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## Catalogue of Gene Symbols for Wheat

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## PREFACE

This 2008 edition of the Catalogue of Gene Symbols for Wheat represents 40 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 300 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 is to continue to evolve the database as new information becomes available and older material becomes less relevant. Consensus maps are not yet adequately integrated with the Catalogue. While we have to adapt to the increasing universality of genetics across species, we must not lose track of our agricultural background and the fact that our organism is 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. Olin Anderson, Craig Morris and Daryl Somers are now part of the curatory team. I acknowledge their contributions as well as thanking Dr Gary Hart and others who, from time to time, have 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 will always be 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 us of omissions, errors, typos so we can fix them and your suggestions on better ways to provide and display wheat genetics information are always welcome.

R.A. McIntosh  
August, 2008

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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 4<sup>th</sup> 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 7<sup>th</sup> 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<sup>+</sup> 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 four-letter 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 non-enzymatic 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.

### 2.3. 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 italicised. 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 intra-chromosomally 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 lower-case 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](http://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 8<sup>th</sup> 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 8<sup>th</sup> IWGS

A nomenclature proposal for AFLP loci has been received from Marc Zabeau at Keygene with the format 'X<sub>xyz</sub>AN<sub>1</sub>N<sub>2</sub>N<sub>3</sub>', 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.; N<sub>1</sub> and N<sub>2</sub> are two-digit numbers identifying standard one, two or three base-pair extensions (standard lists will be provided by Keygene); and N<sub>3</sub> 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 11<sup>th</sup> 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 4<sup>th</sup> 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<sup>m</sup> are listed separately (under 4A<sup>m</sup>S, 4A<sup>m</sup>L, or 4A<sup>m</sup>), due to the several rearrangements that distinguish 4A and 4A<sup>m</sup>.

3. Superscripts appended to locus references designate the species in which loci were analyzed, as follows,

<sup>1</sup> ,	<i>T. aestivum</i> ,
<sup>2</sup> ,	<i>T. turgidum</i> ,
<sup>3</sup> ,	<i>T. monococcum</i> ,
<sup>4</sup> ,	<i>Ae. tauschii</i> , and
<sup>5</sup> ,	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	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
abg	(Barley genomic* clones) Kleinhofs, A. (see abc)	bg	(Barley genomic* clones) Lapitan, N. Department of Soil and Crop Sciences Colorado State University Fort Collins, CO 80526 USA
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)	bgl	Lane, B.G.* Faculty of Medicine University of Toronto Dept. of Biochemistry Medical Sciences Building Toronto, Ontario M5S 1A8 Canada
ak	Kleinhofs, A.* (see abc)	bnl	Burr, B. Brookhaven National Laboratory* Biology Dept. Upton, NY 11973 USA
aww	Langridge, P plangrid@waite.adelaide.edu.au Department of Plant Science Waite Campus* University of Adelaide* Glen Osmond South Australia 5064 Australia	bzh	Dudler, R. Institut fur Pflanzenbiologie* Universitat Zurich Zollikerstrasse 107 CH-8008 Zurich Switzerland
barc	Cregan, P USDA-ARS Beltsville, MA	ccsu	Gupta, P.K. Molecular Biology Laboratory Dept. of Agricultural Botany Ch. Charan Singh University Meerut-250004 India
bcd	(Barley cDNA clones*) Sorrells, M.E. Dept. of Plant Breeding & Biometry Cornell University 252 Emerson Hall Ithaca, NY 14853 USA		

cdo	(Oat cDNA clones) Sorrels, M.E. (see bcd)	csu	Coe, E. Department of Genetics University of Missouri Columbia, Mo 65211 USA
cfb	( <i>Ae. tauschii</i> clones) Bernard, M. michel.Bernard@clermont.inra.fr UMR Amelioration et Sante des plantes INRA-UBP 63039 Clermont-Erard*, Cedex 2 France	DuPw	Petra Wolters Petra.wolters@usa.dupont.com DuPont Company* P.O. Box 6104 Newark, DE 19714-6104 USA
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	fbf	(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*
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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
csl	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	labc	(Barley cDNAs) Shewry, P. IACR-Long Ashton Research Station Long Ashton Bristol, BS18 9AF, UK
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npi	*Grant, D. Pioneer Hi-Bred International 7250 N.W. 62nd Avenue Johnston IA 50131 USA	rz	(rice cDNA clones) Sorrells, M.E. {See bcd}
php	Grant, D. (see npi)	scs	(S. cereale SSRs) Gustafson, P. Dept. of Agronomy 208 Curtis Hall University of Missouri-Columbia Columbia, Missouri 6521, USA
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	Swm, sfr & sfrpr	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 psr)	tav	Breiman, A. Tel Aviv University University Campus Ramat Aviv, Israel
rgc	(Rice cDNA* clones) Sasaki, T. Rice Genome Research Program National Institute of Agrobiological Resources 2-1-2, Kannondai, Tsukuba Ibaraki 305, Japan	ttu	(cDNAs corresponding to stress- responsive 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
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)		

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ucd	Dvorák, J. University of California Dept. of Agronomy and Range Science Davis California CA 95616 USA	wg	(Wheat gDNA clones) Sorrells, M.E. (see bcd)
ucg	Hasselkorn, R. Department of Molecular Genetics and Cell Biology University of Chicago Chicago, Illinois 60637 USA	whe	Anderson, O. USDA ARS-WRRC 800 Buchanan Street Albany CA94710 USA
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## 9 Summary Tables

**Summary Table 1. Symbols including loci detected with 'known function' probes preceded by X**

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-1,2
<i>Aba</i>		Abscisic acid
<i>Aco-1,2</i>	sets	Aconitase-1,2
<i>Acl</i>		Acyl carrier protein
<i>Acl1</i>		Leaf acyl carrier proteins
<i>ACCCc</i>	sets	Acetyl CoA carboxylase - cytosolic form
<i>ACCP</i>	sets	Acetyl CoA carboxylase - plastid form
<i>AcpH-1</i>	set	Acid phosphatase-1
<i>Adh-1</i>	set	Alcohol dehydrogenase-1
<i>Adk-1</i>	set	Adenylate kinase-1
<i>Adpg</i>		ADP-glucose pyrophosphorylase
<i>Ald</i>		Aldolase
<i>Alt</i>		Aluminium tolerance
<i>Amc</i>		Amylase content
<i>Amp-1,2,3</i>	sets	Aminopeptidase-1,2,3
<i>Amp-A3</i>		Aminopeptidase-3
<i>An</i>		Anthocyanin Pigmentation
<i>ATPase</i>		Adenosinetriphosphatase
<i>Ar</i>		Alkylresocinol content in grain
<i>a-Amy-1,2</i>	sets	Alpha-amylase-1,2
<i>b-Amy-1</i>	set	Beta-amylase-1
<i>B-Atp</i>		B-Adenosinetriphosphatase
<i>B</i>		Inhibitor of awns
<i>Ba</i>		Blue aleurone
<i>Bdv</i>		Reaction to barley yellow dwarf virus
<i>b-Gls</i>		Beta-glucosidase
<i>Bg</i>		Black glume colour
<i>bh</i>		Branched spike
<i>Bls</i>		Reaction to <i>Xanthomonas campestris</i> pv <i>undulosa</i>
<i>Bla</i>		Black awns
<i>Bo</i>		Boron tolerance
<i>Br</i>		Brittle rachis
<i>Brz</i>		Bronze
<i>Bs</i>		Inhibitor of basal sterility in speltoides
<i>Bt1 to 10</i>		Reaction to <i>Tilletia</i>
<i>Bza</i>		Histone gene binding protein (bZIP) subfamily 1a
<i>Bza</i>		Basic leucine zipper protein of family 1a
<i>Bzb</i>		Histone gene binding protein (bZIP) 1b
<i>Bzb</i>		Basic leucine zipper protein of family 1b
<i>C</i>		Club spike shape
<i>Caa</i>		Carbonic anhydrase
<i>Cab</i>		Chlorophyll a/b binding protein
Symbol		Trait
<i>Cbp</i>		Chitin-binding protein

**Summary Table 1 (Cont.). Symbols including loci detected with 'known function' probes preceded by X**

Symbol	Trait
<i>Cc</i>	Chocolate chaff
<i>Cdu</i>	Cadmium uptake: low Cadmium uptake
<i>Ce</i>	Copper efficiency
<i>Ch</i>	Hybrid chlorosis
<i>Chi</i>	Chitinase
<i>Chr</i>	Hybrid chlorosis Type 1 gene in rye
<i>Chs</i>	Chalcone synthase
<i>CK2alpha</i>	Casien Kinase 2a 3ubunit
<i>cl</i>	Cleistogamus flowering in durumms
<i>Cm</i>	Reaction to <i>Eriophyes tulipae</i>
<i>Cmc</i>	Resistance to curl mite colonization
<i>CM16</i>	CM16 protein
<i>cn-1</i>	set Chlorina
<i>co</i>	Corroded
<i>Cre1 to 8</i>	Reaction to <i>Heterodera avenae</i>
<i>Crr</i>	Reaction to <i>Cochliobolus sativus</i>
<i>Cs</i>	Hybrid chlorosis Type 2
<i>Cxp</i>	Carboxypeptidase
<i>Cyp</i>	Cyclophilin
<i>Cyp71C</i>	Cytochrome P450 mono-oxygenase CYP71C subfamily
<i>D</i>	Grass-clump dwarfness
<i>Dfg</i>	Difenzoquat insensitivity
<i>Dhn</i>	Dehydrin
<i>Dip-1</i>	set Dipeptidase-1
<i>Dn1 to 9</i>	Reaction to <i>Diuraphis noxia</i>
<i>Eet</i>	Ear emergence time
<i>Eg</i>	Elongated glume
<i>El</i>	Ear length
<i>ELIP</i>	Early light-inducible protein
<i>Em</i>	Early methionine-labelled polypeptide
<i>Embp</i>	b-ZIP class DNA binding protein
<i>Ep-1,2</i>	sets Endopeptidase-1
<i>Eps</i>	Earliness per se
<i>Esi</i>	Early-salt-induced mRNAs
<i>Est-1 to 9</i>	sets Esterase-1,2,3,4,5,6,7,8,9
<i>Fbp</i>	Fructose-1,6-bisphosphatase
<i>Fbpa</i>	Fructose bisphosphate aldolase
<i>Fe</i>	Iron deficiency
<i>Fed</i>	Ferredoxin
<i>Fedr</i>	Ferredoxin-NADP+ reductase
<i>Fgw</i>	50-grain weight
<i>Fhs</i>	Reaction to <i>Fusarium graminearum</i>
<i>Flt</i>	Flowering time
<i>Fmt</i>	Flavonoid O-methyltransferase
<i>Fr</i>	Frost resistance
<i>Ft</i>	Free-threshing habit
<i>Gadp1</i>	Chloroplast glyceraldehyde phosphate dehydrogenase
<i>Gadp2</i>	Cytosolic glyceraldehyde phosphate dehydrogenase
<i>Gai</i>	Gibberellic acid insensitivity



**Summary Table 1 (Cont.). Symbols including loci detected with 'known function' probes preceded by X**

Symbol	Trait
<i>Gb1 to 6</i>	Reaction to <i>Toxoptera graminum</i>
<i>Gc</i>	Gameticidal genes
<i>Gdd</i>	Glycine decarboxylase
<i>Ger</i>	Germin
<i>Glb3</i>	(1-3)-?-glucanase (EC3.2.1.39)
<i>Gli-1,2,3</i>	sets Gliadin-1,2,3
<i>Glo-1</i>	set Salt soluble globulins-1
<i>Glob</i>	7S storage globulin
<i>Glp</i>	Germin-like protein
<i>Glu-1,3</i>	set Glutenin-1,3
<i>Glu-1-1</i>	X-type glutenins
<i>Glu-1-2</i>	Y-type glutenins
<i>Glu-2,4,5</i>	Glutenin-2,4,5
<i>GluTR</i>	set Glutamyl-tRNA reductase
<i>gn</i>	Grain number
<i>Got-1,2,3</i>	sets Glutamic oxaloacetic transaminase-1,2,3
<i>Gpc</i>	Grain protein content
<i>Gpi-1</i>	set Glucose phosphate isomerase-1
<i>Gpp</i>	Green plant percentage
<i>Grp</i>	Grp94 protein (endoplasmic heat shock protein 'endoplasmic')
<i>Gpt-1</i>	set Glutamate-pyruvate transaminase
<i>Gsp-1</i>	set Grain softness protein
<i>Gst</i>	Glutathione S-transferase
<i>Gwe</i>	Grain weight per ear
<i>H1 to 31</i>	Reaction to <i>Mayetiola destructor</i>
<i>Ha</i>	Grain hardness
<i>Hak</i>	High affinity potassium transporter
<i>Hd</i>	Hooded (awns)
<i>Hg</i>	Hairy glume
<i>Hk-1,2</i>	sets Hexokinase-1,2
<i>Hl</i>	Hairy leaf
<i>Hmgp</i>	High mobility group protein
<i>Hn</i>	Hairy node
<i>Hp</i>	Hairy peduncle
<i>Hpr</i>	NAD <sup>+</sup> hydroxypyruvate reductase
<i>Hrp</i>	Hydroxyproline-rich protein
<i>Hs</i>	Hairy leaf sheath
<i>Hsp</i>	Heat shock protein
<i>HstH1-1,2</i>	sets Histone proteins
<i>Ht</i>	Height
<i>Ibf-1</i>	sets Iodine binding factor-1
<i>Ica</i>	Chymotrypsin inhibitor
<i>Igc</i>	Suppressor of gametocidal activity
<i>itv:</i>	Near isogenic tetraploid stocks
<i>Iw</i>	Inhibitor of glaucousness
<i>Iha</i>	set Inhibitor of heterologous $\alpha$ -amylase
<i>Iso</i>	Isoamylase
<i>Isa</i>	set Inhibitor of $\alpha$ -amylase and subtilisin
<i>Kb1 to 6</i>	Reaction to <i>Tilletia indica</i>

**Summary Table 1 (Cont.). Symbols including loci detected with 'known function' probes preceded by X**

Symbol		Trait
<i>Ki</i>		Pollen killer
<i>Kna1</i>		Response to Salinity
<i>Kr</i>		Crossibility with rye
<i>Ld</i>		Lodging
<i>Lec-1</i>	sets	Lectin -1
<i>ler</i>		Leaf erectness
<i>lg</i>		Liguleness
<i>Lhcb</i>		Chlorophyll a/b binding protein CP29 of photosystem II
<i>Lpx-1,2</i>	sets	Lipoxygenase-1,2
<i>Lr1 to 61</i>		Reaction to <i>Puccinia recondita</i>
<i>LRR</i>		Protein that contains a leucine rich repeat
<i>Lrk</i>		Receptor-like kinase associated with <i>Lr</i> locus
<i>Ltn</i>		Leaf tip necrosis
<i>Ltp</i>		Low temperature pairing
<i>L13</i>		Chloroplast ribosomal protein L13
<i>Mal-1</i>	sets	Malic enzyme-1
<i>Mdh-1,3</i>	sets	Malate dehydrogenase-1,3
<i>Ml</i>		Reaction to <i>Blumeria graminis</i> - temporary designation
<i>Mpc1</i>		Myb protein c1
<i>ms</i>		Male sterile
<i>Msg</i>		Megasporogenesis
<i>Msh7</i>		DNA mismatch repair gene
<i>Mtase</i>		DNA (cytosine-5)-methyltransferase
<i>NBS</i>		Protein that contains a nucleotide binding site
<i>Ndh-1,2,3,4</i>	sets	NADH dehydrogenase-1,2,3,4
<i>Ne</i>		Hybrid necrosis
<i>Ner</i>		Hybrid necrosis genes in rye chromosome
<i>Nor</i>		Nucleolar organizer region
<i>Nra</i>		Nitrate reductase activity
<i>or</i>		Osmoregulation
<i>Oxo</i>		Oxalate oxidase
<i>OxoLP</i>		Oxalate oxidase
<i>P</i>		Long glumes (polonicum)
<i>Pa</i>		Pubescent/hairy auricles
<i>Pal</i>		Phenylalanine ammonia lyase
<i>Pan</i>		Purple anthers
<i>Pbc</i>		Pseudo-black chaff
<i>Pc</i>		Purple culm
<i>Pch</i>		Reaction to <i>Psuedocercospora herpotrichoides</i>
<i>Pdc</i>		Pyruvate decarboxylase
<i>Pde-1</i>	sets	Phosphodiesterase-1
<i>Pdi</i>		Protein disulphide isomerase
<i>Pdl</i>		Peduncle length
<i>Pepc</i>		Phosphoenol pyruvate carboxylase
<i>Per-1,2,3,4</i>	sets	Peroxidase-1,2,3,4
<i>Per-D5</i>		Peroxidase-5
<i>Pgd</i>		Phosphogluconate dehydrogenase
<i>Pgk1</i>		Chloroplast phosphoglycerate kinase
<i>Pgk2</i>		Cytosolic phosphoglycerate kinase

**Summary Table 1 (Cont.). Symbols including loci detected with 'known function' probes preceded by X**

Symbol		Trait
<i>Pgm-1</i>	set	Phosphoglucomutase-1
<i>Ph</i>		Pairing homoeologous
<i>Phn</i>		Dormancy seed
<i>Phs</i>		Preharvest sprouting
<i>PhyA</i>		Phytochrome A
<i>Pina</i>		Purindoline a
<i>Pinb</i>		Purindoline b
<i>Pk</i>		Protein kinase
<i>Pki</i>		Protein kinase inhibitor
<i>Plc</i>		Plastocyanin
<i>Pln</i>		Sterol esterification
<i>Pm1 to 39</i>		Reaction to <i>Blumeria graminis</i>
<i>Pp</i>		Purple pericarp
<i>Pp</i>		P protein
<i>Ppc</i>		Phosphoenol pyruvate carboxylase
<i>Ppd</i>		Response to photoperiod
<i>Ppdk</i>		Pyruvate orthophosphate dikinase
<i>Ppo</i>		Polyphenol oxidase
<i>Pr</i>		Pathogenicity related protein
<i>Prk</i>		Phosphoribulokinase
<i>Prp</i>		Proline-rich protein
<i>Pro</i>		Protein in seeds
<i>Psah</i>		10.2 kDa photosystem I polypeptide
<i>Psif</i>		Protein synthesis initiation factor
<i>Psk</i>		Chloroplast photosystem I PSK-I subunit
<i>Pur-1</i>	sets	Lipopurothionin-1
<i>q</i>		Spelt factor
<i>R-1</i>	set	Red grain colour
<i>Ra</i>		Red auricles
<i>Raw</i>		Red awns
<i>Rbca</i>		Rubisco activase
<i>Rbcs</i>		Ribulose-1,5-biphosphate carboxylase small subunit
<i>Rbp</i>		Rubisco binding protein
<i>Rbpa</i>		Rubisco binding protein, a subunit
<i>Rc-1</i>	set	Red coleoptile
<i>Rep</i>	set	DNA replication regulating gene
<i>Rf</i>		Restorer for cytoplasmic male sterility - <i>T. timopheevii</i>
<i>Rfd1</i>		Restorer for cytoplasmic male sterility - <i>Ae. crassa</i>
<i>Rg</i>		Red glume colour
<i>Rht-1</i>	set	Reduced height
<i>Rip</i>		Ribosome inactivating protein
<i>Rkn</i>		Reaction to <i>Meloidogyne</i> spp.
<i>Rlnn</i>		Reaction to <i>Pratylenchus neglectus</i>
<i>Rmg</i>		Reaction to <i>Magnaporthe grisea</i>
<i>5S-Rrna-1,2</i>	sets	5S Ribosomal RNA-1,2
<i>s-1</i>	set	Sphaerococcum factor
<i>Sam</i>		S-adenosyl methionine decarboxylase
<i>Sbe</i>		Starch branching enzyme
<i>Sbp</i>		Sedoheptulose-1,7-bisphosphatase

**Summary Table 1 (Cont.). Symbols including loci detected with 'known function' probes preceded by X**

Symbol		Trait
<i>sc</i>		Seedling chlorosis
<i>scs</i>		Nuclear-cytoplasmic compatibility enhancer
<i>Sd</i>		Segregation distortion
<i>Sdh</i>		Succinate dehydrogenase
<i>Sev</i>		Sedimentation value
<i>Sgp-1,2,3</i>	sets	Starch granule proteins
<i>Shw</i>		Sterility in hybrids with wheat
<i>Si-2</i>	set	Subtilisin inhibitor-2
<i>Skdh-1</i>	set	Shikimate dehydrogenase-1
<i>Sm</i>		Reaction to <i>Sidodiplosis mosellana</i>
<i>Snb</i>		Reaction to <i>Phaeosphaeria nodorum</i>
<i>Sod-1</i>	set	Superoxide dismutase-1
<i>Spn</i>		Spikelet number per ear
<i>Sr1 to 46</i>		Reaction to <i>Puccinia graminis</i>
<i>Ss</i>		Sucrose synthase
<i>SsI-1</i>	set	Starch synthase I
<i>SsII-1</i>	set	Starch synthase II
<i>Stb1 to 8</i>		Reaction to <i>Mycosphaerella graminicola</i>
<i>Su</i>		Insensitivity to chlortoluron
<i>SuLr</i>		Suppressor of leaf rust resistance
<i>SuPm</i>		Suppressor of powdery mildew resistance
<i>Sus</i>		Sucrose synthase
<i>Sut</i>		Sucrose transporter-1
<i>taVp1</i>		Viviparous ( <i>Triticum aestivum</i> )
<i>Tel</i>		Telomere
<i>Tg</i>		Tenacious glumes
<i>Tgw</i>		1000-grain weight
<i>Tha</i>		Thaumatococin
<i>Ti-2</i>	set	Protease inhibitor-2
<i>Tin</i>		Tiller inhibitor
<i>Tlp</i>		Thiolprotease
<i>Tn</i>		Tiller number
<i>Tpi-1,2</i>	sets	Triosephosphate isomerase-1,2
<i>Tria</i>	set	Pollen allergen encoding gene
<i>Tri-1</i>	set	Triticin protein -1
<i>Tsc</i>		Reaction to <i>Pyrenophora tritici-repentis</i> - Resistance to chlorosis induction
<i>tsn</i>		-Insensitivity to tan spot toxin
<i>Uba</i>		Ubiquitin activating enzyme E1
<i>Us</i>		Uniculum stunt
<i>Ut</i>		Reaction to <i>Ustilago tritici</i>
<i>v</i>		Virescent
<i>VAtpB2</i>		V-Adenosinetriphosphatase subunit B
<i>Vdac</i>		Voltage-dependent anion-channel protein
<i>vg</i>		Variagated red seed coat colour
<i>Vgw</i>		Temperature sensitive winter variegation
<i>Vi</i>		Restorer for cytoplasmic male sterility - <i>Ae. Ingissima</i>
<i>Vil</i>		Homologues of Arabidopsis vernalization insensitive gene <i>Vrn3</i> and <i>Vin</i> -like genes

**Summary Table 1 (Cont.). Symbols including loci detected with 'known function' probes preceded by X**

Symbol		Trait
<i>Vrn-1</i>	set	Response to vernalization
<i>W</i>		Glaucousness/waxiness/glossiness
<i>Win</i>		Winter hardiness
<i>Wip</i>		Wound-induced protein
<i>Wcs</i>		Wheat cold-specific genes
<i>Wsip</i>		Water-stress induced protein
<i>Wsm</i>		Reaction to wheat streak mosaic virus
<i>Wsp-1</i>	set	Water soluble proteins-1
<i>Wx-1</i>	set	Waxy endosperm
<i>X</i>		Basic symbol for DNA markers
<i>Yld</i>		Yield
<i>Yr1 to 41</i>		Reaction to <i>Puccinia striiformis</i>
<i>14-3-3</i>		14-3-3 protein
<i>60S</i>		60S ribosomal protein
<i>17D</i>		17kDa protein

**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	Gene	Chromosome	Gene	Chromosome	Gene
Arm		Arm		Arm	
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>Glo-A1</i>		<i>Glo-B1</i>		<i>Glo-D1</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>Per-B1</i>		<i>Per-D1</i>
	<i>Rg-A1</i>		<i>Rg-B1</i>		<i>Rg-D1</i>
	<i>5S-Rrna-A1</i>		<i>5S-Rrna-B1</i>		<i>5S-Rrna-D1</i>
			<i>Si-B2</i>		<i>Si-D2</i>
	<i>Tri-A1</i>				<i>Tri-D1</i>
1AL	<i>Glu-A1</i>	1BL	<i>Glu-B1</i>	1DL	<i>Glu-D1</i>
	<i>Lec-A1</i>		<i>Lec-B1<sup>a</sup></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>
2AS	<i>Est-A6</i>	2BS	<i>Est-B6</i>	2DS	<i>Est-D6</i>
	<i>Per-A2</i>		<i>Per-B2</i>		<i>Per-D2</i>
			<i>Ppd-B1</i>		<i>Ppd-D1</i>
2AL	<i>Est-A7</i>	2BL	<i>Est-B7</i>	2DL	<i>Est-D7</i>
	<i>Isa-A1</i>		<i>Isa-B1</i>		<i>Isa-D1</i>
	<i>Ppd-A1</i>				
	<i>Ppo-A1</i>				<i>Ppo-D1<sup>a</sup></i>
	<i>Sod-A1</i>		<i>Sod-B1</i>		<i>Sod-D1</i>
	<i>Tc1</i>		<i>Tc2</i>		<i>Tc3</i>
3AS	<i>Br-A1</i>	3BS	<i>Br-B1</i>	3DS	<i>Br-D1</i>
	<i>Est-A1</i>		<i>Est-B1</i>		<i>Est-D1</i>
	<i>Est-A9</i>		<i>Est-B9</i>		<i>Est-D9</i>
	<i>Hk-A2<sup>a</sup></i>		<i>Hk-B2</i>		<i>Hk-D2</i>
			<i>Iha-B1</i>		<i>Iha-D1</i>
	<i>Ndh-A4</i>		<i>Ndh-B4</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>
3AL		3BL		3DL	
	<i>Est-A2<sup>a</sup></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>

**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>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>S-A1<sup>a</sup></i>		<i>S-B1<sup>a</sup></i>		<i>S-D1<sup>a</sup></i>
4AL <sup>b</sup>	<i>Adh-A1</i>	4BS	<i>Adh-B1</i>	4DS	<i>Adh-D1</i>
	<i>Amp-A2</i>		<i>Amp-B2</i>		<i>Amp-D2</i>
	<i>Lpx-A1</i>		<i>Lpx-B1</i>		<i>Lpx-D1</i>
	<i>Lpx-A3</i>		<i>Lpx-B3<sup>a</sup></i>		
	<i>Ndh-A1</i>		<i>Ndh-B1</i>		<i>Ndh-D1</i>
	<i>Pdi-A1</i>		<i>Per-B4</i>		<i>Pdi-D1</i>
	<i>Pgm-A1</i>		<i>Pdi-B1</i>		<i>Pgm-D1</i>
	<i>Wx-B1</i>		<i>Rht-B1</i>		<i>Rht-D1</i>
4AS <sup>b</sup>	<i>AcpH-A1</i>	4BL	<i>Aco-B2</i>	4DL	<i>Aco-D2</i>
			<i>AcpH-B1</i>		<i>AcpH-D1</i>
			<i>b-Amy-B1</i>		<i>b-Amy-D1</i>
5AS	<i>Gsp-A1<sup>a</sup></i>	5BS	<i>Gsp-B1<sup>a</sup></i>	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>Pina-A1<sup>a</sup></i>				<i>Pina-D1</i>
	<i>,Pinb-A1<sup>a</sup></i>				<i>,Pinb-D1</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>Ibf-A1</i>		<i>Ibf-B1</i>		<i>Ibf-D1</i>
	<i>HstH1-A1</i>		<i>HstH1-B1,B2</i>		<i>HstH1-D1</i>
	<i>,A2</i>				<i>,D2</i>
	<i>Lpx-A2</i>		<i>Lpx-B2</i>		<i>Lpx-D2</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-A1</i>		<i>Vrn-B1</i>		<i>Vrn-D1</i>
5A	<i>Psy2-A1</i>	5B	<i>Psy2-B1</i>	5D	
6AS	<i>Amp-A1</i>	6BS	<i>Amp-B1</i>	6DS	<i>Amp-D1</i>
			<i>Ep-B2</i>		
	<i>Gli-A2</i>		<i>Gli-B2</i>		<i>Gli-D2</i>
	<i>Got-A1</i>		<i>Got-B1</i>		<i>Got-D1</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
6AL	<i>Aadh-A2</i> <i>Aco-A1</i> <i>AhasL-A1</i> <i>a-Amy-A1</i> <i>Dip-A1</i> <i>Est-A4</i> <i>Got-A2</i>	6BL	<i>Aadh-B2</i> <i>Aco-B1</i> <i>AhasL-B1</i> <i>a-Amy-B1</i> <i>Dip-B1</i> <i>Est-B4</i> <i>Got-B2</i>	6DL	<i>Aadh-D2</i> <i>Aco-D1</i> <i>AhasL-D1</i> <i>a-Amy-D1</i> <i>Dip-D1</i> <i>Est-D4</i> <i>Got-D2</i>
7AS	<i>Amp-A3</i>  <i>Ndh-A2<sup>a</sup></i> <i>Pan2</i> <i>Per-A4</i>  <i>Rc-A1</i> <i>Sgp-A1</i> <i>Sgp-A3</i> <i>Wx-A1</i>	7BS	     <i>Est-B3</i>   <i>Pgip1</i> <i>Rc-B1</i> <i>Sgp-B1</i> <i>Sgp-B3</i>	7DSc	          <i>Est-D3</i> <i>Ndh-D2</i> <i>Pan1</i> <i>Per-D4</i> <i>Pgip2</i> <i>Rc-D1</i> <i>Sgp-D1</i> <i>Sgp-D3</i> <i>Wx-D1</i>
7AL	<i>Adk-A1</i>  <i>a-Amy-A2</i> <i>Cn-A1</i> <i>Ep-A1</i> <i>PsyI-A1</i> <i>Wsp-A1</i>	7BL	<i>Adk-B1</i>  <i>a-Amy-B2</i> <i>Cn-B1</i> <i>Ep-B1</i> <i>PsyI-B1</i> <i>Wsp-B1</i>	7DLc	<i>Adk-D1</i>  <i>a-Amy-D2</i> <i>Cn-D1</i> <i>Ep-D1</i>   <i>Wsp-D1</i>
7A	<i>SsI-A1</i> <i>SsII-A2</i>	7B	<i>SsI-B1</i> <i>SsI-B2</i>	7D	<i>SsI-D1</i> <i>SsI-D2</i>

<sup>a</sup> Arm location is unknown

<sup>b</sup> 4AL is mostly homoeologous to 4BS and 4DS and likewise 4AS is mostly homoeologous to 4BL and 4DL.

<sup>c</sup> The arm designated S is physically longer than the arm designated L.



**Summary Table 3.** Chromosomal locations of wheat genes, that have not been assigned to an orthologous set of Triticeae genes. QTLs are not included.

Chromosome-arm/ Chromosome	Genes
1AS	<i>Gli4, Gli6, H3, H5, H6, H9,H10, H11, H15, Hdic, Hg, Lr10, Nor, Pm3, Pm17, Rf1, Rg3, SuPm8, tin1, Tsc1</i>
1AL	<i>Eps-1Am, Lr59, scs</i>
1A	<i>Cmc3, Gb2, Gb6, kr4, Pm25, YrDa1</i>
1BS	<i>Rf3, Rf4, Snn1, Stb11, Vi, Yr10, Yr15, Yr24/26, YrAlp, YrH52</i>
1BL	<i>Iw3, Lr33, Lr46, Lr51, Nor6, Sr14, Yr29</i>
1B	<i>Bt4, Bt5, Bt6, Dn7, Lr44, Lr55, Ltn2, Pm28, Pm32, Sr31, SrZdar, Yr3, Yr9, Yr21</i>
1DS	<i>Gli-DT1, H22, Lr21, Lr60, Pm24, Sr45</i>
1DL	<i>Dn4, Dn9, Lr38, Sbe11, Sr33.</i>
1D	<i>Glu4, Lr42, Pm10, Ra1, Sr18, Stb10, Yr25</i>
2AS	<i>bh, Cre5, Lr17, Lr37, Lr49, Sr38, Yr17</i>
2AL	<i>b-Gls, Lr38, Pm4, PmPs5A, Snb2, Sr21, Tc1, Yr1, Yr32</i>
2A	<i>Br4, Ch1, lg3, Lr11, Lr45, LrTt1, Pp3, Rht7, Sr32, Sr34, tin2</i>
2BS	<i>Iw1, Lr13, Lr16, Lr23, Ne2, Pm26, Sr19, Sr23, Sr36, Sr40, Tg2, W1, Yr27, Yr31, Yr41, YrSp, Tsc2</i>
2BL	<i>Cre1, D2, Dfq1, Lr50, Lr58, Mlzecl, Pm33, Rht4, Sr9, Sr16, Sr28, Tc2, Yr5, Yr7</i>
2B	<i>Bt1, Gc1, H20, H21, lg1, Lr35, Pm6, Sm1, Sr10, Sr20, Sr32, Sr39, wptms2, wtms1, Yr3, YrSte, YrV23.</i>
2DS	<i>D1, Iw2, Lr2, Lr15, Lr22, Lr39, Per5, Sr6, SuLr23, Snn2, Tg1, YrCK</i>
2DL	<i>Acp2, C, Cre3, D4, Lr54, Rht8, Tc3, YmYF, Yr37</i>
2D	<i>Bt7, Cre4, lg2, Ra1, Sr32, Sr34, Yr8, Yr16</i>
3AS	<i>Stb6</i>
3AL	<i>Eps1, Snb1, SnbTM, Sr35</i>
3A	<i>EpsWi, ms5, Sr27, Tsr4, V2, YrTr2.</i>
3BS	<i>Lr27, Pbc, Rht5, sc, Sr2, Sr12, Stb2, Stb14, Yr30, Yrns1, VI</i>
3BL	<i>Tsn2, Tsr2, Tsr5</i>
3B	<i>Igcl, Pm13, Rkn-mn1, YrS, YrSte</i>
3DS	<i>Lr32, Lr38, Nor8, Ph2</i>
3DL	<i>Ch2, H26, H32, Lr24</i>
3D	<i>H24, Pm13</i>
4AL	<i>D3, Lr28, Lr30, Per4, Phs1, Sr7, Stb7, Stb12</i>
4AS	<i>Hd.</i>
4A	<i>Bo3, H25, Pm16, YrHVII, YrMin, YrND, Wsm1</i>
4BS	<i>Gail, Gai3, Lpx1, Lr25, ms1, Pa</i>
4BL	<i>Cat1, Ce, H11, Hp, Lr31, Lr48, Pm7, Sr37</i>
4B	<i>Bal, H25, Lpx1, Lr12, Lr16, Mld, Ra2, Sr23, YrCle, YrMor, YrYam.</i>
4DS	<i>Gai2, ms2, ms4, Yr28</i>

**Summary Table 3 (Cont.).** Chromosomal locations of wheat genes, that have not been assigned to an orthologous set of Triticeae genes. QTLs are not included.

Chromosome-arm/ Chromosome	Genes
4DL	<i>Alt2, Kna1, Wss1</i>
4D	<i>H26, Sr41, Yr22, Wsm1</i>
5AL	<i>Ar1, B1, Fr1, Hn, kr2, Nor7, Q, Rht9, Yr34</i>
5AS	<i>Lr38, ms3, Nor10</i>
5A	<i>Cs1, H4, H12, H16, H17, H28, H29, Pm23, Rht12</i>
5BS	<i>Ce, H31, Hp, Lr52, Pm30.</i>
5BL	<i>Cdu1, Crr, Eps5, Kr1, Lr18, Ne1, Ph1, Pm36, Stb1, tsn1, Tsr1, Vgw.</i>
5B	<i>Cmc2, Pm16, wptms1, Yr19, YrDru</i>
5DS	<i>Ha, Lr57, Pm2, Pina, Pinb, Pro2, Yr40</i>
5DL	<i>Fr2, Lr1, Pm34, Pm35, Pro1, Snb3, Sr30, Vrn4, Vrn 5</i>
5D	<i>H7, kr3, YrDa2</i>
6AS	<i>Pm21, Rf6, Sr8, Stb15</i>
6AL	<i>Imi3, Mlre, Sr13, Sr26</i>
6A	<i>Cmc2, Pp1, Yr38, YrD, YrDru2, YrH46.</i>
6BS	<i>col, Ep2, Fhb2, Gpc1, Lr36, Lr53, Nor2, Pm11 Rf6, Su1, Yr35, Yr36</i>
6BL	<i>?-Amy1, B2, Cre8, Imi2, Ki, Lr3, Lr9, Pm20, Sr11?</i>
6B	<i>H25, Pm12, Pm14, Pm27, Ra3, Rf4, Su1, Yr4, YrDru</i>
6DS	<i>Cmc1, Cmc4, H13, H23, HWGRC4, Sr5, Sr29, Sr42, Stb3</i>
6DL	<i>H13, H23, H24, Imi1, Lr38, Sr29</i>
6D	<i>Amp1, Cmc2, co2, Hp, Pm24, Rf5, Yr20, Yr23, YrTye, YrTr1</i>
7AS	<i>Amp3, Msg, or, Pan2</i>
7AL	<i>Lr19, Lr20, Mlm3033, Mlm80, mlRd30, P1, Pch2, Pm1, Pm9, Pm37, Rhn1, Sr15, Sr22, Sr25</i>
7A	<i>Gby, Pgd1, Pp2</i>
7BS	<i>cc, Dn1881, Fe2, Hl2, Pc1, Pqip1, Rht9, Rht13, Vrn3, Yr6</i>
than one chromosome	<i>P2, Pm5, Lr14, Lr19, Rfd1, Sbe12, Sd2, Sr17, Stb8, Stb13, Yr39, YrZH84</i>
7B	<i>Bo1, mljy, mlsy, Mlxbd, Pp2, Yr2</i>
7DS	<i>Bvd1, Dn1, Dn2, Dn5, Dn8, DnX, Lr29 Lr34, Pan1, Pc2, Pqip2, Pln, Pm15, Pm38, Sr44, Stb4, Stb5, Yr18</i>
7DL	<i>Bdv2, Dn2, Dn5, Fe1, Gb3, Gb4, Gb7, Gba, Gbb, Gbc, Gbx1, Gbz, Lr19, LrVPM, Nor4, Pch1, Sr25, Sr43</i>
7D	<i>Dnl, Gb3, Glu5, Ltn, Pch1, Pm19, Rf2, Sd1</i>

**Summary Table 4.** Designated wheat genes {including genes assigned temporary designations}  
whose chromosomal locations are unknown.

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*Alt1.*  
*Bls1, 2, 3, 4 & 5.*  
*Bo2.*  
*Bt2, 3, 8, 9, & 10.*  
*Chr1.*  
*Cre2, 6 & 7.*  
*Dn3 & 6.*  
*epsCnn.*  
*Fhs1 & 2.*  
*Gb1.*  
*H1, 2, 4, 8, 18, 19 & 30.*  
*Hs.*  
*Iso1*  
*Kb1, 2, 3, 4, 5 & 6.*  
*Lr40, LrTb, LrTm, LrTr.*  
*Ltp.*  
*MI-Ad, MI-Br, MI-Ga.*  
*Nra.*  
*Pch3.*  
*Pm1 & 29.*  
*Rht6, 11, 14, 15, 16, 17, 18, 19, 20 & 21.*  
*Rkn.*  
*s2.*  
*Sbm1*  
*Shw.*  
*Sr1, 3, 4, SrA, SrTmp, SrWld.*  
*Stb9*  
*Utl, 2, 3, 4, Ut-x.*  
*vg.*  
*Yr11, 12, 13, 14 & 33*

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## 10. Genetic linkages

Unless otherwise indicated, estimates are for *T. aestivum*, *T. turgidum* {**tv**:} and *T. monococcum* {**dv**:}. All genetic recombination values and standard errors {S.E.} from the literature are presented as percentages with references. Where values were converted to map units by authors these values, S.E.s and references appear in appropriate columns. Recombination values of 15% or greater were converted to map units using the Kosambi function:

$$X = 25 \log_e [(1+2y)/(1-2y)]$$

where X is the map distance in centimorgans {cM} and y is the recombination fraction. This function has little effect on values of less than 15%. Obviously, high values with large S.E.s should be treated with caution.

The S.E. for X was computed from the formula:

$$S.E._X = 100 S.E._y / (1-2y^2).$$

As far as possible genes are listed in order from the distal end of the short (S) arm to the distal end of the long (L) arm. Close linkages are listed under m: in the gene lists.

I = genetically independent; cent = centromere.B56

<b>Genes</b>	% Recombination			cM		
	Value	S.E.	Ref	Value	S.E.	Ref
<b>Chromosome 1</b>						
<b>1AS</b>						
	<i>Rg3</i>	-	<i>Hg</i>	0		{1406}
<b>tv:</b>	<i>Hg</i>	-	<i>Bg</i>	1.17	1.4	{1103}
	<i>Hg</i>	-	<i>Bg</i>	1.52	1.88	{1103}
	<i>Hg</i>	-	<i>Bg</i>	1.32	1.15	{1103}
<b>tv:</b>	<i>Hg</i>	-	<i>Bg</i>	2.4		{1519}
	<i>Hg</i>	-	<i>Bg</i>	0		{631}
	<i>Hg</i>	-	<i>Bg</i>	12.33	2.16	{1347}
<b>dv:</b>	<i>Hg</i>	-	<i>Bg</i>	0-16.5		{1393}
	<i>Hg</i>	-	<i>Pm3a</i>	4.81	0.52	{943}
	<i>Hg</i>	-	<i>Pm3a</i>	0.82		{134}
	<i>Hg</i>	-	<i>Gli-A1</i>	3.95	1.38	{559}
	<i>Hg</i>	-	<i>Gli-A1</i>	0.30	0.31	{1406}
	<i>Hg</i>	-	<i>Gli-A1</i>	0.79	0.81	{897}
	<i>Hg</i>	-	<i>Gli-A1</i>	2.24	1.31	{1406}
	<i>Hg</i>	-	<i>Gli-A1</i>	2.64	0.98	{1405}
	<i>Hg</i>	-	<i>Gli-A1</i>	2.97	1.64	{1103}
	<i>Hg</i>	-	<i>Gli-A1</i>	2.31	1.31	{1103}
	<i>Hg</i>	-	<i>Gli-A1</i>	2.97	0.84	{1103}
	<i>Hg</i>	-	<i>Lr10</i>	5.97	1.7	{559}
	<i>Hg</i>	-	<i>Tin</i>	10	3	{1212}
	<i>Hg</i>	-	<i>cent</i>	I		{947}
	<i>Rg3</i>	-	<i>Hg</i>	0		{1406}
	<i>Pm3a</i>	-	<i>Pm25</i>	21		{1343}
	<i>Pm3a</i>	-	<i>cent</i>	I		{947}
	<i>Pm3a</i>	-	<i>Glu-A1</i>	I		{1406}

**Genetic linkages (Cont.)**

<b>Genes</b>			% Recombination			cM			
			Value	S.E	Ref	Value	S.E.	Ref	
	<i>H5</i>	-	<i>H11</i>				4.4	1.8	{1422, 1222}
	<i>Gli-A1</i>	-	<i>Gli-A5</i>				1.94	0.01	{350}
<b>tv:</b>	<i>Gli-A1</i>	-	<i>Bg</i>	<2.33		{1103}			
	<i>Gli-A1</i>	-	<i>Glu-A1</i>	42		{882}	61.1		
	<i>Gli-A1</i>	-	<i>Lr10</i>	2.95	1.18	{559}			
	<i>Gli-A1</i>	-	<i>Gli-A3</i>	31.9	2.27	{1407}	37.7	3.8	
	<i>Gli-A1</i>	-	<i>Gli-A3</i>	22.73	4.07	{1406}			
	<i>Gli-A1</i>		<i>Gli-A3</i>				22.42	3.61	{1075}
	<i>Gli-A1</i>	-	<i>Glu-A3</i>				1.5	0.3	{1227}
	<i>Gli-A1</i>	-	<i>Tri-A1</i>	40.1	2.9	{1357}	55.2	8.1	{1358}
	<i>Gli-A1</i>	-	<i>Glu-A1</i>	I					
	<i>Gli-A3</i>	-	<i>Glu-A1</i>	27.3	2.7	{1407}	30.6	3.9	
	<i>Gli-A3</i>	-	<i>Glu-A1</i>	37.55	5.05	{1406}			
	<i>Tri-A1</i>	-	<i>cent</i>	11	1.8	{1355}			
	<i>Tri-A2</i>	-	<i>cent</i>	11	2	{1358}			
<b>1AL</b>									
	<i>cent</i>	-	<i>Glu-A1</i>				7.7	1.8	{1125}
	<i>cent</i>	-	<i>Glu-A2</i>				33.9	5.4	{1359}
	<i>cent</i>	-	<i>Glu-A3</i>				10.2	3.5	{1359}
<b>Chromosome 1B</b>									
<b>1BS</b>									
	<i>Yr10</i>	-	<i>Gli-B1</i>	5	2.2	{1121}			
	<i>Yr10</i>	-	<i>Glu-B1</i>	47	5	{1121}			
	<i>Yr 10</i>	-	<i>Yr15</i>				23.6	5.5	{10112}
	<i>Yr10</i>	-	<i>Yr24</i>				37.6	10.7	{10112}
	<i>Rg1</i>	-	<i>Yr10</i>	2	0.3	{1002}			
	<i>Rg1</i>	-	<i>Bt4</i>	23		{1005}	24.9		
	<i>Rg1</i>	-	<i>Bt4</i>	14		{1000}			
	<i>Rg1</i>	-	<i>Gli-B1</i>	close		{504}			
	<i>Rg1</i>	-	<i>Gli-B1</i>	1.8	0.8	{1121}			
	<i>Rg1</i>	-	<i>Gli-B1</i>	2.84	1.39	{1405}			
	<i>Rg1</i>	-	<i>Gli-B1</i>	4.05	1.52	{1405}			
	<i>Rg1</i>	-	<i>Gli-B1</i>	0		{1405}			
	<i>Rg1</i>	-	<i>Sr14</i>	I		{933}			
	<i>Rg1</i>	-	<i>Bt5</i>	I		{1000}			
	<i>Rg1</i>	-	<i>Glu-B1</i>	44.3	3.1	{1121}			
<b>tv:</b>	<i>Rg1</i>	-	Gli band 42	7.87	2.39	{792}			
	<i>Glu-B3</i>	-	<i>Gli-B1</i>	1.7	0.8	{1358}			
<b>tv:</b>	<i>Glu-B3</i>	-	Gli band 45	10.32	2.44	{792}			
<b>tv:</b>	<i>Rg 1</i>	-	band 42/45	8.7	1.2	{500}			
	<i>Rg1</i>	-	( <i>Gli-B1</i> )	2	0.6	{500}			
<b>tv:</b>	<i>Rg 1</i>	-	<i>Gli-B1</i>	6.44	1.71	{1103}			
	<i>Gli-B1</i>	-	<i>Glu-B3</i>	1.7		{1355}			
<b>tv:</b>	<i>Gli-B1</i>	-	<i>Glu-B3</i>	2		{1144}			
	<i>Gli-B1</i>	-	<i>Gli-B5</i>	3.5	1.4	{9922}			
	<i>Gli-B1</i>	-	<i>Gli-B3</i>				22.4	6.3	{589}
	<i>Gli-B1</i>	-	<i>Gli-B3</i>				21.72	2.16	{1315}
			<i>Gli-B3</i>						
	<i>Gli-B1</i>	-	(= <i>Gli 1</i> )	25.5	4.3	{422}	28.1	5.8	{422}

**Genetic linkages (Cont.)**

Genes			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
<i>Gli-B1</i>	-	<i>rf3</i>	22.1	6.4	{1399}	23.7	8	
<i>Gli-B1</i>	-	<i>rf3</i>	18.6		{9934}			
<i>Gli-B1</i>	-	<i>Nor-B1</i>	36.8	13.5	{1399}	47.1	29.5	
		<i>Xgwm11</i>						
<i>Gli-B1</i>	-	<i>/Xgwm18-1B</i>	20.7		{0321}			
<i>Gli-B1</i>	-	cent				59.7	7.1	{1358}
<i>Gli-B1</i>	-	cent				56.1	10.3	{1358}
<i>Gli-B1</i>	-	cent	I		{223}			
<b>tv:</b> <i>Gli-B1</i>	-	cent				46.4		{224}
<i>Gli-B1</i>	-	<i>Glu-B1</i>	42	4.9	{1121}			
<i>Gli-B1</i>	-	<i>Glu-B1</i>	42.5	3	{1121}	62.8	10.8	
<i>Gli-B1</i>	-	<i>Glu-B1</i>	41		{882}	57.8		
<i>Gli-B1</i>	-	<i>Glu-B1</i>				39.1		{589}
<i>Gli-B1</i>	-	<i>Glu-B1</i>				66	5.7	{1125}
<i>Gli-B1</i>	-	<i>Glu-B1</i>	37.5	1.9	{422}	48.6	4.3	{422}
<i>Gli-B1</i>	-	<i>Glu-B1</i>	30.8	7.4	{1399}	35.9	11.9	
<i>Gli-B1</i>	-	<i>Glu-B1</i>	I		{422}	53.6	7.9	{422}
<i>XGli-B3</i>	-	<i>Glu-B2</i>				0		{277}
<i>Gli-B3</i>	-	<i>Glu-B1</i>				16.7	5.2	{589}
<i>Gli-B3</i>	-	<i>Glu-B1</i>				22.4	6.3	{589}
<i>Gli-B3</i>	-	<i>Glu-B1</i>	23.5	4.2	{422}	25.5	5.4	{422}
<i>Glu-B3</i>	-	<i>Glu-B1</i>	35.4	4.8	{1358}	44.2	9.6	
<i>Glu-B3</i>	-	<i>Glu-B1</i>	29.9	6	{458}			
<i>rf3</i>	-	<i>Nor-B1</i>	22.6	9.2	{1399}	24.4	11.6	
<i>rf3</i>	-	<i>Glu-B1</i>	34.1	8.5	{1399}	41.6	15.9	
<i>Nor-B1</i>	-	<i>Glu-B1</i>	22.5	9.3	{1399}	24.2	11.7	
<i>Nor-B1</i>	-	<i>Glu-B1</i>				22		{1120}
<i>Nor-B1</i>	-	<i>Rf3</i>	22.3		{9934}			
<i>Bt4</i>	-	<i>Bt5</i>	30		{1000}	34.7		
<i>Bt4</i>	-	<i>Bt6</i>	15.2	1.6	{1274}	15.7	1	
<i>Lr26</i>	-	<i>Lr3</i>	2.6	0.8	{325}			
<b>tv:</b> <i>Yr10</i>	-	<i>Yr15</i>				34.0	2	{969}
<i>Yr15</i>	-	cent				7		{969}
<i>Yr15</i>	-	<i>Yr24</i>				3.7	1.6	{10112}

Probable gene order: *Nor-B1* - *Gli-B3* - *Glu-B1* {589}.

Gene order: *Nor-B1* - *Hk-B1* - *Per-B1* - cent {012}.

*Rg1* and *Gli-B1* are located on the satellite {1120}

Gene order: *Yr10/Rg1* - *Gli-B1* - *Rf3* - *Gli-B3* - *Nor-B1* - cent - *Glu-B1*{1121}.

cent	-	<i>Lr33</i>				3.1	1.2	{325}
cent	-	<i>Glu-B1</i>				10.2	2.4	{1125}
<i>Lr33</i>	-	<i>Lr44</i>	5.4	1.1	{322}			
<b>tv:</b> cent	-	<i>Glu-B1</i>	32.6		{224}	38.9		
cent	-	<i>Glu-B1</i>	28.1	2.8	{1359}	31.8	4.1	
cent	-	<i>Glu-B1</i>	14.1		{223}			
Cent - <i>Lr51</i>	-	<i>Glu-B1</i>	0.41		{0307}	50-86		{0308}

**Genetic linkages (Cont.)**

<b>Genes</b>			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
<b>Chromosome 1D</b>								
<b>1DS</b>								
<i>Gli-D1</i>	-	<i>Gpi-D1</i>	36.2	4.5	{196}	45.8	9.5	
<i>Gli-D1</i>	-	<i>Tri-D1</i>	36.5	3.6	{1357}	46.4	7.7	
<i>Gli-D1</i>	-	<i>Tri-D1</i>	56	7	{478}			
<i>Gli-D1</i>	-	<i>Tri-D1</i>	I		{477}			
<i>Gli-D1</i>	-	cent	I		{477}			
<i>Gli-D1</i>	-	<i>Glu-D1</i>				63.5		{754}
<i>Gli-D1</i>	-	<i>Glu-D1</i>	48.3	2.4	{196}			
<i>Gli-D1</i>	-	<i>Glu-D1</i>	42		{882}	61.1		
<i>Gli-D1</i>	-	<i>Sr33</i>	5.6	2.4	{620}			
<i>Gli-D1</i>	-	<i>Sr33</i>	7.6	2.8	{620}			
<i>Gli-D1</i>	-	cent	37.3	5.1	{620}			
<i>Gli-D1</i>	-	<i>Glu-D1</i>	44.3	5.2	{620}			
<i>Gli-D1</i>	-	<i>Glu-D1</i>	47.2	5.2	{620}			
<i>Gli-D1</i>								
<i>/Glu-D3</i>	-	<i>Tri-D1</i>	55.8	7.4	{1358}			
<i>Sr45</i>	-	Cent.	21	3.4	{894}			
<i>Sr45</i>	-	<i>Sr33</i>				9	1.9	{894}
Most likely order:			Cent - <i>Sr45</i> - <i>Sr33</i> - <i>Lr21</i> {894}.					
<i>Tri-D1</i>	-	cent				15.4	2.1	{1358}
<i>Tri-D1</i>	-	cent	14.1	2.5	{477}			
<i>Gpi-D1</i>	-	<i>Glu-D1</i>	34.5	4.4	{196}	42.4	8.6	
<i>Tri-D1</i>	-	cent	10.1	2.2	{1355}			
<i>Sr33</i>	-	cent	29.6	4.8	{620}			
<i>Sr33</i>	-	<i>Glu-D1</i>	40.9	5.2	{620}			
<i>Sr33</i>	-	<i>Glu-D1</i>	39.5	5.1	{620}			
Gene order: <i>Gli-D1</i> - <i>Gpi-D1</i> - <i>Per-D1</i> - <i>Tri-D1</i> {709}. Last 3 agree with {012} for 1B.								
<i>Sr33</i>	-	<i>Gli-D1</i>				9	3.2	{226}
<i>Lr21</i>	-	<i>Gli-D1</i>				5.6	2.7	{619}
<i>Lr21</i>	-	<i>Gli-D1</i>	18		{448}			
<i>Lr21</i>	-	<i>Rg2</i>				4.2	2.4	{619}
<i>Lr21</i>	-	<i>Glu-D1</i>	I		{619}			
<i>Lr21</i>	-	<i>Lr42</i>	28.6	2.3	{218}	32.5	3.4	
<i>Lr21</i>	-	<i>Lr41</i>	I		{218}			
<i>Rg2</i>	-	<i>Gli-D1</i>				1.4	1.4	{619}
<i>Rg2</i>	-	<i>Glu-D1</i>	I		{619}			
<i>Gli-D1</i>	-	<i>Glu-D1</i>	I		{619}			
<i>Pm22</i>	-	<i>Pm24</i>	I		{0150}			
Gene order: <i>Gli-D1</i> - <i>Rg2</i> - <i>Lr21</i> {619}.								
<b>1DL</b>								
cent	-	<i>Sr18</i>	1.2	0.8	{1175}	10.2	2.4	{1125}
cent	-	<i>Glu-D1</i>				30.9	2.7	{1359}
cent	-	<i>Glu-D1</i>				22	3.5	{1359}
cent	-	<i>Glu-D1</i>				7.7	9.7	{754}
cent	-	<i>Glu-D1</i>	16.5	3.8	{620}			
<i>Rg2</i>	-	<i>Lr21</i>	10.1	2.2	{1241}			

**Genetic linkages (Cont.)**

<b>Genes</b>			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
<i>Rg2</i>	-	<i>Lr21</i>	3.1	1.1	{1241}			
<i>Rg2</i>	-	<i>s</i>	1.7	1	{1241}			
<i>Rg2</i>	-	<i>Sr33</i>	35	5.2	{650}	43.4	10.2	
<i>Rg2</i>	-	<i>Sr33</i>						
<b>1D</b>	<i>Rg2</i>	-	<i>Sr33</i>					
	<i>Lr41</i>	-	<i>Lr24</i>	I	{218}			
<b>Chromosome 1R</b>								
<b>1RS</b>								
	Tel (C-band)	-	<i>SrR</i>			16	4.8	{9919}
	<i>Sec 1</i>	-	Cent			26.1	4.3	{9919}
	<i>Sec 1</i>	-	<i>Sec 3</i>	36.0	4.6	{779}	45.4	9.6
	<i>Sec 1</i>	-	<i>Sec 3</i>	40.8	3.76	{1336}	57.2	11.3
	<i>Sec 1</i>	-	<i>Sec 3</i>	36.0	4.12	{163}	45.4	8.6
	<i>Dn7</i>	-	<i>Lr26</i>			14.5	3.9	{894}
	<i>Dn7</i>	-	<i>Lr26</i>					
	<i>Sr31</i>							
	<i>/Lr26</i>							
	<i>/Yr9</i>	-	Sec1			5.4	1.7	{9919}
<b>1RL</b>								
	cent	-	<i>Glu-R1</i>			4.7	1.0	{1356}
<b>Chromosome 2A</b>								
<b>2AS</b>								
	<i>bh</i>	-	cent			8.5	2.1	{665}
	<i>Lr17a</i>	-	cent	I	{314}			
	<i>Lr17a</i>	-	<i>Lr11</i>	I	{314}			
	<i>Yr1</i>	-	<i>Yr32</i>	I	{10016}	35		{10016}
<i>Sr38, Lr37 and Yr17 were closely linked in coupling and showed close repulsion linkage with Lr17a</i>								
<i>{062}.</i>								
<b>2AL</b>								
	cent	-	<i>Sr21</i>	2.4	0.9	{1464}		
	cent	-	<i>Tc2</i>			46.8	0.9	{10133}
	cent	-	<i>Pm4b</i>	I	{1464}			
	<i>Sr21</i>	-	<i>Pm4b</i>	37.5	1.7	{1464}	48.6	3.9
	<i>Yr1</i>	-	<i>Pm4a</i>			2	0.6	{940}
	<i>Tc2</i>	-	<i>Lg1</i>			11.9		{10133}
<b>Chromosome 2B</b>								
<b>2BS</b>								
	<i>Lr16</i>	-	<i>Sr23</i>	< 0.7		{950}		
	<i>Lr16</i>	-	<i>Sr36</i>	I	{939}			
	<i>Lr16</i>	-	<i>Sr40</i>	34.4	4.1	{302}	42.2	7.8
	<i>W11</i>	-	cent	42-50		{267}	>61.6	
	<i>Ne2</i>	-	cent	9.4	1.5	{1085}		
	<i>Ne2</i>	-	<i>D2</i>	34		{536}	41.5	
	<i>Sr40</i>	-	<i>Sr36</i>	21.9	2.4	{302}	23.5	3
	<i>Sr40</i>	-	<i>Lr13</i>	1	0.6	{302}		



**Genetic linkages (Cont.)**

Genes			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
<i>Sr40</i>	-	<i>Lr23</i>	4.7	1.2	{302}			
<i>Sr40</i>	-	<i>Sr9</i>	28	3.3	{302}	31.6	4.8	
<i>Sr19</i>	-	cent	7.7		{1582}			
<i>Lr23</i>	-	<i>Lr13</i>	close		{939}			
<i>Lr23</i>	-	cent	4		{948}			
<i>Lr23</i>	-	cent				20		{1058}
<i>Lr23</i>	-	<i>Sr9b</i>	22	2	{948}	23.6	2.5	
<i>Lr23</i>	-	<i>Sr9b</i>	22.3	2.4	{932}	24	3	
<i>Lr23</i>	-	<i>Sr9b</i>	24.1	2.2	{932}	26.3	2.9	
<i>Lr23</i>	-	<i>Sr9b</i>	30.6	4.2	{965}	35.6	6.7	
<i>Lr23</i>	-	<i>Sr28</i>	28.5	2.8	{932}	32.4	4.1	
<i>Yr27</i>	-	<i>Lr13</i>				3.6	2	{928}
<i>Lr23</i>								
<i>/Sr36</i>	-	<i>Sr9b/Sr9e</i>	19.6	1.9	{951}	20.7	2.2	
<i>Lr13</i>	-	<i>Sr9b</i>	17.6	3.1	{1370}	18.4	3.5	
<i>Lr13</i>	-	<i>Lr39</i>	I		{647}			
<i>Sr36</i>	-	<i>Sr9d</i>	24	8	{827}	26.1	10.4	
<i>ppd2</i>	-	<i>Sr9g</i>	I		{1269}			
<i>ppd2</i>	-	<i>Dfq1</i>	I		{789}			
<i>Hst2a-B1</i>	-	cent				20		{909}
<b>2BL</b>								
cent	-	<i>Sr9a</i>	10.6		{1307}			
cent	-	<i>Sr9b</i>	18.2	6.7	{944}	19.1	7.7	
cent	-	<i>Yr5</i>				21		{034}
cent	-	<i>Dfq1</i>				30		{789}
cent	-	<i>Tc2</i>				40.7	0.9	{10133}
cent	-	<i>Sr28</i>	34.6	2.8	{932}	42.6	5.4	
cent	-	<i>D2</i>	48.5		{944}			
cent	-	<i>Sr16</i>	I		{932, 1307}			
<i>Sr9g</i>								
<i>/Yr7</i>	-	<i>Dfq1</i>				6		{789}
<i>Sr9a</i>	-	<i>Sr19</i>	24	3	{636}	26.2	3.9	
<i>Sr9a</i>	-	<i>Sr19</i>	24.5	3.2	{1582}	26.8	4.2	
<i>Sr9a</i>	-	<i>Sr16</i>	I		{830}			
<i>Sr9b</i>	-	<i>Sr28</i>	16.8	2.1	{932}	17.5	2.4	
<i>Sr9b</i>	-	<i>D2</i>	42.2		{944}	61.1		
<i>Sr9b</i>	-	<i>Sr16</i>	I		{932}			
<i>Sr9g</i>	-	<i>Yr7</i>	<1.6		{965}			
<i>Sr9g</i>	-	<i>Sr16</i>	35.4	2.3	{965}	44.2	4.6	
<i>Yr7</i>	-	<i>Yr5</i>	allelic		{034}			
<i>Yr7</i>	-	<i>Yr5</i>	not allelic		{605}			
<i>Dfq1</i>	-	<i>Sr16</i>	I		{789}			
<i>Sr20</i>	-	<i>Sr19</i>	I		{029}			
<i>Sr20</i>	-	<i>Sr16</i>	I		{029}			
<i>Sr28</i>	-	<i>Sr16</i>	29.2	4.2	{932}	33.4	6.4	
<i>Sr28</i>	-	<i>Sr16</i>	38.2	1.9	{932}	50.3	4.6	

Gene order: Cent - *Xgwm382-2B* - 8.0 cM - *Xgwm619-2B* - 35.7 cM - *Tc2* - 9.1 cM - *Ig1* {10133}

**Genetic linkages (Cont.)**

<b>Genes</b>			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
<b>2B</b>								
<i>Sr39</i>	-	<i>Lr35</i>	3	1.1	{651}			
<i>Sr39</i>	-	<i>Sr32</i>	I		{647}			
<i>Sr39</i>	-	<i>Lr13</i>	I		{647}			
<b>Chromosome 2D</b>								
<b>2DS</b>								
<i>Lr22a</i>	-	cent	63.6	4.8	{1241}			
<i>Lr22a</i>	-	<i>Tg</i>	33	4	{1240}	39.7	7.1	
<i>Lr22</i>	-	<i>Tg</i>	41.6	4.4	{1240}	59.7	14.3	
<i>Lr22</i>	-	<i>Tg</i>	20.8	3.6	{1241}	22.1	4.4	
<i>Lr22</i>	-	<i>Tg</i>	6	1.5	{311}			
<i>Lr22b</i>	-	<i>W2I</i>	10.6	2.9	{298}			
<i>Lr22b</i>	-	<i>W2I</i>	18.3	2.9	{1240}	19.2	3.3	
<i>Lr22b</i>	-	<i>W2I</i>	41.6	4.4	{1240}	59.7	14.3	
<i>Lr22b</i>	-	<i>W2I</i>	15.6	2.5	{311}	16.1	2.8	
<i>Lr22b</i>	-	<i>Tg</i>	11.6	3.1	{298}			
<i>W2I</i>	-	cent	52.5	5	{1241}			
<i>W2I</i>	-	cent	58.9	4.6	{1241}			
<i>W2I</i>	-	<i>Tg</i>	21.9	4.2	{298}	23.5	5.2	
<i>W2I</i>	-	<i>Tg</i>	22.3	3.9	{1240}	24	4.9	
<i>W2I</i>	-	<i>Tg</i>	28.2	2.7	{1240}	31.9	4	
<i>W2I</i>	-	<i>Tg</i>	21.6	2.7	{1240}	23	3.3	
<i>W2I</i>	-	<i>Tg</i>	20.8	3.6	{1241}	22.1	4.4	
<i>W2I</i>	-	<i>Tg</i>	15.1	2.6	{648}			
<i>Tg</i>	-	cent	39.4	4.9	{1241}	53.3	12.9	
<i>Tg</i>	-	cent	42.9	4.6	{1241}	64.3	17.4	
<i>Tg</i>	-	cent	38.7	4	{652}	51.5	10	
<i>Tg</i>	-	cent	45	4.7	{652}			
<i>Lr15</i>	-	cent	32	5.1	{942}	37.9	8.6	
<i>Lr15</i>	-	<i>Lr2a</i>	allelic		{939, 942}			
<i>Lr15</i>	-	<i>Sr6</i>	0.75	0.34	{942}			
<i>Lr2a</i>	-	<i>C</i>	10	1.2	{843}			
<i>Lr2a</i>	-	<i>Sr6</i>	1.16	0.82	{942}			
<i>Sr6</i>	-	<i>C</i>	33.1, 18.9		{436}	39.8, 19.9	9.9	
<i>Sr6</i>	-	<i>C</i>	18.1		{671}	19		
<i>Sr6</i>	-	cent	28.7	4.8	{942}	32.7	7.2	
<i>Sr6</i>	-	cent	15.5	3.6	{942}	16	4	
<i>Sr6</i>	-	cent	33.1		{436}	39.8		
<i>Sr6</i>	-	cent	18.9		{436}	19.9		
<i>Sr6</i>	-	cent	18.1		{671}	18.8		
<i>Sr6</i>	-	cent	18.69	2.36	{942}	19.6	2.7	
<i>Sr6</i>	-	<i>Ra</i>	0		{1645}			
<i>DI</i>	-	cent	3.2	2.4	{942}			

Gene order: *Tg* - *W2I* - *Lr22* {1240}; *Tg* - *Lr22* - *W2I* {311}. The *DI* - cent linkage was not supported by other genetic data {1000}.

**Genetic linkages (Cont.)**

<u>Genes</u>	% Recombination			cM		
	Value	S.E	Ref	Value	S.E.	Ref
<b>2DL</b>						
cent	-	C	2.26			{1192}
cent	-	<i>Tc3</i>	38.8	5.8		{10131}
<i>C</i>	-	<i>D1</i>	36.7			{1000}
<i>C</i>	-	<i>D4</i>	I			[1000]
<i>Rht8</i>	-	<i>Ppd1</i>	17	4.9		{1598}
<i>Rht8</i>	-	<i>Ppd1</i>	25			{1601}
<i>Rht8</i>	-	<i>Ppd1</i>	16.6			{1601}
<i>Rht8</i>	-	<i>Yr16</i>	44	5		{1598}
<i>Rht8</i>	-	<i>Yr16</i>	38			{1601}
<i>Rht8</i>	-	<i>Ppd1</i>				20.9
<i>Rht8</i>	-	<i>D4</i>	I			{1598}
<i>Ppd1</i>	-	<i>Yr16</i>	36	5		{1598}
<i>Ppd1</i>	-	<i>D4</i>	I			{1598}
<i>Yr16</i>	-	<i>D4</i>	25	1		{1598}
<i>Yr16</i>	-	<i>D54</i>	26	8		{1598}
<i>D4</i>	-	<i>Su-D</i>	I			{1598}

*C* gave no recombination with the centromere in tests involving either arm {939}. Probable gene order:  
*Rht8* - *Ppd1* - *Yr16* - *D4*/*Su-D*.

**Chromosome 3A****3AS**

<i>Br-A1</i>	-	cent				21.1	0.2	{10061}
<i>Br-A1</i>	-	cent				20.6		{10182}

**3AL**

<i>cent</i>	-	<i>Sr35</i>	34	4		{957}	41.5	7.4
<i>Br2</i>	-	<i>R-Alb</i>					44.2	
<i>Sr35</i>	-	<i>R2</i>	1	1		{957}		

**Chromosome 3B****3BS**

<i>Lr27</i>	-	cent	33.6	4.1		{1367}	40.7	7.5
<i>Lr27</i>	-	cent	I			{1367}		
<i>Lr27</i>	-	<i>Sr12</i>	I			{1372}		
<i>Br-B1</i>	-						20.1	0.6
<i>vla</i>	-	cent	0.28			{1297}		
<i>Sr12</i>	-	cent	0			{968}		

**3BL**

<i>Br3</i>	-	<i>R-B1b</i>					47	
								{0130}

**Chromosome 3D****3DS**

<i>Lr32</i>	-	cent	26.8	4		{645}	29.9	5.6
<i>Br-D1</i>	-	cent					20.6	0.3
<i>s1</i>	-	cent	5.7			{1194}		

**Genetic linkages (Cont.)**

Genes	% Recombination			cM		
	Value	S.E	Ref	Value	S.E.	Ref
<b>3DL</b>						
<i>cent</i>	-	<i>Got-D3</i>	4.3			{521}
<i>cent</i>	-	<i>S1</i>	5	2		{692}
<i>cent</i>	-	<i>Ch2</i>	36.1	4		{692}
<i>cent</i>	-	<i>R-Alb</i>	I			{1193}

In Agent and Sears' translocations 3Ag#1 and 3Ag#2, *Lr24*, *Sr24* and red grain colour assumed to be determined by RAg, are completely linked. In translocations 3Ag#3 and 3Ag#14, R1 recombined with *Lr24/Sr24* {930} with linkage of about 20% {939}. This led to the release of white seeded R-D1b derivatives in Australia.

**Chromosome 4A****4AS**

<i>Adh-B1</i>	-	cent	20	3.5		{1197}	21.2	4.2
<i>Hd</i>	-	cent	7.7	3.7		{1195}		

**4AL**

<i>cent</i>	-	<i>Lr30</i>	2.9	1.3		{315}		
<i>cent</i>	-	<i>Lr28</i>	39.2	2.7		{967}	52.8	7
<i>Sr7a</i>	-	<i>Hd</i>	I			{671}		

**Chromosome 4B****4BS**

<i>ms1b</i>	-	cent	I			{064}		
<i>ms1b</i>	-	<i>Lr25</i>	34			{064}	41.5	
<i>ms1c</i>	-	cent	I			{064}		
<i>ms1c</i>	-	<i>Lr25</i>	20			{064}	21	
<i>Adh-Ala</i>	-	<i>Gai/Rht-B1</i>	23.1	4.0		{1442}	25.0	5.1
<i>Gai1</i>	-	<i>Gai3</i>	0			{406}		
<i>Rht-B1</i>								
<i>/Gai1</i>	-	cent	15	3		{698}		
<i>Rht-B1</i>	-	<i>b-Amy-B1</i>	I			{008}		
<i>b-Amy-B1</i>	-	cent	>35			{008}	43.4	
<i>pa</i>	-	<i>Hl</i>					29	2.6
<i>pa</i>	-	<i>Hl</i>					30	

Gene order: *Adh* - *Rht-B1* - cent {1442}.

**4BL**

<i>cent</i>	-	<i>Lr25/Pm7</i>	1			{271}		
<i>cent</i>	-	<i>Hp</i>		30		{275}	34.7	
<i>cent</i>	-	<i>b-Amy-B1</i>	35			{008}	43	
<i>Lr25</i>	-	<i>Pm7</i>		0		{271}		
<i>Rht-B1</i>	-	<i>b-Amy-B1</i>	I			{008}		

**Chromosome 4D****4DS**

<i>ms4</i>	-	cent	I			{0293}		
<i>Ms2</i>	-	<i>Rht-D1c</i>	0.005			{805}		
<i>Ms2</i>	-	cent	31.2			{807,80}	36.5	
<i>Rht-D1</i>								
<i>/Gai2</i>	-	cent	13	4		{698}		

**Genetic linkages (Cont.)**

Genes	% Recombination			cM		
	Value	S.E	Ref	Value	S.E.	Ref

According to {805}, *Ms2* and *Rht-D1c* were closely linked. However, a translocated recombinant male sterile dwarf was isolated.

Gibberellic insensitivity in Ai-Bian 1 possessing *Rht-D1C* was allelic with *Rht-D1*{114}.

**4DL**

<i>Rht2</i>	-	<i>b-Amy-D1</i>	I	{008}		
cent	-	<i>b-Amy-D1</i>	>35	{008}	>43.4	
<i>Alt2</i>	-	<i>Kna1</i>			12.5	{848}

**Chromosome 5A**

**5AS**

<i>Ms3</i>	-	cent	3.1	{622}		
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**5AL**

cent	-	<i>a-Amy-A1</i>			3.8	{1081}
cent	-	<i>a-Amy-A1</i>			8	{599}
<i>B1</i>	-	<i>Rht12</i>	<2.5	{1605}		
<i>B1</i>	-	<i>Xpsr164-5A</i>			57	{9903}
cent	-	<i>Vrn-A1</i>	I	{775}		
cent	-	<i>q</i>	I	{1196}		
<i>Kr2</i>	-	<i>Vrn-A1</i>	4.8	4.66	{1387}	
<i>Kr2</i>	-	<i>q</i>	38.1	10.6	{1387}	50 25.3
<i>Vrn-A1</i>	-	<i>q</i>			34	{1400}
<i>Vrn-A1</i>	-	<i>B1</i>			31	3.3 {925}
<i>Vrn-A1</i>	-	<i>B1</i>			45	4.1 {925}
<i>Vrn-A1</i>	-	<i>B1</i>			47	4.4 {925}
<i>Vrn-A1</i>	-	<i>B1</i>			50	4.3 {925}
<i>Vrn-A1</i>	-	<i>b-Amy-A1</i>	37	{008}		47.5
<i>q</i> (S)	-	<i>Hn</i>	36.2		45.8	
<i>q</i>	-	<i>B1</i> (n)	30	{913}	34.7	
<i>q</i> (S)	-	<i>B1</i> (N)	32.7	{1136}	39	
<i>q</i> (S)	-	<i>B1</i> (B)	37.3	{193}	48.2	
<i>q</i> (K)	-	<i>B1</i>	41	{1550}	57.8	
<i>q</i>	-	<i>B1</i>			25	{1400}
<i>Hn</i>	-	<i>B1</i>	5	{396}		
<i>Hn</i>	-	close		{837}		
<i>B1</i>	-	<i>b-Amy-A1</i>	2.3	2.3	{008}	
<i>B1</i>	-	<i>Ibf-A1</i>	0	{1605}		

Gene order: *b-Amy-A1* - *B1* - *Hn* - *Q* - *Vrn-A1* - *Kr2* {008,1387,1400}.

: cent - *Vrn-A1* - *Q* - *B1* {9903}.

**Chromosome 5A**

<i>H3</i>	-	<i>H6</i>	9	{1105}		
<i>H3</i>	-	<i>H9</i>	15.5	4.8	{1420}	16 5.3
<i>H6</i>	-	<i>H9</i>	2	2.01	{1421}	
<i>H9</i>	-	<i>H10</i>	36		{162}	45.4
	-		I	{1421}		
<i>H9</i>	-	<i>H15</i>	close	{625}		
<i>H28</i>	-	<i>H9</i>			22	{171}

**Genetic linkages (Cont.)**

<b>Genes</b>	% Recombination			cM		
	Value	S.E	Ref	Value	S.E.	Ref
<i>H10</i> - <i>H14</i>			I {625}			
<i>H10</i> - <i>H17</i>				20		{1098}
<i>H16</i> - <i>H12</i>				25		{1098}
<i>H16</i> - <i>H29</i>	close		{1097}			
<i>H17</i> - <i>H16</i>				25		{1098}

Gene order: *H3* - *H6* - *H9*.Gene order: *H9/H15* - *H17* - *H16* - *H12* {1098}**Chromosome 5B****5BS****5BL**

cent	-	<i>Ne1</i>				6		{1021}
cent	-	<i>Ne1</i>				10.5	2	{1085}
<i>Ne1</i>	-	<i>Vg</i>				11		{1021}
<i>Vg</i>	-	<i>IbfB1</i>				35		{1021}
cent	-	<i>Kr1</i>	11.5	3	{762}			
cent	-	<i>Kr1</i>	44.8	3.3	{1387}	72.6	16.6	
cent	-	<i>Crr</i>	42.9	3.4	{765}	64.3	12.9	
cent	-	<i>Crr</i>	36.1	3.3	{765}	45.6	6.9	
cent	-	<i>Ph1</i>	50.7	4.1	{1537}			
								{939, 935}
cent	-	<i>Lr18</i>		I				
<i>Xbcd103</i>	-	<i>tsn1</i>				5.7		{346}
<i>tsn1</i>	-	<i>Xwg583</i>				16.5		{346}

**Chromosome 5D****5DS**

<i>Pm2</i>	-	<i>Lr1</i>		I	{945}			
<i>Pm2</i>	-	<i>Sr30</i>		I	{688}			

**5DL**

cent	-	<i>Lr1</i>	36.7	5.3	{688}	46.9	11.5	
cent	-	<i>Lr1</i>		I	{945}			
cent	-	<i>Sr30</i>		I	{688}			
cent	-	<i>Vrn3</i>		I	{775}			
<i>Lr1</i>	-	<i>Sr30</i>		I	{688}			
<i>Vrn-D5</i>	-	<i>Vrn-D1</i>		I	{10004}			

**Chromosome 6A****6AS**

<i>Xbcd342-6U</i>	-	( <i>Rf6</i> ) cent				31.4		{865}
<i>Sr8a</i>	-	cent	44	5	{929}			
<i>Sr8a</i>	-	<i>Sr13</i>		I	{929}			
<i>Bza3-A1</i>	-	cent				30		{909}
<i>Gli-A2</i>	-	cent				26.2		{599}

**6AL**

cent	-	<i>Sr26</i>		0	{1154}			
cent	-	<i>Ep-A1</i>				1		{599}
cent	-	<i>Sr13</i>		I	{929}			

**Genetic linkages (Cont.)**

<b>Genes</b>			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
<b>Chromosome 6B</b>								
<i>Amp-B2</i>	-	<i>B2</i>		0.9	{0176}			
<i>Amp-B2</i>	-	<i>B2</i>		2.1	{0176}			
<b>6BS</b>								
telomere	-	<i>Lr36</i>		<9.9	{292}			
<i>Lr36</i>	-	cent				46.3	4	{292}
<i>Lr36</i>	-	cent				26	7.9	{292}
<i>Amp-B1</i>	-	cent		<0.6	{1244}			
<i>co</i>	-	cent		I	{1304}			
<i>Gli-B2</i>	-	C band				10.2	4.3	{289}
<i>Gli-B2</i>	-	<i>Nor-B2</i>		16.7	{289}	17.4		
<i>Gli-B2</i>	-	cent				20	5.3	{289}
C band	-	cent				12.2	4.6	{289}
<i>Nor-B2</i>	-	cent				<6.1		{289}
<i>Nor-B2</i>	-	cent				4.1		{599}
<i>Lr9</i>	-	cent		0	{1299}			
<i>Pm11</i>	-	cent				1		{1480}
<i>Pm12</i>	-	<i>a-Amy-S1</i>				1.1		{598}
<i>XCxp3-6B</i>	-	cent				30.1		{599}
<i>Ep-B2</i>	-	cent				33.1		{599}
								{799,
<b>tv:</b>	<i>Nor-B2</i>	-	<i>Xpsr312</i>			24.8		735}
<b>tv:</b>	<i>Xpsr312-6B</i>	-	<i>Su1</i>			5.5		{735}
<b>tv:</b>	<i>Su1</i>	-	<i>a-Amy-1</i>	9		84		{735}
			<i>Xpsr141</i>					
	<i>Su1</i>	-	( <i>Pgk-2</i> )			6.8		{799}
	<i>Su1</i>	-	<i>Xpsr312</i>			5.3		{799}
 <i>Lr36</i> is distal to <i>Gli-B2</i> {292}.								
<b>6BL</b>								
	cent	-	<i>a-Amy-B1</i>	13.8	2.6	{1083}		
	cent	-	<i>a-Amy-B1</i>				4.5	{598}
	cent	-	<i>a-Amy-B3</i>	5.5	1.7	{1083}		
	<i>a-Amy-B1</i>	-	<i>a-Amy-B3</i>	9.3	2.2	{1083}		
<b>tv:</b>	<i>a-Amy-B1</i>	-	<i>a-Amy-B5</i>	<1.0		{1083}		
<b>tv:</b>	<i>a-Amy-B1</i>	-	<i>a-Amy-B4</i>	22.3	3.5	{1083}		
<b>tv:</b>	cent	-	<i>a-Amy-B5</i>	2.1	1.1	{1083}		
<b>tv:</b>	cent	-	<i>a-Amy-B1</i>	13.2	3.5	{1083}		
<b>tv:</b>	cent	-	<i>a-Amy-B4</i>	26.1	5	{1083}		
	<i>X-Amy-1</i>	-	<i>Xpsr149</i>	4.2	2.9	{663}		
	cent	-	<i>a-Amy-B3</i>				5.5	{1081}
	cent	-	<i>a-Amy-B1</i>				13.8	{1081}
	cent	-	<i>a-Amy-B1</i>				4.5	{599}
	cent	-	<i>B2</i>	0.44		{1297}		
	cent	-	<i>B3</i>	0.87		{394}		
	cent	-	<i>a-Amy-B1</i>	19.4	3.8	{398}	20	

**Genetic linkages (Cont.)**

Genes	% Recombination			cM		
	Value	S.E	Ref	Value	S.E.	Ref
<i>Xcdo772</i>				41.2		
/cent - <i>Xbcd1-6B</i>				cM		{9921}
<i>Xbcd-6B</i>						
/Lr3 - <i>Xmwig798</i>				32.1 cM		{9921}
cent - <i>Sr11</i>	45.1		{1297}		74.1	
cent - <i>Lr3</i>	I		{1244}			
<i>B2</i> - <i>Lr9</i>	3.5		{1299}			
<i>B2</i> - <i>Sr11</i>	43.3		{1297}		65.8	
	46.9					
<i>B2</i> - <i>Sr11</i>	(or 43.8)		{1299}	86.1 (or 67.9)		
<i>a-Amy-B3</i> - <i>a-Amy-B1</i>				9.3		{1081}
<i>Sr11</i> - <i>Ki</i>	9		{829}			
<i>Sr11</i> - <i>Ki</i>	10.5		{1306}			
<i>Sr11</i> - <i>Lr9</i>	close		{1297}			
<i>Sr11</i> - <i>Lr3</i>	21.7	7.8	{548}	23.2	9.6	
			{839,			
<i>Sr11</i> - <i>Lr3</i>	0		842}			
<i>Lr3</i> - <i>Ki</i>	11.5		{1306}			

An *Sr11 Lr9* coupling stock was isolated by ER Sears.

**Chromosome 6D**

**6DS**

<i>Sr5</i> - <i>Sr29</i>			I	{313}		
<i>Cmc1</i> - cent			I	{1468}		
<i>Cmc1</i> - <i>Cmc4</i>			I	{0222}		

**6DL**

cent - <i>a-Amy-D1</i>	11.9	2.8		{398}		
cent - <i>a-Amy-D1</i>					11.3	{1081}
				{441}		
cent - <i>H13</i>	35	8	+H641	43.4	15.7	
cent - <i>Sr29</i>	I		{313}			
<i>H13</i> - <i>H23</i>				25	5	{1199}

**Chromosome 7A**

**7AS**

<i>XNra</i> - <i>Per-A4</i>				23.3	6.4	{816}
<i>XNra</i> - <i>Per-A4</i>				20.1	6.5	{816}
<i>Amp-A1</i> - <i>XPepc</i>				24		{179}
<i>Xpsr119-7A</i> - <i>or</i>				13		{1031}

**7AL**

cent - <i>Sr22</i>	27	4.2	{1460}	30.2	5.9	
cent - <i>Cn-A1a</i>	I		{1304}			
cent - <i>Cn-A1b</i>	34		{802}	41.5		
cent - <i>cn-A1d</i>				46.6	3.8	{665}
cent - <i>Pm1</i>	I		{1305}			
<i>Ep-A1b</i> - <i>Xpsr121-7A</i>	3.8	2.1	{228}			
<i>Ep-A1b</i> - <i>Pch2</i>	15	4	{228}			
<i>Rc1</i> - <i>P</i>	20.3		{911}			
<i>Sr22</i> - <i>Cn-A1</i>	2		{1462}			



**Genetic linkages (Cont.)**

<b>Genes</b>			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
		<i>Pm1</i> / <i>Lr20</i>						
	<i>Sr22</i>	- <i>/Sr15</i>	41		{1462}	57.8		
		<i>Pm1</i> / <i>Lr20</i>						
	<i>Sr22</i>	- <i>/Sr15</i>				42		{10263}
	<i>Xpsr121-7A</i>	- <i>Pch2</i>	11.2	3.5	{228}			
<b>dv:</b>	<i>Sr22</i>	- <i>Rc1</i>	42	2.8	{1461}	61.9	9.5	
	<i>Sr22</i>	- <i>Rc1</i>	43	2.7	{1461}	64.7	10.4	
		<i>Pm1</i> / <i>Lr20</i>						
	<i>cn-A1a</i>	- <i>/Sr15</i>	40		{1462}	54.9		
	<i>Pm1</i>	- <i>Pm9</i>	linked		{347}			
	<i>Pm1</i>	- <i>Pm9</i>				8.5		{1287}
<b>tv:</b>	<i>P</i>	- <i>cn-A1d</i> (CDd6)				37.9	3.2	{1547}

**Chromosome 7B**

**7BS**

	<i>cc</i>	- cent				33.5	4.1	{665}
	<i>Vrn5</i>	- <i>Pc</i>	26	5	{771}	28.8	5.6	
	<i>Vrn5</i>	- <i>Lr mod</i>	25.5	4.6	{412}	28.1	6.2	
	<i>Vrn5</i>	- <i>Pm5</i>	26	5	{771}	28.8	6.9	
	<i>Pc</i>	- <i>Lr14a</i>	44	6	{771}			
	<i>Pc</i>	- cent	22.8	5.3	{412}	24.6	6.7	
	<i>Pc</i>	- <i>P2</i>				29.6	7.3	{9990}
	<i>Pc(Rc2)</i>	- cent	16	5	{769}	16.6	5.6	
	<i>Pc</i>	- <i>Lr mod</i>	10.5	3.7	{412}			
	<i>Hl2</i>	- cent	14.3	3.5	{0316}			

Gene order: *Pc* - *Vrn5* (*e1*) - cent {770}; revised to: *Vrn5* - *Pc* - cent {769}.

**7BL**

	cent	- <i>a-Amy-B2</i>	5.9	5.5	{412}			
	cent	- <i>cn-B1a</i>				42.6	4.3	{665}
	cent	- <i>Pm5</i>	37	9	{771}	47.5	19.9	
	cent (5B.7B)	- <i>Ep-B1</i>		I	{708}			
	<i>a-Amy-B2</i>	- <i>Pm5</i>	44.4	5.1	{412}	70.6	24.1	
	<i>a-Amy-B2</i>	- <i>Ep-B1</i>		I	{708}			
	<i>Xpsr129</i>	- <i>Ep-B1</i>				>50		{179}
	<i>Pm5</i>	- <i>Lr14a</i>	20.4	2.4	{1564}	21.7	2.9	
	<i>Pm5</i>	- <i>Lr14a</i>	28	5	{770}	31.6	7.3	
	<i>Pm5</i>	- <i>Lr14a</i>	30.1	4.5	{412}	34.8	7.1	
	<i>Pm5</i>	- <i>Sr17</i>	6	2	{964}			
	<i>Pm5</i>	- <i>Sr17</i>	2	1.1	{964}			
	<i>Lr14a</i>	- <i>Sr17</i>	18.2	4.5	{964}	19.1	5.2	
	<i>Lr14a</i>	- <i>Ep-B1</i>	9.6	3	{708}			
	<i>Xpsr121</i>	- <i>Ep-B1</i>				9		{179}
	<i>Xpsr121</i>	- <i>Wsp-B1</i>				16.6	6.9	{817}
	<i>Ep-B1</i>	- <i>WspB1</i>				31.6	12.1	{817}
	<i>P2</i>	- <i>cn-B1b</i>				36.5	5.6	{9990}

Gene order: cent - *Pm5* - *Lr14a* {770}.

**Genetic linkages (Cont.)**

Genes	% Recombination			cM		
	Value	S.E	Ref	Value	S.E.	Ref
<b>Chromosome 7D</b>						
<b>7DS</b>						
This chromosome arm is physically longer than the arm designated 7DL, but is homoeologous to those arms designated 7AS and 7BS {1571,388}.						
		<i>Lr34</i>				
		<i>/Yr18</i>				
<i>Bdv1</i>	-	<i>/Ltn</i>	0			{1363}
<i>Lr34</i>	-	<i>Lr29</i>	0			{924}
<i>Ltn</i>	-	<i>Lr34/Yr18</i>	<0.013			{1361}
						{1362,
<i>Lr34</i>	-	<i>Yr18</i>	0			937}
<i>Lr34</i>	-	<i>Rc3</i>	30.25	2.88		{924}
<i>Rc3</i>	-	cent	10.3	2.8		{1241}
<i>Rc3</i>	-	cent	9.8	2.8		{1241}
<i>Rc3</i>	-	cent	16	4.2		{1444}
					16.7	4.7
<i>Rc3</i>	-	<i>Adk-D1</i>			24.1	4.5
						{1435}
<i>a-Amy-D2</i>	-	<i>Adk-D1</i>			0.24	5
						{1603}
<i>a-Amy-D2</i>	-	<i>Pch</i>			37	5
						{1603}
		<i>Pch</i>				
<i>a-Amy-D2</i>	-	<i>/Ep-D1b</i>			I	
						{1603}
<i>Pan1</i>	-	<i>Pc2</i>			13.3	2.3
						{921}
<i>Pan1</i>	-	<i>Pc2</i>			14.4	2.7
						{921}
<i>Pm15</i>	-	cent		I		{1480}

**7DL**

Physically shorter than 7DS; see note for 7DS above.

<i>a-Amy-D2</i>	-	<i>Lr</i>			42	6	{1603}
							{417,
<i>a-Amy-D2</i>	-	<i>Pch</i>			I		1603}
<i>Xgwm111-7D</i>	-	<i>Gb3</i>			22.5		{0319}
Cent	-	<i>Dn5</i>		I			{287}
<i>Lr</i>	-	<i>Pch</i>			18	4	{1603}
<i>Pch</i>	-	<i>Ep-D1b</i>			0		{1603}
<i>Lr19/Sr25</i>	-	<i>cn-D1</i>			0		{939}
<i>Dn5</i>	-	<i>Ep-D1</i>		32	4.67		{894}
<i>Dn5</i>	-	<i>cn-D1</i>		37	6.3		{894}
<i>Gb3</i>	-	<i>Xgwm428-7D</i>			33.1		{0319}
<i>Gb3</i>	-	<i>Gb7</i>			8.75		{10169}
<i>Pm29</i>	-	<i>Pm19</i>					{0129}

Gene order: cent - *Xgwm111-7D* - *Gb3* {0319}.

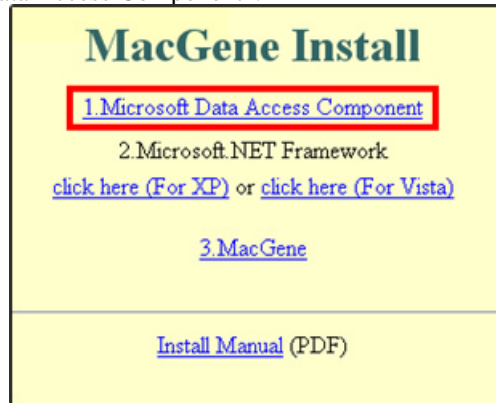
### III. MacGene2008 (Standalone version) quick manual

#### 1. System environment

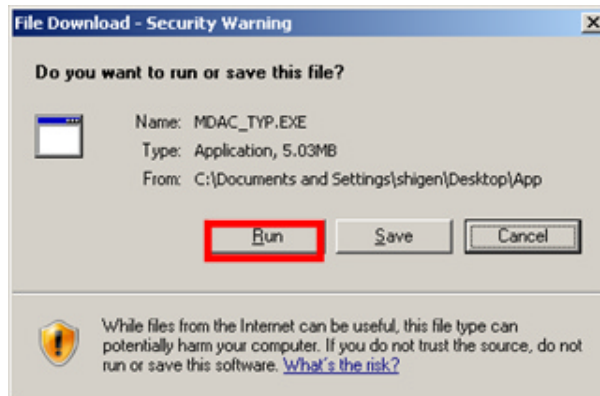
OS: Windows XP or Vista  
Microsoft Office 2003 or 2007

#### 2. Installation

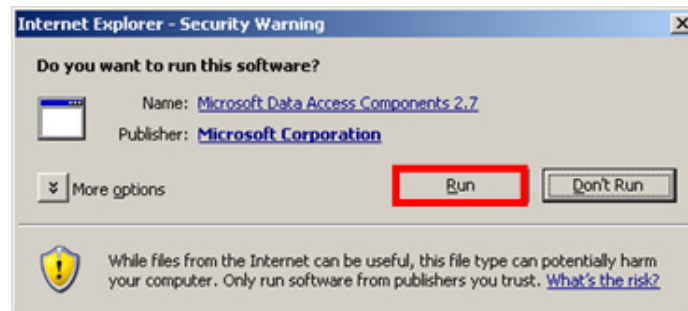
- 2.1. Insert the USB.
- 2.2. Open Install.htm
- 2.3. Click "1: Microsoft Data Access Component".



- 2.4. Click "Run".



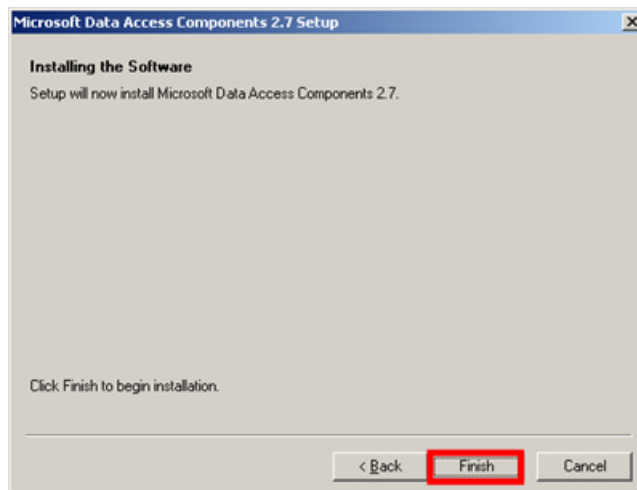
- 2.5. Click "Run".



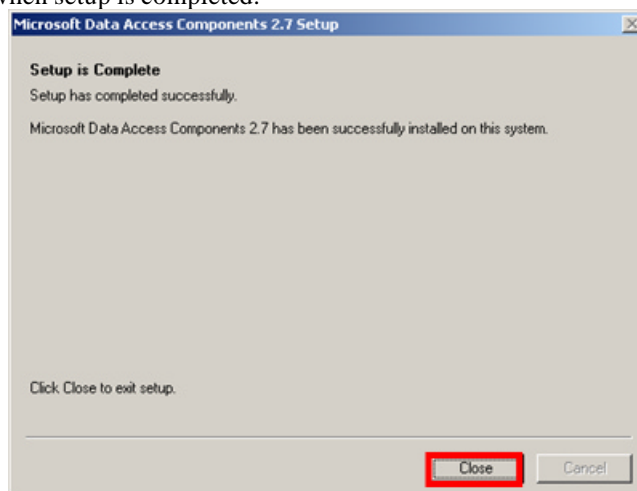
2.6. Click “Next” if you can agree.



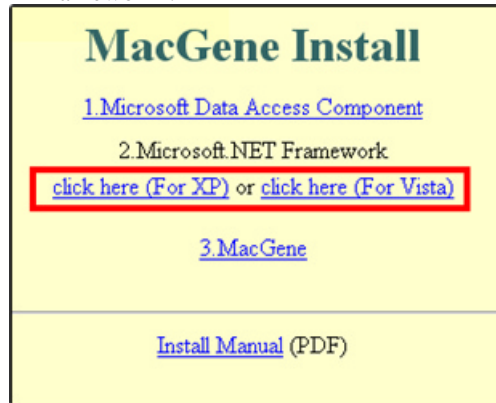
2.7. Click “Finish”.



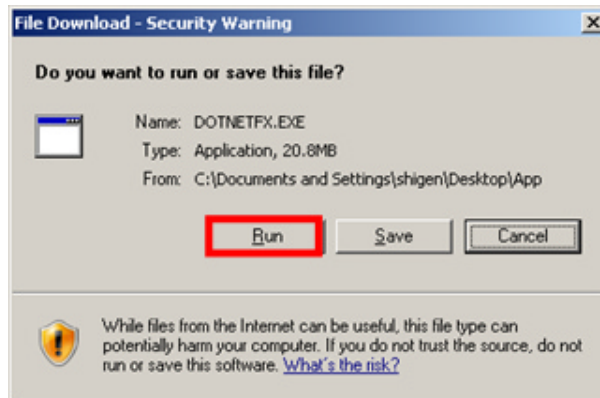
2.8. Click “Close” when setup is completed.



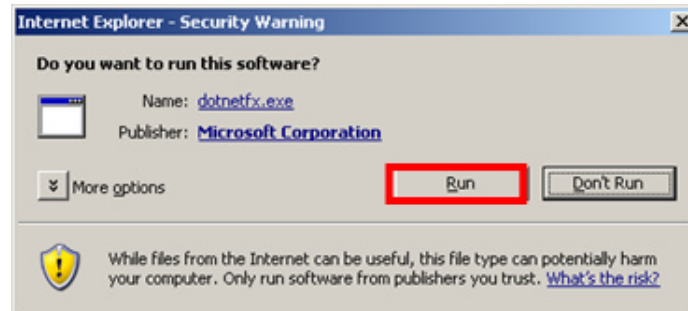
2.9. Click “2.Microsoft .NET Framework”.



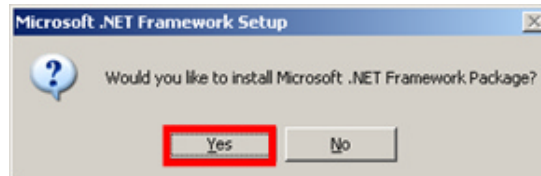
2.10. Click “Run”.



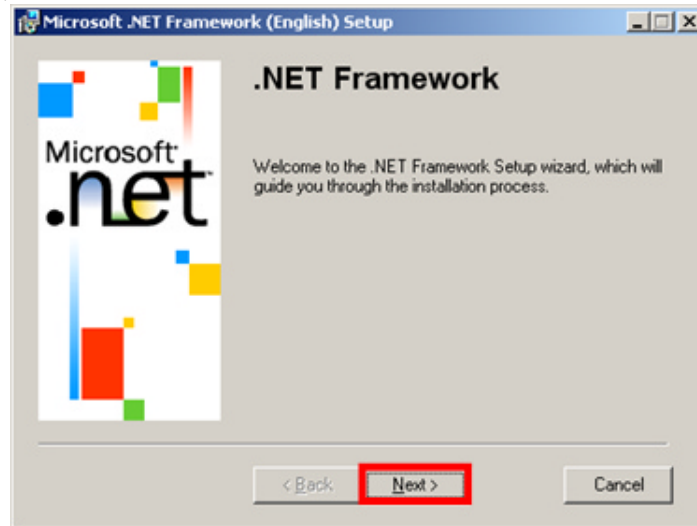
2.11. Click “Run”.



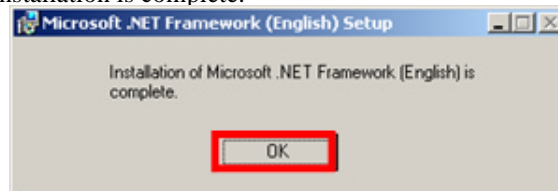
2.12. Click “Yes”.



2.13. Click “Next”.



2.14. Click “OK” when installation is complete.



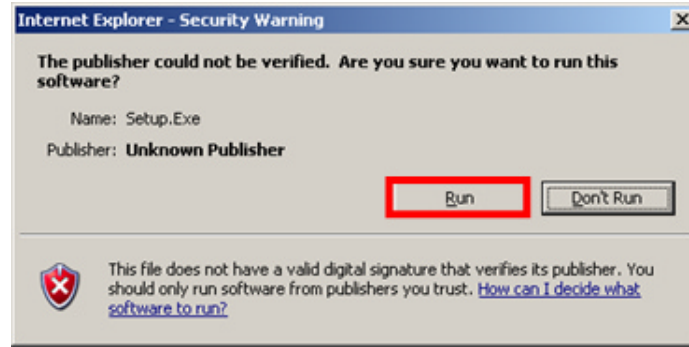
2.15. Click “3.MacGene”.



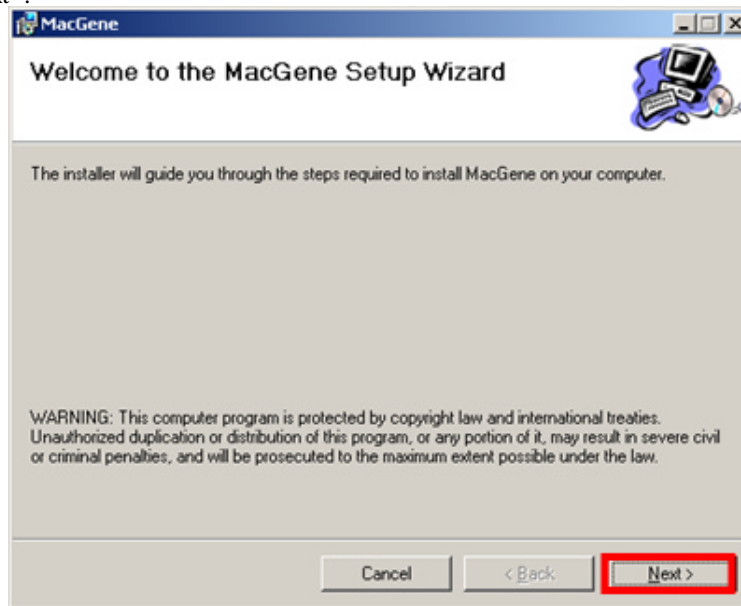
2.16. Click “Run”.



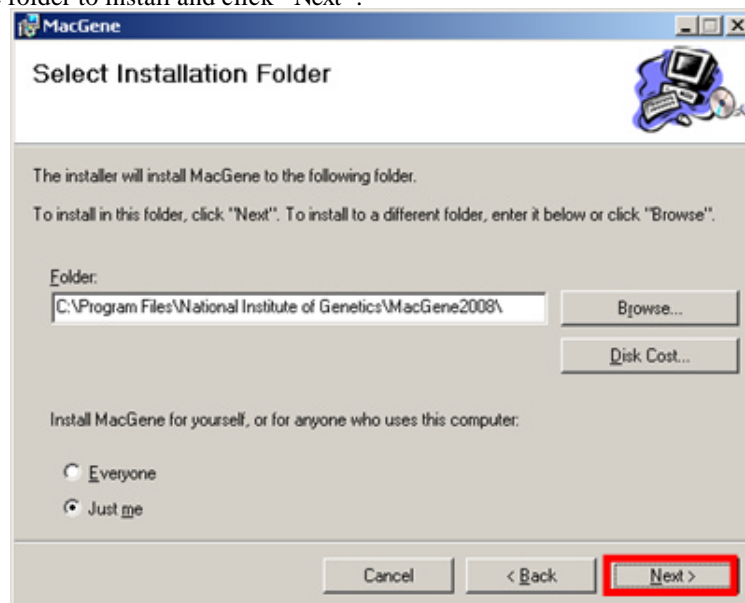
2.17. Click “Run”.



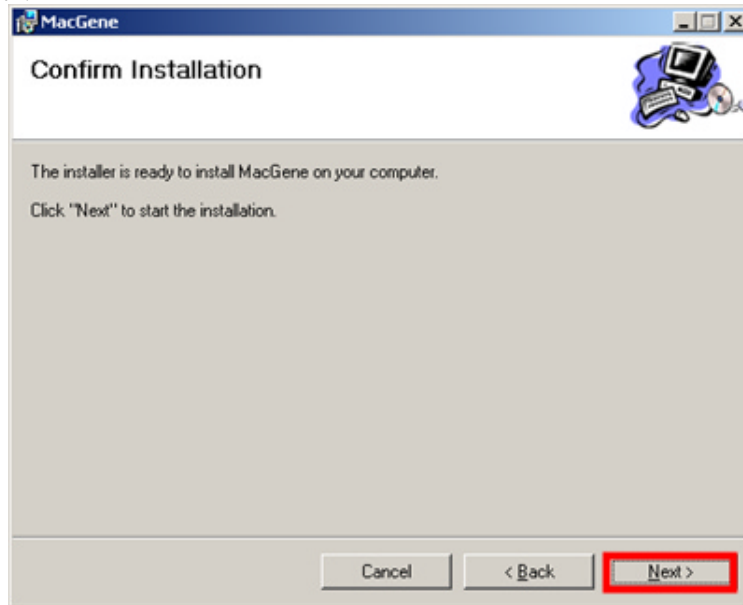
2.18. Click “Next”.



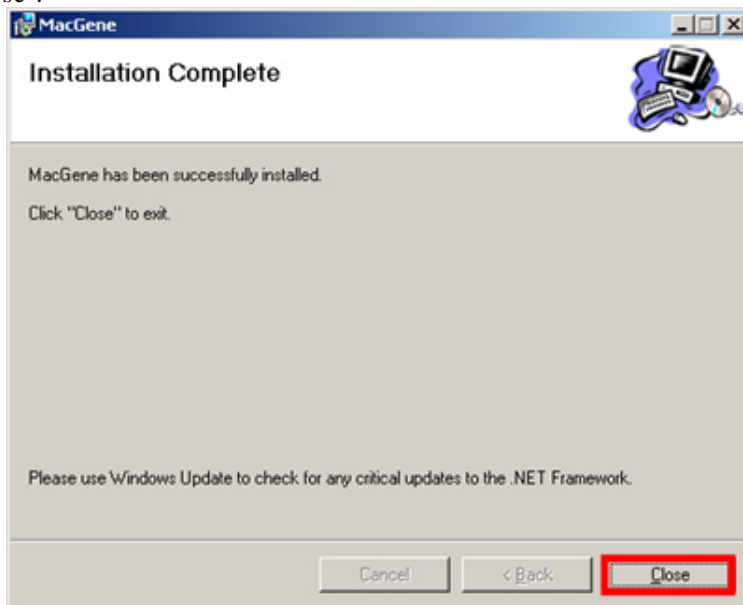
2.19. Define the folder to install and click “Next”.




2.20. Click “Next”.



2.21. Click “Close”.

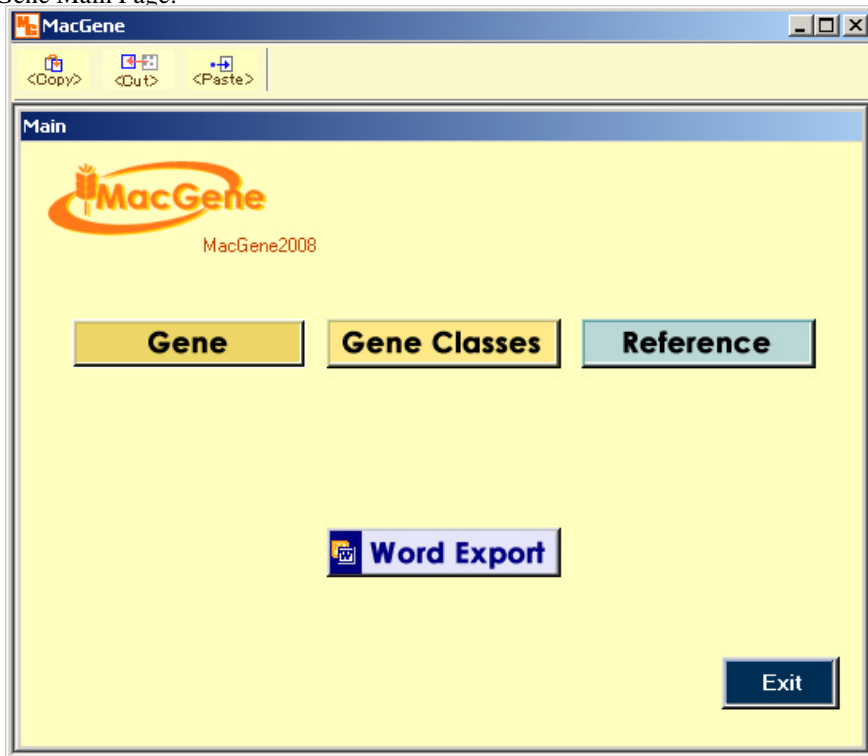


### 3. How to use “MacGene”

3.1. Click “MacGene” icon  on your desktop.



### 3.2. MacGene Main Page.



There are two basic functions, (I) SEARCH (Gene/Reference) and (II) RETRIEVE (Word Export) on the page.

You can follow the same procedure for the two searches.

Click "Gene" for example.

### 3.3. Gene Search.

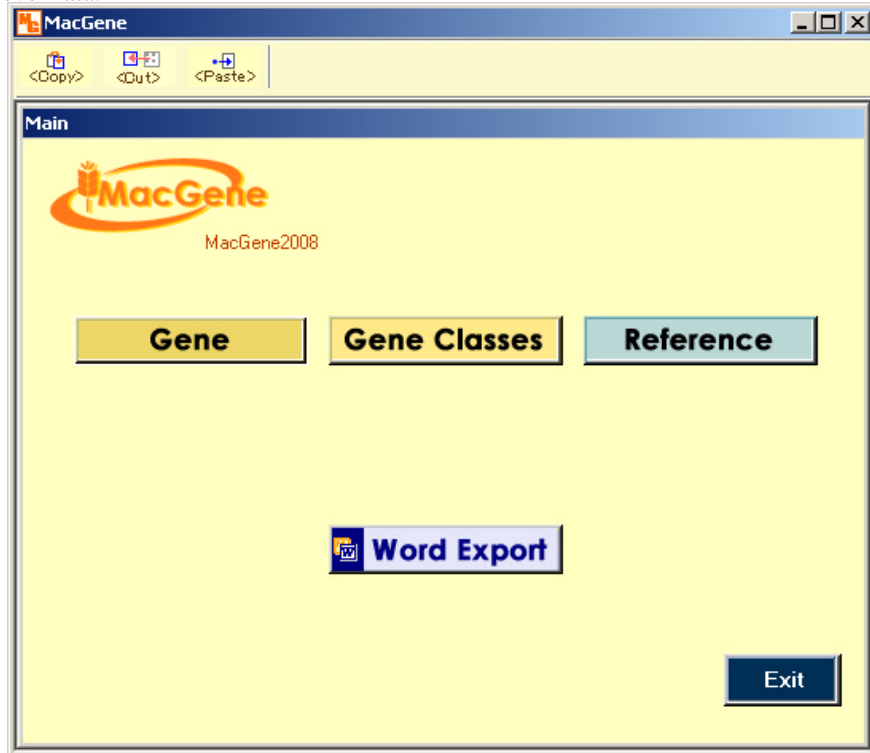
Perfect Match Search      Quick Search      go to Advanced Search

ID	Symbol	Level1Class	Level2Class	Level3Class	Level4Class	Synonyms	Location	Chromosomes	Gemiplasms	PubliYear
1	q	Gross Morphology	Squarehead/spelt			K		5AL	v>Linnon wheats	1998
2	q	Gross Morphology	Squarehead/spelt			K			v'Macha wheats,v	1998
3	C	Gross Morphology	Club/Compact spk			Cd	2D,2DL		iS-615(cup)*c/bu	1998
4	s2	Gross Morphology	Sphaerococcum			sp2			v'Sphaerococcoid	1998
5	bh	Gross Morphology	Branched spike					2AS	lv/P1 349056	1998
6	P1	Gross Morphology	Elongated glume			P.Eg.P-A/cup		7AL,7A or 7B (b	iSaratovskaya29K	1998
7	Al1	Aluminium Toleran							v'ET3 = Carazinho	1998
8	al1	Aluminium Toleran							v'ES3 = Carazinho	1998
9	Al2	Aluminium Toleran				Alt(cub)B/c/		4DL	su/co.T. lugdunv	1998
10	Pan1	Anthocyanin Pigm	Purple anthers.					7D5	vilychevka,vMir	1998
11	Ra1	Anthocyanin Pigm	Purple/Red awicle			Ra		1D Gujveva,2D	v'Kenya 58	1998
12	Ra2	Anthocyanin Pigm	Purple/Red awicle					4B		1998
13	Ra3	Anthocyanin Pigm	Purple/Red awicle					6B		1998
14	An5	Anthocyanin Pigm	Purple/Red awicle					5R		1998
15	Rc-A1a	Anthocyanin Pigm	Red/purple coleopt			Rc1, R		7A,7AS	s:CS(cup)*c/sup	1998
16	Rc-B1a	Anthocyanin Pigm	Red/purple coleopt			Rc2, R2		7B,7BS	s:CS(cup)*c/sup	1998
17	Rc-D1a	Anthocyanin Pigm	Red/purple coleopt			Rc3		7D,7D5	v'Moskovskaya 80	1998
18	Pc1	Anthocyanin Pigm	Purple/red culm/st			Pc		7B,7BS	s:CS(cup)*c/sup	1998
19	Pc2	Anthocyanin Pigm	Purple/red culm/st					7D5	vilychevka,vMir	1998
20	Pp1	Anthocyanin Pigm	Purple grain/perica					6A,7BL	iSaratovskaya 29	1998
21	Pp2	Anthocyanin Pigm	Purple grain/perica					7A	lv/co.T. durumc/o	1998
22	Hd	Awredness	Dominant inhibitor	Hooded				4AS	iS-615(cup)*c/bu	1998

access to Details

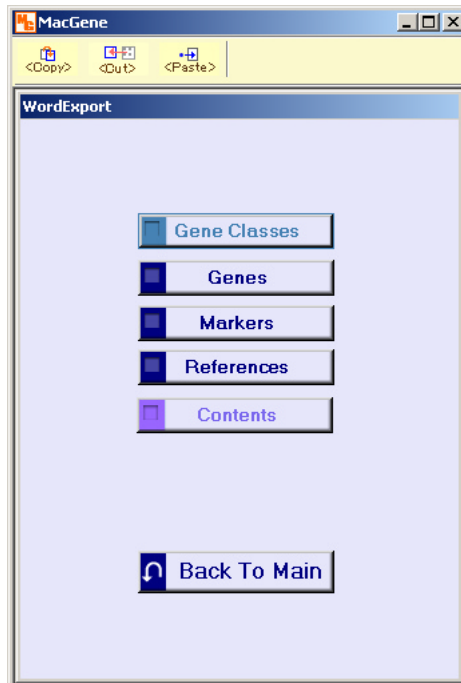
Click on headers to sort data by column

3.4. Retrieve Data.



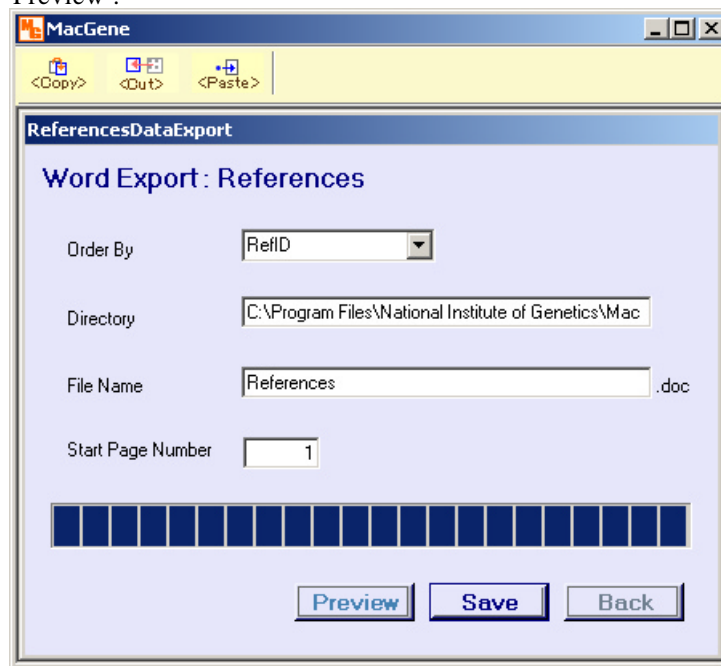
Click "Word Export" on the main page.

3.5. Word Export Options.



You can choose the relevant option.

- 3.6. After you click “Save”, “Preview” appears on the nextscreen. You can immediately view all pages by clicking “Preview”.



- 3.7. Word Output.

You can also retrieve all pages from the saved file without reopening “MacGene”.

1 MORPHOLOGICAL AND PHYSIOLOGICAL TRAITS	1 REFERENCES order by RefID
<p style="text-align: center;"><b>Morphological and Physiological Traits</b></p> <p>Note: Levy and Feldman (797) studied the inheritance of more than 20 morphological and biochemical traits in crosses of four <i>T. dicoccoides</i> lines and <i>T. durum</i>. Similarly, Kuspira et al. (744) studied 12 qualitative characters in <i>T. monococcum</i>. The symbols applied to the characters examined in these studies are not being reserved and listed in the Catalogue. However, both studies should serve as bases for future work. In a large study of 6 agronomic traits in a AC Karma/7E03-S2B1 DH population, 24 QTLs were detected in 12 chromosomes (10434).</p> <p><b>1. Grass Morphology: Spike characteristics</b> Major hexaploid wheat types are categorized into groups with respect to three major gene pairs, viz. <i>Q</i>, <i>C</i> and <i>S1</i> (1038).</p> <ol style="list-style-type: none"> <li>1. Common wheat <i>Q c S1 v. vulgare</i> group.</li> <li>2. Club wheat <i>Q C S1 v. compactum</i> group.</li> <li>3. Soft wheat <i>Q c S1 v. spheroconvexum</i> group.</li> <li>4. Spelt wheat <i>q c S1 and q C S1 v. spelta</i> group (including varislovi).</li> </ol> <p>The majority of hexaploid wheat stocks are already, or can be readily, classified into these groups. Diploid wheat is assumed to be <i>q</i>. Durum and carthagen groups have the genotype <i>Q</i> (1049).</p> <p><b>1.1. Squarehead/spelt</b> <i>Q</i> (881), [K(1550)]. 5AL(1293). <i>v.</i>: Common wheats, CS; Iranian spelts (0140). <i>rv.</i>: <i>T. nurgidum</i> ssp. <i>carthagenum</i>, <i>durum</i> and <i>politicum</i> (10457). <i>ma.</i>: Complete linkage with cDNA clone PTAq22(0127); <i>Q</i> was cloned and shown to have similarity to <i>AtAP2</i> (APEATLA 2); the <i>Q</i> allele was more abundantly transcribed than the <i>q</i> allele transcription factor (10457). <i>q</i> (881), [K(1550)]. <i>v.</i>: Macha wheats; European spelt wheats (10457); <i>varislovi</i> wheats. <i>s.</i>: CS 8 White Spring Spelt SA (1048). <i>rv.</i>: <i>T. nurgidum</i> ssp. <i>dicoccum</i>, <i>dicoccoides</i> (10457). <i>ma.</i>: Cent - <i>Uryg803/Emph</i>-3A - 4.6 cM - <i>Q</i> - 4.3 cM - <i>Xpar370-3A</i> (419). <i>Q</i> was physically mapped in 5AL, fraction length 0.87, bracketed by deletions 5AL-7 and 5AL-23 (446); <i>Q</i> - 9.3 cM - <i>Xpar370-5A</i> (9903). The speltoid phenotype of at least some spelts may be caused by genes at other loci (0140). Fine mapping of the 20 cM region possessing <i>Q</i> and delimited by deletions 5AL -7 and -23 is reported in (0324).</p> <p><b>1.2. Club/Compact spike</b> <i>C</i> (1517), [Cd(047)] 2D(1192) 2DL(1192.1517). <i>i.</i>: S-615*11/Elgin(1500). <i>s.</i>: CS 6 Poso 2D(1304). CS 5 Red Egyptian 2D(1304). <i>v.</i>: Club wheats. QTL/Sat QTLs for spike compactness were detected in Courtot/Chinese Spring but only 4 on chromosome arms 1AL, 2BS, 2DS and 4AS were consistent for at least two years (0114). Two additional QTLs for spike compactness were detected in Courtot/Chinese Spring (10080) on chromosome arms 5DL (<i>QCpJcf-5D</i>) and 6DL (<i>QCpJcf-6D</i>). Markers <i>Xcfd26-5D</i> and <i>Xcfd38-6D</i> explained 13.6% and 12.2% of the variance in spike compactness, respectively (10080). Although gene <i>C</i> may be present in some forms of group <i>macha</i> (1447) and <i>spelta</i> (0623), it is not universally present. Tsunewaki (1500) found that compact spike in one form was controlled by polygenes.</p>	<ol style="list-style-type: none"> <li>1. Ackerman A 1943 (Experiments to increase the yield from spring wheat. I. Crosses with Brunt Schlanstedter [Brunn Schlanstedter] spring wheat with a description of Svalof. Progress spring wheat). <i>Sveriges Utsaedsforenings Tidkrift</i> 53: 51-66. <i>Citad Plant Breeding Abstracts</i> 14: 173, p.42.</li> <li>2. Ackerman A &amp; MacKey J 1949 (Attempts to improve the yield of spring wheat II. Crosses between spring and winter wheat. Descriptions of Svalof's Ella spring wheat). <i>Sveriges Utsaedsforenings Tidkrift</i> 59: 105-117. <i>Citad Plant Breeding Abstracts</i> 20: 197, p.65.</li> <li>3. Acosta AC 1963 The transfer of stem rust resistance from rye to wheat. <i>Dissertation Abstracts</i> 23: 34-35.</li> <li>4. Ahn SN &amp; Tanksley SD 1993 Comparative linkage maps of the rice and maize genomes. <i>Proceedings of the National Academy of Sciences, USA</i> 90: 7980-7984.</li> <li>5. Ainsworth C 1995 Personal communication.</li> <li>6. Ainsworth CC 1983 The genetic control of hexokinase isozymes in wheat. <i>Genetical Research, Cambridge</i> 42: 219-227.</li> <li>7. Ainsworth CC, Doherty P, Edwards KGG, Martensen RA &amp; Gale MD 1985 Allelic variation at <i>a</i>-amylase loci in hexaploid wheat. <i>Theoretical and Applied Genetics</i> 70: 400-406.</li> <li>8. Ainsworth CC, Gale MD &amp; Baird S 1983 The genetics of beta-amylase isozymes in wheat. Allelic variation among hexaploid varieties and intrachromosomal gene locations. <i>Theoretical and Applied Genetics</i> 66: 30-49.</li> <li>9. Ainsworth CC, Gale MD &amp; Baird S 1984 The genetic control of grain esterases in hexaploid wheat. <i>Theoretical and Applied Genetics</i> 68: 219-226.</li> <li>10. Ainsworth CC, Gale MD &amp; Miller TE 1986 Genetic control of grain esterases in hexaploid wheat II. Homoeologous loci in related species. <i>Theoretical and Applied Genetics</i> 72: 219-225.</li> <li>11. Ainsworth CC, Hosein F, Tarvis M, Weir F, Burrell M, Devos KM &amp; Gale MD 1995 Adenosine diphosphate glucose pyrophosphorylase genes in wheat: differential expression and gene mapping. <i>Planta</i> 197: 1-10.</li> <li>12. Ainsworth CC, Johnson HM, Jackson EA, Miller TE &amp; Gale MD 1984 The chromosomal locations of leaf peroxidase genes in hexaploid wheat, rye and barley. <i>Theoretical and Applied Genetics</i> 69: 205-210.</li> <li>13. Ainsworth CC, Miller TE &amp; Gale MD 1987 <i>a</i>-amylase and beta-amylase homoeoloci in species related to wheat. <i>Genetical Research, Cambridge</i> 49: 93-103.</li> <li>14. Aliev EB, Musaev AD &amp; Maystrenko OI 1982 (Identification of the gene <i>R2</i> controlling grain colour in the spring bread wheat variety Damant 2). <i>Izv. SO AN SSSR, Ser. Bio N.</i> (1983) 15: 75-79. <i>In: Referativnyi Zhurnal</i> (1982) 5: 65:107. <i>Citad Plant Breeding Abstracts</i> 54: 798, p.799.</li> <li>15. Allan RE 1970 Differentiating between two Norin 10/Brevor 14 semi-dwarf genes in a common genetic background. <i>Seiken Zho</i> 22: 83-90.</li> <li>16. Allan RE &amp; Vogel OA 1960 F1 monosomic analysis involving a smooth-awn durum wheat. <i>Wheat Information Service</i> 11: 3-4.</li> <li>17. Allan RE &amp; Vogel OA 1965 Monosomic analysis of red seed colour in wheat. <i>Crop Science</i> 5: 475.</li> <li>18. Allan RE, Heyne EG &amp; Jones ET 1956 Relationship of sources of Hessian fly and leaf rust resistance in several wheat crosses involving a white water wheat. <i>Abstracts of the Annual Meeting of the American Society of Agronomy Cincinatti, Ohio, P.I. 119344-9. Citad Plant Breeding Abstracts</i> 1307, p. 224.</li> </ol>

Genes

Reference