		CFD 68F/CFD 68R.	
Xcfd69-7D {0349}.		CFD 69F/CFD 69R.	
Xcfd74-7B {0349}.		CFD 74F/CFD 74R.	
XDuPw254-7A {0366}.		DUPW 254F/DUPW 254R.	
XDuPw398-7B {0366}.		DUPW 398F/DUPW 398R.	
XgbxR53-7A [{0354}].	[*XgbxR053b-7A* {0354}].	gbxR053.	
Xscu55-7D [{0368}].	[*55-TH.2e7-7D* {0368}].	55-TH.2e7 F/R.	

Dormancy (Seed)
Amendments:
Delete *Phs* 7D {9960} and associated text and replace with:
Phs {9960}. 4AL **v:** Soleil {0346}.
ma: Associated with *Xpsr1327-4A* {0346}.

Add:
QTL: QTL for preharverst sprouting were identified on chromosomes 3A (associated with *Xfbb293-3A* at P≤0.01), 3B (associated with *Xgwm403-3B* and *Xbcd131-3B* at P≤0.001), 3D (associated with *Xgwm3-3D* at P≤0.001) and 5A (associated with *Xbcd1871-5A* at P≤0.001) in the population Renan x Récital {0347}. The resistant alleles on the group 3 chromosomes and on 5A were contributed by Renan and Récital, respectively. All QTL for preharvest sprouting co-located with QTL for grain colour {0347}.

Earliness per se
Eps-1A^{m} {0364}. 1AL {0364} [***Eps-A***^{m}***1***]. **dv:** *T. monococcum* {0364}. DV92 allele for late flowering, G3116 early flowering.
ma: 0.8 cM distal to *Xwg241* {0364}.

Grain hardness / Endosperm texture
This section was revised by Craig F. Morris, and is included in its entirety below.

Grain hardness or endosperm texture significantly influences flour milling, flour properties and end-use. The difference in particle size index between a hard wheat (Falcon) and a soft wheat (Heron) was reported by Symes {1452} to be due to a single major gene. Symes {1452} also found evidence for ‘different major genes or alleles’ that explained differences among the hard wheats Falcon, Gabo, and Spica. Using Cheyenne (CNN) substitution lines in CS and a Brabender laboratory mill, Mattern *et al.* {915} showed that the hard wheat milling and flour properties of Cheyenne were associated with 5D. Using Hope 5D substitution line in CS [CS(Hope 5D)] crossed to CS, and CS(Hope 5D) crossed to CS ditelosomic 5DL, Law *et al.* {777} showed that grain hardness was controlled by alleles at a single locus on 5DS. The dominant allele, *Ha*, controlling softness was present in Chinese Spring and the allele for hardness, *ha*, was present in the other varieties mentioned. A similar study using ‘CS (CNN5D)/CS recombinant-inbred lines’ was reported by Morris *et al.* {03106}.

A pleiotropic result of *hardness* is the decreased level of a 15-kD starch-granule protein, friabilin, on the surface of water-isolated starch {470}. In endosperm, soft and hard wheats have similar amounts of friabilin, consequently the distinction between the two textural types depends upon the manner in which the friabilin co-purifies with starch. Friabilin also is referred to by the name ‘Grain Softness Protein’ (GSP) {0380}, and later was shown to be comprised primarily of puroindoline a and puroindoline b {0295}. Grain hardness of reciprocal ‘soft x hard’ F$_1$ kernels was well correlated with friabilin occurrence on starch in triploid endosperm {0381}. See IV, Proteins: 5.8 Puroindoline. GSP-1 genes, which are closely related to puroindolines, are also listed in section 5.8.

Ha {777}. 5DS {777}. Soft phenotype

i: Falcon/7*Heron, Heron/7*Falcon {03109}; Paha*2//Early Blackhull/5*Paha {0203,0298}; Early Blackhull Derivative/5*Nugaines {0203,0298}.

v: Chinese Spring {777,03106}; Cappelle Desprez {470}; Heron {1452,470}; Paha, Nugaines {0203,0298}; NY6432-18 {0241}.

ha {777}. Hard phenotype.

i: Falcon/7*Heron, Heron/7*Falcon {03109}; Paha*2//Early Blackhull/5*Paha {0203,0298}; Early Blackhull Derivative/5*Nugaines {0203,0298}.

s: CS*6/Cheyenne 5D {915}; CS*6/Hope 5D {777}. Cappelle Desprez(Besostaya 5D) {470}.

v: Falcon {1452,470}; Holdfast {470}; Early Blackhull, Early Blackhull Derivative {0203,0298}; Cheyenne {03106}; Clark's Cream {0241}.

ma: *Ha* was closely linked to *Xmta9(Puil)-5D* {1414}.

Single-factor effects on hardness were found for chromosome 2A, 2D, 5B, and 6D, and interactive effects were found for chromosomes 5A, 6D, and 7A {1414}.

The addition of King II rye chromosome 5R converted Holdfast wheat from hard to soft {470}. A 14.5-kD rye analogue also was isolated from 6x triticales which have soft texture {470}. All ryes are thought to have soft texture.

Two genes for grain hardness were reported in {055}.

Hard and soft NILs are listed in {0298}.

QTL: In a DH population of 'Courtot/CS' a major locus in chromosome 5DS coincided with *Ha*; minor QTL mapped in chromosomes 1A (associated with *Xfba92*) and 6D (associated with *Xgwm55*) {0141}. Ten QTL for kernel hardness (54 % of the variation) were mapped in a cross 'Forno/Oberkulmer spelt' {0280}.

Grain Quality Parameters

2. Flour colour

Revise title '**Flour colour**' to '**Flour, semolina and pasta colour**'.

QTL: A major QTL was detected in the distal region of chromosome 7BL in the cross 'Omrabi5/*T. turgidum* subsp. *dicoccoides* 600545'. The QTL explained 53 % of the variation and was completely linked to microsatellite marker *Xgwm344-7B*. Omrabi5 contributed the allele for high level of yellow pigment. Two additional small QTL were detected on 7AL {0365}.

7. Starch characteristics (new catagory)

QTL: QTLs for starch viscosity and swelling were associated with the *Wx-B1* locus in the cross 'Cranbrook (*Wx-B1a*)/ Halberd (null *Wx-B1b*)'. An additional QTL for starch viscosity was found on 7BL between markers *Xgwm344-7B* and *Xwg420-7B* in the first cross. This QTL disappeared when amylase activity was inhibited, indicating that it was determined by the late maturing α-amylase activity contributed by Cranbrook. A QTL for starch viscosity was associated with the *Wx-A1* locus in the cross 'CD87/Katepwa' {0362}.

Hairy Leaf

Hl1 {0316}. *Hl.*

Hl2 {0316}. 7BS {0316}. **v:** Hong-mang-mai {0316}.

Heat Tolerance (new category)

QTL: QTL contributing to grain-filling duration (GFD) under high temperatures were associated with *Xgwm11-1BS* (11 % of variability) and *Xgwm293-5AS* (23 % of variability) in 'Ventnor (tolerant)/Karl 92 (nontolerant)' {0327}.

Height

Reduced Height

Rht-B1

Rht-B1b.

Add: 'The development of allele-specific primers for Rht-B1b has been reported in {0378}.'.

QTL: QTL for reduced plant height, peduncle length and coleoptile length contributed by Cranbrook were associated with *XcsMe1-4B* (up to 49 % of variability for plant height and peduncle length and 27–45 % of variability for coleoptile length) in the cross 'Cranbrook (dwarf)/Halberd (tall)'. The dwarfing effect underlying the QTL is caused by the *Rht-B1b* allele {0379}.

Rht-D1b.

Add: 'The development of allele-specific primers for *Rht-D1b* was reported in {0378}.'.

Rht8

Rht8a. Integrate alphabetically in the **v:** section:

Klasic {0341}; Hartog {0341}; Neepawa {0341}; Millbrook {0341}; Otane {0341}; Monad {0341}; Karamu {0341}; Puma Rye {0341}; Oberkulmer {0341}; CAH106 {0341}; TAM107 {0341}; Pioneer Var25W33 {0341}; Karl {0341}; Thatcher {0341}; Century {0341}; Grandin {0341}; AC Reed {0341}; Opata {0341}; Elite Lepeuple {0341}.

Rht8b. Integrate alphabetically in the **v:** section:

Devoy {0341}; Era {0341}; Regency {0341}; Augusta {0341}; NYBatavia {0341}; Mendon {0341}; Geneva {0341}; Stephens {0341}; Bavaria {0341}; Houser {0341}; NY6432-18 {0341}; Foster {0341}; Caledonia {0341}; Ramrod {0341}; Chelsea {0341}; Frankenmuth {0341}; Cayuga {0341}; Yorkstar {0341}; NY85020-395 {0341}; NY85020-139 {0341}; NY87048W-7387 {0341}; Greer {0341}; Pioneer Var2548 {0341}; Superior {0341}; Cornell 595 {0341}; NY86003-106 {0341}; Clarks Cream {0341}; Genesee {0341}; Brevor {0341}; Losprout {0341}; Marilee {0341}; Harus {0341}; OAC Ariss {0341}; Cadoux {0341}; Heines VIII {0341}; Jennah Katifa {0341}.

Rht8c Integrate alphabetically in the **v:** section:

Pioneer Var2510 {0341}; Bai Huo {0341}; Kanto {0341};

Add:

Rht8i. Associated with a 180-bp fragment of WMS261 {0341}. **v:** Madison {0341}.

Rht8j. Associated with a 198-bp fragment of WMS261 {0341}. **v:** W7984 Synthetic {0341}; TAM200 {0341}.

Rht8k. Associated with a 200-bp fragment of WMS261 {0341}. **v:** Tiritea {0341}.

Rht8l. Associated with a 204-bp fragment of WMS261 {0341}. **v:** Pioneer Var2550 {0341}; Pioneer Var2545 {0341}; Pioneer Var2737W {0341}.

QTL: QTL for reduced plant height, peduncle length and coleoptile length corresponding to *Rht-B1* were identified in the cross 'Cranbrook (dwarf)/Halberd (tall)'. These QTL explained up to 49 % of variability for plant height and peduncle length and 27–45 % of variability for coleoptile length. A QTL for coleoptile length (reduced coleoptile length was contributed by Cranbrook) also was identified on 4BL, associated with *XksuC2-4B* and explaining 15–27 % of the phenotypic variation. The influence of this QTL was greatest at 19°C and decreased with cooler temperatures. This QTL also affected leaf size and coleoptile-tiller size and presence. QTL of smaller effect were identified on 2D, 3D, and 6B for peduncle length and 2B, 3B, 5A, and 6B for coleoptile length {0379}.

Male Sterility

Chromosomal

Sterility in hybrids with wheat

Shw {0331}. 1HL {0331}. **ad:** Additions of 1H and 1HL to wheat and certain translocation lines {0331}.
ma: Located in a 16.4 cM interval flanked by *Xmwg800* and *Xmwg943* {0331}. A possible relationship with *Ncc* genes is discussed {0331}.

Manganese Efficiency (new category)

1. Mangenese deficiency

QTL: Variation associated with *Xcdo583-4B* explained 42 % of the variation for Mn efficiency in the durum cross 'Stojocri 2 (Mn efficient)/Hazar (MN inefficient)' {0320}.

Meiotic Characters

2. Pairing homoeologous

Ph1. **ma:** Add {0359} as reference for 'PCR-based assays for presence and absence of *Ph1* were described {0214, 0217, 9965}'.

Polyphenol Oxidase (PPO) Activity (new category)

3,4 dihydroxyphenylalanine (L-DOPA) was used as a substrate in a nondestructive test of polyphenol oxidase activity in seeds. Chromosome 2D was shown to carry PPO gene(s) based on Langdon/Chinese Spring (2D) substitution lines and nullisomic-tetrasomic analysis {0342}.

QTL: A QTL on 2D, associated with *Xfba314*-2D was identified in an 'M6/Opata 85' population using the L-DOPA assay. The high PPO activity was contributed by M6 {0344}. Markers significantly associated with PPO activity were also detected on chromosomes 2A, 2B, 3B, 3D, and 6B in the population 'NY18/Clark's Cream' {0344}.

Proteins

1. Grain protein content

Amendments:

QPro.mgb-5A**:** Add 'and *Xcdo412-5A* {0343}^{2}.'.
QPro.mgb-6A.2**:** Add 'and *Xpsr627-6A* {0343}^{2}.'.
QPro.mgb-6B**:** Add 'and *Nor-2* {0343}^{2}.'.
QPro.mgb-7B**:** Add 'and *Xutv913-7B* {0343}^{2}.'.

New:

QPro.mgb-7A associated at $P \leq 0.01$ with *Pan2* {0343}^{2}.'.

2. Enzymes

2.11 Lipoxygenase

Lpx-A1 [{516}]. **ma:** *Xksu919(Lpx-1)-4A* {0091}.
Lpx-B1 [{516}]. **ma:** *Xcn110(Lpx-1)-4B* {0269} {0367}.
Lpx-A2 [{516}]. **ma:** *Xksu919(Lpx-2)-5A* {0091}.
Lpx-B2 [{516}]. **ma:** *Xksu919(Lpx-2)-5B* {0091}, *Xcn111(Lpx-2)-5B* {0269}.

2.22. NADH dehydrogenase

Add at the bottom of the *Ndh-1* section:

'Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *Ndh1* (NADH dehydrogenase) and *Dia3* (diaphorase) represent the same locus {0356}.'

Add at the bottom of the *Ndh-2* section:

'Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *Ndh2* (NADH dehydrogenase) and *Dia2* (diaphorase) represent the same locus {0356}.'

Add at the bottom of the *Ndh-3* section:

‘Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *Ndh3* (NADH dehydrogenase), *Dia1* (diaphorase) and *Mnr1* (menadione reductase) represent the same locus {0356}.’

3. Endosperm Storage Proteins

3.1 Glutenins

Add to the end of the preamble:

‘Using proteomic analysis of 2D gels of seed storage proteins in 39 ditelocentric lines of cv. Chinese Spring, 105 protein spots were resolved {03129}. Locations of structural genes controlling 26 spots were identified in 10 chromosomal arms (4 on 1BL, 5 on 1BS, 4 on 1DL, 4 on 1DS, 2 on 6AS, 3 on 6BS, 1 on 6DL, 1 on 6DS, 1 on 3BS, and 1 on 3BL). Multiple regulators of the same protein located on various chromosome arms were observed. Two novel subunits, named 1Bz and 1BDz, were found to have very similar structures to HMW-glutenin subunit 12 (encoded by *Glu-D1-2a* – see the relevant list below) and were located to chromosome arms 1BL and 1DL, respectively.’

Glu-A1

Add:

Glu-A1v [{03137}].	[*Glu-A1-VII* {03137}].	VII {03137}.	**v:**	PI-308879 emmer wheat accession {03137}.

Glu-B1

Replace:

Glu-B1e {1116}.		20 {1116}.	**v:**	Federation.

with:

Glu-B1e {1116}.		20 {1116}; 20+20y {03133}.	**v:**	Federation.

Replace:

Glu-B1j {1116}.		21 {1116}.	**v:**	Dunav (rare).

with:

Glu-B1j {1116}.		21 {1116}; 21x+21y {03116}	**v:**	Dunav (rare); Foison {03116}.

Add:

Glu-B1av [{03116}].	[*Glu-B1r* {03116}].	7-18 {03116}.	**v:**	Triticor hexaploid *Triticale* {03116}.
Glu-B1aw [{03116}].	[*Glu-B1s* {03116}].	6.8-20y {03116}.	**v:**	Carnac hexaploid *Triticale* {03116}.
Glu-B1ax [{03137}].	[*Glu-B1-XV* {03137}].	XV {03137}.	**v:**	PI 190922, BG-012302 emmer wheat accessions {03137}.
Glu-B1ay [{03137}].	[*Glu-B1-XVI* {03137}].	XVI {03137}.	**v:**	PI 277681 emmer wheat accession {03137}.
Glu-B1az [{03137}].	[*Glu-B1-XVII* {03137}].	XVII {03137}.	**v:**	PI 348620 emmer wheat accession {03137}.
Glu-B1ba [{03122}].	[*Glu-B1-XVIII* {03122}].	13*+16 {03122}.	**v:**	PI 348767 spelt wheat accession {03122}.
Glu-B1bb [{03122}].	[*Glu-B1-XIX* {03122}].	6+18´ {03122}.	**v:**	PI 348631 spelt wheat accession {03122}.
Glu-B1bc [{03138}].		6+17 {03138}.	**v:**	ICDW 20975 {03138}.

Glu-B1bd [{03140}].		20+8 {03140}.	**v:**	Abadía {03140}.
Glu-D1				
Replace:				
Glu-D1w [{755}].		2+T1+T2 {755}.	**dv:**	*Ae. tauschii*.
with:				
Glu-D1w [{03124}].		5*+10 {03124}.	**v:**	Fiorello {03124}.
Replace:				
Glu-D1x [{755}].		2+T2 {755}.	**dv:**	*T. tauschii*.
with:				
Glu-D1x [{755}].		2+T2 {755}; 2^{t}+12.2^{t} {03124}.	**dv:**	*Ae. tauschii*.
Replace:				
Glu-D1y [{755}].		3+T2 {755}.	**dv:**	*Ae. tauschii*.
with:				
Glu-D1y [{755}].		3+T2 {755}; 3^{t}+12.2^{t} {03124}.	**dv:**	*Ae. tauschii*.
Replace:				
Glu-D1ae [{1578}].		2.1+T1+T2 {1578}.	**dv:**	*Ae. tauschii*.
with:				
Glu-D1ae [{1578}].		2.1+T2 [{1578}]; 2.1^{t}+12.2^{t} {03124}.	**dv:**	*Ae. tauschii*.
Delete:				
Glu-D1af [{1578}].		3+T1+T2 {1578}.	**dv:**	*Ae. tauschii*.
Designation reserved by WJR.				
Replace:				
Glu-D1ag [{1578}].		1.5+T1+T2 {1578}.	**dv:**	*Ae. tauschii*.
with:				
Glu-D1ag [{1578}].		1.5+T2 [{1578}]; 1.5^{t}+12.2^{t} {03124}.	**dv:**	*Ae. tauschii*.
Add:				
Glu-D1am [{03122}].	[*Glu-D1-I* {03122}].	2+12´ {03122}.	**v:**	PI 348495 spelt wheat accession {03122}.
Glu-D1an [{03122}].	[*Glu-D1-II* {03122}].	2+12* {03122}.	**v:**	PI 348672 spelt wheat accession {03122}.
Glu-D1ao [{03122}].	[*Glu-D1-III* {03122}].	2.4+12 {03122}.	**v:**	PI 348473 spelt wheat accession {03122}.
Glu-D1ap [{03122}].	[*Glu-D1-IV* {03122}].	2.5+12 {03122}.	**v:**	PI 348572 spelt wheat accession {03122}.
Glu-D1aq [{03124}].		1.5^{t}+10.1^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1ar [{03124}].		2^{t}+10.1^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1as [{03124}].		1.5^{t}+10.2^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1at [{03124}].		3^{t}+10.1^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1au [{03124}].		2.1^{t}+10.2^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1av [{03124}].		2^{t}+12.3^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1aw [{03124}].		1^{t}+10^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1ax [{03124}].		1^{t}+12^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1ay [{03124}].		1^{t}+10.1^{t} {03124}.	**dv:**	*Ae. tauschii*.

Glu-D1az [{03124}].	$4^t+12.2^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1ba [{03124}].	$1^t+12.3^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bb [{03124}].	1.5^t+11^t {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bc [{03124}].	$1.5^t+10.3^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bd [{03124}].	1^t+11^t {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1be [{03124}].	$2.1^t+12.4^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bf [{03124}].	$2^t+12.1^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bg [{03124}].	$3^t+10.2^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bh [{03124}].	$4^t+10.1^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bi [{03124}].	$4^t+10.2^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bj [{03124}].	5^t+11^t {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bk [{03124}].	$5^t+10.1^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bl [{03124}].	$5^t+12.2^t$ {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bm [{03124}].	5^{*t}-null {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1bn [{03124}].	$5^{*t}+12$ {03124}.	**dv:**	*Ae. tauschii*.

To the end of the paragraph at the end of the *Glu-D1* section concluding, after an amendment in the 2002 Supplement, with the sentence 'The authors named the locus *Gli-DT1* (see below, section '3.2 Gliadins').', add this sentence: 'Reference to T1 has, consequently, been removed from the *Glu-D1* list.'

After this change, add the following paragraphs:
'In {03124}, null alleles were observed for both *Glu-D1-1* and *Glu-D1-2*, which, naturally, are not necessarily the same as those previously reported for this locus, meaning that composite alleles involving them in this study and corresponding to combinations apparently already listed in the Catalogue, may, in fact, represent novel alleles. It also was found that certain subunits of apparently identical relative mobility in SDS-PAGE showed different surface hydrophobicities in RP-HPLC; and the reverse situation was also observed (the same hydrophobicity but different electrophoretic mobilities).

It has been shown {03126} that the relatively small size of a y-type HMW glutenin subunit, named 12.4^t (encoded by *Glu-D1-1t* [{03124}] – see the relevant list below) and carried by accession CPI110750 of *Ae. tauschii*, is due to the deletion of blocks of repetitive motifs, amounting to approximately 200 amino acids, probably caused by unequal crossing-over.

Note that the cultivar Fiorello is given as a standard for *Glu-D1h* encoding subunits 5+12 and for *Glu-D1w* encoding subunits 5*+10. An attempt to resolve this apparent conflict will be made in a future update.'

Glu-B1-1

Replace:

Glu-B1-1i.	21.	**v:**	Dunav.

with:

Glu-B1-1i.	21; 21x {03116}.	**v:**	Dunav; Foison {03116}.

Add:

Glu-B1-1ac [{03116}].	6.8 {03116}.	**v:**	Carnac hexaploid *Triticale* {03116}.
Glu-B1-1ad [{03122}].	13* {03122}.	**v:**	PI-348767 spelt wheat accession {03122}.

Glu-B1-2

Add:

Glu-B1-2z [{03116}].	20y {03116}.	**v:**	Carnac hexaploid *Triticale* {03116}.

Glu-B1-2aa [{03122}].	18´ {03122}.	**v:**	PI 348631 spelt wheat accession {03122}.
Glu-B1-2ab [{03116}].	21y {03116}.	**v:**	Foison {03116}.

Glu-D1-1

Add:

Glu-D1-1n [{03122}].	2.4 {03122}.	**v:**	PI 348473 spelt wheat accession {03122}.
Glu-D1-1o [{03122}].	2.5 {03122}.	**v:**	PI 348572 spelt wheat accession {03122}.
Glu-D1-1p [{03124}].	1^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1-1q [{03124}].	5^{*t} {03124}.	**dv:**	*Ae. tauschii*.

Glu-D1-2

Add:

Glu-D1-2q [{03122}].	12´ {03122}.	**v:**	PI 348495 spelt wheat accession {03122}.
Glu-D1-2r [{03124}].	12.1^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1-2s [{03124}].	12.3^{t} {03124}.	**dv:**	*Ae. tauschii*.
Glu-D1-2t [{03124}].	12.4^{t} {03124}.	**dv:**	*Ae. tauschii*.

Glu-Hch1.

Add:

Glu-Hch1a {03114}.	1^{Hch} {03114}.	**al:**	Accession H1 *H. chilense* {03114}.
Glu-Hch1b {03114}.	2^{Hch} {03114}.	**al:**	Accession H11 *H. chilense* {03114}.
Glu-Hch1c {03114}.	3^{Hch} {03114}.	**al:**	Accession H7 *H. chilense* {03114}.
Glu-Hch1d {03114}.	4^{Hch} {03114}.	**al:**	Accession H16 *H. chilense* {03114}.
Glu-Hch1e {03114}.	5^{Hch} {03114}.	**al:**	Accession H47 *H. chilense* {03114}.
Glu-Hch1f {03114}.	6^{Hch} {03114}.	**al:**	Accession H220 *H. chilense* {03114}.
Glu-Hch1g {03114}.	7^{Hch} {03114}.	**al:**	Accession H293 *H. chilense* {03114}.
Glu-Hch1h {03114}.	8^{Hch} {03114}.	**al:**	Accession H297 *H. chilense* {03114}.
Glu-Hch1i {03114}.	9^{Hch} {03114}.	**al:**	Accession H252 *H. chilense* {03114}.
Glu-Hch1j {03114}.	10^{Hch} {03114}.	**al:**	Accession H210 *H. chilense* {03114}.

Follow this entry with the paragraph:
‘38 accessions (natural populations) of *Hordeum chilense* carrying these 10 subunits have been used as the maternal parents of 121 lines of primary tritordeum, and evaluations for associations with bread-making quality initiated {03114}. Subunits 1^{Hch}, 2^{Hch}, and 3^{Hch} were previously referred to as $H^{ch}a$, $H^{ch}b$, and $H^{ch}c$ {03112}.’

Glu-R1

Add:

Glu-R1a {03116}.	1^{r}-4^{r} {03116}.	**v:**	Indiana hexaploid *Triticale* {03116}.

Glu-R1b {03116}.	2^r-6.5^r {03116}.	**v:**	Graâl hexaploid *Triticale* {03116}.
Glu-R1c {03116}.	6^r-13^r {03116}.	**v:**	Alamo hexaploid *Triticale* {03116}.
Glu-R1d {03116}.	2^r-9^r {03116}.	**v:**	Olympus hexaploid *Triticale* {03116}.
Glu-R1e {03116}.	6.5^r {03116}.	**v:**	Clercal hexaploid *Triticale* {03116}.
Glu-R1f {03115}.	0.8^r-6^r {03115}.	**v:**	Carmara hexaploid *Triticale* {03115}.
Glu-R1g {03115}.	5.8^r {03115}.	**v:**	Arrayan hexaploid *Triticale* {03115}.

Add the following two lists after the *Glu-R1* list:

Glu-R1-1.	1R, 1RL.		
Glu-R1-1a {03116}.	1^r {03116}.	**v:**	Indiana hexaploid *Triticale* {03116}.
Glu-R1-1b {03116}.	2^r {03116}.	**v:**	Graâl hexaploid *Triticale* {03116}.
Glu-R1-1c {03116}	6^r {03116}.	**v:**	Alamo hexaploid *Triticale* {03116}.
Glu-R1-1d {03115}.	0.8^r {03115}.	**v:**	Carmara hexaploid *Triticale* {03115}.
Glu-R1-1e {03115}.	5.8^r {03115}.	**v:**	Arrayan hexaploid *Triticale* {03115}.

Add:

Glu-R1-2.	1R, 1RL.		
Glu-R1-2a {03116}.	4^r {03116}.	**v:**	Indiana hexaploid *Triticale* {03116}.
Glu-R1-2b {03116}.	6.5^r {03116}.	**v:**	Graâl hexaploid *Triticale* {03116}.
Glu-R1-2c {03116}.	13^r {03116}.	**v:**	Alamo hexaploid *Triticale* {03116}.
Glu-R1-2d {03116}.	9^r {03116}.	**v:**	Olympus hexaploid *Triticale* {03116}.

Followed by:
'There is a difficulty in the assignment of subunit 6^r in the *Glu-R1-1* and *Glu-R1-2* lists, since it appears as an x-type subunit in allele *Glu-R1c* and as a y-type subunit in allele *Glu-R1f*. It is currently provisionally assigned to the *Glu-R1-1* list since, based upon its relative electrophoretic mobility, it is considered more likely to be an x-type subunit. Some of the remaining designations should also be considered as provisional since they too are not free of ambiguity.

From study of chromosome substitutions in bread wheat {03117}, it was found that a chromosome 1R carrying HMW-secalin subunit 6.5^r (*Glu-R1e*), originally derived from the 'Petkus' rye population, was associated with bread-making quality (i) intermediate between chromosome 1A carrying the null allele *Glu-A1c* and chromosome 1A carrying HMW-glutenin subunit 2* encoded by *Glu-A1b*; (ii) equivalent to a chromosome carrying HMW-glutenin subunit 7 encoded by *Glu-B1a*; and (iii) inferior to chromosomes 1D with distinct alleles.

A nomenclature system for prolamin banding patterns of triticale has been proposed in {03139}. Extensive allelic variation in triticale at the *Glu-A1*, *Glu-B1*, *Glu-R1*, and *Gli-R2* loci has been reported in {03121}.'

At the end of the preamble to the *Glu-3* section, which reads: '…it has now been demonstrated that, although the majority of the subunits are indeed controlled by genes on this group, some of the C subunits must be controlled by loci elsewhere in the genome {482}.', add the following paragraphs:

‘A novel type of polymeric protein (M_r approx. 71000) has been reported in the Australian advanced breeding line DD-118 {03125}. It participates in the polymeric structure of glutenin (possibly as a chain terminator), and, with an M_r of approximately 71,000, could be considered as a D-subunit of LMW glutenin. However, N-terminal sequencing suggests it to be a *Gli-B1*-type ω-gliadin that has acquired a cysteine residue through mutation.

In an electrophoretic survey of 51 primary tritordeums {03113}, 20 distinct whole-banding patterns (a–t), each consisting of between one and three bands, were observed for D-zone prolamins exhibiting glutenin-like solubility characteristics.

In 85 Japanese bread wheat cultivars and 61 elite, F_6-breeding lines, three alleles were observed at each of *Glu-A3* and *Glu-B3*, and two alleles at *Glu-D3*, named according to their parental origin in three doubled-haploid mapping populations {03135}.

C-type LMW-glutenin subunits in Chinese Spring have been assigned to chromosome groups 1 and 6, and shown to have sequences very similar to those of α-and γ-gliadins {03134}. The authors suggest that they may be encoded by novel genes at loci tightly linked or present within the *Gli-1* and *Gli-2* loci, unlike other LMW-glutenin subunits encoded by the *Glu-3* loci.

The HMW- and LMW-glutenin subunits carried by chromosome $1A^m$ of *T. monococcum* accession G1777 have been characterised electrophoretically and evaluated for quality characteristics using recombinant chromosome substitution lines with chromosome 1A of Chinese Spring {03142}. The HMW- subunits from G1777 are promising for bread-making quality, while its LMW-subunits are promising for biscuit-making quality.

The bread wheat cv. Salmone has been shown to carry two DNA fragments designated as SF720 and SF750 located on the chromosome 1B satellite and associated with the presence of two LMW-glutenin subunits {03143}. However, the authors suggest that they occur at a locus other than *Glu-B3* due to their relatively high frequency of recombination with *Gli-B3*.

A naming system in which roman numerals are assigned to whole banding patterns for the LMW-glutenin subunits is given in {03131} as an alternative to the LMW-1/-2 system described in {03136}. A further system naming whole banding patterns from LMW-1 to LMW-23 in emmer wheat is described in {03137}.’

***Glu-A3* (original bread wheat listing)**

Add:

Glu-A3g {00113}.			
Glu-A3h [{03116}].	[*Glu-A3d´* {03116}].	**v:**	Magistral hexaploid *Triticale* {03116}.

Add after this *Glu-A3* list:

‘In 112 bread wheat cultivars from Argentina, 11 microsatellite alleles plus a null allele were found at the *Glu-A3* locus {03123}.’

***Glu-B3* (original bread wheat listing)**

Add:

Glu-B3m [{03120}].	[*Glu-B3b´* {03120}].	**v:**	Soissons {03120}.
Glu-B3n [{03120}].	[*Glu-B3c´* {03120}].	**v:**	Courtot {03120}.
Glu-B3o [{03116}].	[*Glu-B3i´* {03116}].	**v:**	Olympus hexaploid *Triticale* {03116}.
Glu-B3p [{03116}].	[*Glu-B3k* {03116}].	**v:**	Alamo hexaploid *Triticale* {03116}.
Glu-B3q [{03115}].	[*Glu-B3h´* {03115}].	**v:**	Torote hexaploid *Triticale* {03115}.

Add after this *Glu-B3* list:

‘Currently there are two nomenclature systems described in the Catalogue for the B-LMW-glutenin subunits encoded by *Glu-A3* and *Glu-B3*, one for bread wheat and triticale (above) and one for durum wheat {00114, 02110} (see separate lists below). In {03116}, it has been suggested that *Glu-B3d* in bread wheat is equivalent to *Glu-B3a* in durum wheat, and that (referring to article {03127}) B-LMW subunits observed in some Portuguese triticales can be of the durum type. There would appear, therefore, to be room for unifying the distinct nomenclature systems currently in use.'

Glu-D3.
Add at the bottom of the section:
'The isolation of a new LMW-glutenin subunit gene, located on chromosome 1D, was reported in {0350}.'.

3.2. Gliadins

At the end of the preamble, which, after an amendment made in the 2001 Supplement, reads: 'The authors placed some of the results in the context of the possible ancestor of the B genome and relationships with the barley C-hordeins and rye w-secalins.', add the following paragraph:
'11 new gliadin alleles have been found in a collection of 52 Spanish landraces of bread wheat {03141}; these will be incorporated into the *Gli-1* and *Gli-2* allelic lists in the next Supplement.'

After the *Gli-A1* list, add:
'An allele *Gli-A1f** is mentioned in {03130}.'

After the *Gli-B1* list, add:
'In 112 bread wheat cultivars from Argentina, 12 microsatellite alleles plus a null allele were found at the *Gli-B1* locus tightly linked to *Glu-B3* {03123}.'

After the entry for *Gli-R1*, add the comment:
'*Sec-12* and *Sec-13* are given as allelic alternatives in T1BL·1RS translocation lines by {03132}.'

Gli-R2
Add:

Gli-R2a {03116}.	d1 {03116}.	**v:**	Carnac hexaploid *Triticale* {03116}.
Gli-R2b {03116}.	d2 {03116}.	**v:**	Mostral hexaploid *Triticale* {03116}.
Gli-R2c {03116}.	t1 {03116}.	**v:**	Alamo hexaploid *Triticale* {03116}.
Gli-R2d {03116}.	null {03116}.	**v:**	Triticor hexaploid *Triticale* {03116}.
Gli-R2e {03115}.	t2 {03115}.	**v:**	Tornado hexaploid *Triticale* {03115}.

5. Other proteins

5.6 Waxy proteins

Wx-A1b. **tv:** MG 826 {03101}.
Add at the end of *Wx-A1* section: 'A variant allele was present in one Iranian and one Italian accession {03101}.'.

Wx- B1. **tv:** A variant allele was present in three accessions {03101}.
Wx-D1d. **v:** One Iranian and one Italian accession {03101}.

At the end of section insert: 'Various hard and soft wheats with the alleles *Wx-A1b*, *Wx-B1b* and *Wx-D1b* are listed in {0304}.

5.8. Puroindolines and Grain Softness Protein

This section was revised by Craig F. Morris, and is included in its entirety below.

Puroindoline a and b are the major components of friabilin, a protein complex that is associated with grain texture (see 'Grain Hardness'). The name 'puroindoline' and the complete amino-acid sequence of puroindoline a were given in {0382} from cv. Camp Rémy. Hard grain texture in hexaploid wheat results from unique changes in the puroindoline amino acid sequence or, currently, four null forms {0295} of the completely linked genes (max. map distance 4.3 cM) {452}. Tetraploid (AABB and AAGG) wheats lack puroindolines and are consequently very hard {03103}. A searchable database of wheat varieties and their puroindoline genotype is available at http://www.wsu.edu/~wwql/php/puroindoline.php. Grain softness protein-1 is a closely related gene that is closely located to the puroindoline genes {03111, 1185}. 'GenBank' and 'dbEST' refer to sequence databases available at NCBI (also available through EMBL and DDBJ).

Pina-A1 {03103, 03108, 03104}. **dv:** *T. urartu* unspecified accession {03103}; TA763 (GenBank AJ302094) {03108,03104}; TA808 (GenBank AJ302095) {03108,03104}.

Pina-D1. 5DS {452}. **v:** CS {452}; Capitole (GenBank X69914) {03110}**.**

Pina-D1a {452}. **v:** Aurelio *Pinb-D1a* {0249}; Bellevue {0249}; Bezostaja *Pinb-D1b* {0249}; Bilancia *Pinb-D1a* {0249}; Bolero *Pinb-D1a* {0249}; Brasilia *Pinb-D1b* {0249}; Centauro *Pinb-D1a* {0249}; Cerere *Pinb-D1b* {0249}; Chinese Spring *Pinb-D1a* {452,0249}; Colfiorito *Pinb-D1b* {0249}; Cologna 21 *Pinb-D1b* {0249}; Courtot {0249}; David *Pinb-D1b* {0249}; Democrat *Pinb-D1b* {0249}; Etruria *Pinb-D1b* {0249}; Fortuna {0249}; Francia *Pinb-D1b* {0249}; Galaxie {0249}; Gemini *Pinb-D1b* {0249}; Genio *Pinb-D1b* {0249}; Gladio *Pinb-D1b* {0249}; Heron {1035}; Lampo *Pinb-D1a* {0249}; Leone *Pinb-D1a* {0249}; Leopardo *Pinb-D1a* {0249}; Libero *Pinb-D1a* {0249}; Livio *Pinb-D1a* {0249}; Marberg *Pinb-D1b* {0249}; Mentana *Pinb-D1a* {0249}; Mieti *Pinb-D1b* {0249}; Mosè *Pinb-D1a* {0249}; Neviana *Pinb-D1a* {0249}; Newana *Pinb-D1b* {0249}; Oscar *Pinb-D1a* {0249}; Pandas *Pinb-D1b* {0249}; Pascal *Pinb-D1b* {0249}; Penawawa *Pinb-D1a* {03104}; Sagittario *Pinb-D1b* {0249}; Salgemma *Pinb-D1b* {0249}; Saliente *Pinb-D1b* {0249}; Salmone *Pinb-D1b* {0249}; Serena *Pinb-D1a* {0249}; Serio *Pinb-D1b* {0249}; Soissons {0249}; Veda *Pinb-D1b* {0249}; Zena *Pinb-D1b* {0249}.

Pina-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats that carry a hardness mutation in puroindoline b {452, 1035, 0082, 0204, 0295}.

dv: *Ae. tauschii* unspecified accession (GenBank AJ249935) {03103}; TA1583 (GenBank AY252029) *Pinb-D1a, Gsp-D1b* {03105}; TA2475 (GenBank AY252037) *Pinb-D1i, Gsp-D1b* {03105}; TA1599 (GenBank AY252011) *Pinb-D1j, Gsp-D1g* {03105}; TA1691 (GenBank AY252013) *Pinb-D1j, Gsp-D1h* {03105}.

Pina-D1b {1035}. Null allele **v:** Amidon *Pinb-D1a* {0249}; Barra *Pinb-D1a* {0249}; Butte 86 {1035}; Ciano *Pinb-D1a* {0249}; Dorico *Pinb-D1a* {0249}; Eridano {0249}; Falcon {1035}; Fortuna (USA) *Pinb-D1a* {0249}; Glenman *Pinb-D1a* {0249}; Golia *Pinb-D1a* {0249}; Guadalupe *Pinb-D1a* {0249}; Inia 66 *Pinb-D1a* {0249}; Jecora *Pinb-D1a* {0249}; Indice *Pinb-D1a* {0249}; Kalyansona {0249}; Manital *Pinb-D1a* {0249}; Mendos *Pinb-D1a* {0249}; Padus *Pinb-D1a* {0249}; Prinqual *Pinb-D1a* {0249}; Sibilia *Pinb-D1a* {0249}; Super X {0249}; Yecora Rojo {0204}.

i: Falcon/7*Heron, Heron/7*Falcon {03109}; Heron/7*Falcon sel.{0298,0203}; Gamenya sib {0298,0203}.

Present only in some hard hexaploid wheats. *Pina-D1b* is associated with harder texture than *Pinb-D1b* {0177, 0206}.

Pina-D1c {03105}. **dv:** *Ae. tauschii* TA2369 (GenBank AY252031) *Pinb-D1h, Gsp-D1c*; TA2527 (GenBank AY252015) *Pinb-D1h, Gsp-D1e*; TA2536 (GenBank AY251998) *Pinb-D1i,Gsp-D1d* {03105}.

Pina-D1d {03105}. **dv:** *Ae. tauschii* PI452131 (GenBank AJ302098) *Pinb-D1i* {03104}; PI554318 (GenBank AJ302099) *Pinb-D1k* {03104}; TA1649 (GenBank AY251963) *Pinb-D1h, Gsp-D1f* {03105}; TA2374 (GenBank AY251948) *Pinb-D1i, Gsp-D1d* {03105}; TA2512 (GenBank AY252042) *Pinb-D1i, Gsp-D1e* {03105}; TA2455 (GenBank AY252022) *Pinb-D1i, Gsp-D1f* {03105}.

Pina-D1e {03105}. **dv:** *Ae. tauschii* TA2458 (GenBank AY252034) *Pinb-D1i, Gsp-D1d* {03105}; TA2495 (GenBank AY252041) *Pinb-D1i, Gsp-D1e* {03105}.

Pina-D1f {03105}. **dv:** *Ae. tauschii* TA2436 (GenBank AY1998) *Pinb-D1i, Gsp-D1d* {03105}.

Pina-A^{m}1 {0083}. 5A^{m}S {0083}. **dv:** *T. monococcum* DV92 (cultivated), G3116 (spp. *aegilopoides)* (GenBank AJ242715) {0083}; unspecified accession (GenBank AJ249933) {03103}; PI277138 (GenBank AJ302093) {03104}; PI418582 (GenBank AJ302092) {03104}; *T. monococcum* spp. *monococcum* TA2025, TA2026, TA2037 {03108}; *T. monococcum* spp. *aegilopoides* TA183, TA291, TA546, TA581 {03108}.

In *T. monococcum Pina-A^{m}1* is completely linked to *Gsp-A^{m}1* {0083}.

Pina-S1 {03108}. **dv:** *Ae. speltoides* PI393494 (GenBank AJ302096) {03104}; PI369616 (GenBank AJ302097) {03104}; *Ae. speltoides* spp. *speltoides* TA2368, TA1789 {03108}; *Ae. speltoides* spp. *ligustica* TA1777 {03108}.

Pina-S^{b}1 {03108}. **dv:** *Ae. bicornis* spp. *typica* TA1954, TA1942 {03108}.

Pina-S^{l}1 {03108}. **dv:** *Ae. longissima* spp. *longissima* TA1912 {03108}; *Ae. longissima* spp. *nova* TA1921 {03108}.

Pina-S^{s}1 {03108}. **dv:** *Ae. searsii* TA1837, TA1355 {03108}.

Pina-S^{sh}1 {03108}. **dv:** *Ae. sharonensis* TA1999 {03108}.

Pinb-A1 {03108,03104}. **dv:** *T. urartu* TA763 (GenBank AJ302103) {03108, 03104}; TA808 (GenBank AJ302104){03108, 03104}

Pinb-D1. 5DS {452}. **v:** CS {452}; Capitole (GenBank X69912) {03110}**.**

Pinb-D1a {452}. **v:** Adder *Pina-D1a* {0317}; Amidon *Pina-D1b* {0249}; Aurelio *Pina-D1a* {0249}; Barra *Pina-D1b* {0249}; Bilancia *Pina-D1a* {0249}; Bolero *Pina-D1a* {0249}; Centauro *Pina-D1a* {0249}; Chinese Spring *Pina-D1a* {452,0249}; Ciano *Pina-D1b* {0249}; Dorico *Pina-D1b* {0249}; Fortuna (USA) *Pina-D1b* {0249}; Glenman *Pina-D1b* {0249}; Golia *Pina-D1b* {0249}; Guadalupe *Pina-D1b* {0249}; Hill 81 {452}; Inia 66 *Pina-D1b* {0249}; Jecora *Pina-D1b* {0249}; Idice *Pina-D1b* {0249}; Karl *Pina-D1a* {0317}; Lampo *Pina-D1a* {0249}; Leone *Pina-D1a* {0249}; Leopardo *Pina-D1a* {0249}; Libero *Pina-D1a* {0249}; Livio *Pina-D1a* {0249}; Manital *Pina-D1b* {0249}; Mendos *Pina-D1b* {0249}; Mentana *Pina-D1a* {0249}; Mosè *Pina-D1a* {0249}; Neviano *Pina-D1a* {0249}; Oscar *Pina-D1a* {0249}; Padus *Pina-D1b* {0249}; Penawawa *Pina-D1a* {03104}; Prinqual *Pina-D1b* {0249}; Serena *Pina-D1a* {0249}; Sibilia *Pina-D1b* {0249} Sigyn II *Pina-D1a* {0317}.

Pinb-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying the *Pina-D1b*, *-D1c*, *-D1d*, *-D1e*, *-D1f*, and *-D1g* mutations {452, 1035, 0082, 0204, 0295}.

dv: *Ae. tauschii* unspecified accession (GenBank AJ249936) {03103}; TA1583 (GenBank AY1981) *Pina-D1a*, *Gsp-D1b* {03105}.

Pinb-D1b {452}. 5DS {452}. **i:** Paha*2//Early Blackhull/5*Paha {0203,0298}; Early Blackhull der./5*Nugaines sel. {0203,0298}; hard sib sel. from Weston {03107}.

s: CS*7/Cheyenne 5D {452}.

v: Bastion *Pina-D1a* {0317}; Bezostaya *Pina-D1a* {0249}; Brasilia *Pina-D1a* {0249}; Cerere *Pina-D1a* {0249}; Colfiorito *Pina-D1a* {0249}; Cologna 21 *Pina-D1a* {0249}; David *Pina-D1a* {0249}; Democrat *Pina-D1a* {0249}; Etruria *Pina-D1a* {0249}; Francia *Pina-D1a* {0249}; Gemini *Pina-D1a* {0249}; Genio *Pina-D1a* {0249}; Gladio *Pina-D1a* {0249}; Marberg *Pina-D1a* {0249}; Mieti *Pina-D1a* {0249}; Newana *Pina-D1a* {0249}; Pandas *Pina-D1a* {0249}; Pascal *Pina-D1a* {0249}; Sagittario *Pina-D1a* {0249}; Salgemma *Pina-D1a* {0249}; Saliente *Pina-D1a* {0249}; Salmone *Pina-D1a* {0249}; Serio *Pina-D1a* {0249}; Thatcher {0204}; Veda *Pina-D1a* {0249}; Wanser {452}; Zena *Pina-D1a* {0249}; hard component of Turkey {0204}.

Pinb-D1b is a 'loss-of-function' mutation resulting from the replacement of a glycine by a serine at position 46 {452}.

Pinb-D1c {0082}. **v:** Avle {0082}; Reno {0082}; Tjalve {0082}; Bjorke {0082}; Portal {0082}.

Pinb-D1c is a 'loss-of-function' mutation resulting from the replacement of a leucine by a proline at position 60 {0082}.

Pinb-D1d {0082}. **v:** Bercy {0082}; Mjolner {0082}.

Pinb-D1d is a 'loss-of-function' mutation resulting from the replacement of a tryptophan by a arginine at position 44 {0082}.

Pinb-D1e {0204}. **v:** Gehun {0204}; Canadian Red {0204}; Chiefkan {0204}.

Pinb-D1e is a 'loss-of-function' mutation resulting from the replacement of a tryptophan by a stop codon at position 39 {0204}.

Pinb-D1f {0204}. **v:** The hard component of Utac {0204}.

Pinb-D1f is a 'loss-of-function' mutation resulting from the replacement of a tryptophan by a stop codon at position 44 {0204}.

Pinb-D1g {0204}. **v:** Andrews {0204}.

Pinb-D1g is a 'loss-of-function' mutation resulting from the replacement of a cysteine by a stop codon at position 56 {0204}.

Pinb-D1h {03105}. **dv:** *Ae. tauschii* TA2369 *Pina-D1c, Gsp-D1c* {03105}; TA2527 *Pina-D1c, Gsp-D1e* {03105}; TA1649 *Pina-D1d, Gsp-D1f* {03105}.

Pinb-D1i {03105}. **dv:** *Ae. tauschii* TA2475 (GenBank AY251989) *Pina-D1a, Gsp-D1b* {03105}; TA2536 (GenBank AY251993) *Pina-D1c, Gsp-D1d* {03105}; TA2374 (GenBank AY1948) *Pina-D1d, Gsp-D1d* {03105}; TA2512 (GenBank AY251992) *Pina-D1d, Gsp-D1e* {03105}; TA2455 (GenBank AY251972) *Pina-D1d, Gsp-D1f* {03105}; TA2458 (GenBank AY1986) *Pina-D1e, Gsp-D1d* {03105}; TA2495 (GenBank AY1991) *Pina-D1e, Gsp-D1e*; TA2436 *Pina-D1f, Gsp-D1d* {03105}.

Pinb-D1j {03105}. **dv:** *Ae. tauschii* TA1599 *Pina-D1a, Gsp-D1g* {03105}; TA1691 *Pina-D1a, Gsp-D1h* {03105}.

Pinb-D1k. **dv:** *Ae. tauschii* PI554318 (GenBank AJ302108) *Pina-D1d* {03104}.

Pinb-A^{m}1 {0083}. 5A^{m}S {0083}. **dv:** *T. monococcum* DV92 (cultivated), G3116 (spp. *aegilopoides)* (GenBank AJ242716){0083}; unspecified accession (GenBank AJ249934){03103} is identical to allele *Pina-D1h* {03105}; PI277138 (GenBank AJ302102) {03104}; PI418582 (GenBank AJ302101) {03104}.

In *T. monococcum Pinb-A^{m}1* is 0.1 cM proximal to *Pina-A^{m}1* and both loci are less than 36 kb apart {0083}.

Pinb-S1 {03108}. **dv:** *Ae. speltoides* PI393494 (GenBank AJ302105) {03104}; PI369616 (GenBank AJ302106) {03104}; *Ae. speltoides* spp. *speltoides* TA2368, TA1789 {03108}; *Ae. speltoides* spp. *ligustica* TA1777 {03108}.

Pinb-S^{b}1 {03108}. **dv:** *Ae. bicornis* spp. *typica* TA1954, TA1942 {03105}.

Pinb-S^{l}1 {03108}. **dv:** *Ae. longissima* spp. *longissima* TA1912 {03108}; *Ae. longissima* spp. *nova* TA1921 {03108}.

Pinb-S^{s}1 {03108}. **dv:** *Ae. searsii* TA1837, TA1355 {03105}.

Pinb-S^{sh}1 {03108}. **dv:** *Ae. sharonensis* TA1999 {03105}.

Pinb-D1b, Pinb-D1c, Pinb-D1d, Pinb-D1e, Pinb-D1f, or *Pinb-D1g* were present in hard hexaploid wheats not carrying the *Pina-D1b* (null) mutation {452, 1035, 0082, 0204, 0295}.

Wheats with *Pinb-D1b* were slightly softer and slightly superior to those with *Pina-D1b* in milling and bread-making characteristics although there was considerable overlap {0206}.

Transgenic rice with the *Pina-D1a* and *Pinb-D1a* alleles possessed softer grain {0207}.

Genotypes for a selection of North American wheats are given in {0204}.

Gsp-1 {1185}.

Gsp-A1 {614}. 5A {614, 0383}. **v:** CS {614, 0383}; Rosella (GenBank AF177218) {0383}.

In {1185} partial-sequence clone TSF61 from cv. Soft Falcon (GenBank X80380) is identical to this allele.

Gsp-B1 {614}. 5B {614}. **v:** CS {614}; Glenlea {0385}.

In {1185} sequence of clone TSF33 from cv. Soft Falcon (GenBank X80379) is identical to this allele, as are ESTs for cv. CS (dbEST BJ235798) and cv. CNN (dbEST BE423845).

Gsp-D1 {614}. 5DS {614}. **v:** CS {614}; Glenlea {0385}.

ma: Cosegregation of *Gsp-D1* and *Ha* {614}.

dv: *Ae. tauschii* CPI110799 (GenBank AF177219) {0383}.

In {1185} sequence of clone TSF69 from cv. Soft Falcon (GenBank S72696) is identical, as are ESTs for cv. CS (dbEST BJ237450) and cv. CNN (dbEST BE422565).

Gsp-D1b {03105}. **dv:** *Ae. tauschii* TA1583 (GenBank AY252079) *Pina-D1a, Pinb-D1a* {03105}; TA2475 (GenBank AY252087) *Pina-D1a, Pina-D1i* {03105}.

Gsp-D1c {03105}. **dv:** *Ae. tauschii* TA2369 (GenBank AY252081) *Pina-D1c, Pinb-D1h* {03105}; CPI110799 (GenBank AF177219) {0383}.

Gsp-D1d. **dv:** *Ae. tauschii* TA2536 (GenBank AY252093) *Pina-D1c, Pinb-D1i* {03105}; TA2374 (GenBank AY252046) *Pina-D1d, Pinb-D1i* {03105}; TA2458 (GenBank AY252084) *Pina-D1e, Pinb-D1i* {03105}; TA2436 (GenBank AY252048) *Pina-D1f, Pinb-D1i* {03105}.

Gsp-D1e. **dv:** *Ae. tauschii* TA2527 (GenBank AY252066) *Pina-D1c, Pinb-D1h* {03105}; TA2512 (GenBank AY252092) *Pina-D1d, Pinb-D1i* {03105}; TA2495 (GenBank AY252091) *Pina-D1e, Pinb-D1i* {03105}.

Gsp-D1f. **dv:** *Ae. tauschii* TA1649 (GenBank AY252063) *Pina-D1d, Pinb-D1h* {03105}; TA2455 (GenBank AY252073) *Pina-D1d, Pinb-D1i* {03105}.

Gsp-D1g. **dv:** *Ae. tauschii* TA1599 (GenBank AY252062) *Pina-D1a, Pinb-D1j* {03105}.

Gsp-D1h. **dv:** *Ae. tauschii* TA1691 (GenBank AY252064) *Pina-D1a, Pinb-D1j* {03105}.

Response to Vernalization

Vrn-B1.

At the end of the introductory paragraph add: 'On the other hand Japanese workers {0305} claim that *Vrn-B1* corresponds only to the former *Vrn2* and not to *Vrn4*.'.

At the end of the second paragraph add: '*Vrn-A*^{m}*1* was mapped to the *Xcdo504-5A* – *Xpsr426-5A* region {0312}. In the opinion of the curators this location may not be correct.

At the bottom of the section add: 'The development of a dCAPS marker from RFLP marker WG644 as a molecular tag for *Vrn-B1* was reported in {0305}.'.

ma: *Xwg644-5B* – 1.7 cM – *Vrn-B1* {0305}; *Vrn-B1* – 2.5 cM – *Xgwm408-5B* {0337}.

Vrn2.

At the end of the first paragraph add: '*Vrn-A*^{m}*2* was mapped to the distally located *Xwg114-5A* – *Xwec87-5A* region {0312}.'.

Restorers for Cytoplasmic Male Sterility

3. Restorers for photoperiod-sensitive *Aegilops crassa* cytoplasm

Rfd1.

At end of section add: 'Several Japanese wheats carry a similar or equally effective gene combination {0335}.'.

Pathogenic Disease/Pest Reaction

Reaction to *Blumeria tritici* (formerly *Erysiphe graminis*)

Pm1.

Pm1a. **ma:** Complete cosegregation of several markers including *Xcdo347-7A, Xpsr121-7A, Xpsr680-7A, Xpsr687-7A, Xbzh232(Tha)-7A, Xrgc607-7A,* and *Xsts638-7A* with *Pm1* and *Lr20* was reported in {0323}.

Pm1e {0322}. **v:** See earlier listings under *Pm22.*

Pm3. **ma:** *Xgdm33-1A* – 2.3cM – *Pm3/Xpsp2999-1A* {0313}.
Genotype list: {0313}.

Pm3d. **v:** Axona {0313}; Cornette {0313}; Indian 4 {0313}; Kadett {0313}; Kleiber {0313}.

Pm3g. 1AS (0363) **v:** Champêtre {0313}; Lutin {0313}; Oradian {0313}: Rubens {0313}; Soissons {0313}; Valois {0313}.
ma: Add: '*Pm3g* is completely linked to microsatellite *Xpsp2999* in {0363}.'.

Pm4.

Pm4b. **ma:** *Xgwm382-2A* – ±10 cM – *Pm4b* – ±2 cM – *XgbxG303* [{0354}].

Pm22 {1134}. 1D {1134}. Transfer **v:** listings to *Pm1e* and delete comment at the end of *Pm22* section.

Pm29. **ma:** *Pm29* co-segregates with several markers {0129}.

Pm31 {0301}. **v:** G-305-M/781//3*Jing 411 {0301}. **tv:** *T. dicoccoides* G-305-M {0301}.

mljy {0339}. 7B {0339}. **v:** Jieyan 94-1-1 *Pm8* {0339}.
Recessive, hemizygous-effective {0339}.

mlsy {0339}. 7B {0339}. **v:** Siyan 94-2-1 {0339}.
Recessive, hemizygous-effective {0339}.

QTL: QTL on chromosomes 1A, 2A, 2B, 3A, 5D, 6A, and 7B were detected in a RE714/Festin population in multiple locations and over multiple years. The QTL on chromosome 5D was detected in all environments and all years and is associated with markers *Xgwm639-5D* and *Xgwm174-5D*. Resistance was contributed by RE714. A QTL coinciding with *MlRE* on 6A also was detected in all environments. The QTL on chromosomes 5D and 6A accounted for 45 % to 61 % of the phenotypic variation {0354}.

Reaction to *Diuraphis noxia*

Dn2. **ma:** Add '*XksuA1-7D* – 9.9 cM – *Dn2* – 2.8 cM – *Xgwm437-7D* {0353}.'.

Dn4. **ma:** Add '*Xgwm106-1D* – 7.4 cM – *Dn4* – 12.9 cM – *Xgwm337-1D* {0352}.'.

Dn6. **ma:** Add '*Dn6* – 3.0 cM – *Xgwm111* {0352}.'.

Reaction to *Fusarium graminearum*

QFhs.ndsu-3AS {0372}. 3AS {0372}. **tv:** *T. turgidum* var. *dicoccoides*. Recombinant substitution lines LDN and LDN(Dic-3A). The resistant allele was contributed by dicoccoides {0372}.
ma: Associated with *Xgwm2-3A* (explained 37 % of the phenotypic variation) {0372}.

QTL: QTLs were located in 3BS, 2BL and 2AS in Ning 7840/Clark. The most effective QTL was probably in an interval, flanked by deletions 3BS-3 and -8 and was close to *Xgwm533-3B* and *Xbarc147-3B* {0328}.

Reaction to *Heterodera avenae*

CreR {0318}. 6RL. **ad:** Wheat + 6R {0318}; Wheat + 6RL {0318}; Various deletion stocks {0318}.
al: Triticale T-701
ma: Deletion mapping indicated *CreR* was located near *Got-R2* {0318}.

Reaction to *Magnaporthe grisea*

M. grisea is a pathogen of blast on many graminaceous species, the best known of which is rice. In Brazil it has become a pathogen of wheat. The wheat pathotype(s) is different from those attacking other species such as rice, oats, millets, and weeping lovegrass.

Rmg1 {0333}. *Rwt4* {0302}. **v:** Norin 4 {0302}.

A second gene designated *Rwt3* {0302} was present in Chinese Spring and Norin 4. Genes *Rwt3* and *Rwt4* were detected using hybrids of *Triticum*-virulent and *Avena*-virulent pathogen isolates.

Reaction to *Mayetiola destructor*

H21. **ma:** A STS primer set SJ07 was developed to identify 2RL, and hence *H21* {0233}.

H30 {0256}. Derived from *Ae. triuncialis* {0256}.
v: TR-3531 {0256}. **al:** *Ae. triuncialis* {0256}.

H31 {0332}. 5BS {0332}. **v:** P961696 {0332}. **tv:** CI3984 {0332}.
ma: STS marker *Xupw148-5B* – 3 cM – *H31* {0332}.

Reaction to *Mycosphaerella graminicola*

Stb6. **v:** Add: 'Bezostaya {0187}; Hereward {0187}; Shafir {0187}; Vivant {0187}.'
ma: *Stb6* – 2cM – *Xwgm369-3A* {0187}.

Stb7 {0311}. 4AL {0311}. **v:** ST6 = Estanzuela Federal {0310,0311}.
ma: *Xwmc219-4A* – 0.8cM – *Xwmc-4A* – 0.3cM – *Stb7* {0311}.

Stb8 {0326}. 7BL {0326}. **v:** Synthetic hexaploid W7984 (parent of ITMI population) {0326}.
ma: *Xgwm146* – 3.5cM – *Stb8* – 5.3cM – *Xgwm577* {0326}.

Reaction to *Pratylenchus spp.*

1. Reaction to *Pratylenchus neglectus*

Rlnn1 **ma:** Mapped between markers *Xpsr121-7A* and *Xgwm344-7A* and 9 cM proximal to *Lr20* {0374}.

Reaction to *Puccinia graminis* Pers.

Sr2. **ma:** *Xgwm389-3B* – 2.7 cM – *Sr2* – 1.1 cM – *Xglk683* {0358}.
Sr15. **ma:** Associated with clustered markers {0323}.
Sr24. 3DL. **v:** At the end of section add: 'List of Australian genotypes {0340}.'.
Sr31. **ma:** Several markers tightly linked with *Sr31* were identified in {0377}.
Sr33. **ma:** *Xmwg60-1D* – 5.8 cM – *Sr33* – 2.2 cM – *Xwmg2083-1D* {0360}.
SrR. **ma:** Several markers tightly linked with *SrR* were identified in {0377}.

Reaction to *Puccinia striiformis* Westend.

Yr5. **v:** By 33 {03102}.
ma: *Yr5* – 10.5 & 13.3 cM – *Xgwm501-2B* {03102}.
Yr9. **ma:** Several markers tightly linked with *Yr9* were identified in {0377}.
Yr10. **ma:** *Yr10* – 1.2 cM – *Xpsp3000-1B* – 4.0 cM – *Gli-B1* {0321}.Cosegregation between a RGA marker *RgaYr10a* and *Yr10* was reported in {0376}.
Yr15. **v:** Add: 'Boson {0330}; Agrestis {0330}.'
Yr25. **v:** Add: 'Tugela {0314}; Tugela-DN {0314}.'
Yr29 {0119}. Add: 'See *Lr46*.'.
Yr31 {0325}. 2BS {0325}. **v:** Pastor {0325}.
ma: recombination values: *Yr31* – *Yr27* 0.148; *Yr31* – *Lr23* 0.295; Yr27 – *Lr23* 0.131 {0325}.
YrMor. **ma:** The development of an STS marker, derived from an AFLP fragment, that co-segregates with *YrMor* was reported in {0357}.

Add at the end of this section:

QTL: Two QTL in 'Camp Remy/Michigan Amber' were located on chromosomes 2BL (*QYR1*, LOD score 12) and 2AL (*QYR2*, 2.2) {0304}. Four QTL were scored in the ITMI population. The most effective (*QYR3*, 7.4) on chromosome 2BS was probably *Yr27*, the others were located on 7DS (*QYR4*, 3.4), 5A (*QYR5*, 2.8), 3D (*QYR6*, 2.8), and 6DL (*QYR7*, 2.4) {0304}.

Reaction to *Puccinia triticina* (formerly *P. recondita tritici*)

Lr10. **v:** At the end of section add: 'See also {0337}.'.
Lr17a. **v:** Jagger {0338}.
At the end of *Lr17* section add: ' {0337} (European cultivars).
***Lr20*.** **ma:** Complete cosegregation of several markers including *Xcdo347-7A*, *Xpsr121-7A*, *Xpsr680-7A*, *Xpsr687-7A*, *Xbzh232(Tha)-7A*, *Xrgc607-7A*, and *Xsts638-7A* with *Pm1* and *Lr20* was reported in {0323}.
Lr21. **ma:** Add at the end of the sentence starting 'All members of the *Lr21* family …':'*XksuD14-1D* was reported to map 1.8 cM proximal to *Lr21* in {0375}.'*Lr21* – 0 cM – *rgaYr10b* – 0.6 cM – *Xgdm33-1D* {0360}.

Lr24. 3DL **v:** At the end of section add: 'List of Australian genotypes {0340}.'.
Lr26. **ma:** Several markers tightly linked with *Lr26* were identified in {0377}.
Lr46. **ma:** An AFLP marker associated with *Lr46* with a recombination value of about 10% was identified in {0119}.
Lr48. 4BL {0329}. **v:** Dove *Lr34* {0329}.
Lr49. 2AS (0329}. **v:** Tonichi *Lr34* { 0329}.
Lr51 {0308}. 1BL {0308}. **i:** Express*7/T1 {0308}; Kern*7/T1 {0308}; UC1037*7/T2 {0308}.
v: Neepawa*6/ *Ae. speltoides* F-7, selections 3 and 12 {0306}. Interstitial translocations T1AS·1AL-1S#F7-12L-1AL {0308} = T1; T1BS·1BL-1S#F7L-1BL {0306}.
al: *Ae. speltoides* F-7 selections 3 and 12 {0306}.
ma: linked with RFLP markers *Xmwg710 – XAga7* {0308}.
Genotype lists: Add {0334} to (U.S.A. cultivars).

Reaction to *Pyrenophora tritici repentis*

2. Resistance to chlorosis induction

Tsc1. Add: '*Tsc1*, or a closely associated gene, confers insensitivity to Ptr ToxC {see 0315}'. Inoculation with purified toxin Ptr ToxC was used to map this locus 5.7 cM proximal to *XGli-1A* {0315}.
ma: *Gli1* – 5.7cM – *Tsc1* ('Ptr ToxC') {0315}.

Reaction *to Schizaphis graminum*

Gb3. 7DL {0319}. **v:** TAM110 {0319}; TXGBE373 {0319}.
ma: Completely associated with 2 AFLP markers {0319}. These also were present in germ plasm line KS89WGRC4, implying the likelihood of *Gb3* or a closely linked resistance gene {0319}.

Reaction to *Sitodiplosis mosellana*

Pest: Add at the end of the pest common names: 'This pest should not be confused with *Contarinia tritici*, the yellow blossom wheat midge.'.

Reaction to *Tapesia yallundae* (formerly *Pseudocosporella herpotrichoides)*

Pch2. Add after the present entry: 'According to {0380}, this gene is not effective at the adult plant stage. Instead, the adult resistance of Cappelle-Desprez was controlled by a gene on chromosome 5A with the possibility of two less effective genes on 1A and 2B.

Genetic Linkages

Chromosome 1BS

Gli-B1 – *Xgwm11/Xgwm18-1B* 20.7 cM {0321}.

Chromosome 1BL

Cent – *Lr51* 0.41 {0307}, 50 – 86 cM {0308}.

Chromosome 7BS

Hl2 – cent 0.143 ± 0,035 {0316}.

Chromosome 7DL

Cent . . . *Xgwm111-7D* – *Gb3* 22.5 cM {0319}.
Gb3 – *Xgwm428-7D* 33.1 cM {0319}.
Pm29 – *Pm19* Independent {0129}.

Additions to Summary Table 1

Add:

CK2a	Casein Kinase 2*a* subunit.
Cyp71C	Cytochrome P450 mono-oxygenase CYP71C subfamily.
Msh7	DNA mismatch repair gene.
Sut-1	Sucrose transporter-1.

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Amendments.

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1185. Replace 'puroindol-like' with 'puroindoline-like' in the reference title.
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VI. 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 mosaci 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 = *Rhonpalosiphum padi* = bird cherry-oat aphid
S. tritici = *Septorai 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. dicoccom*
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. *dicoccom = *Triticum dicoccum*
T. urartu = *Triticum urartu*
Th. bessarabicum = *Thinopyrum bassarabicum*

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
m^3 = 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 = quantative 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-HPLE = 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 tagges 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

VII. ADDRESSES OF CONTRIBUTORS.

The E-mail addresses of contributors denoted with a '*' are included in section VIII.

DAKOTA GROWERS PASTA COMPANY One Pasta Avenue, P.O. Box 21, Carrington ND 58421, U.S.A. James Quick* and Brad Miller.

STOLLER ARGENTINA S.A. Av. Malagueño s/n-Complejo Industrial U. CO. MA. Ferreyra, C.P. X5020CST, Córdoba, Argentina. W. Londero, L.E. Torres*, and Ricardo H. Maich*.

ARGENTINA

UNIVERSIDAD NACTIONAL DE CÓRDOBA College of Agriculture, Avenida Valparaíso s.n. Ciudad Universitaria, P.O. Box 509, Casilla de Correo 509, 5000 Córdoba, Argentina. (051) 334116/7 (TEL), (051) 334118 (FAX). S. Patricia Gil*, L.I. Mas, A. Semino, R.H. Maich*, M.M. Cerana*, Gabriel Manera*, María E. Dubois*, and Z. Gaido.

INSTITUTO DE BIOTECHNOLÓGICA – INTA Castelar, CC25, Pcia. de Buenos Aires, Argentina. 54-1-621-5663/0125/1684 (Tel), 54-11-4621-6903 (FAX). F. del Viso, Andrea F. Puebla*, R.A. Heinz, and H.E. Hopp.

AUSTRALIA

NEW SOUTH WALES

THE UNIVERSITY OF ADELAIDE Waite Campus, Department of Plant Science, Glen Osmond, 5064, SA, Australia. Daryl J. Mares*, Anna Campbell, and Kolumbina Mrva.

BRAZIL

NATIONAL RESEARCH CENTER FOR WHEAT – EMBRAPA Centro Nacional de Pesquisa de Trigo, Rodovia BR 285, km 174, Caixa Postal 569, 99001-970, Passo Fundo, Rio Grande do Sul, Brazil. (54) 312-3444 (TEL), (54) 311 3617 (FAX). Cantído N.A. de Sousa*, Leo de J.A. Del Duca*, Pedro L. Scheeren, Márcio Só e Silva, Alfredo do Nascimento Jr., Aroldo G. Linhares, Gilberto Cunha, Diego Pegoraro, Eliana M. Guarienti, Leila M. Costamilan, Maria Imaculada P.M. Lima, Martha Miranda, Márcio Sóe Silva, Osmar Rodrigues, and Renato S. Fontaneli.

CROATIA

Bc INSTITUTE FOR BREEDING AND PRODUCTION OF FIELD CROPS d.d. Zageb, Marulicev trg 5/I, 10 000 Zagreb, Croatia. 385-1-65-45-576 (TEL); 385-1-65-45-579 (FAX). http://www.bc.institut.hr. Slobodan Tomasovic*, Rade Mlinar, Ivica Ikic, Kristijan Pusaric, and Branko Palavercic.

ESTONIA

ESTONIAN AGRICULTURAL UNIVERSITY Institute of Experimental Biology, Department of Plant Genetics, 76902, Harku, Estonia. Oskar Priilinn*, T. Enno, and H. Peusha.

GERMANY

INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG (IPK) Corrensstraße 3, 06466 Gatersleben, Germany. (049) 39482 5229 (TEL); (049) 39482 280/5139 (FAX). Andreas Börner*, A. Bálint, K.F.M. Salem, E. Pestsova, M.S. Röder, and E.K. Khlestkina.

HUNGARY

AGRICULTURAL RESEARCH INSTITUTE OF THE HUNGARIAN ACADEMY OF SCIENCES Brunszvik str. 2, Martonvásár, H-2462, Hungary. 36/22-569-500 (TEL); 36/22-460-213 (FAX). Z. Bedö*, L. Láng*, L. Szunics, Ottó Veisz*, G. Vida, I. Karsai*, K. Mészáros, A. Juhász, M. Rakszegi, P. Szücs, K. Puskás, C. Kuti, M. Megyeri, M. Gál, I. Nagy, J. Sutka, G. Galiba, M. Molnár-Láng*, G. Kocsy, G. Kovács, G. Linc, A. Vágújfalvi, E.D. Nagy, A.F. Bálint, B. Tóth, I. Molnár, B. Barnabás, L. Sági, I. Takács, É. Szakács, I. Timár, É. Darkó, and F. Bakos.

KARCAG RESEARCH INSTITUTE OF DEBRECEN UNIVERSITY 5301 Karcag, Hungary. M. Fazekas*, L. Balla, Gy. Chrappán, and Á. Czimbalmas.

INDIA

BHABHA ATOMIC RESEARCH CENTRE Nuclear Agriculture and Biotechnology and Molecular Biology and Computer Divisions, Mumbai–400085, India. B.K. Das, S.G. Bhagwat*, A. Saini, N. Jawali, E. Nalini, J.K. Sainis, S.P. Shouche, and R. Rastogi.

BHARATHIAR UNIVERSITY Cytogenetics Laboratory, Department of Botany, Coimbatore–641 046, Tamil Nedu, India. 091-422222 Ext. 359 (TEL), 091-422-422387 (FAX). V. Rama Koti Reddy and G. Kalaiselvi*.

CH. CHARAN SINGH UNIVERSITY Wheat Biotechnology Project, Department of Agricultural Botany, Meerut–250 004 (U.P.), India. 91-121-768195/770335 (TEL); 91-121-767018/760577/764070 (FAX). P. K. Gupta*, H.S. Balyan, M. Prasad, J.K. Roy, R. Bandopadhyay, N. Kumar, S. Sharma, P.L. Kulwal, S. Rustgi, R. Singh, A. Goyal, A. Kumar, and S.N. Prashanth.

CHAUDHARY CHARAN SINGH HARYANA AGRICULTURAL UNIVERSITY Department of Plant Pathology, Hisar–125004, India. Rajender Singh*, S.S. Karwasra, and M.S. Beniwal.

DIRECTORATE OF WHEAT RESEARCH Karnal-132 001, India. Gyanendra P. Singh*, Ravish Chatrath, S. Nagarajan, Jag Shoran, Gyanendra Singh, and S.K. Singh.

INDIAN AGRICULTURAL RESEARCH INSTITUTE REGIONAL STATION Wellington–643 231, The Nilgiris, Tamilnadu, India. R.N. Brama*, M. Sivasamy, Aloka Saikia, K.A. Nayeem, S.G. Bhagwat, and P.J. Kulkarni.

INDIAN AGRICULTURAL RESEARCH INSTITUTE REGIONAL STATION Genetics Division, New Delhi–110012, India. (011)-5783077, 5781481 (TEL). B.S. Malik*, A.P. Sethi*, Vinod Tewari*, R.K. Sharma, V.C. Sinha, S.S. Singh*, J.B. Sharma, P. Bahadur, Anita Baranwal, J.B. Singh*, Lal M. Ahamed*, Javed S. Salim, Reza Haghparast*, Nirupma Singh*, and Sohan Pal Sharma.

ITALY

EXPERIMENTAL INSTITUTE FOR CEREAL RESEARCH Via Mulino 3, 26866 S. Angelo Lodigiano, Italy. 39-0371-211261 (TEL); 39-0371-210372 (FAX). M. Perenzin, M. Corbellini, Gaetano Boggini*, M. Cattaneo, P. Vaccino, C. Concaro, N.E. Pogna*, L. Gazza, G. Boggini, M. Corbellini, P. Vaccino, and E. Ponzoni, A. Brandolini, G. Reffo, and G. Bruschi.

JAPAN

GIFU UNIVERSITY Faculty of Agriculture, 1-1 Yanagido, Gifu 501-11, Japan. Nobuyoshi Watanabe*.

JAPAN INTERNATIONAL RESEARCH CENTER FOR AGRICULTURAL SCIENCES (JIRCAS) Tsukuba, Ibaraki 305-8686, Japan. 81-298-38-6358 (TEL/FAX). Hiro Nakamura*.

MEXICO

INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER (CIMMYT INT.) Lisboa 27, Colonia Juárez, Apdo. Postal 6-641, 06600 México, D.F., México. (52-5) 726-9091 (TEL); (52-5) 726 75-58/9 (FAX). R.L. Villareal, O.T. Bañuelos, S. Rajaram, A. Mujeeb-Kazi*, R.M. Trethowan, J. Borja, M. Zaharieva, A. Cortés, V. Rosas, S. Cano, R. Delgado, K. Suenaga, and H.M. William.

PAKISTAN

REGIONAL AGRICULTURAL RESEARCH INSTITUTE Model Town-A, Bahawalpur, Punjab, Pakistan. Altaf Hussain Tariq, Saeed Ahmad, Muhammad Arshad Hussain, Muhammad Ziaullah, Lal Hussain Akhtar, Sabir Zameer Siddiqi*, Abdul Rashid, Habib Ahmad Saeed, Lal Hussain Akhtar*, Mushtaq Ahmad, Manzoor Hussain, Ghulam Hussain, Muhammad Aslam, Muhammad Safdar, Muhammad Rafiq, and Liaquat Ali.

ROMANIA

S.C.A.—AGRICULTURAL RESEARCH STATION Turda, 3350, str. Agriculturii 27 Jud Cluj, Romania. 00-40-64-311134 (TEL/FAX). Vasile Moldovan*, Maria Moldovan, and Rozalia Kadar.

RUSSIAN FEDERATION

AGRICULTURAL RESEARCH INSTITUTE OF THE CENTRAL REGION OF NON-CHENOZEM ZONE 143026, Nemchinovka-1, Moscow region, Russian Federation. V.G. Kyzlasov*, A.E. Druzhin*, A.V. Borozdina, S.N. Sibikeev, S.A. Voronina, V.A. Krupnov, A.Yu. Buyenkov, M.R. Abdryaev, and O.V. Subkova*.

AGRICULTURAL RESEARCH INSTITUTE FOR SOUTH-EAST REGIONS – ARISER Toulaikov Str., 7, Saratov, 410020, Russian Federation. 8452-64-76-88 (FAX). Yuri V. Lobachev*, I.F. Lapochkina, E.D. Kovalenko, A.I. Zhemchuzhina, and T.M. Kolomietz.

ALL RUSSIA RESEARCH INSTITUTE OF PHYTOPATHOLOGY 143053, Bol´shie Vyazemy, Moscow region, Russian Federation. D.A. Solomatin.

INSTITUTE OF COMPLEX ANALYSIS OF REGIONAL PROBLEMS Karl Marx str., 105 A, kb. 167, Khabarovsk, 680009, Russian Federation. Ivan M. Shindin, Elizoveta N. Meshkova, and Olga V. Lokteva.

OMSK STATE PEDAGOGICAL UNIVERSITY Chemico-Biological Faculty, nab. Tuchachevskogo, 14, Omsk, 644099, Russian Federation. Natalia A. Kuzmina*.

PRYANISHNIKOV ALL RUSSIAN RESEARCH INSTITUTE OF AGRICULTURE AND SOIL SCIENCE Pryanishnikova, 31. Moscow 127550, Russian Federation. N.V. Poukhalskaya* and A.I. Gurin.

SHEMYAKIN AND OVCHINNIKOV INSTITUTE OF BIOORGANIC CHEMISTRY, RUSSIAN ACADEMY OF SCIENCES Ul. Miklukho-Maklaya 16/10, Moscow, Russian Federation. Ts.A. Egorov and A.K. Musolyamov.

SIBERIAN INSTITUTE OF PLANT PHYSIOLOGY AND BIOCHEMISTRY Lermontov str., 132, 664033, Irkutsk-33, P.O. Box 1243, Russian Federation. O.I. Grabelnych*, S.P. Funderat, T.P. Pobezhimova, A.V. Kolesnichenko*, V.K. Voinikov, N.I. Rekoslavskaya*, R.K. Salyaev*, V.M. Sumzova, T.V. Kopytina, A.M. Sobenin, Gennadii B. Borovskii*, A.Yu. Yakovlev, S.V. Vladimirova, A.K. Glyanko*, N.V. Mironova, and G.G. Vasilieva.

VAVILOV INSTITUTE OF GENERAL GENETICS Gubkin str. 3, 117809 Moscow, Russian Federation. 7-095-3304022 (Tel), 7-095-3307301 (FAX). T.I. Odintsova,V.A. Pukhalsky*, S.P. Martynov, and E.N. Bilinskaya.

N.I. VAVILOV RESEARCH INSTITUTE OF PLANT INDUSTRY B. Morskaya Str. 44, St. Petersburg, 190000, Russian Federation. Sergei P. Martynov* and T.V. Dobrotvorskaya.

SOUTH AFRICA

SMALL GRAIN INSTITUTE Private Bag X29, Bethlehem 9700, Republic of South Africa. 27 58 3073444 (TEL), 27 58 3033952 (FAX). J.C. Aucamp, D.J. Exley, H.A. Smit, W.H.P. Boshoff, T. van A. Bredenkamp, M.V. van Wyk, A.F. Malan, R. Prins, V.P. Ramburan, A. Barnard, K. Naudé, W.M. Otto, K.B. Majola, M.L.T. Moloi, M.M. Raderbe, N.E.M. Mtjale, C.N. Matla, M.M. Mofokeng, M.L. Dhlamini, N.M. Mtshali, and L. Visser.

UNIVERSITY OF FREE STATE Plant Pathology Department, Republic of South Africa. Z.A. Pretorius.

UNIVERSITY OF STELLENBOSCH Department of Genetics, Private Bax X1, Matieland 7602, Republic of South Africa. 27-21-8085829 (TEL), 27-21-8085833 (FAX). G. Frans Marais*, H.S. Roux, A.S. Marais, W.C. Botes, and J.H. Louw.

SPAIN

UNIVERSITY OF LLEIDA Center of R&D, Alcalde Rovira Roure 177, 25198 Lleida, Spain. 34-973-702569 (Tel), 34-973-238301 (FAX). J.A. Martín-Sánchez*, E. Sin, C. Martínez, and A. Michelena.

UNIVERSIDAD POLITÉCNICA DE MADRID Departamento de Biotecnología, E.T.S. Ingenieros Agrónomos, Ciudad Universitaria, 28040 Madrid, Spain. A. Delibes*, I. López-Braña, M.J. Montes, and C. Gonzalez-Belinchon.

JUNTA DE EXTREMADURA Servicio de Investigación Agraria, Finca La Orden, 06187 Guadajira, Badajoz, Spain. J. del Moral, F. Perez–Rojas, F.J. Espinal, and M. Senero.

SYRIA

ICARDA International Center for Agricultural Research in Dry Areas, P.O. Box 5466, Aleppo. M. Mousaad and A. Yahyaoui.

TURKEY

CIMMYT–TURKEY P.K. 39 Emek, 06511 Ankara, Turkey. 90-312-287-3595 (TEL); 90-312-287-7006/8955 (FAX); www.cimmyt.org. Hans-Joachim Braun*, Arne R. Hede*, Julie Nicol*, and B. Akin.

MINISTRY OF AGRICULTURE AND RURAL AFFAIRS M. Keser, N. Bolat, N. Colak, H. Ekiz, S. Taner, S. Ceri, F. Partigoc, L. Cetin, S. Albustan, F. E. Donmez, Dusunceli, S. Yazar, I. Ozseven, I. Ozturk, and T. Yildirim.

THE UKRAINE

INSTITUTE OF PLANT PRODUCTION N.A. V. YA. YURJEV National Centre for Plant Genetic Resources of Ukraine, Yurjev Plant Production Institute, Moskovsky prospekt, 142, 310060 Kharkov, Ukraine. 00380 (0572) 920354 (TEL/FAX). R.V. Rozhkov, O.O. Kushchenko, Yu.G. Krasilovets*, N.V. Kouzmenko, A.E. Litvinov, V.A. Tzyganko, O.V. Golik, Vladimir V. Sotnikov, T.M. Yevlanova, S.V. Rabinovich*, V.P. Petrenkova, I .M. Chernyaeva, and L.N. Chernobay.

UNITED KINGDOM

JOHN INNES CENTRE Crop Genetics Department, Norwich Research Park, Colney Lane, Norwich NR4 7UH, United Kingdom. 44-1603-450611 (TEL); 44-1603-450023/450045 (FAX). Robert M.D. Koebner*, G. Xia, P. Nicholson, E. Chandler, N. Chapman, R. Draeger, D. Simpson, A. Steed, M. Thomsett, A. Wilson, R. Bradburne, A. Turner, L. Fish, and John Snape.

THE UNITED STATES

COLORADO

COLORADO STATE UNIVERSITY Department of Agronomy, Ft. Collins, CO 80523, USA. S. Haley*, J. Stromberger, B. Clifford, S. Clayschulte, T. Mulat, E. Ball, A. Brown, F. Pardina-Malbrán, M. Collins, and J. Butler.

GEORGIA / FLORIDA

UNIVERSITY OF GEORGIA Department of Agronomy, Griffin, GA 30212-1197, USA. 770-228 7321 (TEL), 770-229-3215 (FAX). Jerry W. Johnson*, R.D. Barnett, B.M. Cunfer, and G.D. Buntin.

IDAHO

UNIVERSITY OF IDAHO Plant and Soil Science Department, Moscow, ID 83343, USA and the Agricultural Experiment Station, P.O. Box AA, Aberdeen, ID 83210, USA. R. Zemetra*, E. Souza, S. Guy, L. Robertson, B. Brown, N. Bosque-Pérez, J. Hansen, K. O'Brien, M. Guttieri, D. Schotzko, T. Koehler, L. Sorensen, J. Clayton, Zhiwu Li, and M. Rehman.

USDA–ARS NATIONAL SMALL GRAINS GERMPLASM RESEARCH FACILITY P.O. Box 307, Aberdeen, ID 83210, USA. H.E. Bockelman*, D.M. Wesenberg, C.A. Erickson, and B.J. Goates.

INDIANA

PURDUE UNIVERSITY

Departments of Agronomy, 915 W. State Street, West Lafayette, IN 47907, USA. 317-494-8072 (TEL), 317-496-2926 (FAX). Herbert W. Ohm*, F.L. Patterson, Hari C. Sharma*, and J. Uphaus.

Department of Botany and Plant Pathology G. Buechley, D.M. Huber*, G. Shaner*, and J.R. Xu.

Department of Entomology J.J. Stuart*.

USDA–ARS J.M. Anderson*, S.E. Cambron, C.C. Collier, C. Crane, S.B. Goodwin*, A. Johnson, J.A. Nemacheck, S. Scofield, R.H. Ratcliffe*, R.H. Shukle, and C.E. Williams*.

KANSAS

KANSAS DEPARTMENT OF AGRICULTURE U.S. Department of Agriculture, 632 SW Van Buren, Rm. 200. P.O. Box 3534, Topeka, KS 66601-3534, USA. 913-233-2230 (TEL). http://www.nass.usda.gov/ks/. E.J. Thiessen, Sherri Hand, and Ron Sitzman.

KANSAS STATE UNIVERSITY

Environmental Physics Group Department of Agronomy, Kansas State University, Waters Hall, Manhattan, KS 66502, USA. 913-532-5731 (TEL); 913-532-6094 (FAX). M.S. Liphadzi and M.B. Kirkham*.

The Wheat Genetics Resource Center Departments of Plant Pathology and Agronomy and the USDA–ARS, Throckmorton Hall, Manhattan, KS 66506-5502, USA. 913-532-6176 (TEL); 913 532-5692 (FAX). B.S. Gill*, W.J. Raupp*, B. Friebe*, D.L. Wilson*, G.M. Paulsen, J. Wang, L. Huang*, and S.A. Brooks*.

U.S. GRAIN MARKETING AND PRODUCTION RESEARCH CENTER — USDA, Agricultural Research Service, Manhattan, KS 66502, USA. O.K. Chung*, Scott R. Bean*, M. Tilley*, G.L. Lookhart*, F.E. Dowell*, M.S. Ram*, L.M. Seitz*, M.E. Casada*, J.B. Ohm*, S.H. Park*, B.W. Seabourn*, M.S. Caley*, E.B. Maghirang, J.D. Wilson*, D.B. Bechtel*, T.C. Pearson, F.H. Arthur, R.K. Lyne, D. L. Brabec, J.E. Throne*, J.E. Baker*, J.D. Hubbard*, and J.M. Downing*.

MINNESOTA

CEREAL DISEASE LABORATORY, USDA–ARS University of Minnesota, 1551 Lindig, St. Paul, MN 55108, USA. 612-625-6299 (TEL); 612-649-5054 (FAX). http://www.edl.umn.edu D.L. Long, J.A. Kolmer, Mark E. Hughes*, and L.A. Wanschura.

MISSOURI

UNIVERSITY OF MISSOURI Department of Agronomy and the USDA–ARS, 106 Curtis Hall, Columbia, MO 65211, USA. 1-572-882-7708 (TEL); 1-573-884-7850 (FAX). http://www.psu.missouri.edu/agronomy/index.stm. A.L. McKendry*, J. Perry Gustafson*, K. Ross, D.N. Tague, Jessica Tremain, R.L. Wright, S. Liu, Z. Abate, T. Chikmawati, X. Ma, A. Mahmoud, Miftahuddin, and M. Rodriguez.

NEBRASKA

UNIVERSITY OF NEBRASKA Department of Agronomy, Lincoln, NE 68583, USA. P.S. Baenziger*, B. Beecher, D. Baltensperger, L. Nelson, I. Dweikat, M. Dickman, A. Mitra, T. Clemente, and J. Watkins.

USDA–ARS Wheat, Sorghum and Forage Unit, Keim Hall, Lincoln, NE 68583, USA. 402-472-1563 (TEL); 402-472-4020 (FAX). Robert A. Graybosch*, R. French, and D. Stenger.

NORTH DAKOTA

USDA–ARS CEREAL CROPS RESEARCH UNIT Northern Crop Science Laboratory, Fargo, ND 58078-5051, USA. Justin D. Faris*, Timothy Friesen, Steven Xu, James Miller, Daryl Klindworth, Leonard Joppa, Karri Haen, Erik Doehler, and Huangjun Lu.

OKLAHOMA

OKLAHOMA STATE UNIVERSITY Department of Plant and Soil Sciences, 368 Ag Hall, Stillwater, OK 74078-6028, USA. Brett F. Carver*, E.G. Krenzer*, A.K. Klatt*, and Arron C. Guenzi*.

SOUTH DAKOTA

SOUTH DAKOTA STATE UNIVERSITY AND THE USDA–ARS Plant Science Department and the Northern Grain Insect Research Laboratory (NGIRL), Brookings, SD 57007, USA. http://triticum.sdstate.edu 605-688-4453 (TEL), 605-688-4452 (FAX). A.M.H. Ibrahim*, S.A. Kalsbeck, R.S. Little, D. Gustafson, S.A. Kalsbeck, L. Hesler, W. Riedell, S. Osborne, W. Riedell, L. Osborne, and R. Gelderman.

VIRGINIA

VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY Department of Crop and Soil Environmental Sciences and Department of Plant Pathology, Physiology and Weed Science, 419A Smyth Hall, Blacksburg, VA 24061–0404, USA. 540-231-7624 (Tel), 540-231-3431 (FAX). Wendy L. Rohrer*, Carl A. Griffey*, J.A. Wilson, D. Nabati, J. Chen, T.H. Pridgen, E.G. Rucker, and D.E. Brann.

WASHINGTON

USDA–ARS WHEAT GENETICS, QUALITY, PHYSIOLOGY AND DISEASE RESEARCH Department of Crop & Soil Sciences and Plant Pathology, Washington State University, P.O. Box 646420, 209 Johnson Hall, Pullman, WA 99164-6420, USA. 509-335-3632 (TEL); 509-335-2553 (FAX). Xianming Chen*, David A. Wood, Mary K. Moore, Paul Ling, Vihanga Pahalawatta, R.E. Allan*, Kimberly Garland Campbell*, Robert E. Allan, Todd Linscott, Kay Walker-Simmons, Eric Weir, Daniel Z. Skinner, and Kwang-Hyun Baek.

USDA–ARS WESTERN WHEAT QUALITY LABORATORY E-202 Food Science & Human Nutrition Facility East, Washington State University, Pullman, WA 99164-6394, USA. 1-509-335-4062 (TEL), 1-509-335-8573 (FAX). Craig F. Morris*, A.D. Bettge, D.A. Engle, M.L. Baldridge, R.L. Engle, G.E. King, G.L. Jacobson, A.N. Masa, I. Eujayl, E.P. Fuerst, K.R. Gedye, C.C. Burke, J.F.Connett, W.J Kelley, M.J. Freston, P.K. Boyer, L. Nguyen, E.E. Galli, S.M. Finnie, C.A. Oliver, S.M. Leach, and Y. Haruta.

WASHINGTON STATE UNIVERSITY Spring Wheat Breeding and Genetics Program, Department of Crop and Soil Sciences, 201 Johnson Hall, P.O. Box 646420, Pullman, WA 99164-6420, USA. 509-335-7247 (TEL). K.G. Kidwell*, G. Shelton, V. DeMacon, M. McClendon, J. Baley, R. Higgonbotham, and T. Paulitz.

VIII. E-MAIL DIRECTORY OF SMALL GRAINS WORKERS.

Acevedo, Alberto	aacevedo@unq.edu.ar, aacevedo@inta.gov.ar	INTA, Castelar, Argentina
Ahamed, Lal M	lal–pdl@yahoo.com	IARI, New Delhi, India
Akhtar, Lal H	lhakhtar@yahoo.com	Reg Agr Res Inst, Bahawalpur, Pakistan
Aldana, Fernando	fernando@pronet.net.gt	ICTA, Guatemala
Allan, Robert E	allanre@mail.wsu.edu	USDA–ARS, Pullman, WA
Altenbach, Susan	altnbach@pw.usda.gov	USDA–WRRE, Albany, CA
Altman, David	dwa1@cornell.edu	ISAAA–Cornell University, Ithaca, NY
Alvarez, Juan B	alvarez@unitus.it	Univeristy of Córdoba, Argentina
Anderson, Jim M	ander319@tc.umn.edu	University of Minnesota, St. Paul
Anderson, Joseph M	janderson@purdue.edu	Purdue University, W. Lafayette, IN
Anderson, Olin	oandersn@pw.usda.gov	USDA-WRRE, Albany, CA
Appels, Rudi	rudi@pican.pi.csiro.au	CSIRO–Div of Plant Industry, Australia
Armstrong, Ken	armstrongkc@em.agr.ca	AAFC–Ottawa, Ontario, Canada
Aung, T	taung@mbrswi.agr.ca	AAFC–Winnipeg, Canada
Babaoglu, Metin	metin_babaoglu@edirne.tagem.gov.tr	Thrace Ag Research Institute, Turkey
Bacon, Robert	rb27412@uafsysb.uark.edu	University of Arkansas, Fayetteville
Baenziger, P Stephen	agro104@unlnotes.unl.edu	University of Nebraska, Lincoln
Baker, Cheryl A	cbaker@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Baker, JE	baker@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Barnard, Anri D	anri@kgs1.agric.za	Small Grain Institute, South Africa
Barreto, D	dbarreto@cnia.inta.gov.ar	INTA, Buenos Aires, Argentina
Barker, Susan	sbarker@waite.adelaide.edu.au	Waite, University Adelaide, Australia
Bariana, Harbans	harbansb@camden.usyd.edu.au	PBI Cobbitty, Australia
Barkworth, Mary	uf7107@cc.usu.edu	USDA–ARS, Pullman, WA
Bartos, Pavel	bartos@hb.vruv.cv	RICP, Prague, Czech Republic
Bhagwat, SG	sbhagwat@apsara.barc.ernet.in	Bhaba Atomic Res Cen, Mumbai, India
Buerstmayr, Hermann	buerst@ifa-tulln.ac.at	IFA–Tulln, Austria
Bean, Scott R	scott@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Beazer, Curtis	cbeazer@dcwi.com	AgriPro Seeds, Inc., Lafayette, IN
Bechtel DB	don@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Bedö, Zoltan	bedoz@buza.mgki.hu	Martonvásár, Hungary
Bentley, Stephen	bentleys@phibred.com	Pioneer Hi-Bred–Frouville, France
Bergstrom, Gary	gcb3@cornell.edu	Cornell University, Ithaca, NY
Berzonsky, William A	berzonsk@badlands.nodak.edu	North Dakota State University, Fargo
Bhagwat, SG	sbhagwat@apsara.barc.ernet.inn	Bhabha Atomic Res Center, India
Bhatta, MR	rwp@nwrp.mos.com.np	Natl Wheat Research Program, Nepal
Blake, Nancy	nblake@montana.edu	Montana State University, Bozeman
Blake, Tom	isstb@montana.edu	Montana State University, Bozeman
Blanco, Antonia	blanco@afr.uniba.it	Institue of Plant Breeding, Bari, Italy
Blum, Abraham	vcablm@volcani.agri.gov.il	Volcani Center, Israel
Bockelman, Harold E	hbockelman@ars-grin.gov	USDA–ARS, Aberdeen, ID
Boggini, Gaetano	cerealicoltura@iscsal.it	Exp Inst Cereal Research, Italy
Boguslavskiy, Roman L	bogus@ncpgru.relcom.kharkov.ua	Kharkov Inst Plant Protection, Ukraine
Börner, Andreas	boerner@ipk-gatersleben.de	IPK, Gatersleben, Germany
Borovskii, Genadii	borovskii@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Bowden, Robert	rbowden@plantpath.ksu.edu	Kansas State University, Manhattan
Boyko, Elena	olena@plantpath.ksu.edu	Kansas State University, Manhattan
Brahma, RN	amaljoe@rediffmail.com	Indian Agric Res Inst, Wellington
Brown, John S	john.brown@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Brammer, Sandra P	sandra@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Bradová, Jane	bradova@hb.vurv.cz	RICP, Prague, Czech Republic
Braun, Hans J	H.J.Braun@cgiar.org	CIMMYT–Turkey, Ankara
Brennan, Paul	paulb@qdpit.sth.dpi.qld.gov.au	Queensland Wheat Res Inst, Australia
Brooks, Steven A	sbrooks@plantpath.ksu.edu	USDA–ARS, Manhattan, Kansas

Brown, Douglas	dbrown@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Brown, James	jbrown@bbsrc.ac.uk	JI Centre, Norwich, UK
Brown-Guedira, Gina	gbg@ksu.edu	USDA–ARS, Manhattan, KS
Bruckner, Phil	bruckner@montana.edu	Montana State University, Bozeman
Bruns, Rob	rbruns@frii.com	AgriPro Wheat, Berthoud, CO
Buerstmayr, Hermann	buerst@ifa-tulln.ac.at	IFA, Tulln, Austria
Burd, John D	jdburd@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Busch, Robert	Robert.H.Busch-1@umn.edu	USDA–ARS, St. Paul, MN
Byrne, Pat	pbyrne@lamar.colostate.edu	Colorado State University, Ft. Collins
Caley, MS	margo@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Cambron, Sue	sue_cambron@entm.purdue.edu	Purdue University, W. Lafayette, IN
Campbell, Kimberly G	kgcamp@wsu.edu	USDA–ARS, Pullman, WA
Carmona, M	mcarmona@sion.com.ar	University of Buenos Aires, Argentina
Carver, Brett F	bfc@mail.pss.okstate.edu	Oklahoma State University, Stillwater
Cerana, María M	macerana@agro.uncor.edu	Córdoba National University, Argentina
Casada, ME	casada@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Chapin, Jay	jchapin@clust1.clemson.edu	Clemson University
Chapon, Michel	michel-chapon@wanadoo.fr	Bourges, France
Chen, Xianming	xianming@mail.wsu.edu	USDA–ARS, Pullman, WA
Chung, OK	okchung@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Cisar, Gordon L	glcisa@ccmail.monsanto.com	Hybritech–Lafayette, IN
Clark, Dale R	dclark@westbred.com	Western Plant Breeders, Bozeman, MT
Corke, Harold	harold@hkuxa.hku.hk	Hong Kong University
Czarnecki, E	eczarnecki@mbrswi.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Davydov, VA	gluten@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Das, BK	bkdas@magnum.barc.ernet.in	Bhaba Atomic Res Cen, Mumbai, India
Del Duca, Leo JA	delduca@cnpt.embrapa.br	EMBRAPA, Brazil
Delibes, A	adelibes@bit.etsia.upm.es	Univ Politécnica de Madrid, Spain
del Moral, J.	moral@inia.es	Junta de Extramadura Servicio, Spain
Dempster, RE	rdempster@aibonline.org	Amer Inst Baking, Manhattan, KS
de Sousa, Cantído NA	cantidio@cnpt.embrapa.br	EMBRAPA, Brazil
DePauw, Ron	depauw@em.agr.ca	AAFC–Swift Current
Devos, Katrien	devos@bilbo.bi.purdue.edu	Purdue University, W. Lafayette, IN
Dill-Macky, Ruth	ruthdm@puccini.crl.umn.edu	University Of Minnesota, St. Paul
Dotlacil, Ladislav	dotlacil@hb.vurv.cz	RICP, Prague, Czech Republic
Dorlencourt, Guy	dorlencourt@phibred.com	Pioneer Hi-bred–Frouville France
Dowell, FE	fdowell@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Downing, JM	jdowning@atrixlab.frii.com	
Dreccer, F	fernanda.dreccer@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Druzhin, AE	elkonin@mail.saratov.ru	Agric Res Inst SE Reg, Saratov, Russia
Dubcovsky, Jorge	jdubcovsky@ucdavis.edu	Univesity of California, Davis
Dubin, Jesse	JDubin@cimmyt.mx	CIMMYT, Mexico
Dubois, María E	mdubois@agro.uncor.edu	Córdoba National University, Argentina
Dundas, Ian	idundas@waite.adelaide.edu.au	University of Adelaide, Australia
Dunphy, Dennis	dennis.j.dunphy@monsanto.com	Monsanto Corp., Lafayette, IN
Dvorak, Jan	jdvorak@ucdavis.edu	Univesity of California, Davis
Eastwood, Russell	russell.eastwood@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Edge, Benjamin	bedge@clemson.edu	Clemson University, SC
Edwards, Ian	iane@biotest.com.au	Grain Biotech Australia, Joondalup
Egorov, Tsezi	egorov@imb.ac.ru	Englehardt Institute, Moscow, Russia
Elias, Elias	elias@prairie.nodak.edu	North Dakota State University, Fargo
Elliott, Norman C	nelliott@ag.gov	USDA–ARS, Stillwater, OK
Endo, Takashi R	endo@kais.kyoto-u.ac.jp	Kyoto University, Japan
Faberova, Iva	faberova@genbank.vurv.cz	RICP, Prague, Czech Republic
Fahima, Tzion	rabi310@haifauvm.bitnet	University of Haifa, Israel
Faris, Justin D	justin.faris@ndsu.nodak.edu	UDSA–ARS–NCRL, Fargo, ND
Fazekas, Miklós	forizsne@dateki.hu	Karcag Research Institute, Hungary

Fedak, George	fedakga@em.agr.ca	AAFC–Ottawa, Ontario
Federov, AK	meraserv@mega.ru	Russian Univ People Friend, Moscow
Feldman, Moshe	lpfeld@weizmann.weizmann.ac.il	Weizmann Institute, Rehovot, Israel
Fellers, John P	jpf@alfalfa.ksu.edu	USDA–ARS, Manhattan, KS
Fox, Paul	pfox@alphac.cimmyt.mx	CIMMYT–Mexico
Fogelman Jr, J Barton	jbarton@ipa.net	AgriPro Seeds, Inc., Jonesboro, AK
Frank, Robert W	frankr@idea.ag.uiuc.edu	University of Illinois, Urbana
Fritz, Alan K	akf@ksu.edu	Kansas State University, Manhattan
Friebe, Bernd	friebe@ksu.edu	Kansas State University, Manhattan
Gale, Mike	gale@bbsrc.ac.uk	JI Centre, Norwich, UK
Giese, Henriette	h.giese@risoe.dk	Risoe National Lab, DK
Gilbert, Jeannie	jgilbert@mbrswi.agr.ca	Agriculture Canada–Winnipeg
Gil, S Patricia	patrigil@agro.uncor.edu	University of Córdoba, Argentina
Gill, Bikram	bsgill@ksu.edu	Kansas State University, Manhattan
Giroux, Mike	mgiroux@montana,edu	Montana State University, Bozeman
Gitt, Michael	mgitt@pw.usda.gov	USDA–ARS–WRRC, Albany, CA
Glyanko, AK	ustaft@sifibr.irk.ru	Siberian Inst Pl Physio Biochem, Russia
Gonzalez-de-Leon, Diego	dgdeleon@alphac.cimmyt.mx	CIMMYT–Mexico
Gooding, Rob	rgooding@magnus.acs.ohio-state.edu	Ohio State University, Wooster
Goodwin, Steve	goodwin@btny.purdue.edu	Purdue University, W. Lafayette, IN
Gothandam, KM	gothandam@yahoo.com	Bharathiar University, Coimbatore, India
Grabelnych, OI	grolga@sifibr.irk.ru	Siber Inst Plant Physiol, Irkutsk, Russia
Grausgruber, Heinrich	grausgruber@ipp.boku.ac.at	Univ of Agriculture Sciences, Vienna
Graham, W Doyce	dgraham@clust1.clemson.edu	Clemson University, SC
Graybosch, Bob	rag@unlserve.unl.edu	USDA–ARS, Lincoln, NE
Greenstone Matthew H	mgreenstone@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Grienenberger, Jean M	grienen@medoc.u-strasbg.fr	University of Strasberg, France
Griffey, Carl	cgriffey@vt.edu	Virginia Tech, Blacksburg
Griffin, Bill	griffinw@lincoln.cri.nz	DSIR, New Zealand
Groeger, Sabine	probstdorfer.saatzucht@netway.at	Probstdorfer Saatzucht, Austria
Guenzi, Arron	acg@soilwater.agr.okstate.edu	Oklahoma State University, Stillwate
Guidobaldi, Héctor A.	guidobaldi@uol.com.ar	Univrsity of Córdoba, Argentina
Gupta, PK	pkgupta36@vsnl.com	Ch. Charan Singh Univ, Meerut, India
Gustafson, Perry	pgus@showme.missouri.edu	USDA–ARS, University of Missouri
Haber, Steve	shaber@agr.gc.ca	Winnipeg, Manitoba, Canada
Haghparast, Reza	rezahaghparast@yahoo.com	IARI, New Delhi, India
Haley, Scott	scott.haley@colostate.edu	Colorado State University, Ft. Collins
Hancock, June	june.hancock@seeds.Novartis.com	Novartis Seeds Inc., Bay, AR
Harrison, Steve	sharris@lsuvm.sncc.lsu.edu	Louisiana State University, Baton Rouge
Harder, Don	dharder@mbrswi.agr.ca	Winnipeg, Manitoba, Canada
Hart, Gary E	ghart@acs.tamu.edu	Texas A & M Univ, College Station
Hays, Dirk B	dhays@ag.gov	USDA–ARS, Stillwater, OK
Hayes, Pat	hayesp@css.orst.edu	Oregon State University, Corvallis
Hearnden, PR	phillippa.hearden@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Hede, Arne R	a.hede@cgiar.org	CIMMYT–Turkey, Ankara
Henzell, Bob	bobh@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland, AU
Hershman, Don	dhershman@ca.uky.edu	University Of Kentucky, Lexington
Heslop-Harrison, JS (Pat)	hharrison@bbsrc.ac.uk	JI Centre, Norwich, UK
Hoffman, David	A03dhoffman@attmail.com	USDA–ARS, Aberdeen, ID
Hohmann, Uwe	uhemail@botanik.biologie.unimuenchen.de	Botanical Institute, Munich, Germany
Hoisington, David	dhoisington@cimmyt.mx	CIMMYT–Mexico
Hole, David	dhole@mendel.usu.edu	Utah State University, Logan
Howes, Neil	nhowes@mbrswi.agr.ca	Winnipeg, Manitoba, Canada
Hubbard, JD	john@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Huber, Don M	huber@btny.purdue.edu	Purdue University, W. Lafayette, IN
Hucl, Pierre	hucl@sask.usask.ca	University of Saskatchewan
Hughes, Mark E	markh@umn.edu	USDA–ARS–CDL, St. Paul, MN

Hulbert, Scot	shulbrt@plantpath.ksu.edu	Kansas State University, Manhattan
Hunger, Robert	rmh@okstate.edu	Oklahoma State University, Stillwater
Ibrahim, Amir	amir_ibrahim@sdstate.edu	South Dakota State Univ, Brookings
Isaac, Peter G	mbnis@seqnet.dl.ac.uk	Nickerson Biocem, UK
Jacquemin, Jean	stamel@fsagx.ac.be	Cra-Gembloux, Belgium
Jelic, Miodrag	miodrag@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Jiang, Guo-Liang	dzx@njau.edu.cn	Nanjing Agricultural University, China
Jin, Yue	jiny@ur.sdstate.edu	South Dakota State Univ, Brookings
Johnson, Doug	djohnson@ca.uky.edu	University of Kentucky, Lexington
Johnson, Jerry	jjohnso@griffin.peachnet.edu	University of Georgia, Griffin
Johnston, Paul	paulj@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland, AU
Jones, Steven S	joness@wsuvm1.csc.wsu.edu	Washington State University, Pullman
Joppa, Leonard	joppa@badlands.nodak.edu	USDA–ARS, Fargo, ND
Kalaiselvi, G	kalaipugal@rediffmail.com	Bharathiar Univ, Coimbatore, India
Karabayev, Muratbek	mkarabayev@astel.kz	CIMMYT, Kazakhstan
Karow, Russell S	Russell.S.Karow@orst.edu	Oregon State University, Corvallis
Karsai, Ildiko	karsai@buza.mgki.hu	ARI, Martonvasar, Hungary
Kasha, Ken	kkasha@crop.uoguelph.ca	University of Guelph, Canada
Keefer, Peg	peg_keefer@entm.purdue.edu	Purdue University, West Lafayette, IN
Keller, Beat	bkeller@botinst.unizh.ch	University of Zurich, Switzerland
Kidwell, Kim	kidwell@wsu.edu	Washington State University, Pullman
Kindler, S Dean	sdkindler@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Kirkham, MB	mbk@ksu.edu	Kansas State University, Manhattan
Kisha, Theodore	tkisha@dept.agry.purdue.edu	Purdue University, W. Lafayette, IN
Klatt, Art	aklatt@mail.pss.okstate.edu	Oklahoma State University, Stillwater
Kleinhofs, Andy	coleco@bobcat.csc.wsu.edu	Washington State University, Pullman
Knezevic, Desimir	deskok@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Koebner, Robert	robert.koebner@bbsrc.ac.uk	JI Centre, Norwich, UK
Koemel, John Butch	jbk@soilwater.agr.okstate.edu	Oklahoma State University, Stillwater
Kokhmetova, Alma	kalma@ippgb.academ.alma-ata.su	Kazakh Research Institute of Agriculture
Kolb, Fred	fkolb@ux1.cso.uiuc.edu	University Of Illinois, Urbana
Kolesnichenko, AV	akol@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Koppel, R	Reine.Koppel@jpbi.ee	Jõgeva Plant Breeding Institute, Estonia
Korol, Abraham	rabi309@haifauvm.bitnet	University of Haifa
Kovalenko, ED	kovalenko@vniif.rosmail.com	Russian Res Inst Phytopath, Moscow
Krasilovets, Yuri G	ncpgru@kharkov.ukrtel.net	Inst Plant Production, Karkiv, Ukraine
Krenzer, Gene	egk@agr.okstate.edu	Oklahoma State University, Stillwater
Kronstad, Warren E	kronstaw@css.orst.edu	Oregon State University, Corvallis
Krupnov, V	imu@ssau.saratov.ru	Agric Res Inst SE Reg, Saratov, Russia
Kuhr, Steven L	slkuhr@ccmail.monsanto.com	Hybritech–Mt. Hope, KS
Kuzmina, Natalia	natakuzmina@yandex.ru	Omsk State Pedagogical Univ, Russia
Kyzlasov, VG	nemchin@cityline.ru	ARI, Moscow, Russia
Lafferty, Julia	lafferty@edv1.boku.ac.at	Saatzucht Donau, Austria
Lagudah, Evans	e.lagudah@pi.csiro.au	CSIRO, Australia
Lankevich, SV	laser@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Láng, László	langl@penguin.mgki.hu	HAAS, Martonvásár, Hungary
Langridge, Peter	plangridge@waite.adelaide.edu.au	University of Adelaide, Australia
Lapitan, Nora LV	nlapitan@lamar.colostate.edu	Colorado State University, Ft. Collins
Lapochkina, Inna F	lapochkina@chat.ru	Research Inst of Agric, Moscow, Russia
Laskar, Bill	laskarb@phibred.com	Pioneer Hi-Bred–Windfall, IN
Leach, Jan E	jeleach@ksu.edu	Kansas State University, Manhattan
Leath, Steve	steven_leath@ncsu.edu	USDA–ARS, Raleigh, NC
Leonard, Kurt J	kurtl@puccini.crl.umn.edu	USDA–ARS, St. Paul, MN
Leroy, Philippe	leroy@valmont.clermont.inra.fr	INRA, Clermont
Lewis, Hal A	halewi@ccmail.monsanto.com	Hybritech–Corvallis OR
Lewis, Silvina	slewis@cirn.inta.gov.ar	CNIA–INTA, Buenos Aires, Argentina
Li, Wanlong	wli@plantpath.ksu.edu	Kansas State University, Manhattan

Liang, GH	ghliang@ksu.edu	Kansas State University, Manhattan
Line, RF	rline@wsu.edu	USDA–ARS, Pullman, WA
Liu, Dajun	djliu@public1.ptt.js.cn	Nanjing Agricultural University, China
Lively, Kyle	livelyk@phibred.com	Pioneer Hi-Bred–Windfall, IN
Lobachev, Yuri V	lobachev@ssau.saratov.ru	Agric Res Inst SE Reg, Saratov, Russia
Long, David	davidl@puccini.crl.umn.edu	USDA St. Paul, MN
Lookhart, George	george@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Luckow, Odean	alvkow@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Lukaszewski, Adam	ajoel@ucrac1.ucr.edu	University of California–Riverside
Maas, Fred	fred_maas@entm.purdue.edu	Purdue University, West Lafayette, IN
Mackay, Michael	mackaym@quord.agric.nsw.gov.au	AWEE, Tamworth, NSW, Australia
Maich, Ricardo H.	rimaich@agro.uncor.edu	University of Córdoba, Argentina
Malik, BS	bsmalik2000@yahoo.com	IARI, New Delhi, India
Manera, Gabriel	gamanera@agro.uncor.edu	University of Córdoba, Argentina
Manifesto, María M	mmanifes@cicv.intgov.ar	INTA Castelar, Argentina
Marais, G Frans	gfm@sun.ac.za	University of Stellenbosch, R.S.A.
Mares, Daryl J	daryl.mares@adelaid.edu.au	University of Adelaide, Australia
Marshall, David	d-marshall@tamu.edu	Texas A & M University, Dallas
Marshall, Gregory C	marshallg@phibred.com	Pioneer Hi-Bred–Windfall, IN
Martin, Erica	erica.martin@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Martín-Sánchez, JA	JuanAntonio.Martin@irta.es	IRTA, Lleida, Spain
Martynov, Sergei	sergej_martynov@mail.ru	Vavilov Inst Plant Prod, St. Petersburg
Mather, Diane	indm@musicb.mcgill.ca	McGill University, Canada
Matthews, Dave	matthews@greengenes.cit.cornell.edu	Cornell University, Ithaca, NY
McCallum, John	mccallumj@lan.lincoln.cri.nz	Crop & Food Res. Ltd, NZ
McGuire, Pat	pemcguire@ucdavis.edu	University of California, Davis
McIntosh, Robert A	bobm@camden.usyd.edu.au	PBI Cobbitty, Australia
McKendry, Anne L	mckendrya@missouri.edu	University of Missouri, Columbia
McKenzie, RIH	rmckenzie@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
McVey, Donald	donm@puccini.crl.umn.edu	USDA–ARS, St. Paul, MN
Mi, Q.L.	qlm@ksu.edu	Kansas State University, Manhattan
Milach, Sandra	mila0001@student.tc.umn.edu	University of Minnesota, St. Paul
Miller, James	millerid@fargo.ars.usda.gov	USDA–ARS, Fargo, ND
Milovanovic, Milivoje	mikim@knez.uis.kg.ac.yu	ARI Center Small Grains, Yugoslavia
Milus, Gene	gmilus@comp.uark.edu	University of Arkansas, Fayetteville
Miskin, Koy E	miskin@dcwi.com	AgriPro Wheat, Berthoud, CO
Mochini, RC	rmoschini@inta.gov.ar	INTA, Castelar, Argentina
Moffat, John	apwheat@frii.com	AgriPro Wheat, Berthoud, CO
Moldovan, Vasile	scaturda@rdslink.ro	Agric Research Station, Turda, Romania
Molnár-Láng, Marta	molnarm@fsnew.mgki.hu	Martonvásár, Hungary
Moore, Paul	ejh@uhccvx.uhcc.hawaii.edu	University of Hawaii, Honolulu
Moreira, João C.S.	moreira@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Morgounov, Alexei	amorgounov@astel.kz	CIMMYT, Kazakhstan
Morino-Sevilla, Ben	bmoreno-sevilla@westbred.com	Western Plant Breeders, Lafayette, IN
Mornhinweg, Dolores W	dmornhin@ag.gov	USDA–ARS, Stillwater, OK
Morris, Craig	morrisc@wsu.edu	USDA–ARS–WWQL, Pullman, WA
Morrison, Laura	alura@peak.org	Oregon State University, Corvallis
Moser, Hal	hsmoser@iastate.edu	Iowa State University, Ames
Mujeeb-Kazi, A	mkazi@cimmyt.mx	CIMMYT, Mexico
Mukai, Yasuhiko	ymukai@cc.osaka-kyoiku.ac.jp	Osaka Kyoiku University, Japan
Murphy, Paul	njpm@unity.ncsu.edu	North Carolina State University
Murray, Tim	tim_murray@wsu.edu	Washington State University, Pullman
Muthukrishnan, S	smk@ksu.edu	Kansas State University, Manhattan
Nakamura, Hiro	hiro@jircas.affrc.go.jp	Japan Inter Res Cen Agric Sci, Tsukuba
Nass, Hans	nassh@em.agr.ca	AAFC–Prince Edward Island, Canada
Nelson, Lloyd R	lr-nelson@tamu.edu	Texas A & M University
Nevo, Eviatar	rabi301@haifauvm.bitnet	University of Haifa, Israel

Nicol, Julie	j.nicol@cgiar.org	CIMMYT–Turkey, Ankara
Nguyen, Henry T	bwlab@ttacs1.ttu.edu	Texas Tech University, Lubbock
Noll, John S	jnoll@em.agr.ca	AAFC–Winnipeg, Canada
Nyachiro, Joseph	jnyachir@gpu.srv.ualberta.ca	University of Alberta
O'Donoughue, Louise	em220cyto@ncccot2.agr.ca	AAFC–Canada
Ogbonnaya, Francis C	fc.ogbonnaya@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Ohm, Herbert W	hohm@purdue.edu	Purdue Univ, West Lafayette, IN
Ohm, Jay B	jay@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Oman, Jason	jason.oman@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Osipova, AV	gluten@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Paelo, Antonio D	adiazpaleo@cnia.inta.gov.ar	CRN INTA Castelar, Argentina
Park, SH	seokho@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Payne, Thomas	t.payne-t@cgiar.org	CIMMYT, Addis Ababa, Ethiopia
Penix, Susan	agsusan@mizzou1.missouri.edu	University of Missouri, Columbia
Permyakov, AV	gluten@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Perry, Keith	perry@btny.purdue.edu	Purdue University, W. Lafayette, IN
Perry, Sid	sidgsr@southwind.com	Goertzen Seed Research, Haven, KS
Pérez, Beatríz A	baperez@inta.gov.ar	INTA, Castelar, Argentina
Peterson, CJ	cjp@orst.edu	Oregon State University, Corvallis
Pickering, Richard	pickeringr@crop.cri.nz	Christchurch, NZ
Pomazkina, L	agroeco@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Pogna, Norberto	isc.gen@iol.it	Inst Exper Cereal, Rome, Italy
Porter, David	dporter@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Poulsen, David	davep@qdpit.sth.dpi.qld.gov.au	Warwick, Queensland AU
Poukhalskaya, Nina V	adiletnin@mtu-net.ru	Pryanishnikov Rus Res Inst, Moscow
Priillin, Oskar	ebi@ebi.ee	Estonian Agricultural University, Harku
Puebla, Andrea F	apuebla@cicv.inta.gov.ar	INTA, Castelar, Argentina
Pukhalsky, VA	pukhalsk@vigg.su	N.I. Vavilov Institute, Moscow
Qi, Lili	qilili@plantpath.ksu.edu	Kansas State University, Manhattan
Qualset, Cal	coqualset@ucdavis.edu	University of California–Davis
Quick, Jim	jim.quick@colostate.edu	Dakota Grow Pasta Co, Carrington, ND
Rabinovych, Svitlana	ppi@kharkov.ukrtel.net	Inst Plant Production, Karkiv, Ukraine
Rajaram, Sanjaya	srajaram@cimmyt.mx	CIMMYT, Mexico
Ram, MS	ramms@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Ratcliffe, Roger H	roger_ratcliffe@entm.purdue.edu	USDA–ARS, W. Lafayette IN
Ratti, C	cratte@tin.it	Istit Patologia Vegetale, Bologna, Italy
Raupp, W John	jraupp@ksu.edu	Kansas State University, Manhattan
Rayapati, John	nanster@iastate.edu	Iowa State University, Ames
Reddy, VRK	botany@bharathi.ernet.in	Bharathiar University, Coimbatore, India
Rekoslavskaya, NI	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Reisner, Alex	reisner@angis.su.oz.au	Australia
Rekoslavskaya, Natalya I	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Riera-Lizarazu, Oscar	oscar.rierd@orst.edu	Oregon State University, Corvallis
Roberts, John	jrobert@gaes.griffin.peachnet.edu	USDA–ARS, Griffin, GA
Rodríguez, Daniel	daniel.rodriguez@nre.vic.gov.au	Victorian Inst Dryland Agric, Australia
Rohrer, Wendy L	wrohrer@vt.edu	Virginia Tech, Blacksburg
Romig, Robert W	bobromig@aol	Trigen Seed Services LLC, MN
Rosa, OS	ottoni@ginet.com.br	OR Seed Breeding Co., Brazil
Rudd, Jackie	j-rudd@tamu.edu	Texas A&M Agric Res Cen, Amarillo
Rubies-Autonell, C	crubies@agrsci.unibo.it	Istit Patologia Vegetale, Bologna, Italy
Safranski, Greg	greg_safranski@entm.purdue.edu	Purdue University, W. Lafayette, IN
Salyaev, RK	phytolab@sifibr.irk.ru	Siberian Inst Plant Physiology, Russia
Sãulescu, Nicolae	saulescu@valhalla.racai.ro	Fundulea Institute, Romania
Schwarzacher, Trude	schwarza@bbsrc.ac.uk	JI Centre, Norwich, UK
Seabourn, BW	brad@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Sears, Rollie	rsears@flinthills.com	AgriPro Wheat, Junction City, KS
Seitz, LM	larry@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS

Sethi, Amit P	amit_sethi@hotmail.com	IARI, New Delhi, India
Shaner, Greg	shaner@btny.purdue.edu	Purdue University, W. Lafayette, IN
Sharma, Hari	hsharma@purdue.edu	Purdue University, W. Lafayette, IN
Sharp, Peter	peters@camden.usyd.edu.au	PBI Cobbitty, Australia
Sheppard, Ken	ksheppard@waite.adelaide.edu.au	University of Adelaide, Australia
Shields, Phil	shieldsp@phibred.com	Pioneer Hi-Bred, St. Matthews, SC
Shroyer, Jim	jshroyr@ksuvm.edu	Kansas State University, Manhattan
Shufran, Kevin A	kashufran@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Shukle, Rich	rich_shukle@entm.purdue.edu	Purdue University, West Lafayette, IN
Siddiqi, Sabir Z	dirrari@mul.paknet.com.pk	Reg Agr Res Inst, Bahawalpur, Pakistan
Singh, Gyanendra P	dwrpratap@rediffmail.com	IARI, New Delhi, India
Singh, JB	jbsingh1@rediffmail.com	IARI, New Delhi, India
Singh, Nirupma	nirupmasingh@rediffmail.com	IARI, New Delhi, India
Singh, Rajender	rsb@hau.nic.in	Ch Ch Singh Haryana Agric Univ, India
Singh, SS	singhss@rediffmail.ocm	IARI, New Delhi, India
Sinnot, Quinn	quinn@prime.ars-grin.gov	USDA–ARS, Beltsville, MD
Síp, Vaclav	sip@hb.vurv.cz	RICP, Prague, Czech Republic
Skovmand, Bent	bskovmand@cimmyt.mx	CIMMYT–Mexico
Smith, Joe A	jasmith@frii.com	AgriPro Seeds, Inc., Berthoud, CO
Snape, John	john.snape@bbsrc.ac.uk	JI Centre, Norwich, UK
Sorrells, Mark	mark_sorrells@qmrelay.mail.cornell.edu	Cornell University, Ithaca, NY
Sotnikov, Vladimir V	ncpgru@kharkov.ukrtel.net	Inst Plant Production, Kharkov, Ukraine
Spetsov, Penko	iws@eos.dobrich.acad.bg	Inst Wheat and Sunflower, Bulgaria
Steffenson, Brian	bsteffen@badlands.nodak.edu	North Dakota State University, Fargo
Stehno, IZ	stehno@vurv.cz	RICP, Prague, Czech Republic
Stift, G.	stift@ifa-tulln.ac.at	IFA-Tulln, Austria
Stoddard, Fred	stoddard@extro.ucc.edu.oz.ua	University of Sydney, Australia
Stuart, Jeffery J	jeff_stuart@entm.purdue.edu	Purdue University, W. Lafayette, IN
Stupnikova, IV	irina@sifibr.irk.ru	Siberian Inst Plant Physiology, Irkutsk
Subkova, OV	ariser@mail.saratov.ru	Agric Res Inst SE Reg, Saratov, Russia
Suchy, Jerry	isuchy@em.arg.ca	AAFC–Winnipeg, Manitoba, Canada
Sun, Mei	meisun@hkucc.hku.hk	Hong Kong University
Szabo, Les	lszabo@puccini.crl.umn.edu	USDA–ARS, University of Minnesota
Talbert, Luther	usslt@montana.edu	Montana State University, Bozeman
Therrien, Mario C	therrien@mbrsbr.agr.ca	AAFC–Manitoba, Canada
Throne, JE	throne@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Tewari, Vinod	vinodtiwari_iari@rediffmail.com	IARI, New Delhi, India
Tilley, M	mtilley@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Tinker, Nick	cznt@agradm.lan.mcgill.ca	McGill University, Canada
Tkachenko, OV	agm@ssau.saratov.ru	Saratov State Agrarian Univ, Russia
Tohver, Maimu	maimu.tohver@mail.ee	Estonian Agricultural University, Harku
Tomasovic, Slobodan	slobodan.tomasovic@zg.hinet.hr	Bc Institute, Zagreb, Croatia
Townley-Smith, TF	tsmith@em.agr.ca	AAFC–Winnipeg, Manitoba, Canada
Trottet, Maxime	mtrottet@rennes.inra.fr	INRA, Le Rheu Cedex, France
Torres, Lorena	letorres_k@yahoo.com.ar	University of Córdoba, Argentina
Tranquilli, Gabriela	granqui@cirn.inta.gov.ar	INTA Castelar, Argentina
Tsehaye, Yemane	yemtse@yahoo.com	Inst Biodiversity Conservation, Ethiopia
Tsujimoto, Hisashi	tsujimot@yokohama-cu.ac.jp	Kihara Institute, Japan
Urbano, Jose Maria	urbano@phibred.com	Pioneer Hi-Bred, Sevilla, Spain
D'utra Vaz, Fernando B	ferbdvaz@pira.cena.usp.br	University De Sao Paulo, Brazil
Vallega, Victor	vallegavictor@mclink.it	Exp Inst Cerealicoltura, Rome, Italy
Vassiltchouk, NS	ariser@mail.saratov.ru	ARISER, Saratov, Russia
Van Sanford, Dave	agr38@pop.uky.edu	University of Kentucky, Lexington
Varshney, Rajeev K	kumar@ipk-gatersleben,de	IPK, Gatersleben, Germany
Varughese, George	g.varughese@cgnet.com	CIMMYT, Mexico
Veisz, Ottó	veiszo@penguin.mgki.hu	ARI–HAS, Martonvásár, Hungary
Verhoeven, Mary C	Mary.C.Verhoeven@orst.edu	Oregon State University, Corvallis

Vida, Gyula	h8607vid@ella.hu	ARI–HAS, Martonvásár, Hungary
Von Allmen, Jean-Marc	bvonal@abru.cg.com	Ciba-Geigy, Basel, Switzerland
Voss, Márcio	voss@cnpt.embrapa.br	EMBRAPA, Passo Fundo, Brazil
Waines, Giles	waines@ucrac1.ucr.edu	University of California, Riverside
Walker-Simmons, MK	ksimmons@wsu.edu	USDA–ARS, Pullman, WA
Wang, Richard	rrcwang@cc.usu.edu	Utah State University, Logan
Ward, Richard	wadri@pilot.msu.edu	Michigan State University, East Lansing
Watanabe, Nobuvoshi	watnb@cc.gifu-u.ac.jp	Gifu University, Japan
Webster, James A	jwebster@pswcrl.ars.usda.gov	USDA–ARS, Stillwater, OK
Wesley, Annie	awesley@rm.agr.ca	AAFC–Winnipeg, Manitoba
Wildermuth, Graham	wilderg@prose.dpi.gld.gov.au	Leslie Research Centre, Australia
Williams, Christie	christie_williams@entm.purdue.edu	Purdue University, W. Lafayette, IN
Wilson, Dean	trio@feist.com	Trio Research, Wichita, KS
Wilson, Duane L	dlwil@ksu.edu	Kansas State University, Manhattan
Wilson, James A	trio@feist.com	Trio Research, Wichita, KS
Wilson, Jeff D	jdw@gmprc.ksu.edu	USDA–ARS–GMPRC, Manhattan, KS
Wilson, Paul	wilsonp@phibred.com	Pioneer Hi-bred, Northants, UK
Wilson, Peter	hwaust@mpx.com.au	Hybrid Wheat Australia, Tamworth
Worrall, David	agripro@chipshot.net	AgriPro Seeds, Berthoud, CO
Yen, Yang	yeny@ur.sdstate.edu	South Dakota State Univ, Brookings
Zeller, Frederich	zeller@mm.pbz.agrar.tu-muenchen.de	Technical University Munich, Germany
Zemetra, Robert	rzemetra@uidaho.edu	University of Idaho, Moscow
Zhang, Peng	pzhang@plantpath.ksu.edu	Kansas State University, Manhattan
Zhu, Yu Cheng	zhuyc@ag.gov	USDA–ARS, Stillwater, OK

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Grain Marketing Production and Research Center, USDA–ARS, Hard Red Winter Wheat Quality Laboratory, 1515 College Ave., Manhattan, KS 66502, USA.
M.B. Kirkhan, Departmrnt of Agonomy, Kansas State University, Manhattan, ID 66506-5501, USA.
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Fred L. Patterson, Purdue University, Department of Agronomy, 105 Lilly Hall, W. Lafayette, IN 47907, USA.
Patsy Sperry, 209 Johnson Hall, USDA–ARS Washington State University, Pullman, 99164-6420 WA, USA.

Contributions to $50
Harold Bockelman, USDA–ARS, P.O. Box 307, Aberdeen, ID 83210, USA.
Gaetano Boggini, Via Mulino 3, Instituto Sperimentale per la Cerealicoltura, S. Angelo Lodigiano, LO 26866, ITALY.
Phil Bruckner, Department of Plant Sciences and Plant Pathology, Montana State University, Bozeman, MT 59717 USA.
Xianming Chen, 361 Johnson Hall, P.O. Box 646430, Washington State University, Pullman, WA 99164-6430 USA.
Ahmed Mushtaq, B-2 Agricultural Colony, Regional Agricultural Research Institute, Bahawalpur, PAKISTAN.
Byrd C. Curtis, 1904 Sequoia Street, Ft. Collins, CO 80525-1540, USA.
Enzo Deambrogio, Via Macaro, 1, Producttoir Sementi S.P.A., Argelato (Bo) 44042, ITALY.
Jesse Dubin, 9705 Fleetwood Way, Frederick, MD 21701, USA.
Robert Graybosch, USDA–ARS, 1332 N. 38th St., Lincoln, NE 68503, USA.
Russell Karow, 107 Crop Science Building, Oregon State University, Corvallis, OR 97331-3002, USA.
Art Klatt, Department of Plant and Soil Sciences, 274 Ag Hall, Oklahoma State University, Stillwater, OK 74078, USA.
M.M. Kohli, CIMMYT, Andes 1365 #314, Montevideo 111000, URUGUAY.
Ricardo Hector Maich, Faculty of Ciencias Agropecuarias, Universidad Nacional Casillia de Correro, 509-C Central, 5000 Córdoba, ARGENTlNA.
D. Mares, Plant Science, Waite Campus, University of Adelaide, Glen Osmond 5064, AUSTRALIA.
Robert A. McIntosh, Plant Breeding Institute, Cobbitty, Private Bag 1, Camden NSW 2570, AUSTRALIA.
Craig Morris, USDA–ARS Western Wheat Quality Laboratory, E202 Food Quality Building, Washington State University, Pullman, WA 99164-6394, USA.
Hiro Nakamura, Japan International Research Center for Agricultural Sciences, Tsukuba Ibaraki, 305-8686, JAPAN.
Herbert W. Ohm, Purdue University, Department of Agronomy, 105 Lilly Hall, W. Lafayette, IN 47907, USA.
James S. Quick, Soil and Crop Sciences Department, Colorado State University, Ft. Collins, CO 80525, USA.
Ralf Schachschneider, Nordsaat Saatzucht GMBH, Hauptstrasse 1, D-38895 Bohnshausen, GERMANY.
Michael Tilley, USDA–ARS, U.S. Grain Marketing Production and Research Center, 1515 College Ave., Manhattan, KS 66502,USA.
Wayne E. Vian, 1207 Harrison Street, Grand Island, NE 68803-6352, USA.
Nobuyoshi Watanabe, Faculty of Agriculture, Gifu Univ., 1-1 Yanagido, Gifu 501-11, JAPAN.

X. VOLUME 50 MANUSCRIPT GUIDELINES.

Manuscript guidelines for the *Annual Wheat Newsletter*, volume 50. The required format for Volume 50 of the *Annual Wheat Newsletter* will be similar to Volume 49 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.

FORMATTING & SUBMITTING MANUSCRIPTS:

Follow the format in volume 44–49 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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DISTRIBUTION:

The primary method of distribution of Volume 50 will be CD-ROM in HTML format. These files can be read with any internet browser. A hard copy will be sent only if requested by 1 March, 2004, and will cost $40.

The *Annual Wheat Newsletter* will continue to be available (Vol. 37–49) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/ and Internet gopher access at "greengenes.cit.cornell.edu".

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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 $15 to $30 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 2004. The address for contibutions is Dr. Brett Carver, Department of Agronomy, Oklahoma State University, Stillwater, OK 74078, U.S.A.