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Catalogue of Gene Symbols for Wheat

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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

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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 *Enzyme 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 reading 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 primer(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 Plant Science Research 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 *HindIII*. 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*. R² 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 'X_{xyz}ANIN₂N₃, 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 *Pst*I, 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 11th IWGS

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 541 in 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. **Pleiotropic 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. Chromosome 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:	=	Cultivar hexaploid stocks in increasing order of genetic complexity.
v2 :	=	Cultivar 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'	<i>T. aestivum</i> ,
'2'	<i>T. turgidum</i> ,
'3'	<i>T. monococcum</i> ,
'4'	<i>Ae. tauschii</i> , 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	bg	(Barley genomic* clones) Lapitan, N. Department of Soil and Crop Sciences Colorado State University Fort Collins, CO 80526 USA
abg	(Barley genomic* clones) Kleinhofs, A. (see abc)	bgl	Lane, B.G.* Faculty of Medicine University of Toronto Dept. of Biochemistry Medical Sciences Building Toronto, Ontario M5S 1A8 Canada
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)	bnl	Burr, B. Brookhaven National Laboratory* Biology Dept. Upton, NY 11973 USA
ak	Kleinhofs, A.* (see abc)	bzh	Dudler, R. Institut fur Pflanzenbiologie* Universitat Zurich Zollikerstrasse 107 CH-8008 Zurich Switzerland
aww	Langridge, P plangrid@waite.adelaide.edu.au Department of Plant Science Waite Campus* University of Adelaide* Glen Osmond South Australia 5064 Australia	ccsu	Gupta, P.K. Molecular Biology Laboratory Dept. of Agricultural Botany Ch. Charan Singh University Meerut-250004 India
barc	Cregan, P USDA-ARS Beltsville, MA	cdo	(Oat cDNA clones) Sorrells, M.E. (see bcd)
bcd	(Barley cDNA clones*) Sorrells, M.E. Dept. of Plant Breeding & Biometry Cornell University 252 Emerson Hall Ithaca, NY 14853 USA	cfid	(<i>Ae. tauschii</i> clones) Bernard, M. michel.Bernard@clermont.inra.fr UMR Amelioration et Sante des plantes INRA-UBP 63039 Clermont-Errand*, Cedex 2 France
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		

cmwg	(Barley cDNA* clones) Graner, A. (see mwg)	fba	(cv Courtot clones) Leroy, P. Station d'Amelioration des Plantes de Clermont-Ferrand INRA, Domaine de Crouelle F-63039 Clermont-Ferrand Cedex France
cr	Robinson, C. Dept. of Biological Sciences University of Warwick Coventry, CV4 7AR UK	ffb	(cv Chinese Spring clones) Leroy, P. (see fba)
crc	Procunier, J.D. dprocunier@agr.gc.ca Cereal Research Centre Agriculture and Agri-Food Canada 195 Dafoe Road Winnipeg, MB R3T 2M9 Canada	fdp	DuPont, F.M. USDA-ARS Western Regional Research Center 800 Buchanan Street Albany, CA 94710, USA
cs	Appels, R. (see csb)	fra	Bernard, Michel INRA Station d'Amelioration des Plantes 234, Avenue du Brezet 63039 Clermont-Ferrand Cedex 2 France*
csb	Appels, R. rappels@agric.wa.gov.au Formerly, CSIRO Division of Plant Industry CSIRO*, GPO Box 1600 Canberra ACT 2601 Australia	gbx	Jacquemin, J.M. Centre de Recherches Agronomiques Station d'Amelioration des Plantes 4, rue du Bordia B-5030 Gembloux* Belgium
csc	Chandler, P.M. CSIRO Division of Plant Industry GPO Box 1600 Canberra ACT 2601 Australia	gdm	Röder, M.S. (Gatersleben D-genome microsatellite*) Institut fuer Pflanzengenetik und Kulturpflanzenforschung (IPK) Corrensstr. 3 06466 Gatersleben Germany
csd	Dennis, L.* Division of Plant Industry Institute of Plant Production and Processing CSIRO*, GPO Box 1600 Canberra ACT 2601 Australia	ggo	Jakobsen, K.S. Division of General Genetics University of Oslo Pb. 1031 Blinders N-0316, Norway
csf	Lagudah, E.S. CSIRO Division of Plant Industry GPO Box 1600 Canberra ACT 2601 Australia	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
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gwm	Roder, M.S. Institut fuer Pflanzengenetik und Kulturpflanzenforschung (IPK) Corrensstr. 3 06466 Gatersleben Germany	logt	Volckaert, G. Laboratory of Gene Technology* Katholieke Universiteit Leuven Willem de Croylaan 42 B-3001 Leuven Belgium
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ksu	Gill, B.S. Dept. of Plant Pathology Throckmorton Hall Kansas State University* Manhattan, Kansas 66506-5502, USA	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
kuj	Mori, Naoki Laboratory of Plant Genetics Faculty of Agriculture Kobe University 1 Rokkodai-cho Nada-ku Kobe 657 Japan	ndsu	Anderson, J. A. ander319@tc.umn.edu Formerly, USDA-ARS P.O. Box 64620 Washington State University Pullman, WA 99164-6420 USA
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lars	Holdsworth, M.J. IACR - Long Ashton Research Station* Department of Agricultura l Sciences University of Bristol Long Ashton, Bristol BS18 9AF UK	php	Grant, D. (see npi)

pkg	Gausung, K. Department of Molecular Biology Aarhus University C.F. Møllers Allé, Bldg. 130 DK. 8000 Århus Denmark	scu	Henry, R.J. Centre for Plant Conservation Genetics Southern Cross University* P.O. Box 157 Lismore NSW 2480 Australia
psb	(Barley clones*) Laurie, D. John Innes Centre Norwich Research Park Colney, Norwich NR4 7UH UK	<i>swm</i> , <i>sfr</i> & <i>sfrpr</i>	Keller, B. Institute of Plant Biology University of Zürich Zollikerstrasse 107 CH-8008 Zürich Switzerland
psp	(PCR markers) Gale, M.D. John Innes Centre Norwich Research Park Colney, Norwich NR4 7UH UK	tam	(Wheat DNA clones) *Hart, G.E. Retired, Soil and Crop Sciences Department Texas A&M University* College Station, TX 77843 USA
psr	(Wheat clones) Gale, M.D. (see <i>psr</i>) <i>rgc</i> (Rice cDNA* clones) Sasaki, T. Rice Genome Research Program National Institute of Agrobiological Resources 2-1-2, Kannondai, Tsukuba Ibaraki 305, Japan	tav	Breiman, A. Tel Aviv University University Campus Ramat Aviv, Israel
rgg	(Rice gDNA* clones) Sasaki, T. (see <i>rgc</i>)	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
rgr	(Rice root* cDNA clones) Sasaki, T. (see <i>rgc</i>)	ubp	Spagnoletti, P. Dip. Biologia, Difesa e Biotecnologie Agro-Forestali Universita della Basilicata 85 Via N. Sauro I-85100 Potenza, Italy
rgy	(Rice YAC* end clone) Sasaki, T. (see <i>rgc</i>)	ucb	Quail, P. Department of Plant Biology Plant Gene Expression Center University of California -Berkeley* Berkeley, CA 94720, USA
rsq	*Quatrano, R.* Dept. of Biology The University of North Carolina CB# 3280 Coker Hall Chapel Hill NC 27599-3280 USA	ucd	Dvorák, J. University of California Dept. of Agronomy and Range Science Davis California CA 95616 USA
rz	(rice cDNA clones) Sorrells, M.E. {See <i>bcd</i> }		
scs	(<i>S. cereale</i> SSRs) Gustafson, P. Dept. of Agronomy 208 Curtis Hall University of Missouri-Columbia Columbia, Missouri 6521, USA		

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uta	Browning, Karen Department of Chemistry University of Texas* Austin*, Texas USA	wsu	*Walker-Simmons, M.K. Wheat Genetics, Quality and Disease Research Unit 209 Johnson Hall Washington State University Pullman WA 99164-6420, USA
utv	D'Ovidio, R. Università della Tuscia Dipartimento di Agrobiologia e Agrochimica Via S. Camillo de Lellis 01100 Viterbo Italy	wsuj	Jones*, S.S. Department of Crop and Soil Sciences Washington State University* Pullman, WA 99164 USA
waxc	(Barley cDNA clones) von Wettstein-Knowles, P. Carlsberg Laboratory Dept. of Physiology Gamle Carlsberg VEJ 10 DK-2500 Copenhagen Valby, Denmark	wye	Ainsworth, C. Wye College* University of London Wye, Ashford, Kent TN25 5AH, UK
wg	(Wheat gDNA clones) Sorrells, M.E. (see bcd)	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
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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
<i>Aadh-1,2</i>	sets	Aromatic alcohol dehydrogenase
<i>a-Amy1,2</i>	sets	Alpha-amylase
<i>Aco-1,2</i>	sets	Aconitase
<i>AcpH-1</i>	sets	Acid phosphatase
<i>Adh-1</i>	sets	Alcohol dehydrogenase (Aliphatic)
<i>Adk-1</i>	sets	Adenylate kinase
<i>AhasL-1</i>	sets	Acetohydroxyacid synthase (EC 4.1.3.18)
<i>Alt1,2</i>		Aluminium Tolerance
<i>Amp-1,2,3</i>	sets	Aminopeptidase
<i>An5</i>		Anthocyanin Pigmentation
<i>Apd1,2</i>		Hybrid Weakness
<i>Ar1</i>		Alkylresocinol Content in Grain
<i>B1,2</i>		Awnedness
<i>Ba1,2</i>		Blue Aleurone
<i>b-Amy-1</i>	sets	Beta-amylase
<i>Bdv1,2,3</i>		Reaction to Barley Yellow Dwarf Virus
<i>b-Gls</i>		Beta-glucosidase
<i>bh-1</i>	sets	Gross Morphology: Spike characteristics
<i>Bla1</i>		Glume Colour and Awn Colour
<i>Bls1,2,3,4,5</i>		Reaction to <i>Xanthomonas campestris</i> pv. <i>undulosa</i>
<i>Bo1,2,3</i>		Boron Tolerance
<i>Br1,4</i>		Brittle Rachis
<i>Bt1 to 10</i>		Reaction to <i>Tilletia caries</i> (D.C.)Tul., <i>T. foetida</i> (Wallr.) Liro, <i>T. controversa</i>
<i>C</i>		Club/Compact spike
<i>Cat-B1</i>		Catalase
<i>cc</i>		Glume Colour and Awn Colour
<i>Cdu1</i>		Cadmium Uptake
<i>Ce</i>		Copper Efficiency
<i>Ch1,2</i>		Hybrid Weakness
<i>Cmc1,2,3,4</i>		Resistance to Colonization by <i>Eriophyes tulipae</i> (<i>Aceria tulipae</i>)
<i>Cn-1</i>	sets	Chlorophyll Abnormalities
<i>co1,2</i>		Corroded
<i>Cre1 to 8</i>		Reaction to <i>Heterodera avenae</i> Woll.
<i>Crr</i>		Reaction to <i>Cochliobolus sativus</i> Ito & Kurib.
<i>Cs1,2</i>		Hybrid Weakness
<i>D1,2,3,4</i>		Grass-Clump Dwarfness/Grass Dwarfness
<i>Dfq1</i>		Herbicide Response
<i>Dip-1</i>	sets	Dipeptidase
<i>Dn1 to 9</i>		Reaction to <i>Diuraphis noxia</i> (Mordvilko)
<i>Dreb-1</i>	sets	Abiotic Stress Responses:Dehydrin-response Element Binding Factors
<i>Ep-1</i>	sets	Endopeptidase
<i>Ep-1</i>		Endopeptidase
<i>Est1 to 9</i>	sets	Esterase
<i>F3h-1</i>	sets	Flavone 3-hydroxylase (EC 1.14.11.9)
<i>Fe1,2</i>		Iron Deficiency
<i>Fhb1,2,3,4,5</i>		Reaction to <i>Fusarium</i> spp.
<i>Fhs1,2</i>		Reaction to <i>Fusarium</i> spp.
<i>Fr1,2</i>		Frost Resistance
<i>Gai1,2,3</i>		Gibberellic Acid Response (insensitivity)
<i>Gb1 to 7</i>		Reaction to <i>Schizaphis graminum</i> Rond. (<i>Toxoptera graminum</i> Rond.)
<i>Gc1,2,3</i>		Gametocidal Genes
<i>Gli-1,2,3,5,6,7</i>	sets	Gliadins
<i>Gllu-A3y</i>		Glutenins

Summary Table 1 (Cont.). Symbols with ‘known function’

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

Summary Table 1 (Cont.). Symbols with ‘known function’

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

Summary Table 1 (Cont.). Symbols with ‘known function’

Symbol		Trait
<i>SsI-1</i>	sets	Starch synthase
<i>SsII-1</i>	sets	Starch synthase
<i>Stb1 to 18</i>		Reaction to <i>Mycosphaerella graminicola</i> (Fuckel) Schroeter
<i>Su1</i>		Herbicide Response
<i>SuLr23</i>		Reaction to <i>Puccinia triticina</i>
<i>SuPm8</i>		Reaction to <i>Blumeria graminis</i> DC.
<i>TaCwi-A1</i>		Yield and Yield Components
<i>TaGW2-6A</i>		Yield and Yield Components
<i>Tc1,2,3</i>		Phenol Colour Reaction of Kernels
<i>Tg1,2</i>		Tenacious Glumes
<i>Ti-1,2</i>	sets	Trypsin inhibition
<i>tin1,2,3</i>		Tiller Inhibition
<i>Tpi-1,2</i>	sets	Triosephosphate isomerase
<i>Tri-1</i>	sets	Other endosperm storage proteins
<i>Tsc1,2</i>		Reaction to <i>Pyrenophora tritici-repentis</i> (anamorph: <i>Drechlera tritici-repentis</i>)
<i>Tsn1,2</i>		Reaction to <i>Phaeosphaeria nodorum</i> (E. Muller) Hedjaroude (anamorph: <i>Stagonospora nodorum</i> (Berk.) Castellani & E.G. Germano)
<i>Tsr1 to 6</i>		Reaction to <i>Pyrenophora tritici-repentis</i> (anamorph: <i>Drechlera tritici-repentis</i>)
<i>Ut1,2,3,4</i>		Reaction to <i>Ustilago tritici</i> (Pers.) Rostrup
<i>V1,2</i>		Chlorophyll Abnormalities
<i>vg</i>		Variegated Red Grain Colour
<i>Vgw</i>		Temperature-Sensitive Winter Variegation
<i>Vi</i>		Restorers for Cytoplasmic Male Sterility
<i>Vil-1,2,3</i>		Response to Vernalization
<i>Vp-1</i>	sets	Dormancy (Seed)
<i>Vrn1,2,3,5</i>	sets	Response to Vernalization
<i>W1,2</i>		Glaucousness (Waxiness/Glossiness)
<i>wptms1,2</i>		Male Sterility
<i>Ws</i>		Glaucousness (Waxiness/Glossiness)
<i>Wsm1,2,3</i>		Reaction to Wheat Streak Mosaic Virus
<i>Wsp-1</i>	sets	Water soluble proteins
<i>Wss1</i>		Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)
<i>wtms1</i>		Male Sterility
<i>Wx-1</i>	sets	Waxy proteins
<i>X</i>		Basic symbol for DNA markers
<i>Ym</i>		Reaction to Wheat Yellow Mosaic Virus
<i>Yr1 to 53</i>		Reaction to <i>Puccinia striiformis</i> Westend.
<i>Zds-1</i>	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	<i>Gli-A1</i>	1BS	<i>Gli-B1</i>	1DS	<i>Gli-D1</i>
	<i>Gli-A3</i>		<i>Gli-B3</i>		
	<i>Gli-A5</i>		<i>Gli-B5</i>		
	<i>Gli-A6</i>				
					<i>Gli-A7</i>
	<i>Glo-A1</i>		<i>Glo-B1</i>		<i>Glo-D1</i>
			<i>Glu-B2</i>		
	<i>Glu-A3</i>		<i>Glu-B3</i>		<i>Glu-D3</i>
	<i>Gpi-A1</i>		<i>Gpi-B1</i>		<i>Gpi-D1</i>
	<i>Gpt-A1</i>		<i>Gpt-B1</i>		<i>Gpt-D1</i>
			<i>Hk-B1</i>		<i>Hk-D1</i>
	<i>Nor-A1</i>		<i>Nor-B1</i>		
	<i>Nor-A9</i>				
			<i>Per-B1</i>		<i>Per-D1</i>
	<i>Rg-A1</i>		<i>Rg-B1</i>		
			<i>Si-B2</i>		<i>Si-D2</i>
	<i>5S-Rrna-A1</i>		<i>5S-Rrna-B1</i>		<i>5S-Rrna-D1</i>
	<i>Tri-A1</i>				<i>Tri-D1</i>
1AL	<i>Eps-1A^m</i>	1BL		1DL	
	<i>Glu-A1</i>		<i>Glu-B1</i>		<i>Glu-D1</i>
	<i>Lec-A1</i>				<i>Lec-D1</i>
	<i>Mdh-A1</i>		<i>Mdh-B1</i>		<i>Mdh-D1</i>
			<i>Nor-B6</i>		
	<i>Pur-A1</i>		<i>Pur-B1</i>		<i>Pur-D1</i>
	<i>Spa-A1</i>		<i>Spa-B1</i>		<i>Spa-D1</i>
1A		1B		1D	<i>Glu-D4</i>
			<i>Lec-B1</i>		
	<i>Rg-A1c</i>			1DL,1DS	<i>Rg-D1</i>
2AS	<i>bh-A1</i>	2BS		2DS	<i>bh-D1</i>
	<i>Est-A6</i>		<i>Est-B6</i>		<i>Est-D6</i>
	<i>Per-A2</i>		<i>Per-B2</i>		<i>Per-D2</i>
					<i>Per-D5</i>
			<i>Ppd-B1a</i>		<i>Ppd-D1a</i>
2AL		2BL		2DL	<i>Acph-D2</i>
	<i>Est-A7</i>		<i>Est-B7</i>		<i>Est-D7</i>
	<i>F3h-A1</i>		<i>F3h-B1</i>		<i>F3h-D1</i>
			<i>F3h-B2</i>		
	<i>Hyd-A1</i>		<i>Hyd-B1</i>		<i>Hyd-D1</i>
	<i>Isa-A1</i>		<i>Isa-B1</i>		<i>Isa-D1</i>
	<i>Ppd-A1</i>				
	<i>Ppo-A1</i>				
	<i>Sod-A1</i>		<i>Sod-B1</i>		<i>Sod-D1</i>
					<i>Zds-D1</i>
2A		2B	<i>Gcl-B1a</i>	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
			<i>Gc1-B1b</i>		
3AS	<i>Zds-A1</i>	3BS	<i>Zds-B1</i>	3DS	<i>Br-D1</i>
	<i>Br-A1</i>		<i>Br-B1</i>		<i>Est-D1</i>
	<i>Est-A1</i>		<i>Est-B1</i>		<i>Est-D9</i>
	<i>Est-A9</i>		<i>Est-B9</i>		<i>Hk-D2</i>
			<i>Hk-B2</i>		<i>Iha-D1</i>
			<i>Iha-B1.1</i>		
			<i>Iha-B1.2</i>		
	<i>Ndh-A4</i>		<i>Ndh-B4</i>		
					<i>Nor-D8</i>
	<i>Pde-A1</i>		<i>Pde-B1</i>		<i>Pde-D1</i>
	<i>Tpi-A1</i>		<i>Tpi-B1</i>		<i>Tpi-D1</i>
			<i>Yrns-B1</i>		
3AL		3BL	<i>Dreb-B1</i>	3DL	
	<i>Eps-A1a</i>				
			<i>Est-B2</i>		<i>Est-D2</i>
	<i>Est-A5</i>		<i>Est-B5</i>		<i>Est-D5</i>
	<i>Est-A8</i>		<i>Est-B8</i>		<i>Est-D8</i>
	<i>Got-A3</i>		<i>Got-B3</i>		<i>Got-D3</i>
	<i>Mal-A1</i>		<i>Mal-B1</i>		<i>Mal-D1</i>
	<i>Ndh-A3</i>		<i>Ndh-B3</i>		<i>Ndh-D3</i>
	<i>Per-A3</i>		<i>Per-B3</i>		<i>Per-D3</i>
	<i>R-A1</i>		<i>R-B1</i>		<i>R-D1</i>
	<i>Vp-A1</i>				<i>Vp-D1</i>
					<i>Vp-D1a</i>
3A	<i>Dreb-A1</i>	3B		3D	<i>Dreb-D1</i>
	<i>Est-A2</i>				
	<i>Hk-A2</i>				
	<i>S-A1</i>		<i>S-B1</i>		<i>S-D1</i>
4AS	<i>AcpH-A1</i>	4BS		4DS	
			<i>Adh-B1</i>		<i>Adh-D1</i>
			<i>Amp-B2</i>		<i>Amp-D2</i>
			<i>Lpx-B1</i>		<i>Lpx-D1</i>
			<i>Lpx-B1.1</i>		
			<i>Ndh-B1</i>		<i>Ndh-D1</i>
			<i>Pdi-D1</i>		<i>Pdi-B1</i>
					<i>Pgm-D1</i>
			<i>Rht-B1</i>		<i>Rht-D1</i>
					<i>Rht-D1b</i>
4AL		4BL	<i>Aco-B2</i>	4DL	<i>Aco-D2</i>
			<i>AcpH-B1</i>		<i>AcpH-D1</i>
	<i>Adh-A1</i>				
			<i>b-Amy-B1</i>		<i>b-Amy-D1</i>
	<i>Amp-A2</i>				

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
			<i>Cat-B1</i>		
			<i>Hyd-B2</i>		<i>Hyd-D2</i>
	<i>Lpx-A1</i>				
	<i>Lpx-A3</i>				
	<i>Ndh-A1</i>				
	<i>Pdi-A1</i>				
	<i>Per-B4</i>				
	<i>Pgm-A1</i>				
	<i>Wx-B1</i>				
4A		4B	<i>Lpx-B1.2</i>	4D	
		4B	<i>Lpx-B3</i>		
5AS		5BS		5DS	<i>Gsp-D1</i>
	<i>Mdh-A3</i>		<i>Mdh-B3</i>		<i>Mdh-D3</i>
	<i>Nor-A3</i>				<i>Nor-D3</i>
	<i>Nor-A10</i>				<i>Pina-D1</i>
	<i>Pina-A^m1</i>				<i>Pinb-D1</i>
	<i>Pinb-A^m1</i>				<i>Pinb-D1b</i>
	<i>5S-Rrna-A2</i>		<i>5S-Rrna-B2</i>		<i>5S-Rrna-D2</i>
	<i>Skdh-A1</i>		<i>Skdh-B1</i>		<i>Skdh-D1</i>
5AL	<i>Aadh-A1</i>	5BL	<i>Aadh-B1</i>	5DL	<i>Aadh-D1</i>
	<i>Aco-A2</i>				
	<i>b-Amy-A1</i>				
			<i>Eps-5BL.1</i>		
			<i>Eps-5BL.2</i>		
	<i>HstH1-A1</i>		<i>HstH1-B1</i>		<i>HstH1-D1</i>
	<i>HstH1-A2</i>		<i>HstH1-B2</i>		<i>HstH1-D2</i>
	<i>Hyd-A2</i>				
	<i>Ibf-A1</i>		<i>Ibf-B1</i>		<i>Ibf-D1</i>
	<i>Lpx-A2</i>		<i>Lpx-B2</i>		<i>Lpx-D2</i>
	<i>Nor-A7</i>				
	<i>Srp-A1</i>		<i>Srp-B1</i>		<i>Srp-D1</i>
	<i>Ti-A2</i>		<i>Ti-B2</i>		<i>Ti-D2</i>
	<i>Tpi-A2</i>		<i>Tpi-B2</i>		<i>Tpi-D2</i>
	<i>Vrn-A1a</i>		<i>Vrn-B1a</i>		<i>Vrn-D1</i>
					<i>Vrn-D5a</i>
5A	<i>Gsp-A1</i>	5B	<i>Gsp-B1</i>	5D	
	<i>Psy2-A1</i>		<i>Psy2-B1</i>		
6AS	<i>Amp-A1</i>	6BS	<i>Amp-B1</i>	6DS	<i>Amp-D1</i>
			<i>Ep-B2</i>		

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