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Catalogue of Gene Symbols for Wheat

RA McINTOSH[1], Y YAMAZAKI[2], J DUBCOVSKY[3], J ROGERS[4], C MORRIS[5], R APPELS[6] and XC Xia[7]

[1] The University of Sydney, Plant Breeding Institute Cobbitty, PMB 11, Camden, N.S.W., Australia, 2570. bobm@camden.usyd.edu.au

[2] National Institute of Genetics, 111 Yata Mishima, Shizuoka 411-8540 Japan. yyamazak@nig.ac.jp

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

[4] Catedra de Genetica y Fitotecnia, Facultad de Agronomia, Universidad Nacional del Centro de la Provincia de Buenos Aires, Argentina. Av. Rep. Italia 780, CC47 73 Azul, Provincie de Buenos Aires, Argentina. rogers@faa.unicen.edu.ar

[5] USDA-ARS Western Wheat Laboratory, Pullman, WA 99164-6394, U.S.A. craig.morris@ars.usda.gov

[6] Molecular Plant Breeding Research Centre, Biological Sciences, Murdoch University and Department of Agriculture, Locked Bag 4, Bentley Delivery Centre W.A. 6983, Australia. rappels@agric.wa.gov.au

[7] Institute of Crop Science, National Wheat Improvement Centre, Chinese Academy of Agricultural Sciences, 12 Zhongguancun South St, Beijing 100081, China. xiaxianchun@yahoo.com

PREFACE

This 2013 edition of the Catalogue of Gene Symbols for Wheat represents 45 years of curation of wheat genetic information which began with my appointment as Curator at the Third International Wheat Genetics Symposium held in Canberra, Australia, in 1968. Prior to that time there was a reference catalogue of 17 pages {047} published in Agronomy Journal. The current Catalogue exceeds 400 pages of information and references.

The objective of this Catalogue is to have a document that is helpful to a wide range of people, from 'coal-face' researchers to extension workers, and even farmers. Different sections of the Catalogue were prepared in different ways and a major challenge for our Japanese colleagues has been to continue to evolve the database as new information became available and as older material became less relevant. Consensus maps are not yet adequately integrated with the Catalogue. As we adapt to the increasing universality of genetics across species, we must not lose track of our agricultural background and the fact that our main target organism is polyploid wheat. Farmers grow wheat!

Annual supplements continue to be published in Annual Wheat Newsletter as well as displayed on the GrainGenes and Komugi websites. In the future it may be possible to update the entire database on an annual basis. I acknowledge the contributions of past members of the curation team, especially Drs Yukiko Yamazaki, Gary Hart, Mike Gale and Katrien Devos, as well as others, who from time to time helped with sectional revisions. Curators tend to do their best work on sections with which they are most familiar. In order to encompass the full breadth of wheat genetics and to present data in the best way, the suggestions and advice of all wheat workers are appreciated and suggested revision to any section are always welcome. I thank the University of Sydney and the Director of the Plant Breeding Institute, Professor Peter Sharp, for allowing me to continue to work in an honorary capacity.

My usual request for advice on the Catalogue (your catalogue!) is as imperative as in the past. Please advise omissions, errors, typos so we can fix them and your suggestions on better ways to provide and display wheat genetics information will always be welcome.

I would especially like to acknowledge and thank Dr Yukiko Yamazaki the tremendous effort in developing and maintaining the MacGene database and for provided the online updates over the past 14 years. Dr Yamazaki will be stepping down from that responsibility following this meeting.

R.A. McIntosh
September, 2013

CONTENTS

I. Gene Nomenclature

II. Catalogue of Gene Symbols for Wheat 2008

CATALOGUE INDEX

GeneClass

Morphological and Physiological Traits

    - 30.6. Mixograph peak time
    - 30.7. Starch characteristics
    - 30.8. Loaf volume
    - 30.9. Dough rheological properties
    - 30.10. Grain fructan content
    - 30.11. Water absorption
    - 30.12. Chinese dry noodle quality
31. Grass-Clump Dwarfness/Grass Dwarfness
32. Grain Weight
33. Growth Rate and Early Vigour
34. Hairy/Pubescent Auricles
35. Hairy Glume
36. Hairy Leaf
37. Hairy Leaf Sheath
38. Hairy Neck/Pubescent Peduncle
39. Hairy Node/Pubescent Node
40. Heat tolerance
41. Height
    - 41.1. Reduced Height : GA-insensitive
    - 41.2. Reduced Height : GA-sensitive
    - 41.3. Reduced Height : QTL
42. Herbicide Response
    - 42.1. Difenzoquat insensitivity
    - 42.2. 2,4-D tolerance
    - 42.3. Chlortoluron Insensitivity
    - 42.4. Imidazolinone resistance
43. Hybrid Weakness
    - 43.1. Hybrid necrosis
    - 43.2. Hybrid chlorosis type 1
    - 43.3. Hybrid chlorosis type 2
    - 43.4. Apical lethality
44. Iron Deficiency
45. Lack of Ligules
46. Leaf Erectness
47. Leaf Tip Necrosis
48. Lesion Mimicry
49. Lodging
50. Male Sterility
    - 50.1. Chromosomal
    - 50.2. Sterility in hybrids with wheat
    - 50.3. Photoperiod and/or temperature-sensitive male sterility (PTGMS)
51. Manganese Efficiency
52. Maturity time
53. Megasporogenesis
    - 53.1. Control of megasporogenesis
54. Meiotic Characters
    - 54.1. Low-temperature pairing
    - 54.2. Pairing homoeologous
    - 54.3. Inhibitor of pairing homoeologous
55. Nitrate Reductase Activity
56. Nuclear-Cytoplasmic Compatability Enhancers
57. Nucleolus Organizer Regions
    - 57.1. 18S - 5.8S - 26S rRNA genes
58. Osmoregulation
59. Phenol Colour Reaction of Kernels
60. Pollen Killer
61. Polyphenol Oxidase (PPO) Activity

62. Red Grain Colour
63. Reaction to Black-Point of Grain
64. Response to Photoperiod
65. Response to Salinity
   65.1. K+/Na+ discrimination
   65.2. Salt tolerance
   65.3. Sodium exclusion
66. Response to Tissue Culture
67. Response to Vernalization
68. Restorers for Cytoplasmic Male Sterility
   68.1. Restorers for *T. timopheevi* cytoplasm
   68.2. Restorers for *Aegilops longissima* cytoplasm
   68.3. Restorers for photoperiod-sensitive *Aegilops crassa* cytoplasm
69. Ribosomal RNA
   69.1. 5S rRNA genes
70. Seedling Leaf Chlorosis
71. Segregation Distortion
72. Soft Glumes
73. Sterol Esterification in Kernels - Synthesis of b-Sitosterol Esters
74. Stem solidness
75. Temperature-Sensitive Winter Variegation
76. Tenacious Glumes
77. Tiller Inhibition
78. Uniculm Stunt
79. Variegated Red Grain Colour
80. Yield and Yield Components
   80.1. Grain number per spike
   80.2. Grain volume weight
   80.3. Grain weight
      80.3.1. 50-grain weight
      80.3.2. 1000-grain weight
      80.3.3. Test weight
   80.4. Grain weight/ear
   80.5. Grain yield
   80.6. Kernel number per square metre
   80.7. Spikelet number/ear
   80.8. Spike number per plant
   80.9. Spike number per square metre
   80.10. Spike length
   80.11. Tiller number/plant
81. Yellow Berry Tolerance

Proteins

82. Proteins
   82.1. Grain protein content
   82.2. Enzymes
      82.2.1. Acid phosphatase
      82.2.2. Alcohol dehydrogenase (Aliphatic)
      82.2.3. Aminopeptidase
      82.2.4. Alpha-amylase
      82.2.5. Beta-amylase
      82.2.6. Endopeptidase
      82.2.7. Esterase
      82.2.8. Glucosephosphate isomerase
      82.2.9. Glutamic oxaloacetic transaminase
      82.2.10. Hexokinase

        - 82.2.11. Lipoxygenase
        - 82.2.12. Malate dehydrogenase
        - 82.2.13. Peroxidase
        - 82.2.14. Phosphodiesterase
        - 82.2.15. Phosphogluconate dehydrogenase
        - 82.2.16. Phosphoglucomutase
        - 82.2.17. Shikimate dehydrogenase
        - 82.2.18. Superoxide dismutase
        - 82.2.19. Triosephosphate isomerase
        - 82.2.20. Aromatic alcohol dehydrogenase
        - 82.2.21. Aconitase
        - 82.2.22. NADH dehydrogenase
        - 82.2.23. Dipeptidase
        - 82.2.24. Malic enzyme
        - 82.2.25. Adenylate kinase
        - 82.2.26. Glutamate-pyruvate transaminase
        - 82.2.27. Catalase
        - 82.2.28. Beta-glucosidase
        - 82.2.29. Starch branching enzyme I
        - 82.2.30. Starch branching enzyme II
        - 82.2.31. Benzoxinones
        - 82.2.32. Acetohydroxyacid synthase (EC 4.1.3.18)
        - 82.2.33. Phytoene synthase
        - 82.2.34. Polyphenol oxidase
        - 82.2.35. Protein disulfide isomerase (EC 5.3.4.1)
        - 82.2.36. Isoamylase 1
        - 82.2.37. Polygalacturonase-inhibiting proteins
        - 82.2.38. Flavone 3-hydroxylase (EC 1.14.11.9)
        - 82.2.39. Zeta-carotene desaturase
        - 82.2.40. Carotenoid beta-hydroxylase (non-heme di-iron type)
    - 82.3. Endosperm storage proteins
        - 82.3.1. Glutenins
        - 82.3.2. Gliadins
        - 82.3.3. Other endosperm storage proteins
    - 82.4. Enzyme Inhibitors
        - 82.4.1. Inhibitors of alpha-amylase and subtilisin
        - 82.4.2. Inhibitors (dimeric) of heterologous alpha-amylases
        - 82.4.3. Subtilisin inhibition
        - 82.4.4. Trypsin inhibition
    - 82.5. Other proteins
        - 82.5.1. Grain softness protein
        - 82.5.2. Histone H1 Proteins
        - 82.5.3. Iodine binding factor
        - 82.5.4. Lipopurothionins
        - 82.5.5. Lectins
        - 82.5.6. Puroindolines and grain softness protein
        - 82.5.7. Endosperm-specific wheat basic region leucine zipper (bZIP) factor storage activator
        - 82.5.8. Salt soluble globulins
        - 82.5.9. Serine protease inhibitors
        - 82.5.10. Starch granule proteins
        - 82.5.11. Starch synthase
        - 82.5.12. Water soluble proteins
        - 82.5.13. Waxy proteins

Pathogenic Disease/Pest Reaction

I Gene Nomenclature

1. Recommended Rules for Gene Symbolization in Wheat

Adapted from the International Rules of Genetic Nomenclature and compiled by R.A. McIntosh;approved at the 4th IWGS

1.1. In naming hereditary factors, the use of languages of higher internationality should be given preference.

1.2. Symbols of hereditary factors, derived from their original names, should be written in italics, or in Roman letters of distinctive type.

1.3. Whenever unambiguous, the name and symbol of a dominant should begin with a capital letter and those of a recessive with a small letter (see also special rules for symbolizing biochemical and DNA loci and host:pathogen/pest systems).

1.4. All letters and numbers used in symbolization should be written on one line; as far as possible no superscripts or subscripts should be used.

1.5. The plus sign (+) will not be used in symbolization of hereditary factors in wheat.

1.6. Two or more genes having phenotypically similar effects should be designated by a common basic symbol. Non-allelic loci (mimics, polymeric genes, etc.) will be designated in accordance with two procedures:
(i) in sequential polymeric series where an Arabic numeral immediately follows the gene symbol; e.g., *Sr9*.
(ii) in orthologous sets where the basic symbol is followed by a hyphen ("-") followed by the locus designation taking the form of the accepted genome symbol and a homoeologous set number represented by an Arabic numeral; e.g., *Adh-A1* designates the A-genome member of the first *Adh* set. Different alleles, or alleles of independent mutational origin, are designated by a lower-case Roman letter following the locus number designation; e.g., *Sr9a, Adh-Ala.* (See also guidelines for nomenclature of biochemical and DNA loci).

1.7. Temporary symbol designations: Where linkage data are not available, provision has been made for temporary symbols. These shall consist of the basic symbol followed by an abbreviation for the line or stock and an Arabic number referring to the gene; e.g., *SrFr1*, *SrFr2*, etc., refer to two genes for reaction to *Puccinia graminis* in cultivar Federation. It is recommended that official records of temporary designations be kept, but it is not essential that subsequent numbers from other laboratories (e.g., *SrFr3*) be checked against earlier numbers either phenotypically or genetically.

1.8. Inhibitors, suppressors, and enhancers are designated by the symbols *I, Su,* and *En*, or by *i, su,* and *en* if they are recessive, followed by a space and the symbol of the allele affected.

1.9. In wheat and related species, linkage groups and corresponding chromosomes are designated by an Arabic numeral (1-7) followed by genome designated by a capital Roman letter; i.e., for hexaploid wheat of group *aestivum* (Morris and Sears {1038}), 1A-7D. This system supersedes the original designations using Roman numerals; i.e., I-XXI. The designations for homoeologous group 4 chromosomes of wheat are as agreed at Workshop I, 7th International Wheat Genetics Symposium, Cambridge, UK (see Proceedings, Miller TE & Koebner RMD eds. pp. 1205-1211); that is, the previously designated chromosome 4A was redesignated 4B and the previous 4B was redesignated 4A. Consequently, the former 4AS became 4BS and the former 4AL is 4BL. Likewise, the former 4BS and 4BL were redesignated 4AS and 4AL, respectively. Chinese Spring is accepted as having the standard chromosome arrangement. Chromosome arms (or telocentric chromosome derivatives) are designated S (short), L (long), on the basis of relative arm length within the chromosome. In the case of equal arms they are arbitrarily designated S or L on the basis of homoeology with the short or long arms of the other chromosomes of their homoeologous group (see Workshop I Proceedings of the 7th International Wheat Genetics Symposium).

1.10. Genetic formulae may be written as fractions, with the maternal alleles given first or above. Each fraction corresponds to a single linkage group.

1.11. Chromosomal aberrations should be indicated by the abbreviations Df for deficiency, Dp for duplication, In for inversion, T for translocation, and Tp for transposition. In wheat there are a number of genes derived from related species by introgression. Such genes in different instances reside at different locations. One location may be taken as standard. Other locations will be considered as transpositions relative to a designated standard. When a gene does not reside in its standard chromosome position, the new chromosome designation may be given in brackets following the gene designation; e.g., Hp (Tp 6D) refers to a line carrying the introgressed "hairy neck" gene on chromosome 6D instead of 4B which is taken as standard. Alternatively, the chromosome involved may be described as a translocation. Guidelines for the description of translocated chromosomes both within wheat, and between wheat and alien chromosomes are provided in {705}.

1.12. The zygotic number of chromosomes is indicated by 2n, the gametic number by n and the basic number by x.

1.13. Symbols for extra-chromosomal factors should be enclosed within brackets and precede the genetic formula.

2. Guidelines for Nomenclature of Biochemical Molecular Loci in Wheat and Related Species

Developed by G.E. Hart and M.D. Gale {515} and approved at the 7th IWGS

2.1 Biochemical nomenclature: Biochemical nomenclature should be in accordance with the rules of the Joint Commission of Biochemical Nomenclature (JCBN) of the International Union of Pure and Applied Chemistry. The nomenclature recommended by the JCBN is published periodically in major international biochemical journals, such as the Journal of Biological Chemistry and the European Journal of Biochemistry. Also, for enzymes, the publication Enzy me Nomenclature {035,036} may be consulted. Enzymes and other macromolecules have both formal and trivial names. The formal name should be given the first time a macromolecule is mentioned in a publication; the trivial name or an abbreviated name may be used subsequently. For example, ADH is the commonly used abbreviation for aliphatic alcohol dehydrogenase (E.C.1.1.1.1; Alcohol: NAD+oxidoreductase).

2.2 Symbols for gene loci and alleles

2.2.1 *Basic symbol*: The basic symbol for a gene locus should consist of a two-, three-, or fourletter abbreviation of the trivial name of the enzyme, protein, or other macromolecule affected. The initial letter should be a capital and all characters in the symbol should be italicised.

2.2.2 *Loci specifying the structure of similar macromolecules*: Non-allelic gene loci that specify the structure of similar non-enzymatic proteins, of enzymes that catalyse the same or similar reactions, or of similar RNA molecules should be assigned the same basic symbol. The remainder of the symbol for each such locus should be formulated in accordance with one or the other of two procedures, depending upon whether or not evidence is available to assign the locus to an homologous set.

2.2.2.1 Loci that are members of an orthologous set. The basic symbol should be followed by a hyphen (-), the accepted symbol for the genome to which the locus belongs and an homologous set number in the form of an Arabic numeral. For example, *Adh-A1*, *Adh-B1*, *Adh-D1* and *Adh-E1* designate the A-, B-, D-, and E- genome members, respectively, of the first-designated homologous set of aliphatic alcohol dehydrogenase structural gene loci. Identification of a minimum of two members of a set is required to use this nomenclature.

2.2.2.2 Other loci. In the absence of evidence to assign loci to an homologous set, they should be designated in sequential series by a common basic symbol followed immediately by an Arabic numeral. If evidence to assign the loci to an homologous set is obtained subsequently, the loci should be re-designated in accordance with the procedures in section 2.2.2.1.

Rye loci should be designated in accordance with these procedures (see {1448}). For barley loci, the procedures described in section 2.2.2.1 should be used when designation of a locus as a member of an homologous set of Triticeae loci is desired; otherwise, barley genetic nomenclature should be employed. Thus, for example, *Adh-H1* and *Adh-R1* designate the H- and R- genome members, respectively, of the *Adh-1* set of loci.

Evidence regarding phylogenetic relationships among structural genes may be obtained by comparative studies of (1) nucleotide sequences and other molecular properties of genes, (2) physical and/or biochemical properties of gene products, and (3) intra-chromosomal map positions and/or physical locations of genes in homoeologous chromosomes or segments. Criteria for determining whether or not gene loci that encode isozymes are homologous and, for homologous gene loci, whether they belong to the same or different homologous sets, are described in {512}. Most of the criteria are also applicable to nonenzymatic proteins. The evidence that is the basis for designating gene loci as members of an homologous set should be stated in the publication in which symbols for the loci are proposed.

2.2.3 *Alleles*: Different alleles are designated by a lower case italic letter following the locus designation. For example, *a-Amy-A1a* and *a-Amy-A1b* are two alleles of the A genome *a-Amy-1* locus. One strain should be designated the prototype strain for each allele discovered, since variation that has not been detected by the methods used may be present within each allelic class. Currently, Chinese Spring should be the prototype for allele 'a'. If an apparently identical allele in other strains is found by new methods to be different from that in the prototype strain, it should be assigned a new lower case italic letter and a prototype strain designated. This system allows the orderly assignment of symbols to newly-identified alleles and allows ready comparisons of new variants with previously reported variants.

2.2.4 Haplotypes Alleles are based on phenotype. Haplotypes refer to DNA sequences of unspecified length within alleles, or anonymous DNA; for example, incomplete gene sequences, open treading frames, and may include variable upstream and downstream regions. Haplotypes designated sequentially within alleles should be specific to particular projects or publications.

2.3. Gene complexes

Gene complexes, also called compound loci, consist of a number of functionally related genes that are genetically closely linked. Whether composed of a few or many genes, a gene complex should be assigned one symbol, in accordance with the procedures described in section 2.2. The individual genes that compose gene complexes may be designated by adding a hyphen (-) and an Arabic numeral to the locus designation. For example, *Glu-A1-1* and *Glu-B1-1* designate, respectively, the A- and B- genome genes that encode the x-type glutenin-1 proteins while *Glu-A1-2* and *Glu-B1-2* designate, respectively, the A- and B-genome genes that encode the y-type glutenin-1 proteins. Different alleles of genes that are components of gene complexes may be designated following the system described in section 2.2.2, but with the lower-case italic letter following the gene designation rather than the locus designation. For example, *Glu-A1-1a* designates the Chinese Spring A genome allele that encodes the x- type glutenin-1 protein. Triticeae enzyme and protein gene loci are commonly initially identified and assigned designations based on studies of aneuploid strains that lack and/or contain extra copies of whole chromosomes or telosomes. Consequently, evidence may be obtained for the production of two or more similar enzyme or protein promoters by one chromosome arm without genetic evidence as to whether or not the promoters are the products of one gene, of different genes that are members of a gene complex, or of two or more genes that are not members of one gene complex. In these situations, only one locus designation for similar proteins or enzymes should be assigned to a chromosome arm until recombination evidence indicates otherwise.

2.4. Phenotype symbols

The basic symbol for a macromolecule should be identical to the basic symbol for the locus or loci that encode the macromolecule (see Section 2.2.1) except that each letter in the symbol should be a capital Roman letter. For a macromolecule encoded by the members of a homologous set of loci, the phenotype symbol should consist of the basic symbol followed by a hyphen (-) and the same Arabic numeral as is contained in the genotype symbol. For example, the products of the *Adh-1* set of gene loci are designated ADH-1.

2.5. Symbols for DNA markers and alleles

This section describes nomenclature for genetic markers that are detected at the DNA level, including those detected by hybridization with DNA probes [e.g., RFLPs (restriction-fragment-length polymorphisms)) and by amplification with primers [e.g. RAPDs (random-amplified-polymorphic DNAs) and STSs (sequence-tagged sites, including loci detected with sequenced RFLP clones, sequenced RAPDs and clones containing micro- and mini-satellites).

2.5.1 *Basic symbol*: The basic symbol for DNA markers of unknown function should be 'X'

2.5.1.1 Locus symbols : The ‘X’ should be followed by a laboratory designator (see section 8), a number that identifies the probe or primer(s) used to detect the locus, a hyphen (-), and the symbol for the chromosome in which the locus is located. The laboratory designator and number should be assigned by the laboratory that produced the clone or sequenced the primer(s) or, if that laboratory chooses not to do so, then by the laboratory that mapped the locus. The number should consist of one or more Arabic numerals and should begin with a numeral other than zero, i.e. numbers such as ‘01', ‘001', and ‘002' should not be used. The number assigned to a probe need bear no relationship to the name of the clone used to produce the probe and, likewise, the number assigned to a primer(s) need bear no relationship to any name that may have been assigned to the prime r(s). The letters in the laboratory designator should be lower-case and all characters in the locus symbol should be italicized. For example, *Xpsr119-7A* designates an RFLP locus located in chromosome 7A detected with *P*lant *S*cience *R*esearch probe 119 of the John Innes Centre. DNA markers detected in different chromosomes with the same probe or primer(s) should be assigned the same symbol except for the chromosome designation. For example, *Xpsr119-7D* and *Xpsr119-4A* designate other loci detected with probe 119.

2.5.1.2 Locus symbols for DNA markers detected with ‘known-function’ probes or with primers that amplify genes: The locus symbols for RFLP markers of unknown function that are detected with ‘known-function’ probes may include, in parentheses following the probe number, a symbol for the gene from which the probe was obtained. For example, *Xpsr804(Sbp)-3A* designates a chromosome 3A locus detected with a sedoheptulose-1,7-bisphosphatase gene probe. Likewise, when the primers used to amplify a DNA marker of unknown-function are of sufficient length and similarity to a known gene to amplify the gene, the DNA-marker symbol may include the gene symbol in parentheses following the number assigned to the primers. For genes for which the Commission on Plant Gene Nomenclature has assigned mnemonic designations, the set number and other numbers assigned by the Commission may also be included inside the parentheses immediately after the gene symbol.

2.5.2 *'Known-function' DNA Markers*: Loci that are detected with a DNA probe or DNA primers and whose function has been demonstrated should be designated with a symbol that indicates the function of the locus, as described in either Section 2 or in the Recommended Rules for Gene Symbolization in Wheat. It must be emphasized, however, that some clones and primers are likely to detect both loci whose function is known (proven, for example, by a segregational test against allelic forms of a gene encoding a protein) and additional loci of unknown (i.e. unproven) function (either pseudogenes or unrelated loci whose sequence homology to the probe or primers is sufficient to allow detection by it). In this case, the two types of loci require different nomenclature, namely, that described in Section 2, or in the Recommended Rules for Gene Symbolization in Wheat and in Section 2.5.1, respectively.

2.5.3 *Duplicate DNA-marker loci*: DNA markers located in the same chromosome that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the addition of a period and an Arabic numeral immediately after the chromosome designation. For example, *Xpsr933-2A.1* and *Xpsr933-2A.2* designate duplicate loci located in 2A that are detected with probe PSR933. As when two or more enzyme or protein promoters are produced by one chromosome arm, multiple DNA fragments from one chromosome arm that hybridize to one probe or that are amplified by one pair of primers (or by one primer) should be assigned to only one locus until recombination evidence indicates otherwise. As noted in Section 2.5.1, DNA markers located in different chromosomes that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the chromosome designation.

2.5.4 *Allele symbols*: Alleles should be designated as outlined in Section 2.2.3 with the exception that restriction-enzyme-specific alleles, e.g. RFLP- and indirect-STS alleles, should be designated with the name of the restriction enzyme followed by a lower-case letter. For example, *Xtam-5A-HindIIIa* denotes an allele detected with *Hind*III. Where possible, Chinese Spring should be the prototype for allele ‘a’. When a double-digest is used to detect an allele, both restriction enzymes should be listed, separated by a slash.

The name and source of the probe or primer(s) and the length(s) of the DNA fragment(s) detected normally should be stated in the first publication describing an allele.

2.5.5 *Abbreviation of locus and allele symbols*: The chromosome designation is an integral part of the locus symbol for DNA markers. Nevertheless, on chromosome maps and in a limited number of other contexts, the chromosome designation and the hyphen preceding it may be omitted. For example, *Xpsr35-3A* may be abbreviated as *Xpsr35* on a map of chromosome 3A, *Xpsr933-2A.1* and *Xpsr933-2A.2* may be abbreviated as *Xpsr933.1* and *Xpsr933.2*, respectively, on a map of 2A, and *Xpsr804(Sbp)-3A* may be abbreviated as *Xpsr804(Sbp)* on a map of 3A. Also the chromosome designation and the hyphen preceding it may be omitted on chromosome maps from the symbols for intrachromosomally duplicated loci that are detected with a ‘known-function’ probe (or with primers that amplify a gene) but that do not include a gene symbol. For example, if *Xtam200-1A.1* and *Xtam200-1A.2* were the symbols for duplicated loci detected with a ‘known-function’ clone designated TAM200, the symbols could be abbreviated as *Xtam200.1* and *Xtam200.2* respectively, on a map of 1A.

Finally, *Xbgl485(Ger)-4D.2* may be abbreviated on a map of 4D by omission of the hyphen, the chromosome designation and the period, i.e. as *Xbgl485(Ger)2*. In some contexts it will also be possible to abbreviate the symbols for alleles as, for example, *BamH1b*, or even simply *b*.

2.5.6 *Laboratory designators*: Laboratory designators should consist of from two to four and preferably three letters. When used in locus symbols, all of the letters should be lowercase and italicized (see Section 6.1.2).

Laboratory designators should be chosen carefully to insure that they differ both from those used by other laboratories and from those that compose gene symbols. As an aid in this regard, a list of laboratory designators that have appeared in the literature is available electronically via the Internet Gopher from host greengenes.cit.cornell.edu, port 70, menu “Grains files to browse” / “Reserved Laboratory Designators for DNA Probes, Primers and Markers”.

Laboratories that are investigating DNA markers in different species and/or of different types, e.g., RFLPs, STS, and RAPDs, may choose to use more than one designator. For example, oat and barley cDNA clones isolated at Cornell University have been designated with the prefixes CDO and BCD, respectively, and *cdo* and *bcd*, respectively, are appropriately used as laboratory designators in symbols for loci detected with these clones.

Likewise, *tam* and *txs*, respectively, are being used as laboratory designators in symbols for loci detected with wheat and sorghum DNA clones isolated at Texas A&M University, and the John Innes Centre is using *psr* and *psm* as laboratory designators in the symbols for DNA markers detected with wheat and millet probes, respectively, and *psp* for wheat PCR markers.

2.5.7 *Clone designations*: Clone designations should minimally identify the type of vector, the species from which the cloned DNA was obtained, and the source laboratory and cloned DNA, in that order. p = plasmid, l = lambda, c = cosmid, and m = M13 should be used to identify vectors. Initials of the species name, e.g., TA = *Triticum aestivum* and SC = *Secale cereale*, should be used to designate the source of the cloned DNA and a unique letter-number combination chosen by the source laboratory should be used to designate the source laboratory and the cloned DNA.

3. Symbols for Loci and Alleles Controlling Quantitative Characters

Developed largely by G.E. Hart and approved at the 8th IWGS

3.1 Genes identified by segregational analysis: Symbols for loci and alleles controlling quantitative characters that are identified by segregational analysis should be in accord with the Recommended Rules for Gene Symbolization in Wheat.

3.2 Quantitative trait loci (QTLs): QTLs are loci controlling quantitative characters whose allelic classes do not exhibit discontinuous variation or clear segregational patterns. They are identified by association with one or more linked markers.

3.2.1 *Basic symbol*: The basic symbol for QTLs should be ‘*Q*’.

3.2.2. *Locus symbols*: The ‘*Q*’ should be followed by a trait designator, a period, a laboratory designator (see Section 8), a hyphen (-) and the symbol for the chromosome in which the QTL is located. The trait designator should consist of no more than four and preferably three letters, the first of which is capitalized. Different QTLs for the same trait that are identified in one chromosome should be assigned the same symbol except for the addition of a period and an Arabic numeral after the chromosome designation. All characters in the locus symbol should be italicized. For example, *QYld.psr-7B.*1 and *QYld.psr-7B.2* would designate two yield QTLs identified in chromosome 7B by the John Innes Centre. On a map of 7B, these could be abbreviated as *QYld.psr.1* and *QYld.psr.2*. R^2 values,where given, indicate the proportion of variation explained by the QTL.

3.2.3 *Allele symbols*: Alleles at QTL loci should be designated by a lower-case italic letter following the locus designation.

4. AFLP: Amplified Fragment Length Polymorphism

Developed largely by M.D. Gale and approved at the 8th IWGS

A nomenclature proposal for AFLP loci has been received from Marc Zabeau at Keygene with the format '*XxyzAN1N2N3*, where '*X*' is the usual symbol for a DNA marker of unknown function; 'xyz' is the usual laboratory designator (e.g., *kg* for Keygene); A is a single upper-case letter denoting the rare-cutter enzyme used, e.g., P for *PstI*, etc.; N1 and N2 are two-digit numbers identifying standard one, two or three base-pair extensions (standard lists will be provided by Keygene); and N3 is a three-digit number corresponding to the molecular weight of the fragment.

The foregoing should be considered only as a proposal at this time as no AFLPs are listed in the catalogue. Comments regarding the proposal are welcomed and should be sent to the authors.

5. Single Nucleotide Polymorphism

Submitted for approval at the 11IWGS

Single nucleotide polymorphisms (SNP) will be designated using the Genebank accession number followed by a dash (-) and the nucleotide position. For example, *BF482680-541-4B* will represent an SNP at position 541in the alpha tubulin gene on chromosome 4B. Where appropriate, *SNP* and *-4B* can be deleted.

6. Guidelines for Nomenclature of Genes for Reaction to Pathogenic Diseases and Pests

Approved at the 4th IWGS

6.1. Symbol: All genes for resistance (low reaction) will be designated with a capital letter, even though they behave as recessive alleles. Moreover, the dominance of individual alleles may vary with the environment, the genetic background and the particular culture of the pathogen. Symbols for disease/pest-reaction genes are used by people of many disciplines, and since they are frequently communicated verbally, dominance relationships are not clear. Those alleles initially designated with a lower-case letter have tended to be miswritten with a capital. For example, the usually recessive resistance allele *Sr17* was initially designated *sr17* but its presentation in some reports was confusing.

6.2. Pleiotrophic genes: Where no recombination occurs between genes conferring resistance to more than one pathogen, the gene(s) segment shall be designated separately for each disease; e.g. *Pm1, Sr15* and *Lr20.*

6.3. Alleles: Where recombination occurs between two closely linked factors for reaction to a pathogen, the recombined ‘allele’ may be designated as a combination of the separate alleles; e.g. the recombined ‘allele’ obtained by combining *Lr14a* and *Lr14b* was designated as *Lr14ab*. The decision as to whether a designation should be as a combination or as separate genes shall be at the discretion of particular workers. A maximum value of 1 crossover unit for designation as an ‘allele’ is suggested.

Although the need to consider uniform symbolization of corresponding genes in pathogens is recognized, no recommendations are proposed.

7. Organisation of the Catalogue

7.1. Data listing

Information is given in the following order, where possible:

1. Gene symbol, with principal reference to the particular gene or gene symbol in parenthesis.
2. Synonyms (with reference(s) in parenthesis).
3. Chromo some and chromosome-arm location, if known, with references in parenthesis.
4. Stocks carrying the particular gene in order of presentation.

i: = Near-isogenic stocks, with number of backcrosses indicated.
s: = Homologous chromosome-substitution stocks, with number of backcrosses indicated.
tr: = Translocation line of common wheat.
v: = Cultivaral hexaploid stocks in increasing order of genetic complexity.
v2 : = Cultivaral hexaploid stocks with two or more genes affecting the trait.
ad: = Alien chromosome addition line.
su: = Alien chromosome substitution line.
itv: = Near-isogenic tetraploid stocks.
tv: = Tetraploid stocks.
tv2: = Tetraploid stocks with two or more genes affecting the trait.
idv: = Near-isogenic line of diploid wheat.
dv: = Diploid stocks.
al: = Alien species.
ma: = Reference to mapping information involving agronomic and morphological traits and molecular markers under gene entries will generally be restricted to values of less than 10 cM. Values higher than this would be of less use in genetics and plant breeding and, in any case, should be available from the genetic linkage section of the Catalogue or from genetic maps. Higher values will be used in the case of flanking markers.
c: = Cloning details and gene structure

Where more than a single gene affecting a character is listed, e.g., Gabo *D3* {645} under *D1*, the reference refers to the literature source reporting *D1* in Gabo, and not necessarily to *D3*. Abbreviations: CS =Chinese Spring; Tc = Thatcher.

7.2 DNA Markers

See 'Genetic nomenclature proposal' in Introduction for a proposal for the naming of AFLP loci.

The following list catalogues DNA-marker loci that (1) were detected either by Southern hybridization of DNA restriction fragments or as sequence-tagged-sites by amplification of DNA fragments with primers and (2) have been localized to specific wheat chromosomes. The formal listings of the 5S-RNA or 18S-5.8S-26S rRNA (Nor) loci are included elsewhere in the catalogue. No attempt has been made to list orthologous loci in related species, although many have been identified {e.g., 1329,1330}. In addition we list genes that appear on consensus maps prepared by Dr R. Appels and various colleagues.

The nomenclature used is that originally published in the 1994 Supplement, except for some loci detected with 'known-function' clones for which other nomenclature has been used in the publications cited. The reference(s) that follow the locus symbols designate the publication(s) in which the chromosomal locations or map positions of the loci were first reported. References that are in parentheses { } contain the listed locus symbol. Temporary symbols for a few DNA markers detected with known-function DNA probes are marked with an asterisk, *, ; these are temporary, pending assignment of the laboratory designator.' Synonyms are listed in parentheses [ ] in the second column. Where symbols were assigned by the curators to comply with nomenclature guidelines the same reference numbers follow the gene symbol and the synonym. Other chromosomes bearing markers detected with the same probe or the same primers are indicated in parentheses after the probe or the primers. To permit flexibility in using the database, each homoeologous group is bracketed separately.

Three revisions were made in the organization of the DNA Markers section, as follows:

1. Markers in homoeologous chromosome groups 4, 5 and 7 (with the exception of those in T. monococcum chromosome 4Am; see #2 below) are listed in groups composed of loci located in homoeologous segments. The groups include the six classical homoeologous arm groups, namely, 4S (4AL:4BS:4DS), 4L (4AS:4BL:4DL), 5S (5AS:5BS:5DS), 5L (5AL:5BL:5DL), 7S (7AS:7BS:7DS) and 7L (7AL:7BL:7DL), and five new groups, 4AL:4BL:4DL, 5AL:4BL:4DL,

4AL:5BL:5DL, 7BS:5BL:7DS, and 7AS:4AL:7DS. Evidence is not available regarding the correct group location for a few of the markers listed in groups 4S, 4L, and 7S; a double asterisk (**) after the locus reference identifies these markers.

2. Markers in T. monococcum $4A_m$ are listed separately (under $4A_mS$, $4A_mL$, or $4A_m$), due to the several rearrangements that distinguish 4A and $4A_m$.
3. Superscripts appended to locus references designate the species in which loci were analyzed, as follows,

'1'	*T. aestivum,*
'2'	*T. turgidum,*
'3'	*T. monococcum,*
'4'	*Ae. tauschii*, and
'5'	Species hybrid,

with the exception that the superscript is omitted for markers studied only in *T. aestivum*.

'a' Designates primer pairs that identify loci that cap the genetic maps. The forward primer is a degenerate telomeric sequence and the reverse primer is a specific sequence. Each primer combination identified multiple loci; however, only telomeric *(Tel)* loci are included {888}.
'b' Designates loci detected by hybridization with DNA clones whose sequences are largely homologous with known gene in the EMBL database (1392).

STS's from RFLP clones: Certain STS markers are listed using sequences from previously listed RFLP clones. The convention adopted is to add a 'p' to the laboratory designator. The 'References' to PCR markers refer, however, to the paper(s) which reported the first chromosomal location detected by this PCR marker.

Order of presentation: Gene, synonym, map location (approximate distance in cM from the terminal end of the short arm), probe, all known locations in homoeologous groups. In the output files genes appear in alphabetical order with locus numbers in ascending order.

Note: Due to limitations with the database, Greek symbols were converted to words or Roman letters (alpha or a, beta or b, etc). For author names with accents or special letters, the most similar Roman letter
was used.

8. Laboratory Designators

* In part indicates basis for name.

abc (Barley cDNA* clones)
Kleinhofs, A.
North American* Barley*
Genome Mapping Project
Dept. of Agronomy & Soils
Washington State University
Pullman, WA 99164
USA

abg (Barley genomic* clones)
Kleinhofs, A. (see abc)

abl *Forster, J.W.
Institute of Biological Sciences
Sir George Stapleton Building
University of Wales
Aberystwyth
Dyfed SY23 3DD
UK
(current address: Plant Biotechnology
Centre, La Trobe University,
Bundoora, Melbourne)

ak Kleinhofs, A.* (see abc)

aww Langridge, P
plangrid@waite.adelaide.edu.au
Department of Plant Science
Waite Campus*
University of Adelaide*
Glen Osmond
South Australia 5064
Australia

barc Cregan, P
USDA-ARS
Beltsville, MA

bcd (Barley cDNA clones*)
Sorrells, M.E.
Dept. of Plant Breeding
& Biometry
Cornell University
252 Emerson Hall
Ithaca, NY 14853
USA

bfc Nomura, T.
thiadi@kais.kyoto-u.ac.jp
Biofunction Chemistry
Division of Applied Life Sciences
Graduate School of Agriculture
Kyoto University
Kyoto 606-8502, Japan

bg (Barley genomic* clones)
Lapitan, N.
Department of Soil and Crop
Sciences
Colorado State University
Fort Collins, CO 80526
USA

bgl Lane, B.G.*
Faculty of Medicine
University of Toronto
Dept. of Biochemistry
Medical Sciences Building
Toronto, Ontario M5S 1A8
Canada

bnl Burr, B.
Brookhaven National
Laboratory*
Biology Dept.
Upton, NY 11973
USA

bzh Dudler, R.
Institut fur
Pflanzenbiologie*
Universitat Zurich
Zollikerstrasse 107
CH-8008 Zurich
Switzerland

ccsu Gupta, P.K.
Molecular Biology Laboratory
Dept. of Agricultural Botany
Ch. Charan Singh University
Meerut-250004
India

cdo (Oat cDNA clones)
Sorrels, M.E. (see bcd)

cfd (*Ae.* tauschii clones)
Bernard, M.
michel.Bernard@clermont.inra.fr
UMR Amelioration et Sante des
plantes
INRA-UBP
63039 Clermont-Errand*, Cedex 2
France

cmwg (Barley cDNA* clones)
Graner, A. (see mwg)

cr Robinson, C.
Dept. of Biological Sciences
University of Warwick
Coventry, CV4 7AR
UK

crc Procunier, J.D.
dprocunier@agr.gc.ca
Cereal Research Centre
Agriculture and Agri-Food Canada
195 Dafoe Road
Winnipeg, MB R3T 2M9
Canada

cs Appels, R. (see csb)

csb Appels, R.
rappels@agric.wa.gov.au
Formerly, CSIRO
Division of Plant Industry
CSIRO*, GPO Box 1600
Canberra ACT 2601
Australia

csc Chandler, P.M.
CSIRO Division of Plant Industry
GPO Box 1600
Canberra ACT 2601
Australia

csd Dennis, L.*
Division of Plant Industry
Institute of Plant
Production and Processing
CSIRO*, GPO Box 1600
Canberra ACT 2601
Australia

csl Lagudah, E.S
CSIRO Division of Plant Industry
GPO Box 1600
Canberra ACT 2601
Australia

csu Coe, E.
Department of Genetics
University of Missouri
Columbia, Mo 65211
USA
DuPw Petra Wolters
Petra.wolters@usa.dupont.com
DuPont Company*
P.O. Box 6104
Newark, DE 19714-6104
USA

fba (cv Courtot clones)
Leroy, P.
Station d’Amelioration des
Plantes de Clermont-Ferrand
INRA, Domaine de Crouelle
F-63039 Clermont-Ferrand Cedex
France

fbb (cv Chinese Spring clones)
Leroy, P. (see fba)

fdp DuPont, F.M.
USDA-ARS
Western Regional Research Center
800 Buchanan Street
Albany, CA 94710, USA

fra Bernard, Michel
INRA
Station d'Amelioration des Plantes
234, Avenue du Brezet
63039 Clermont-Ferrand Cedex 2
France*

gbx Jacquemin, J.M.
Centre de Recherches
Agronomiques
Station d'Amélioration des Plantes
4, rue du Bordia
B-5030 Gembloux*
Belgium

gdm Röder, M.S.
(Gatersleben D-genome
microsatellite*)
Institut fuer Pflanzengenetik und
Kulturpflanzenforschung (IPK)
Corrensstr. 3
06466 Gatersleben
Germany

ggo Jakobsen, K.S.
Division of General Genetics
University of Oslo
Pb. 1031 Blinders
N-0316, Norway

glk (Wheat gDNA clones)
Tsunewaki, K.
Tunewaki@tpu.ac.jp
Formerly, Laboratory of Genetics*
Faculty of Agriculture
Kyoto* University
Sakyo-ku
Kyoto 606-01, Japan

gwm
Roder, M.S.
Institut fuer Pflanzengenetik und
Kulturpflanzenforschung (IPK)
Corrensstr. 3
06466 Gatersleben
Germany

hhu
Westhoff, P.
Institut fur Entwicklungsund
Molekularbiologie der
Pflanzen
Heinrich-Heine-Universitat*
Universitats strasse 1/
Geb. 26.03.02
D-40225 Dusseldorf, Germany

iag
Wricke, G.
office@mbox.genetik.unihannover.de
Institut fur Angewandte Genetic*
Universitat Hanover
Herrenhauser Strasse 2
3000 Hannover 21
Germany

ipk
Borner, A.
Institut fuer Pflanzengenetik und
Kulturpflanzenforschung (IPK)
Corrensstr. 3
06466 Gatersleben
Germany

ksu
Gill, B.S.
Dept. of Plant Pathology
Throckmorton Hall
Kansas State University*
Manhattan, Kansas
66506-5502, USA

kuj
Mori, Naoki
Laboratory of Plant Genetics
Faculty of Agriculture
Kobe University
1 Rokkodai-cho
Nada-ku
Kobe 657
Japan

labc
(Barley cDNAs)
Shewry, P.
IACR-Long Ashton Research
Station
Long Ashton
Bristol, BS18 9AF, UK

lars
Holdsworth, M.J.
IACR - Long Ashton Research
Station*
Department of Agricultura l
Sciences
University of Bristol
Long Ashton, Bristol BS18 9AF
UK

logt
Volckaert, G.
Laboratory of Gene Technology*
Katholieke Universiteit Leuven
Willem de Croylaan 42
B-3001 Leuven
Belgium

mgb
Blanco, A
Institute of Plant Breeding
University of Bari
via Amendola 165/A
I-70126
Bari, Italy

msu
*Raikhel, N.
MSU-DOE Plant Research
Laboratory
Michigan State University*
East Lansing
Michigan 48824-1312, USA

mta &
mtd
Joudrier, P.
Unite de Biochimie et de
Biology Moleculaire
INRA
2, Place Pierre Viala
34060 Montpellier Cedex 01
France

mwg
(Barley gDNA* clones)
Graner, A.
a_graner@IPK-Gatersleben.de
Formerly, Institute for Resistance
Genetics
Federal Biological Research
Center for Agriculture and
Forestry
W-8059 Grunbach
Germany

ndsu
Anderson , J. A.
ander319@tc.umn.edu
Formerly, USDA-ARS
P.O. Box 64620
Washington State University
Pullman, WA 99164-6420
USA

npi
*Grant, D.
Pioneer Hi-Bred
International
7250 N.W. 62nd Avenue
Johnston IA 50131
USA

php
Grant, D. (see npi)

pkg
Gausing, K.
Department of Molecular Biology
Aarhus University
C.F. Møllers Allé, Bldg. 130
DK. 8000 Århus
Denmark

psb
(Barley clones*)
Laurie, D.
John Innes Centre
Norwich Research Park
Colney, Norwich NR4 7UH
UK

psp
(PCR markers)
Gale, M.D.
John Innes Centre
Norwich Research Park
Colney, Norwich NR4 7UH
UK

psr
(Wheat clones)
Gale, M.D. (see psr)
rgc (Rice cDNA* clones)
Sasaki, T.
Rice Genome Research
Program
National Institute of
Agrobiological Resources
2-1-2, Kannondai, Tsukuba
Ibaraki 305,
Japan

rgg
(Rice gDNA* clones)
Sasaki, T. (see rgc)

rgr
(Rice root* cDNA clones)
Sasaki, T. (see rgc)

rgy
(Rice YAC* end clone)
Sasaki, T. (see rgc)

rsq
Quatrano, R.
Dept. of Biology
The University of
North Carolina
CB# 3280 Coker Hall
Chapel Hill NC 27599-3280
USA

rz
(rice cDNA clones)
Sorrells, M.E. {See bcd}

scs
(S. cereale SSRs)}
Gustafson, P.
Dept.of Agronomy
208 Curtis Hall
University of Missouri-Columbia
Columbia, Missouri 6521, USA

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

swm, sfr
& sfrpr
Keller, B.
Institute of Plant Biology
University of Zürich
Zollikerstrasse 107
CH-8008 Zürich
Switzerland

tam
(Wheat DNA clones)
*Hart, G.E.
Retired, Soil and Crop Sciences
Department
Texas A&M University*
College Station, TX 77843
USA

tav
Breiman, A.
Tel Aviv University
University Campus
Ramat Aviv, Israel

Ttu
(cDNAs corresponding to stressresponsive
proteins and
`known-function' genes)
Nguyen, H.
nguyenhenry@missouri.edu
Formerly, Department of Plant and
Soil Science
Texas Tech University
Box 42122
Lubbock, TX 79409-2122, USA

ubp
Spagnoletti, P.
Dip. Biologia, Difesa e Biotecnologie
Agro-Forestali
Universita della Basilicata
85 Via N. Sauro
I-85100 Potenza, Italy

ucb
Quail, P.
Department of Plant Biology
Plant Gene Expression Center
University of California -Berkeley*
Berkeley, CA 94720, USA

ucd
Dvorák, J.
University of California
Dept. of Agronomy and Range
Science
Davis
California CA 95616
USA

ucg Hasselkorn, R.
Department of Molecular Genetics
and Cell Biology
University of Chicago
Chicago, Illinois 60637 USA

ucw Dubcovsky, J.
Department of Agronomy and
Range Science
University of California*-Davis
One Shields Avenue
Davis, California 95616-8515
USA

umc Coe, E.H.
University of Missouri,
Columbia*
Columbia, MO 65211
USA

unl Gill, K.
ksgill@wsu.edu
Formerly, Department of Agronomy
362H Plant Science
P.O. Box 830915
University of Nebraska, Lincoln
Lincoln NE68583-0915
USA

uta Browning, Karen
Department of Chemistry
University of Texas*
Austin*, Texas
USA

utv D’Ovidio, R.
Università della Tuscia
Dipartimento di Agrobiologia
e Agrochimica
Via S. Camillo de Lellis
01100 Viterbo
Italy

waxc (Barley cDNA clones)
von Wettstein-Knowles, P.
Carlsberg Laboratory
Dept. of Physiology
Gamle Carlsberg VEJ 10
DK-2500 Copenhagen
Valby, Denmark

wg (Wheat gDNA clones)
Sorrells, M.E. (see bcd)

whe Anderson, O.
USDA
ARS-WRRC
800 Buchanan Street
Albany CA94710
USA

whs Mohler, V.
mohler@wzw.tum.de
Lehrstuhl für Pflanzenbau und
Pflanzenzüchtung
Wissenschaftszentrum
Weihenstephan*
Technische Universität München
Am Hogancher 2
85350 Freising
Germany

wia Fincher, G.
Dept. of Agronomy
Waite Agricultural
Research Institute*
University of Adelaide
South Australia 5065
Australia

wmc (wheat microsatellites)
Isaac, Peter G.
Agrogene
620 rue Blaise Pascal
Z.I. 77550
Moissy Cramayel
France

wpg Feldman, M.
Department of Plant Genetics
Weizmann Institute of Science
Rehovot 76100
Israel

wsu *Walker-Simmons, M.K.
Wheat Genetics, Quality and
Disease Research Unit
209 Johnson Hall
Washington State University
Pullman WA 99164-6420, USA

wsuj Jones*, S.S.
Department of Crop and Soil
Sciences
Washington State University*
Pullman, WA 99164
USA

wye Ainsworth, C.
Wye College*
University of London
Wye, Ashford, Kent
TN25 5AH, UK

ycu Ogihara, Y.
ogihara@yokohama-cu.ac.jp
Kihara Institute for Biological
Research
Yokohama City University*
Nakamura-cho 2-120-3, Yokohama
Kanagawa Pref., 232
JAPAN

zens	*Schuch, W. Zeneca Plant Science Jeolatts Hill Research Station Bracknell Berkshire RG12 6BY, UK

9. Summary Table

Summary Table 1. Symbols with 'known function'

The term set(s) indicates that the loci have been grouped into one or (more than one) orthologous (='homoeologous') sets.

Symbol		Trait
Aadh-1,2	sets	Aromatic alcohol dehydrogenase
a-Amy1,2	sets	Alpha-amylase
Aco-1,2	sets	Aconitase
Acph-1	sets	Acid phosphatase
Adh-1	sets	Alcohol dehydrogenase (Aliphatic)
Adk-1	sets	Adenylate kinase
AhasL-1	sets	Acetohydroxyacid synthase (EC 4.1.3.18)
Alt1,2		Aluminium Tolerance
Amp-1,2,3	sets	Aminopeptidase
An5		Anthocyanin Pigmentation
Apd1,2		Hybrid Weakness
Ar1		Alkylresocinols Content in Grain
B1,2		Awnedness
Ba1,2		Blue Aleurone
b-Amy-1	sets	Beta-amylase
Bdv1,2,3		Reaction to Barley Yellow Dwarf Virus
b-Gls		Beta-glucosidase
bh-1	sets	Gross Morphology: Spike characteristics
Bla1		Glume Colour and Awn Colour
Bls1,2,3,4,5		Reaction to *Xanthomonas campestris* pv. *undulosa*
Bo1,2,3		Boron Tolerance
Br1,4		Brittle Rachis
Bt1 to 10		Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*
C		Club/Compact spike
Cat-B1		Catalase
cc		Glume Colour and Awn Colour
Cdu1		Cadmium Uptake
Ce		Copper Efficiency
Ch1,2		Hybrid Weakness
Cmc1,2,3,4		Resistance to Colonization by *Eriophyes tulipae* (*Aceria tulipae*)
Cn-1	sets	Chlorophyll Abnormalities
co1,2		Corroded
Cre1 to 8		Reaction to *Heterodera avenae* Woll.
Crr		Reaction to *Cochliobolus sativus* Ito & Kurib.
Cs1,2		Hybrid Weakness
D1,2,3,4		Grass-Clump Dwarfness/Grass Dwarfness
Dfq1		Herbicide Response
Dip-1	sets	Dipeptidase
Dn1 to 9		Reaction to *Diuraphis noxia* (Mordvilko)
Dreb-1	sets	Abiotic Stress Responses:Dehydrin-response Element Binding Factors
Ep-1	sets	Endopeptidase
Ep-1		Endopeptidase
Est1 to 9	sets	Esterase
F3h-1	sets	Flavone 3-hydroxylase (EC 1.14.11.9)
Fe1,2		Iron Deficiency
Fhb1,2,3,4,5		Reaction to *Fusarium* spp.
Fhs1,2		Reaction to *Fusarium* spp.
Fr1,2		Frost Resistance
Gai1,2,3		Gibberellic Acid Response (insensitivity)
Gb1 to 7		Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)
Gc1,2,3		Gametocidal Genes
Gli-1,2,3,5,6,7	sets	Gliadins
Gllu-A3y		Glutenins

Summary Table 1 (Cont.). Symbols with 'known function'

Symbol		Trait
Glo-1	sets	Salt soluble globulins
Glu-1,3	sets	Glutenins
Glu-1-1	sets	Glutenins
Glu-1-2	sets	Glutenins
Got-1,2,3	sets	Glutamic oxaloacetic transaminase
Gpc-1		Grain protein content
Gpi-1	sets	Glucosephosphate isomerase
Gpt-1	sets	Glutamate-pyruvate transaminase
Gsp-1	sets	Grain softness protein
H_{WGRC4}		Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)
Ha		Grain Hardness/Endosperm Texture
Hd		Awnedness
Hg		Hairy Glume
Hk-1,2	sets	Hexokinase
Hl1,2		Hairy Leaf
Hn		Hairy Node/Pubescent Node
Hp		Hairy Neck/Pubescent Peduncle
Hs		Hairy Leaf Sheath
HstH1-1,2	sets	Histone H1 Proteins
Hyd-1,2	sets	Carotenoid beta-hydroxylase (non-heme di-iron type)
Ibf-1	sets	Iodine binding factor
Igc1		Gametocidal Genes
Iha-1		Inhibitors (dimeric) of heterologous alpha-amylases
Imi1,2,3		Herbicide Response
Isa-1	sets	Inhibitors of alpha-amylase and subtilisin
Iso-1		Isoamylase 1
Iw1,2,3		Glaucousness (Waxiness/Glossiness)
Kb1,2,3,4,5,6		Reaction to *Tilletia indica* Mitra
Ki		Pollen Killer
Kna1		Response to Salinity
Kr1,2,3,4		Crossability with Rye and *Hordeum* and *Aegilops* spp.
Lec-1	sets	Lectins
lg1,2,3		Lack of Ligules
lm		Lesion Mimicry
Lpx-1,2,3	sets	Lipoxygenase
Lr1 to 71		Reaction to *Puccinia triticina*
Ltn1,2		Leaf Tip Necrosis
ltp		Meiotic Characters
Lvl1		Grain Quality Parameters
Mal-1	sets	Malic enzyme
Mdh-1,2,3,4	sets	Malate dehydrogenase
Mg5		Reaction to *Magnaporthe grisea* (Herbert) Barr
Ml		Reaction to *Blumeria graminis* DC.
ms1,2,3,4,5		Male Sterility
Nax1,2		Response to Salinity
Ndh-1,2,3,4	sets	NADH dehydrogenase
Ne1,2		Hybrid Weakness
Ner1,2		Hybrid Weakness
Nor1 to 10	sets	Nucleolus Organizer Regions
Nra		Nitrate Reductase Activity
Or		Osmoregulation
P1,2		Gross Morphology: Spike characteristics
Pa		Hairy/Pubescent Auricles
Pan1,2		Anthocyanin Pigmentation
Pbc		Glume Colour and Awn Colour
Pc1,2		Anthocyanin Pigmentation
Pch1,2,3		Reaction to *Tapesia yallundae*. (Anomorph: *Pseudocerosporella herpotrichoides* (Fron) Deighton)

Summary Table 1 (Cont.). Symbols with 'known function'

Symbol		**Trait**
Pde-1	sets	Phosphodiesterase
Pdi-1	sets	Protein disulfide isomerase (EC 5.3.4.1)
Per-1,2,3,4,5	sets	Peroxidase
Pg		Anthocyanin Pigmentation
Pgd1		Phosphogluconate dehydrogenase
PgdR1,2		Phosphogluconate dehydrogenase
Pgip1,2		Polygalacturonase-inhibiting proteins
Pgm-1	sets	Phosphoglucomutase
Ph1,2		Meiotic Characters
Phs1		Dormancy (Seed)
Pina1	sets	Puroindolines and grain softness protein
Pinb1	sets	Puroindolines and grain softness protein
Pis1		Gross Morphology: Spike characteristics
Plb		Anthocyanin Pigmentation
Pln		Sterol Esterification in Kernels - Synthesis of b-Sitosterol Esters
Pm1 to 47		Reaction to *Blumeria graminis* DC.
Pp1,2,3		Anthocyanin Pigmentation
Ppd-1,2	sets	Response to Photoperiod
Ppo-1	sets	Polyphenol oxidase
Pro1,2		Grain protein content
Psy2-1	sets	Phytoene synthase
Pur-1	sets	Lipopurothionins
Q		Squarehead/spelt
R-1	sets	Red Grain Colour
Ra1,2,3		Anthocyanin Pigmentation
Rc1	sets	Anthocyanin Pigmentation
Rf1 to 6		Restorers for Cytoplasmic Male Sterility
Rg-1,3	sets	Glume Colour and Awn Colour
Rht1 to 22	sets	Height
Rkn1,2,3		Reaction to *Meloidogyne* spp.
Rlnn1		Reaction to *Pratylenchus* spp.
Rmg1,2,3,4		Reaction to *Magnaporthe grisea* (Herbert) Barr
5S-Rna-1,2	sets	5S Ribosomal RNA-1,2
Rot1		Reaction to *Rhizoctonia* spp.
S1,2	sets	Sphaerococcum
Sa1		Reaction to *Sitobion avenae*
Sb1		Reaction to *Bipolaris sorokiniana*
SbeI1,2		Starch branching enzyme I
SbeII		Starch branching enzyme II
Sbm1		Reaction to Soil-Borne Cereal Mosaic Virus
sc		Seedling Leaf Chlorosis
scs		Nuclear-Cytoplasmic Compatability Enhancers
Sd1,2		Gametocidal Genes
Sgp-1,2,3	sets	Starch granule proteins
Shw		Male Sterility
Si-1,2	sets	Subtilisin inhibition
Skdh-1	sets	Shikimate dehydrogenase
Sm1		Reaction to *Sitodiplosis mosellana* (Gehin)
Snb1,2,3		Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano)
Snn1,2,3,4		Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano)
Sod-1	sets	Superoxide dismutase
Sog		Soft Glumes
Spa-1	sets	Endosperm-specific wheat basic region leucine zipper (bZIP) factor storage activator
Sr1 to 57		Reaction to *Puccinia graminis* Pers.
Srp-1	sets	Serine protease inhibitors

Summary Table 1 (Cont.). Symbols with 'known function'

Symbol		Trait
SsI-1	sets	Starch synthase
SsII-1	sets	Starch synthase
Stb1 to 18		Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter
Su1		Herbicide Response
SuLr23		Reaction to *Puccinia triticina*
SuPm8		Reaction to *Blumeria graminis* DC.
TaCwi-A1		Yield and Yield Components
TaGW2-6A		Yield and Yield Components
Tc1,2,3		Phenol Colour Reaction of Kernels
Tg1,2		Tenacious Glumes
Ti-1,2	sets	Trypsin inhibition
tin1,2,3		Tiller Inhibition
Tpi-1,2	sets	Triosephosphate isomerase
Tri-1	sets	Other endosperm storage proteins
Tsc1,2		Reaction to *Pyrenophora tritici-repentis* (anomorph: *Drechlera tritici*-repentis)
Tsn1,2		Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano)
Tsr1 to 6		Reaction to *Pyrenophora tritici-repentis* (anomorph: *Drechlera tritici*-repentis)
Ut1,2,3,4		Reaction to *Ustilago tritici* (Pers.) Rostrup
V1,2		Chlorophyll Abnormalities
vg		Variegated Red Grain Colour
Vgw		Temperature-Sensitive Winter Variegation
Vi		Restorers for Cytoplasmic Male Sterility
Vil-1,2,3		Response to Vernalization
Vp-1	sets	Dormancy (Seed)
Vrn1,2,3,5	sets	Response to Vernalization
W1,2		Glaucousness (Waxiness/Glossiness)
wptms1,2		Male Sterility
Ws		Glaucousness (Waxiness/Glossiness)
Wsm1,2,3		Reaction to Wheat Streak Mosaic Virus
Wsp-1	sets	Water soluble proteins
Wss1		Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)
wtms1		Male Sterility
Wx-1	sets	Waxy proteins
X		Basic symbol for DNA markers
Ym		Reaction to Wheat Yellow Mosaic Virus
Yr1 to 53		Reaction to *Puccinia striiformis* Westend.
Zds-1	sets	Zeta-carotene desaturase

Summary Table 2. Chromosomal locations of wheat genes that are known to be members of orthologous sets of Triticeae genes.

GENOME A		**GENOME B**		**GENOME D**	
Chromosome		**Chromosome**		**Chromosome**	
Arm	***Gene***	**Arm**	***Gene***	**Arm**	***Gene***
1AS	*Gli-A1*	1BS	*Gli-B1*	1DS	*Gli-D1*
	Gli-A3		*Gli-B3*		
	Gli-A5		*Gli-B5*		
	Gli-A6				
					Gli-A7
	Glo-A1		*Glo-B1*		*Glo-D1*
			Glu-B2		
	Glu-A3		*Glu-B3*		*Glu-D3*
	Gpi-A1		*Gpi-B1*		*Gpi-D1*
	Gpt-A1		*Gpt-B1*		*Gpt-D1*
			Hk-B1		*Hk-D1*
	Nor-A1		*Nor-B1*		
	Nor-A9				
			Per-B1		*Per-D1*
	Rg-A1		*Rg-B1*		
			Si-B2		*Si-D2*
	5S-Rrna-A1		*5S-Rrna-B1*		*5S-Rrna-D1*
	Tri-A1				*Tri-D1*
1AL	*Eps-1A*^{m}	1BL		1DL	
	Glu-A1		*Glu-B1*		*Glu-D1*
	Lec-A1				*Lec-D1*
	Mdh-A1		*Mdh-B1*		*Mdh-D1*
			Nor-B6		
	Pur-A1		*Pur-B1*		*Pur-D1*
	Spa-A1		*Spa-B1*		*Spa-D1*
1A		1B		1D	*Glu-D4*
			Lec-B1		
	Rg-A1c			1DL,1DS	*Rg-D1*
2AS	*bh-A1*	2BS		2DS	*bh-D1*
	Est-A6		*Est-B6*		*Est-D6*
	Per-A2		*Per-B2*		*Per-D2*
					Per-D5
			Ppd-B1a		*Ppd-D1a*
2AL		2BL		2DL	*Acph-D2*
	Est-A7		*Est-B7*		*Est-D7*
	F3h-A1		*F3h-B1*		*F3h-D1*
			F3h-B2		
	Hyd-A1		*Hyd-B1*		*Hyd-D1*
	Isa-A1		*Isa-B1*		*Isa-D1*
	Ppd-A1				
	Ppo-A1				
	Sod-A1		*Sod-B1*		*Sod-D1*
					Zds-D1
2A		2B	*Gc1-B1a*	2D	

Summary Table 2. (Cont.) : Chromosomal locations of wheat genes that are known to be members of orthologous sets of Triticeae genes.

GENOME A		**GENOME B**		**GENOME D**	
Chromosome		**Chromosome**		**Chromosome**	
Arm	***Gene***	**Arm**	***Gene***	**Arm**	***Gene***
			Gc1-B1b		
	Zds-A1		*Zds-B1*		
3AS	*Br-A1*	3BS	*Br-B1*	3DS	*Br-D1*
	Est-A1		*Est-B1*		*Est-D1*
	Est-A9		*Est-B9*		*Est-D9*
			Hk-B2		*Hk-D2*
			Iha-B1.1		*Iha-D1*
			Iha-B1.2		
	Ndh-A4		*Ndh-B4*		
					Nor-D8
	Pde-A1		*Pde-B1*		*Pde-D1*
	Tpi-A1		*Tpi-B1*		*Tpi-D1*
			Yrns-B1		
3AL		3BL	*Dreb-B1*	3DL	
	Eps-A1a				
			Est-B2		*Est-D2*
	Est-A5		*Est-B5*		*Est-D5*
	Est-A8		*Est-B8*		*Est-D8*
	Got-A3		*Got-B3*		*Got-D3*
	Mal-A1		*Mal-B1*		*Mal-D1*
	Ndh-A3		*Ndh-B3*		*Ndh-D3*
	Per-A3		*Per-B3*		*Per-D3*
	R-A1		*R-B1*		*R-D1*
	Vp-A1				*Vp-D1*
					Vp-D1a
3A	*Dreb-A1*	3B		3D	*Dreb-D1*
	Est-A2				
	Hk-A2				
	S-A1		*S-B1*		*S-D1*
4AS	*Acph-A1*	4BS		4DS	
			Adh-B1		*Adh-D1*
			Amp-B2		*Amp-D2*
			Lpx-B1		*Lpx-D1*
			Lpx-B1.1		
			Ndh-B1		*Ndh-D1*
			Pdi-D1		*Pdi-B1*
					Pgm-D1
			Rht-B1		*Rht-D1*
					Rht-D1b
4AL		4BL	*Aco-B2*	4DL	*Aco-D2*
			Acph-B1		*Acph-D1*
	Adh-A1				
			b-Amy-B1		*b-Amy-D1*
	Amp-A2				

Summary Table 2. **(Cont.) :** Chromosomal locations of wheat genes that are known to be members of orthologous sets of Triticeae genes.

GENOME A		**GENOME B**		**GENOME D**	
Chromosome		**Chromosome**		**Chromosome**	
Arm	***Gene***	**Arm**	***Gene***	**Arm**	***Gene***
			Cat-B1		
			Hyd-B2		*Hyd-D2*
	Lpx-A1				
	Lpx-A3				
	Ndh-A1				
	Pdi-A1				
	Per-B4				
	Pgm-A1				
	Wx-B1				
4A		4B	*Lpx-B1.2*	4D	
		4B	*Lpx-B3*		
5AS		5BS		5DS	*Gsp-D1*
	Mdh-A3		*Mdh-B3*		*Mdh-D3*
	Nor-A3				*Nor-D3*
	Nor-A10				*Pina-D1*
	Pina-A^{m}1				*Pinb-D1*
	Pinb-A^{m}1				*Pinb-D1b*
	5S-Rrna-A2		*5S-Rrna-B2*		*5S-Rrna-D2*
	Skdh-A1		*Skdh-B1*		*Skdh-D1*
5AL	*Aadh-A1*	5BL	*Aadh-B1*	5DL	*Aadh-D1*
	Aco-A2				
	b-Amy-A1				
			Eps-5BL.1		
			Eps-5BL.2		
	HstH1-A1		*HstH1-B1*		*HstH1-D1*
	HstH1-A2		*HstH1-B2*		*HstH1-D2*
	Hyd-A2				
	Ibf-A1		*Ibf-B1*		*Ibf-D1*
	Lpx-A2		*Lpx-B2*		*Lpx-D2*
	Nor-A7				
	Srp-A1		*Srp-B1*		*Srp-D1*
	Ti-A2		*Ti-B2*		*Ti-D2*
	Tpi-A2		*Tpi-B2*		*Tpi-D2*
	Vrn-A1a		*Vrn-B1a*		*Vrn-D1*
					Vrn-D5a
5A	*Gsp-A1*	5B	*Gsp-B1*	5D	
	Psy2-A1		*Psy2-B1*		
6AS	*Amp-A1*	6BS	*Amp-B1*	6DS	*Amp-D1*
			Ep-B2		

Summary Table 2. **(Cont.) :** Chromosomal locations of wheat genes that are known to be members of orthologous sets of Triticeae genes.

GENOME A		**GENOME B**		**GENOME D**	
Chromosome		**Chromosome**		**Chromosome**	
Arm	***Gene***	**Arm**	***Gene***	**Arm**	***Gene***
	Gli-A2		*Gli-B2*		*Gli-D2*
	Got-A1		*Got-B1*		*Got-D1*
			Gpc-B1b		
			Nor-B2		
6AL	*Aadh-A2*	6BL	*Aadh-B2*	6DL	*Aadh-D2*
	a-Amy-A1		*a-Amy-B1*		*a-Amy-D1*
	Aco-A1		*Aco-B1*		*Aco-D1*
	AhasL-A1		*AhasL-B1*		*AhasL-D1*
	Dip-A1		*Dip-B1*		*Dip-D1*
	Est-A4		*Est-B4*		*Est-D4*
	Got-A2		*Got-B2*		*Got-D2*
6A		6B	*Nor-B2a*	6D	
7AS	*Amp-A3*	7BS		7DS	
			Est-B3		*Est-D3*
					Ndh-D2
	Per-A4				*Per-D4*
			Pgip-B1		*Pgip-D1*
			Ppd-B2		
	Rc-A1a		*Rc-B1a*		*Rc-D1a*
	Sgp-A1		*Sgp-B1*		*Sgp-D1*
	Sgp-A3		*Sgp-B3*		*Sgp-D3*
			Vrn-B3		
	Wx-A1				*Wx-D1*
7AL	*a-Amy-A2*	7BL	*a-Amy-B2*	7DL	*a-Amy-D2*
	Adk-A1		*Adk-B1*		*Adk-D1*
	Cn-A1		*Cn-B1*		*Cn-D1*
	Ep-A1		*Ep-B1*		*Ep-D1*
					Nor-D4
	Psy1-A1		*Psy1-B1*		*Psy1-D1*
	Wsp-A1		*Wsp-B1*		*Wsp-D1*
7A		7B		7D	*Glu-D5*
	Ndh-A2				
	SsI-A1		*SsI-B1*		*SsI-D1*
	SsII-A1		*SsII-B1*		*SsII-D1*