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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 4th IWGS

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

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

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

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

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

1.6. Two or more genes having phenotypically similar effects should be designated by a common basic symbol. Non-allelic loci (mimics, polymeric genes, etc.) will be designated in accordance with two procedures:
(i) in sequential polymeric series where an Arabic numeral immediately follows the gene symbol; e.g., *Sr9*.
(ii) in orthologous sets where the basic symbol is followed by a hyphen ("-") followed by the locus designation taking the form of the accepted genome symbol and a homoeologous set number represented by an Arabic numeral; e.g., *Adh-A1* designates the A-genome member of the first *Adh* set. Different alleles, or alleles of independent mutational origin, are designated by a lower-case Roman letter following the locus number designation; e.g., *Sr9a, Adh-A1a*. (See also guidelines for nomenclature of biochemical and DNA loci).

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

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

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

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

1.11. Chromosomal aberrations should be indicated by the abbreviations Df for deficiency, Dp for duplication, In for inversion, T for translocation, and Tp for transposition. In wheat there are a number of genes derived from related species by introgression. Such genes in

different instances reside at different locations. One location may be taken as standard. Other locations will be considered as transpositions relative to a designated standard. When a gene does not reside in its standard chromosome position, the new chromosome designation may be given in brackets following the gene designation; e.g., Hp (Tp 6D) refers to a line carrying the introgressed "hairy neck" gene on chromosome 6D instead of 4B which is taken as standard. Alternatively, the chromosome involved may be described as a translocation. Guidelines for the description of translocated chromosomes both within wheat, and between wheat and alien chromosomes are provided in {705}.

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

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

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

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

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

2.2 Symbols for gene loci and alleles

2.2.1 *Basic symbol*: The basic symbol for a gene locus should consist of a two-, three-, or 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 *P*lant *S*cience *R*esearch probe 119 of the John Innes Centre. DNA markers detected in different chromosomes with the same probe or primer(s) should be assigned the same symbol except for the chromosome designation. For example, *Xpsr119-7D* and *Xpsr119-4A* designate other loci detected with probe 119.

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

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

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

amplified by one pair of primers (or by one primer) should be assigned to only one locus until recombination evidence indicates otherwise. As noted in Section 2.5.1, DNA markers located in different chromosomes that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the chromosome designation.

2.5.4 *Allele symbols*: Alleles should be designated as outlined in Section 2.2.3 with the exception that restriction-enzyme-specific alleles, e.g. RFLP- and indirect-STS alleles, should be designated with the name of the restriction enzyme followed by a lower-case letter. For example, *Xtam-5A-HindIIIa* denotes an allele detected with *Hind*III. Where possible, Chinese Spring should be the prototype for allele 'a'. When a double-digest is used to detect an allele, both restriction enzymes should be listed, separated by a slash. The name and source of the probe or primer(s) and the length(s) of the DNA fragment(s) detected normally should be stated in the first publication describing an allele.

2.5.5 *Abbreviation of locus and allele symbols*: The chromosome designation is an integral part of the locus symbol for DNA markers. Nevertheless, on chromosome maps and in a limited number of other contexts, the chromosome designation and the hyphen preceding it may be omitted. For example, *Xpsr35-3A* may be abbreviated as *Xpsr35* on a map of chromosome 3A, *Xpsr933-2A.1* and *Xpsr933-2A.2* may be abbreviated as *Xpsr933.1* and *Xpsr933.2*, respectively, on a map of 2A, and *Xpsr804(Sbp)-3A* may be abbreviated as *Xpsr804(Sbp)* on a map of 3A. Also the chromosome designation and the hyphen preceding it may be omitted on chromosome maps from the symbols for 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, port 70, menu "Grains files to browse" / "Reserved Laboratory Designators for DNA Probes, Primers and Markers".

Laboratories that are investigating DNA markers in different species and/or of different types, e.g., RFLPs, STS, and RAPDs, may choose to use more than one designator. For example, oat and barley cDNA clones isolated at Cornell University have been designated with the prefixes CDO and BCD, respectively, and *cdo* and *bcd*, respectively, are appropriately used as laboratory designators in symbols for loci detected with these clones. Likewise, *tam* and *txs*, respectively, are being used as laboratory designators in symbols for loci detected with wheat and sorghum DNA clones isolated at Texas A&M University, and the John Innes Centre is using *psr* and *psm* as laboratory designators in the symbols for DNA markers detected with wheat and millet probes, respectively, and *psp* for wheat PCR markers.

2.5.7 *Clone designations*: Clone designations should minimally identify the type of vector, the species from which the cloned DNA was obtained, and the source laboratory and cloned

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

3. Symbols for Loci and Alleles Controlling Quantitative Characters

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

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

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

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

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

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

4. AFLP: Amplified Fragment Length Polymorphism

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

A nomenclature proposal for AFLP loci has been received from Marc Zabeau at Keygene with the format '*XxyzAN1N2N3*, where '*X*' is the usual symbol for a DNA marker of unknown function; 'xyz' is the usual laboratory designator (e.g., *kg* for Keygene); A is a single upper-case letter denoting the rare-cutter enzyme used, e.g., P for *PstI*, etc.; N1 and N2 are two-digit numbers identifying standard one, two or three base-pair extensions (standard lists will be provided by Keygene); and N3 is a three-digit number corresponding to the molecular weight of the fragment.
The foregoing should be considered only as a proposal at this time as no AFLPs are listed in the catalogue. Comments regarding the proposal are welcomed and should be sent to the authors.

5. Single Nucleotide Polymorphism

Submitted for approval at the 11IWGS

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

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

Approved at the 4th IWGS

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

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

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

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

7. Organisation of the Catalogue

7.1. Data listing

Information is given in the following order, where possible:

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

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

7.2 DNA Markers

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

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

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

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

1. Markers in homoeologous chromosome groups 4, 5 and 7 (with the exception of those in T. monococcum chromosome 4Am; see #2 below) are listed in groups composed of loci located in homoeologous segments. The groups include the six classical homoeologous arm groups, namely, 4S (4AL:4BS:4DS), 4L (4AS:4BL:4DL), 5S (5AS:5BS:5DS), 5L (5AL:5BL:5DL), 7S (7AS:7BS:7DS) and 7L (7AL:7BL:7DL), and five new groups, 4AL:4BL:4DL, 5AL:4BL:4DL, 4AL:5BL:5DL, 7BS:5BL:7DS, and 7AS:4AL:7DS. Evidence is not available regarding the correct group location for a few of the markers listed in groups 4S, 4L, and 7S; a double asterisk (**) after the locus reference identifies these markers.

2. Markers in T. monococcum $4A^m$ are listed separately (under $4A^mS$, $4A^mL$, or $4A^m$), due to the several rearrangements that distinguish 4A and $4A^m$.

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

,1,	*T. aestivum*,
,2,	*T. turgidum*,
,3,	*T. monococcum*,
,4,	*Ae. tauschii*, and
,5,	Species hybrid,

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

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

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

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

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

8. Laboratory Designators

* In part indicates basis for name.

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

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

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

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

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

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

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

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

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

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

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

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

Symbol		Trait
Vrn-1	set	Response to vernalization
W		Glaucousness/waxiness/glossiness
Win		Winter hardiness
Wip		Wound-induced protein
Wcs		Wheat cold-specific genes
Wsip		Water-stress induced protein
Wsm		Reaction to wheat streak mosaic virus
Wsp-1	set	Water soluble proteins-1
Wx-1	set	Waxy endosperm
X		Basic symbol for DNA markers
Yld		Yield
Yr1 to 41		Reaction to *Puccinia striiformis*
14-3-3		14-3-3 protein
60S		60S ribosomal protein
17D		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 Arm	Gene	Chromosome Arm	Gene	Chromosome Arm	Gene
1AS	*Gli-A1*	1BS	*Gli-B1*	1DS	*Gli-D1*
	Gli-A3		*Gli-B3*		
	Gli-A5		*Gli-B5*		
	Glo-A1		*Glo-B1*		*Glo-D1*
	Glu-A3		*Glu-B3*		*Glu-D3*
	Gpi-A1		*Gpi-B1*		*Gpi-D1*
	Gpt-A1		*Gpt-B1*		*Gpt-D1*
			Hk-B1		*Hk-D1*
	Nor-A1		*Nor-B1*		
			Per-B1		*Per-D1*
	Rg-A1		*Rg-B1*		*Rg-D1*
	5S-Rrna-A1		*5S-Rrna-B1*		*5S-Rrna-D1*
			Si-B2		*Si-D2*
	Tri-A1				*Tri-D1*
1AL	*Glu-A1*	1BL	*Glu-B1*	1DL	*Glu-D1*
	Lec-A1		*Lec-B1*[a]		*Lec-D1*
	Mdh-A1		*Mdh-B1*		*Mdh-D1*
			Nor-B6		
	Pur-A1		*Pur-B1*		*Pur-D1*
2AS	*Est-A6*	2BS	*Est-B6*	2DS	*Est-D6*
	Per-A2		*Per-B2*		*Per-D2*
			Ppd-B1		*Ppd-D1*
2AL	*Est-A7*	2BL	*Est-B7*	2DL	*Est-D7*
	Isa-A1		*Isa-B1*		*Isa-D1*
	Ppd-A1				
	Ppo-A1				*Ppo-D1*[a]
	Sod-A1		*Sod-B1*		*Sod-D1*
	Tc1		*Tc2*		*Tc3*
3AS	*Br-A1*	3BS	*Br-B1*	3DS	*Br-D1*
	Est-A1		*Est-B1*		*Est-D1*
	Est-A9		*Est-B9*		*Est-D9*
	Hk-A2[a]		*Hk-B2*		*Hk-D2*
			Iha-B1		*Iha-D1*
	Ndh-A4		*Ndh-B4*		
	Pde-A1		*Pde-B1*		*Pde-D1*
	Tpi-A1		*Tpi-B1*		*Tpi-D1*
3AL					
	Est-A2[a]	3BL	*Est-B2*	3DL	*Est-D2*
	Est-A5		*Est-B5*		*Est-D5*
	Est-A8		*Est-B8*		*Est-D8*
	Got-A3		*Got-B3*		*Got-D3*
	Mal-A1		*Mal-B1*		*Mal-D1*

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
	Ndh-A3		*Ndh-B3*		*Ndh-D3*
	Per-A3		*Per-B3*		*Per-D3*
	R-A1		*R-B1*		*R-D1*
	S-A1[a]		*S-B1*[a]		*S-D1*[a]
4AL[b]	*Adh-A1*	4BS	*Adh-B1*	4DS	*Adh-D1*
	Amp-A2		*Amp-B2*		*Amp-D2*
	Lpx-A1		*Lpx-B1*		*Lpx-D1*
	Lpx-A3		*Lpx-B3*[a]		
	Ndh-A1		*Ndh-B1*		*Ndh-D1*
			Per-B4		
	Pdi-A1		*Pdi-B1*		*Pdi-D1*
	Pgm-A1				*Pgm-D1*
			Rht-B1		*Rht-D1*
	Wx-B1				
4AS[b]		4BL	*Aco-B2*	4DL	*Aco-D2*
	Acph-A1		*Acph-B1*		*Acph-D1*
			b-Amy-B1		*b-Amy-D1*
5AS	*Gsp-A1*[a]	5BS	*Gsp-B1*[a]	5DS	*Gsp-D1*
	Mdh-A3		*Mdh-B3*		*Mdh-D3*
	Nor-A3				*Nor-D3*
	Pina-A1[a] ,*Pinb-A1*[a]				*Pina-D1* ,*Pinb-D1*
	5S-Rrna-A2		*5S-Rrna-B2*		*5S-Rrna-D2*
	Skdh-A1		*Skdh-B1*		*Skdh-D1*
5AL	*Aadh-A1*	5BL	*Aadh-B1*	5DL	*Aadh-D1*
	Aco-A2				
	b-Amy-A1				
	Ibf-A1		*Ibf-B1*		*Ibf-D1*
	HstH1-A1 ,*A2*		*HstH1-B1*,*B2*		*HstH1-D1* ,*D2*
	Lpx-A2		*Lpx-B2*		*Lpx-D2*
	Ti-A2		*Ti-B2*		*Ti-D2*
	Tpi-A2		*Tpi-B2*		*Tpi-D2*
	Vrn-A1		*Vrn-B1*		*Vrn-D1*
5A	*Psy2-A1*	5B	*Psy2-B1*	5D	
6AS	*Amp-A1*	6BS	*Amp-B1*	6DS	*Amp-D1*
			Ep-B2		
	Gli-A2		*Gli-B2*		*Gli-D2*
	Got-A1		*Got-B1*		*Got-D1*

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 Arm	Gene	Chromosome Arm	Gene	Chromosome Arm	Gene
6AL	*Aadh-A2*	6BL	*Aadh-B2*	6DL	*Aadh-D2*
	Aco-A1		*Aco-B1*		*Aco-D1*
	AhasL-A1		*AhasL-B1*		*AhasL-D1*
	a-Amy-A1		*a-Amy-B1*		*a-Amy-D1*
	Dip-A1		*Dip-B1*		*Dip-D1*
	Est-A4		*Est-B4*		*Est-D4*
	Got-A2		*Got-B2*		*Got-D2*
7AS	*Amp-A3*	7BS		7DSc	
			Est-B3		*Est-D3*
	Ndh-A2[a]				*Ndh-D2*
	Pan2				*Pan1*
	Per-A4				*Per-D4*
			Pgip1		*Pgip2*
	Rc-A1		*Rc-B1*		*Rc-D1*
	Sgp-A1		*Sgp-B1*		*Sgp-D1*
	Sgp-A3		*Sgp-B3*		*Sgp-D3*
	Wx-A1				*Wx-D1*
7AL	*Adk-A1*	7BL	*Adk-B1*	7DLc	*Adk-D1*
	a-Amy-A2		*a-Amy-B2*		*a-Amy-D2*
	Cn-A1		*Cn-B1*		*Cn-D1*
	Ep-A1		*Ep-B1*		*Ep-D1*
	Psy1-A1		*Psy1-B1*		
	Wsp-A1		*Wsp-B1*		*Wsp-D1*
7A	*Ss1-A1*	7B	*SsI-B1*	7D	*SsI-D1*
	SsII-A2		*SsI-B2*		*SsI-D2*

[a] Arm location is unknown

[b] 4AL is mostly homoeologous to 4BS and 4DS and likewise 4AS is mostly homoeologous to 4BL and 4DL.

[c] 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	*Gli4, Gli6, H3, H5, H6, H9,H10, H11, H15, Hdic, Hg, Lr10, Nor, Pm3, Pm17, Rf1, Rg3, SuPm8, tin1, Tsc1*
1AL	*Eps-1Am, Lr59, scs*
1A	*Cmc3, Gb2, Gb6, kr4, Pm25, YrDa1*
1BS	*Rf3, Rf4, Snn1, Stb11, Vi, Yr10, Yr15 , Yr24/26, YrAlp, YrH52*
1BL	*Iw3, Lr33, Lr46, Lr51, Nor6, Sr14, Yr29*
1B	*Bt4, Bt5, Bt6, Dn7, Lr44, Lr55, Ltn2, Pm28, Pm32, Sr31, SrZdar, Yr3,Yr9, Yr21*
1DS	*Gli-DT1, H22, Lr21, Lr60, Pm24, Sr45*
1DL	*Dn4, Dn9, Lr38, SbeI1, Sr33.*
1D	*Glu4, Lr42, Pm10, Ra1, Sr18, Stb10, Yr25*
2AS	*bh, Cre5, Lr17, Lr37, Lr49, Sr38, Yr17*
2AL	*b-Gls, Lr38, Pm4, PmPs5A, Snb2, Sr21, Tc1, Yr1, Yr32*
2A	*Br4, Ch1, lg3, Lr11, Lr45, LrTt1, Pp3, Rht7, Sr32, Sr34, tin2*
2BS	*Iw1, Lr13, Lr16, Lr23, Ne2, Pm26, Sr19, Sr23,Sr36, Sr40, Tg2, W1, Yr27, Yr31, Yr41,YrSp, Tsc2*
2BL	*Cre1, D2, Dfq1, Lr50, Lr58, Mlzec1, Pm33, Rht4, Sr9, Sr16,Sr28, Tc2, Yr5, Yr7*
2B	*Bt1, Gc1, H20, H21, lg1, Lr35, Pm6, Sm1, Sr10, Sr20, Sr32,Sr39, wptms2, wtms1, Y r3, YrSte , YrV23.*
2DS	*D1, Iw2, Lr2, Lr15, Lr22, Lr39, Per5, Sr6, SuLr23, Snn2, Tg1, YrCK*
2DL	*Acph2, C, Cre3, D4, L r54, Rht8, Tc3, YmYF, Yr37*
2D	*Bt7, Cre4, lg2, Ra1, Sr32, Sr34, Yr8, Yr16*
3AS	*Stb6*
3AL	*Eps1, Snb1, SnbTM, Sr35*
3A	*EpsWi, ms5, Sr27, Tsr4, V2, YrTr2 .*
3BS	*Lr27, Pbc, Rht5, sc, Sr2, Sr12, Stb2, Stb14, Yr30, Yrns1, V1*
3BL	*Tsn2, Tsr2, Tsr5*
3B	*Igcl, Pm13, Rkn-mn1, YrS, YrSte*
3DS	*Lr32, Lr38, Nor8, Ph2*
3DL	*Ch2, H26, H32, Lr24*
3D	*H24, Pm13*
4AL	*D3, Lr28, Lr30, Per4, Phs1, Sr7, Stb7, Stb12*
4AS	*Hd.*
4A	*Bo3, H25, Pm16, YrHVII, YrMin, YrND, Wsm1*
4BS	*Gail, Gai3, Lpx1, Lr25, ms1, Pa*
4BL	*Cat1, Ce, Hl1, Hp, Lr31, Lr48, Pm7, Sr37*
4B	*Ba1, H25, Lpx1, Lr12, Lr16, Mld, Ra2, Sr23, YrCle, YrMor, YrYam .*
4DS	*Gai2, ms2, ms4, Yr28*

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	*Alt2, Kna1, Wss1*
4D	*H26, Sr41, Yr22, Wsm1*
5AL	*Ar1, B1, Fr1, Hn, kr2, Nor7, Q, Rht9, Yr34*
5AS	*Lr38, ms3, Nor10*
5A	*Cs1, H4, H12, H16, H17, H28, H29, Pm23, Rht12*
5BS	*Ce, H31, Hp, Lr52, Pm30.*
5BL	*Cdu1, Crr, Eps5, Kr1, Lr18, Ne1, Ph1, Pm36, Stb1, tsn1, Tsr1, Vgw .*
5B	*Cmc2, Pm16, wptms1, Yr19, YrDru*
5DS	*Ha, Lr57, Pm2, Pina, Pinb, Pro2, Yr40*
5DL	*Fr2, Lr1, Pm34, Pm35, Pro1, Snb3, Sr30, Vrn4, Vrn 5*
5D	*H7, kr3, YrDa2*
6AS	*Pm21, Rf6, Sr8, Stb15*
6AL	*Imi3, Mlre, Sr13, Sr26*
6A	*Cmc2, Pp1, Yr38, YrD, YrDru2, YrH46.*
6BS	*col, Ep2, Fhb2, Gpc1, Lr36, Lr53, Nor2, Pm11 Rf6, Su1, Yr35, Yr36*
6BL	*?-Amy1, B2, Cre8, Imi2, Ki, Lr3, Lr9, Pm20, Sr11?*
6B	*H25, Pm12, Pm14, Pm27, Ra3, Rf4, Su1, Yr4, YrDru*
6DS	*Cmc1, Cmc4 , H13, H23, HWGRC4, Sr5, Sr29, Sr42, Stb3*
6DL	*H13, H23, H24, Imi1, Lr38, Sr29*
6D	*Amp1, Cmc2, co2, Hp, Pm24, Rf5, Yr20, Yr23, YrTye, YrTr1*
7AS	*Amp3, Msg, or, Pan2*
7AL	*Lr19, Lr20, Mlm3033, Mlm80, mlRd30, P1, Pch2, Pm1, Pm9, Pm37, Rhn1, Sr15, Sr22, Sr25*
7A	*Gby, Pgd1, Pp2*
7BS	*cc, Dn1881, Fe2, Hl2, Pc1, Pgip1, Rht9, Rht13, Vrn3, Yr6*
than one chromosome	*P2, Pm5, Lr14, Lr19, Rfd1, SbeI2, Sd2, Sr17, Stb8, Stb13, Yr39, YrZH84*
7B	*Bo1, mljy, mlsy, Mlxbd, Pp2, Yr2*
7DS	*Bvd1, Dn1, Dn2, Dn5, Dn8, DnX, Lr29 Lr34, Pan1, Pc2, Pgip2, Pln, Pm15, Pm38, Sr44, Stb4, Stb5, Yr18*
7DL	*Bdv2, Dn2, Dn5, Fe1, Gb3,Gb4, Gb7, Gba, Gbb, Gbc, Gbx1, Gbz, Lr19, LrVPM, Nor4, Pch1, Sr25, Sr43*
7D	*Dnl, Gb3, Glu5, Ltn, Pch1, Pm19, Rf2, Sd1*

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

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.
Ml-Ad, Ml-Br, Ml-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
Ut1, 2, 3, 4, Ut-x.
vg.
Yr11, 12, 13, 14 & 33

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

Genes				% Recombination			cM		
				Value	S.E	Ref	Value	S.E.	Ref
Chromosome 1									
1AS									
	Rg3	-	*Hg*	0		{1406}			
tv:	*Hg*	-	*Bg*	1.17	1.4	{1103}			
	Hg	-	*Bg*	1.52	1.88	{1103}			
	Hg	-	*Bg*	1.32	1.15	{1103}			
tv:	*Hg*	-	*Bg*	2.4		{1519}			
	Hg	-	*Bg*	0		{631}			
	Hg	-	*Bg*	12.33	2.16	{1347}			
dv:	*Hg*	-	*Bg*	0-16.5		{1393}	0-17.4		
	Hg	-	*Pm3a*	4.81	0.52	{943}			
	Hg	-	*Pm3a*	0.82		{134}			
	Hg	-	*Gli-A1*	3.95	1.38	{559}			
	Hg	-	*Gli-A1*	0.30	0.31	{1406}			
	Hg	-	*Gli-A1*	0.79	0.81	{897}			
	Hg	-	*Gli-A1*	2.24	1.31	{1406}			
	Hg	-	*Gli-A1*	2.64	0.98	{1405}			
	Hg	-	*Gli-A1*	2.97	1.64	{1103}			
	Hg	-	*Gli-A1*	2.31	1.31	{1103}			
	Hg	-	*Gli-A1*	2.97	0.84	{1103}			
	Hg	-	*Lr10*	5.97	1.7	{559}			
	Hg	-	*Tin*	10	3	{1212}			
	Hg	-	*cent*	I		{947}			
	Rg3	-	*Hg*	0		{1406}			
	Pm3a	-	*Pm25*	21		{1343}			
	Pm3a	-	*cent*	I		{947}			
	Pm3a	-	*Glu-A1*	I		{1406}			

Genetic linkages (Cont.)

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

Genetic linkages (Cont.)

Genes				% Recombination			cM		
				Value	S.E	Ref	Value	S.E.	Ref
	Gli-B1	-	*rf3*	22.1	6.4	{1399}	23.7	8	
	Gli-B1	-	*rf3*	18.6		{9934}			
	Gli-B1	-	*Nor-B1*	36.8	13.5	{1399}	47.1	29.5	
	Gli-B1	-	*Xgwm11 /Xgwm18-1B*	20.7		{0321}			
	Gli-B1	-	cent				59.7	7.1	{1358}
	Gli-B1	-	cent				56.1	10.3	{1358}
	Gli-B1	-	cent	I		{223}			
tv:	*Gli-B1*	-	cent				46.4		{224}
	Gli-B1	-	*Glu-B1*	42	4.9	{1121}			
	Gli-B1	-	*Glu-B1*	42.5	3	{1121}	62.8	10.8	
	Gli-B1	-	*Glu-B1*	41		{882}	57.8		
	Gli-B1	-	*Glu-B1*				39.1		{589}
	Gli-B1	-	*Glu-B1*				66	5.7	{1125}
	Gli-B1	-	*Glu-B1*	37.5	1.9	{422}	48.6	4.3	{422}
	Gli-B1	-	*Glu-B1*	30.8	7.4	{1399}	35.9	11.9	
	Gli-B1	-	*Glu-B1*	I		{422}	53.6	7.9	{422}
	XGli-B3	-	*Glu-B2*				0		{277}
	Gli-B3	-	*Glu-B1*				16.7	5.2	{589}
	Gli-B3	-	*Glu-B1*				22.4	6.3	{589}
	Gli-B3	-	*Glu-B1*	23.5	4.2	{422}	25.5	5.4	{422}
	Glu-B3	-	*Glu-B1*	35.4	4.8	{1358}	44.2	9.6	
	Glu-B3	-	*Glu-B1*	29.9	6	{458}			
	rf3	-	*Nor-B1*	22.6	9.2	{1399}	24.4	11.6	
	rf3	-	*Glu-B1*	34.1	8.5	{1399}	41.6	15.9	
	Nor-B1	-	*Glu-B1*	22.5	9.3	{1399}	24.2	11.7	
	Nor-B1	-	*Glu-B1*				22		{1120}
	Nor-B1	-	*Rf3*	22.3		{9934}			
	Bt4	-	*Bt5*	30		{1000}	34.7		
	Bt4	-	*Bt6*	15.2	1.6	{1274}	15.7	1	
	Lr26	-	*Lr3*	2.6	0.8	{325}			
tv:	*Yr10*	-	*Yr15*				34.0	2	{969}
	Yr15	-	cent				7		{969}
	Yr15	-	*Yr24*				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	-	*Lr33*				3.1	1.2	{325}
	cent	-	*Glu-B1*				10.2	2.4	{1125}
	Lr33	-	*Lr44*	5.4	1.1	{322}			
tv:	cent	-	*Glu-B1*	32.6		{224}	38.9		
	cent	-	*Glu-B1*	28.1	2.8	{1359}	31.8	4.1	
	cent	-	*Glu-B1*	14.1		{223}			
	Cent - *Lr51*	-	*Glu-B1*	0.41		{0307}	50-86		{0308}

Genetic linkages (Cont.)

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

Genetic linkages (Cont.)

Genes				% Recombination			cM		
				Value	S.E	Ref	Value	S.E.	Ref
	Rg2	-	*Lr21*	3.1	1.1	{1241}			
	Rg2	-	*s*	1.7	1	{1241}			
	Rg2	-	*Sr33*	35	5.2	{650}	43.4	10.2	
	Rg2	-	*Sr33*						
1D	*Rg2*	-	*Sr33*						
	Lr41	-	*Lr24*	I		{218}			
Chromosome 1R									
1RS									
	Tel (C-band)	-	*SrR*				16	4.8	{9919}
	Sec 1	-	Cent				26.1	4.3	{9919}
	Sec 1	-	*Sec 3*	36.0	4.6	{779}	45.4	9.6	
	Sec 1	-	*Sec 3*	40.8	3.76	{1336}	57.2	11.3	
	Sec 1	-	*Sec 3*	36.0	4.12	{163}	45.4	8.6	
	Dn7	-	*Lr26*				14.5	3.9	{894}
	Dn7	-	*Lr26*						
	Sr31 /Lr26 /Yr9	-	Sec1				5.4	1.7	{9919}
1RL									
	cent	-	*Glu-R1*				4.7	1.0	{1356}
Chromosome 2A									
2AS									
	bh	-	cent				8.5	2.1	{665}
	Lr17a	-	cent	I		{314}			
	Lr17a	-	*Lr11*	I		{314}			
	Yr1	-	*Yr32*	I		{10016}	35		{10016}

Sr38, *Lr37* and *Yr17* were closely linked in coupling and showed close repulsion linkage with *Lr17a* {062}.

2AL									
	cent	-	*Sr21*	2.4	0.9	{1464}			
	cent	-	*Tc2*				46.8	0.9	{10133}
	cent	-	*Pm4b*	I		{1464}			
	Sr21	-	*Pm4b*	37.5	1.7	{1464}	48.6	3.9	
	Yr1	-	*Pm4a*				2	0.6	{940}
	Tc2	-	*Lg1*				11.9		{10133}
Chromosome 2B									
2BS									
	Lr16	-	*Sr23*	< 0.7		{950}			
	Lr16	-	*Sr36*	I		{939}			
	Lr16	-	*Sr40*	34.4	4.1	{302}	42.2	7.8	
	W1I	-	cent	42-50		{267}	>61.6		
	Ne2	-	cent	9.4	1.5	{1085}			
	Ne2	-	*D2*	34		{536}	41.5		
	Sr40	-	*Sr36*	21.9	2.4	{302}	23.5	3	
	Sr40	-	*Lr13*	1	0.6	{302}			

Genetic linkages (Cont.)

Genes			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
Sr40	-	*Lr23*	4.7	1.2	{302}			
Sr40	-	*Sr9*	28	3.3	{302}	31.6	4.8	
Sr19	-	cent	7.7		{1582}			
Lr23	-	*Lr13*	close		{939}			
Lr23	-	cent	4		{948}			
Lr23	-	cent				20		{1058}
Lr23	-	*Sr9b*	22	2	{948}	23.6	2.5	
Lr23	-	*Sr9b*	22.3	2.4	{932}	24	3	
Lr23	-	*Sr9b*	24.1	2.2	{932}	26.3	2.9	
Lr23	-	*Sr9b*	30.6	4.2	{965}	35.6	6.7	
Lr23	-	*Sr28*	28.5	2.8	{932}	32.4	4.1	
Yr27	-	*Lr13*				3.6	2	{928}
Lr23 /Sr36	-	*Sr9b/Sr9e*	19.6	1.9	{951}	20.7	2.2	
Lr13	-	*Sr9b*	17.6	3.1	{1370}	18.4	3.5	
Lr13	-	*Lr39*	I		{647}			
Sr36	-	*Sr9d*	24	8	{827}	26.1	10.4	
ppd2	-	*Sr9g*	I		{1269}			
ppd2	-	*Dfq1*	I		{789}			
Hst2a-B1	-	cent				20		{909}
2BL								
cent	-	*Sr9a*	10.6		{1307}			
cent	-	*Sr9b*	18.2	6.7	{944}	19.1	7.7	
cent	-	*Yr5*				21		{034}
cent	-	*Dfq1*				30		{789}
cent	-	*Tc2*				40.7	0.9	{10133}
cent	-	*Sr28*	34.6	2.8	{932}	42.6	5.4	
cent	-	*D2*	48.5		{944}			
cent	-	*Sr16*	I		{932, 1307}			
Sr9g /Yr7	-	*Dfq1*				6		{789}
Sr9a	-	*Sr19*	24	3	{636}	26.2	3.9	
Sr9a	-	*Sr19*	24.5	3.2	{1582}	26.8	4.2	
Sr9a	-	*Sr16*	I		{830}			
Sr9b	-	*Sr28*	16.8	2.1	{932}	17.5	2.4	
Sr9b	-	*D2*	42.2		{944}	61.1		
Sr9b	-	*Sr16*	I		{932}			
Sr9g	-	*Yr7*	<1.6		{965}			
Sr9g	-	*Sr16*	35.4	2.3	{965}	44.2	4.6	
Yr7	-	*Yr5*	allelic		{034}			
Yr7	-	*Yr5*	not allelic		{605}			
Dfq1	-	*Sr16*	I		{789}			
Sr20	-	*Sr19*	I		{029}			
Sr20	-	*Sr16*	I		{029}			
Sr28	-	Sr16	29.2	4.2	{932}	33.4	6.4	
Sr28	-	Sr16	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 - *lg1* {10133}

Genetic linkages (Cont.)

Genes			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
2B								
Sr39	-	*Lr35*	3	1.1	{651}			
Sr39	-	*Sr32*	I		{647}			
Sr39	-	*Lr13*	I		{647}			
Chromosome 2D								
2DS								
Lr22a	-	cent	63.6	4.8	{1241}			
Lr22a	-	*Tg*	33	4	{1240}	39.7	7.1	
Lr22	-	*Tg*	41.6	4.4	{1240}	59.7	14.3	
Lr22	-	*Tg*	20.8	3.6	{1241}	22.1	4.4	
Lr22	-	*Tg*	6	1.5	{311}			
Lr22b	-	*W2I*	10.6	2.9	{298}			
Lr22b	-	*W2I*	18.3	2.9	{1240}	19.2	3.3	
Lr22b	-	*W2I*	41.6	4.4	{1240}	59.7	14.3	
Lr22b	-	*W2I*	15.6	2.5	{311}	16.1	2.8	
Lr22b	-	*Tg*	11.6	3.1	{298}			
W2I	-	cent	52.5	5	{1241}			
W2I	-	cent	58.9	4.6	{1241}			
W2I	-	*Tg*	21.9	4.2	{298}	23.5	5.2	
W2I	-	*Tg*	22.3	3.9	{1240}	24	4.9	
W2I	-	*Tg*	28.2	2.7	{1240}	31.9	4	
W2I	-	*Tg*	21.6	2.7	{1240}	23	3.3	
W2I	-	*Tg*	20.8	3.6	{1241}	22.1	4.4	
W2I	-	*Tg*	15.1	2.6	{648}			
Tg	-	cent	39.4	4.9	{1241}	53.3	12.9	
Tg	-	cent	42.9	4.6	{1241}	64.3	17.4	
Tg	-	cent	38.7	4	{652}	51.5	10	
Tg	-	cent	45	4.7	{652}			
Lr15	-	cent	32	5.1	{942}	37.9	8.6	
Lr15	-	*Lr2a*	allelic		{939, 942}			
Lr15	-	*Sr6*	0.75	0.34	{942}			
Lr2a	-	*C*	10	1.2	{843}			
Lr2a	-	*Sr6*	1.16	0.82	{942}			
Sr6	-	*C*	33.1, 18.9		{436}	39.8, 19.9	9.9	
Sr6	-	*C*	18.1		{671}	19		
Sr6	-	cent	28.7	4.8	{942}	32.7	7.2	
Sr6	-	cent	15.5	3.6	{942}	16	4	
Sr6	-	cent	33.1		{436}	39.8		
Sr6	-	cent	18.9		{436}	19.9		
Sr6	-	cent	18.1		{671}	18.8		
Sr6	-	cent	18.69	2.36	{942}	19.6	2.7	
Sr6	-	*Ra*	0		{1645}			
D1	-	cent	3.2	2.4	{942}			

Gene order: *Tg* - *W2I* - *Lr22* {1240}; *Tg* - *Lr22* - *W2I* {311}. The *D1* - cent linkage was not supported by other genetic data {1000}.

Genetic linkages (Cont.)

Genes			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
2DL								
cent	-	C	2.26		{1192}			
cent	-	*Tc3*	38.8	5.8	{10131}			
C	-	*D1*	36.7		{1000}	46.9		
C	-	*D4*	I		[1000}			
Rht8	-	*Ppd1*	17	4.9	{1598}	17.7	4.5	
Rht8	-	*Ppd1*	25		{1601}	27.5		
Rht8	-	*Ppd1*	16.6		{1601}		17.3	
Rht8	-	*Yr16*	44	5	{1598}	68.8	22.2	
Rht8	-	*Yr16*	38		{1601}	49.8		
Rht8	-	*Ppdl*				20.9		{00106}
Rht8	-	*D4*	I		{1598}			
Ppd1	-	*Yr16*	36	5	{1598}	45.4	10.4	
Ppd1	-	*D4*	I		{1598}			
Yr16	-	*D4*	25	1	{1598}	27.5	1.3	
Yr16	-	*D54*	26	8	{1598}	28.8	11	
D4	-	*Su-D*	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

Br-A1	-	cent				21.1	0.2	{10061}
Br-A1	-	cent				20.6		{10182}

3AL

cent	-	*Sr35*	34	4	{957}	41.5	7.4	
Br2	-	*R-Alb*				44.2		{0130}
Sr35	-	*R2*	1	1	{957}			

Chromosome 3B

3BS

Lr27	-	cent	33.6	4.1	{1367}	40.7	7.5	
Lr27	-	cent	I		{1367}			
Lr27	-	*Sr12*	I		{1372}			
Br-B1	-					20.1	0.6	{10061}
vla	-	cent	0.28		{1297}			
Sr12	-	cent	0		{968}			

3BL

Br3	-	*R-Blb*				47		{0130}

Chromosome 3D

3DS

Lr32	-	cent	26.8	4	{645}	29.9	5.6	
Br-D1	-	cent				20.6	0.3	{10061}
s1	-	cent	5.7		{1194}			

Genetic linkages (Cont.)

Genes			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
3DL								
cent	-	*Got-D3*	4.3		{521}			
cent	-	*S1*	5	2	{692}			
cent	-	*Ch2*	36.1	4	{692}	45.6	8.4	
cent	-	*R-Alb*	I		{1193}			

In Agent and Sears' translocations 3*Ag#1* and 3*Ag#2*, *Lr24*, *Sr24* and red grain colour assumed to be etermined 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-Dlb derivatives in Australia.

Chromosome 4A

4AS

Adh-B1	-	cent	20	3.5	{1197}	21.2	4.2	
Hd	-	cent	7.7	3.7	{1195}			

4AL

cent	-	*Lr30*	2.9	1.3	{315}			
cent	-	*Lr28*	39.2	2.7	{967}	52.8	7	
Sr7a	-	*Hd*	I		{671}			

Chromosome 4B

4BS

ms1b	-	cent	I		{064}			
ms1b	-	*Lr25*	34		{064}	41.5		
ms1c	-	cent	I		{064}			
ms1c	-	*Lr25*	20		{064}	21		
Adh-Ala	-	*Gai/Rht-B1*	23.1	4.0	{1442}	25.0	5.1	
Gai1	-	*Gai3*	0		{406}			
Rht-B1 /*Gai1*	-	cent	15	3	{698}			
Rht-B1	-	*b-Amy-B1*	I		{008}			
b-Amy-B1	-	cent	>35		{008}	43.4		
pa	-	*Hl*				29	2.6	{921}
pa	-	*Hl*				30		{042}

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

4BL

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

Chromosome 4D

4DS

ms4	-	cent	I		{0293}			
Ms2	-	*Rht-D1c*	0.005		{805}			
Ms2	-	cent	31.2		{807,80}	36.5		
Rht-D1 /*Gai2*	-	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-DIC* was allelic with *Rht-D*1{114}.								
4DL								
Rht2	-	*b-Amy-D1*	I		{008}			
cent	-	*b-Amy-D1*	>35		{008}	>43.4		
Alt2	-	*Kna1*				12.5		{848}
Chromosome 5A								
5AS								
Ms3	-	cent	3.1		{622}			
5AL								
cent	-	*a-Amy-A1*				3.8		{1081}
cent	-	*a-Amy-A1*				8		{599}
B1	-	*Rht12*		<2.5	{1605}			
B1	-	*Xpsr164-5A*				57		{9903}
cent	-	*Vrn-A1*	I		{775}			
cent	-	*q*	I		{1196}			
Kr2	-	*Vrn-A1*	4.8	4.66	{1387}			
Kr2	-	*q*	38.1	10.6	{1387}	50	25.3	
Vrn-A1	-	*q*				34		{1400}
Vrn-A1	-	*B1*				31	3.3	{925}
Vrn-A1	-	*B1*				45	4.1	{925}
Vrn-A1	-	*B1*				47	4.4	{925}
Vrn-A1	-	*B1*				50	4.3	{925}
Vrn-A1	-	*b-Amy-A1*	37		{008}		47.5	
q (S)	-	*Hn*	36.2			45.8		
q	-	*B1* (n)	30		{913}	34.7		
q (S)	-	*B1* (N)	32.7		{1136}	39		
q (S)	-	*B1* (B)	37.3		{193}	48.2		
q (K)	-	*B1*	41		{1550}	57.8		
q	-	*B1*				25		{1400}
Hn	-	*B1*	5		{396}			
Hn	-	close			{837}			
B1	-	*b-Amy-A1*	2.3	2.3	{008}			
B1	-	*Ibf-A1*	0		{1605}			
Gene order: *b-Amy-A1* - *B1* - *Hn* - *Q* - *Vrn-A1* - *Kr2* {008,1387,1400}.								
: cent - *Vrn-A1* - *Q* - *B1* {9903}.								
Chromosome 5A								
H3	-	*H6*	9		{1105}			
H3	-	*H9*	15.5	4.8	{1420}	16	5.3	
H6	-	*H9*	2	2.01	{1421}			
H9	-	*H10*	36		{162}	45.4		
	-		I		{1421}			
H9	-	*H15*	close		{625}			
H28	-	*H9*				22		{171}

Genetic linkages (Cont.)

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

Gene order: *H3 - H6 - H9*.

Gene order: *H9/H15 - H17 - H16 - H12* {1098}

Chromosome 5B

5BS

5BL

cent	-	*Ne1*				6		{1021}
cent	-	*Ne1*				10.5	2	{1085}
Ne1	-	*Vg*				11		{1021}
Vg	-	*Ibf-B1*				35		{1021}
cent	-	*Kr1*	11.5	3	{762}			
cent	-	*Kr1*	44.8	3.3	{1387}	72.6	16.6	
cent	-	*Crr*	42.9	3.4	{765}	64.3	12.9	
cent	-	*Crr*	36.1	3.3	{765}	45.6	6.9	
cent	-	*Ph1*	50.7	4.1	{1537}			
cent	-	*Lr18*	I		{939, 935}			
Xbcd103	-	*tsn1*				5.7		{346}
tsn1	-	*Xwg583*				16.5		{346}

Chromosome 5D

5DS

Pm2	-	*Lr1*	I		{945}			
Pm2	-	*Sr30*	I		{688}			

5DL

cent	-	*Lr1*	36.7	5.3	{688}	46.9	11.5	
cent	-	*Lr1*	I		{945}			
cent	-	*Sr30*	I		{688}			
cent	-	*Vrn3*	I		{775}			
Lr1	-	*Sr30*	I		{688}			
Vrn-D5	-	*Vrn-D1*	I		{10004}			

Chromosome 6A

6AS

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

6AL

cent	-	*Sr26*	0		{1154}			
cent	-	*Ep-A1*				1		{599}
cent	-	*Sr13*	I		{929}			

Genetic linkages (Cont.)

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

Lr36 is distal to *Gli-B2* {292}.

Genetic linkages (Cont.)

Genes			% Recombination			cM		
			Value	S.E	Ref	Value	S.E.	Ref
Xcdo772 /cent	-	*Xbcd1-6B*				41.2 cM		{9921}
Xbcd-6B /Lr3	-	*Xmwg798*				32.1 cM		{9921}
cent	-	*Sr11*	45.1		{1297}		74.1	
cent	-	*Lr3*	I		{1244}			
B2	-	*Lr9*	3.5		{1299}			
B2	-	*Sr11*	43.3		{1297}		65.8	
B2	-	*Sr11*	46.9 (or 43.8)		{1299}	86.1 (or 67.9)		
a-Amy-B3	-	*a-Amy-B1*				9.3		{1081}
Sr11	-	*Ki*	9		{829}			
Sr11	-	*Ki*	10.5		{1306}			
Sr11	-	*Lr9*	close		{1297}			
Sr11	-	*Lr3*	21.7	7.8	{548}	23.2	9.6	
Sr11	-	*Lr3*	0		{839, 842}			
Lr3	-	*Ki*	11.5		{1306}			

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

Chromosome 6D

6DS

Sr5	-	*Sr29*	I		{313}			
Cmc1	-	cent	I		{1468}			
Cmc1	-	*Cmc4*	I		{0222}			

6DL

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

Chromosome 7A

7AS

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

7AL

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

Genetic linkages (Cont.)

Genes				% Recombination			cM		
				Value	S.E	Ref	Value	S.E.	Ref
	Sr22	-	*Pm1 /Lr20 /Sr15*	41		{1462}	57.8		
	Sr22	-	*Pm1 /Lr20 /Sr15*				42		{10263}
	Xpsr121-7A	-	*Pch2*	11.2	3.5	{228}			
dv:	*Sr22*	-	*Rc1*	42	2.8	{1461}	61.9	9.5	
	Sr22	-	*Rc1*	43	2.7	{1461}	64.7	10.4	
	cn-A1a	-	*Pm1 /Lr20 /Sr15*	40		{1462}	54.9		
	Pm1	-	*Pm9*	linked		{347}			
	Pm1	-	*Pm9*				8.5		{1287}
tv:	*P*	-	*cn-A1d* (CDd6)				37.9	3.2	{1547}
Chromosome 7B									
7BS									
	cc	-	cent				33.5	4.1	{665}
	Vrn5	-	*Pc*	26	5	{771}	28.8	5.6	
	Vrn5	-	*Lr* mod	25.5	4.6	{412}	28.1	6.2	
	Vrn5	-	*Pm5*	26	5	{771}	28.8	6.9	
	Pc	-	*Lr14a*	44	6	{771}			
	Pc	-	cent	22.8	5.3	{412}	24.6	6.7	
	Pc	-	*P2*				29.6	7.3	{9990}
	Pc(*Rc2*)	-	cent	16	5	{769}	16.6	5.6	
	Pc	-	*Lr* mod	10.5	3.7	{412}			
	Hl2	-	cent	14.3	3.5	{0316}			
Gene order: *Pc* - *Vrn5 (e1)* - cent {770}; revised to: *Vrn5* - *Pc* - cent {769}.									
7BL									
	cent	-	*a-Amy-B2*	5.9	5.5	{412}			
	cent	-	*cn-B1a*				42.6	4.3	{665}
	cent	-	*Pm5*	37	9	{771}	47.5	19.9	
	cent (5B.7B)	-	*Ep-B1*	I		{708}			
	a-Amy-B2	-	*Pm5*	44.4	5.1	{412}	70.6	24.1	
	a-Amy-B2	-	*Ep-B1*	I		{708}			
	Xpsr129	-	*Ep-B1*				>50		{179}
	Pm5	-	*Lr14a*	20.4	2.4	{1564}	21.7	2.9	
	Pm5	-	*Lr14a*	28	5	{770}	31.6	7.3	
	Pm5	-	*Lr14a*	30.1	4.5	{412}	34.8	7.1	
	Pm5	-	*Sr17*	6	2	{964}			
	Pm5	-	*Sr17*	2	1.1	{964}			
	Lr14a	-	*Sr17*	18.2	4.5	{964}	19.1	5.2	
	Lr14a	-	*Ep-B1*	9.6	3	{708}			
	Xpsr121	-	*Ep-B1*				9		{179}
	Xpsr121	-	*Wsp-B1*				16.6	6.9	{817}
	Ep-B1	-	*WspB1*				31.6	12.1	{817}
	P2	-	*cn-B1b*				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
Chromosome 7D								
7DS								
This chromosome arm is physically longer than the arm designated 7DL, but is homoeologous to those arms designated 7AS and 7BS {1571,388}.								
Bdv1	-	*Lr34 /Yr18 /Ltn*	0		{1363}			
Lr34	-	*Lr29*	0		{924}			
Ltn	-	*Lr34/Yr18*	<0.013		{1361}			
Lr34	-	*Yr18*	0		{1362, 937}			
Lr34	-	*Rc3*	30.25	2.88	{924}			
Rc3	-	cent	10.3	2.8	{1241}			
Rc3	-	cent	9.8	2.8	{1241}			
Rc3	-	cent	16	4.2	{1444}	16.7	4.7	
Rc3	-	*Adk-D1*				24.1	4.5	{1435}
a-Amy-D2	-	*Adk-D1*				0.24	5	{1603}
a-Amy-D2	-	*Pch*				37	5	{1603}
a-Amy-D2	-	*Pch /Ep-D1b*				I		{1603}
Pan1	-	*Pc2*				13.3	2.3	{921}
Pan1	-	*Pc2*				14.4	2.7	{921}
Pm15	-	cent	I		{1480}			
7DL								
Physically shorter than 7DS; see note for 7DS above.								
a-Amy-D2	-	*Lr*				42	6	{1603}
a-Amy-D2	-	*Pch*				I		{417, 1603}
Xgwm111-7D	-	*Gb3*				22.5		{0319}
Cent	-	*Dn5*	I		{287}			
Lr	-	*Pch*				18	4	{1603}
Pch	-	*Ep-D1b*				0		{1603}
Lr19/Sr25	-	*cn-D1*	0		{939}			
Dn5	-	*Ep-D1*	32	4.67	{894}			
Dn5	-	*cn-D1*	37	6.3	{894}			
Gb3	-	*Xgwm428-7D*				33.1		{0319}
Gb3	-	*Gb7*				8.75		{10169}
Pm29	-	*Pm19*			{0129}			

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

III. MacGene2008 (Standalone version) quick manual

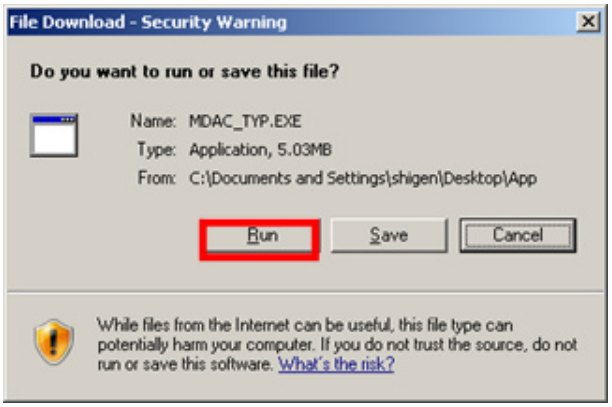
1. System environment

OS: Windows XP or Vista
Microsoft Office 2003 or 2007

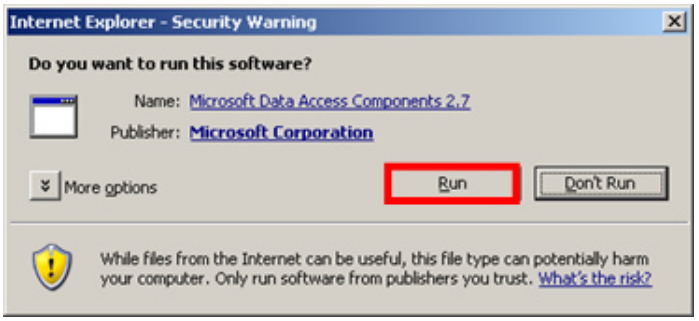
2. Installation

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

2.4. Click "Run".

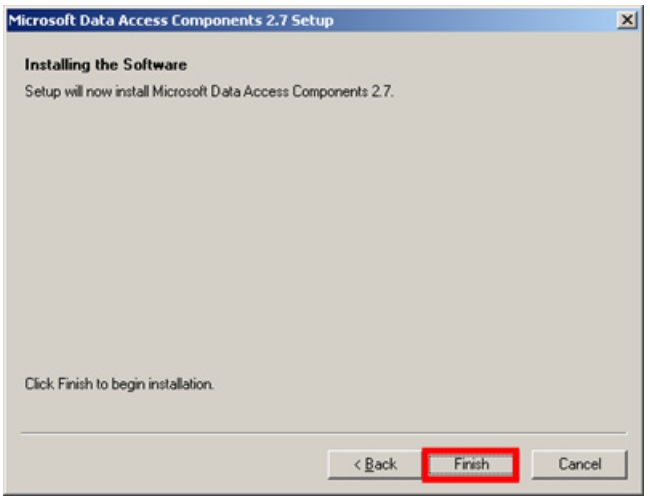


2.5. Click "Run".

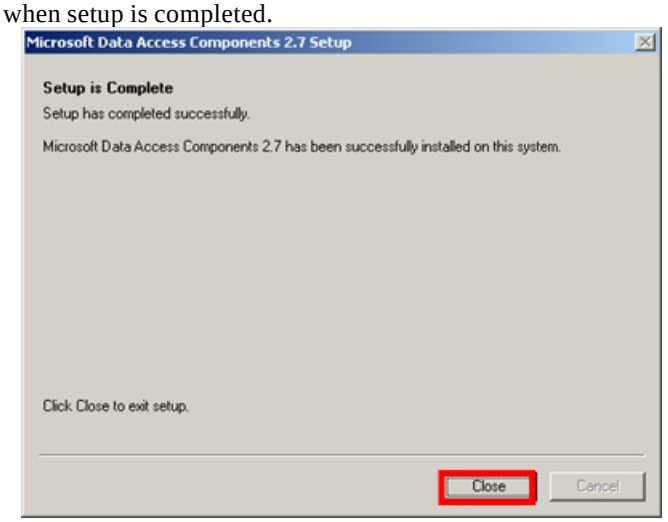


2.6. Click “Next” if you can agree.

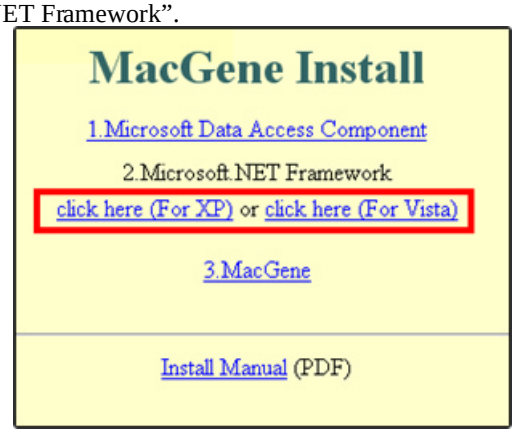
2.7. Click “Finish”.



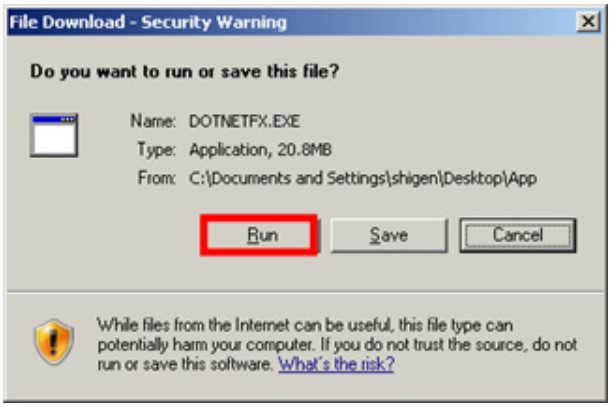
2.8. Click “Close” when setup is completed.



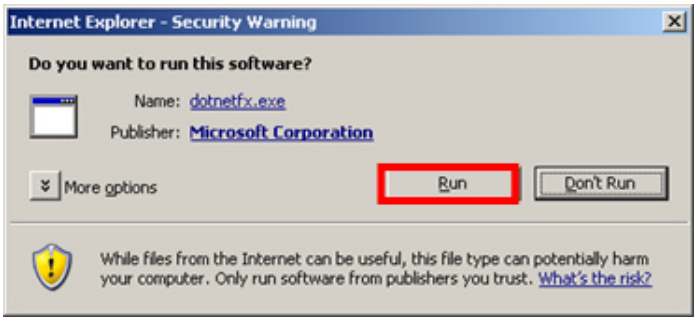
2.9. Click “2.Microsoft .NET Framework”.



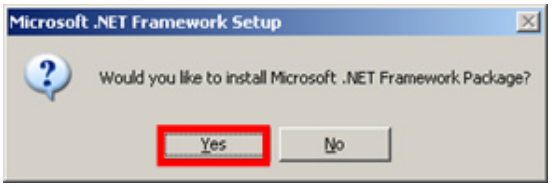
2.10. Click “Run”.



2.11. Click “Run”.

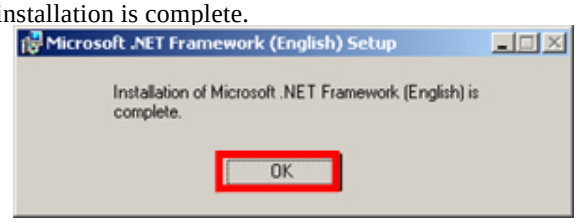


2.12. Click “Yes”.

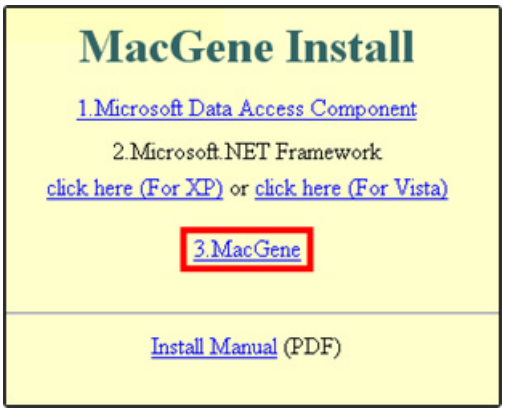


2.13. Click “Next”.

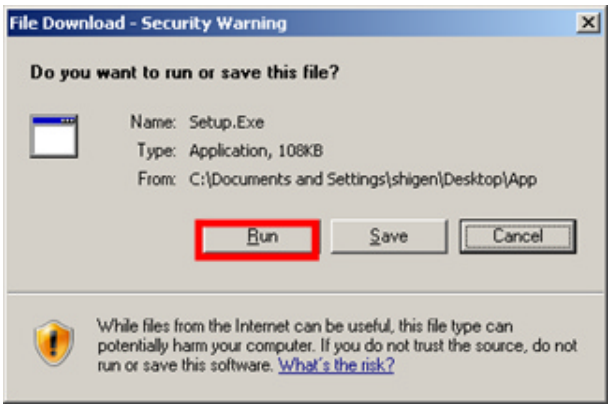
2.14. Click “OK” when installation is complete.



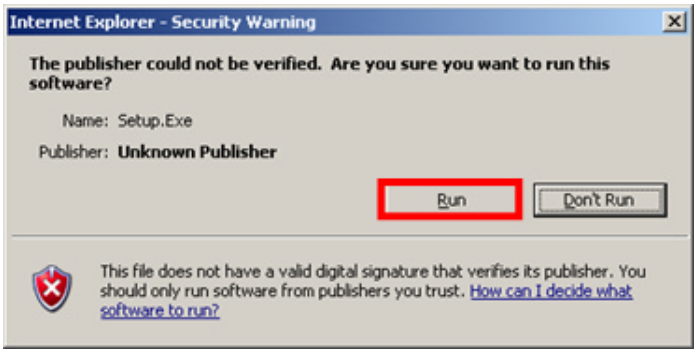
2.15. Click “3.MacGene”.



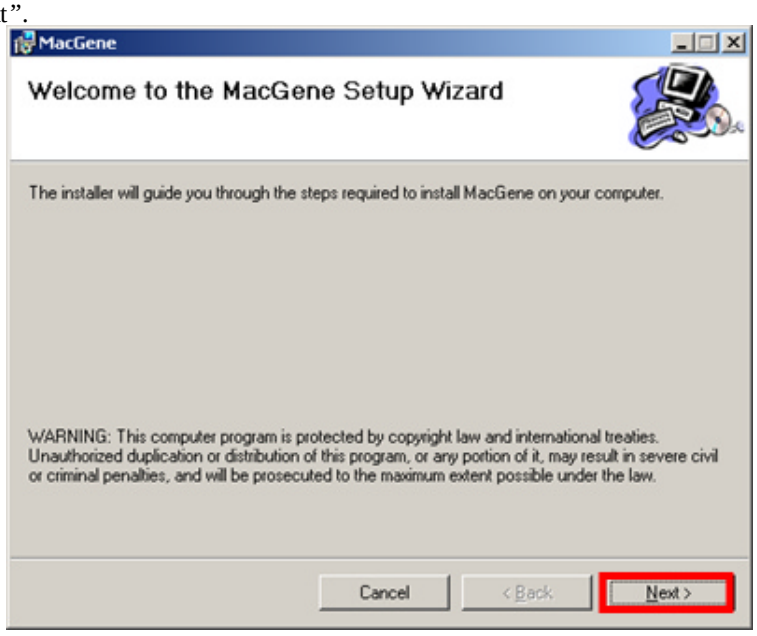
2.16. Click “Run”.



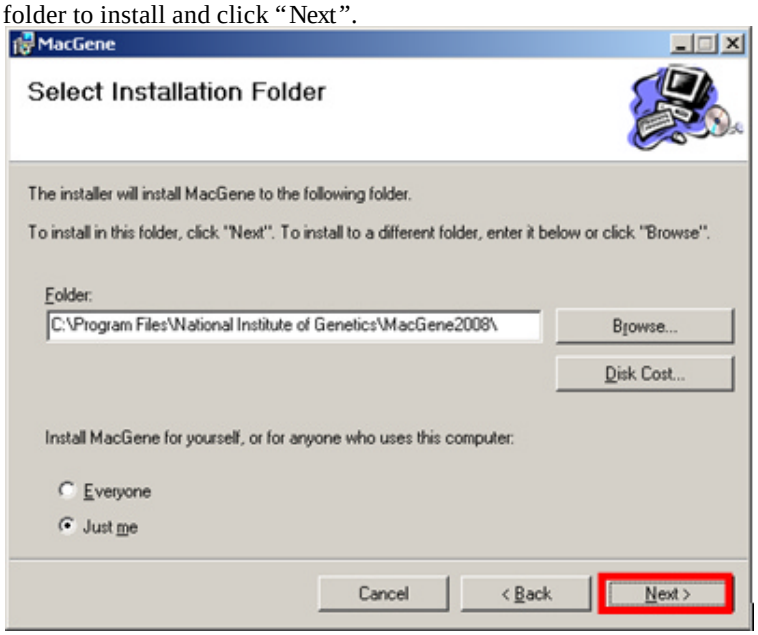
2.17. Click “Run”.



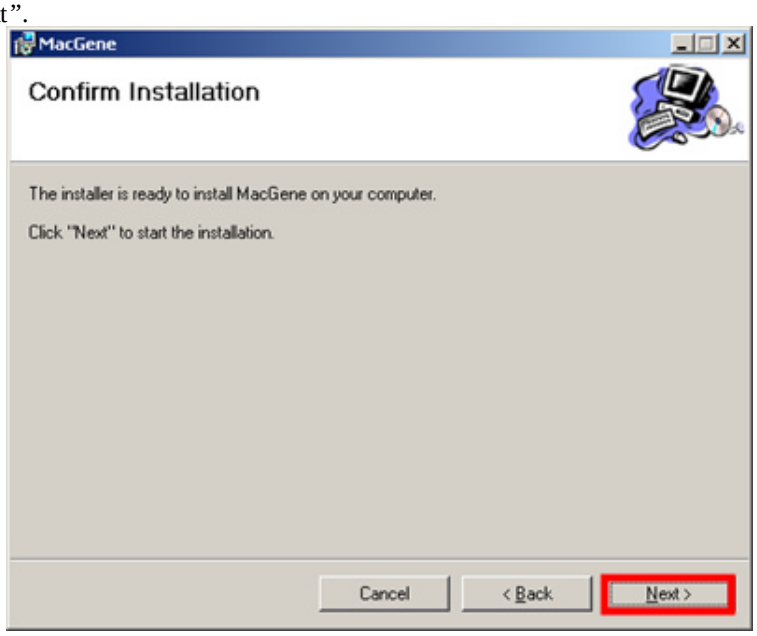
2.18. Click “Next”.



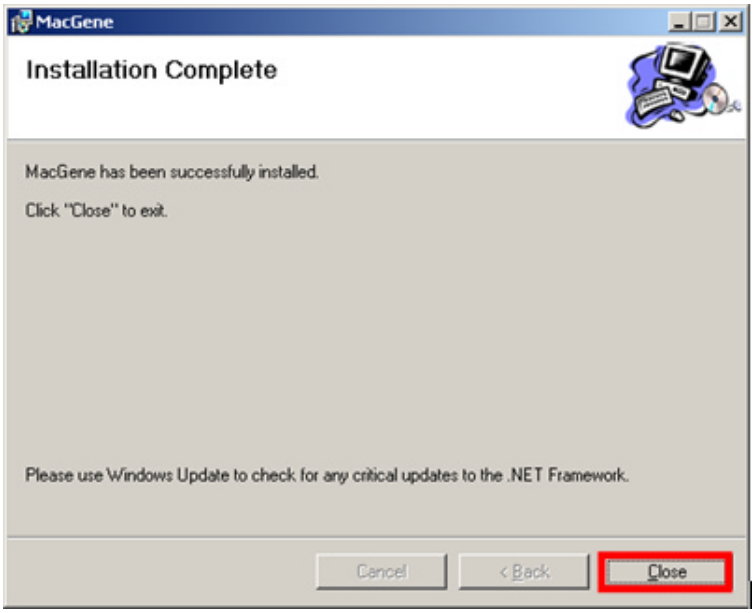
2.19. Define the folder to install and click “Next”.



2.20. Click “Next”.



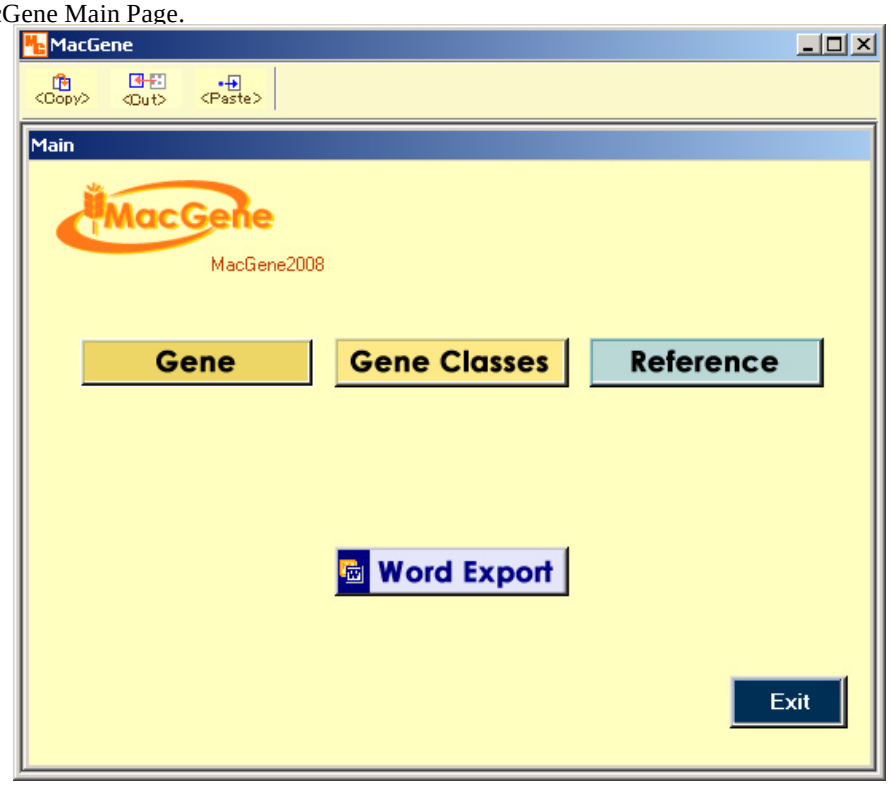
2.21. Click “Close”.



3. How to use “MacGene”

3.1. Click “MacGene” icon  on your desktop.

3.2. MacGene Main Page.

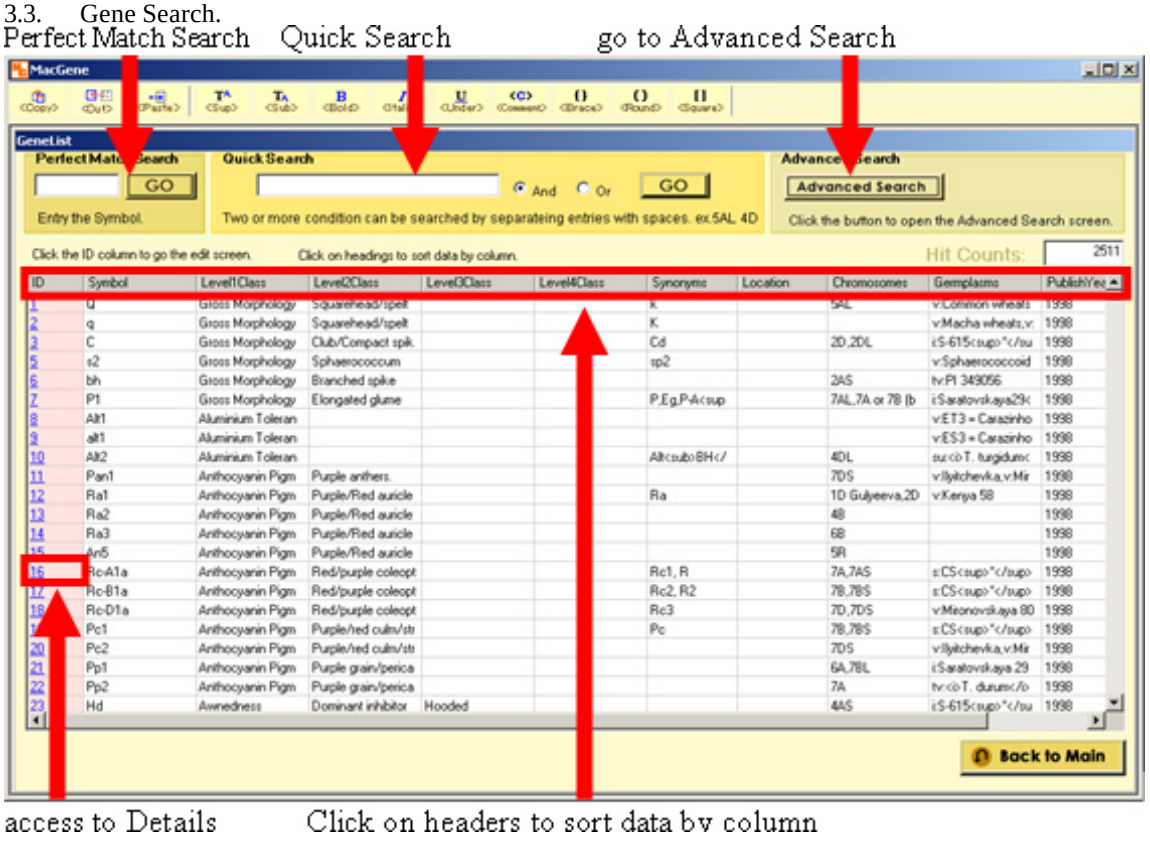


There are two basic functions, (I) SEARCH (Gene/Reference) and (II) RETRIEVE (Word Export) on the page.

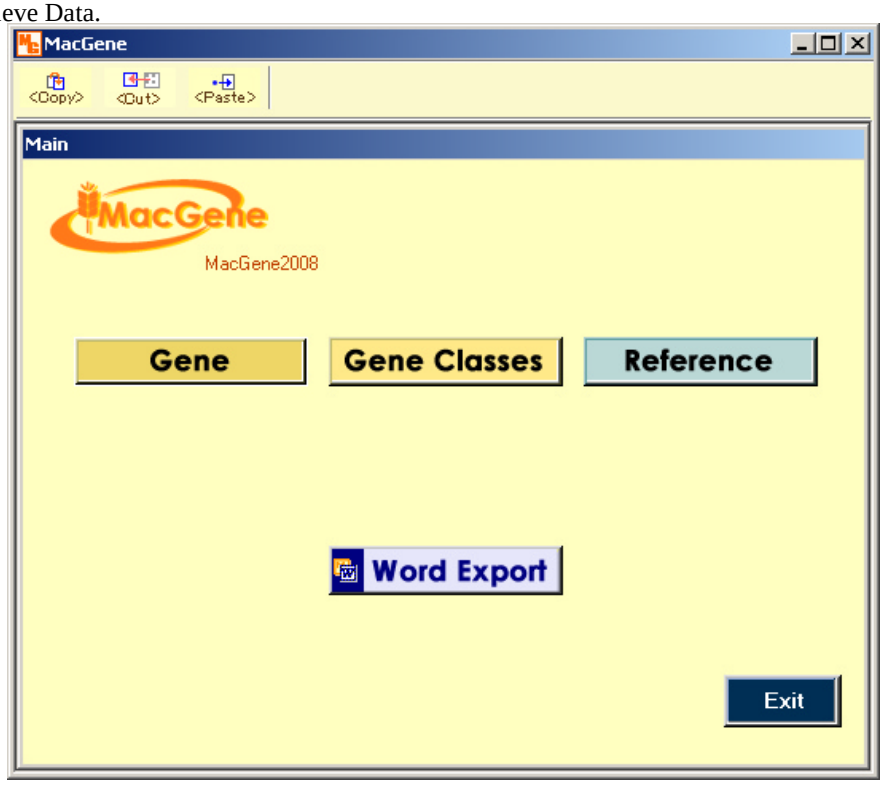
You can follow the same procedure for the two searches.

Click "Gene" for example.

3.3. Gene Search.

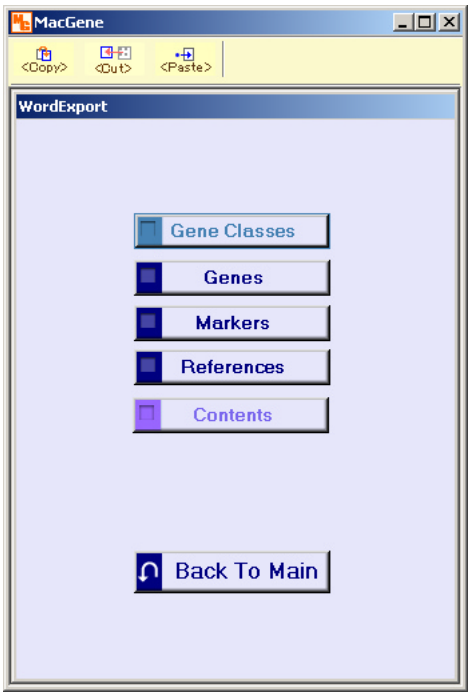


3.4. Retrieve Data.



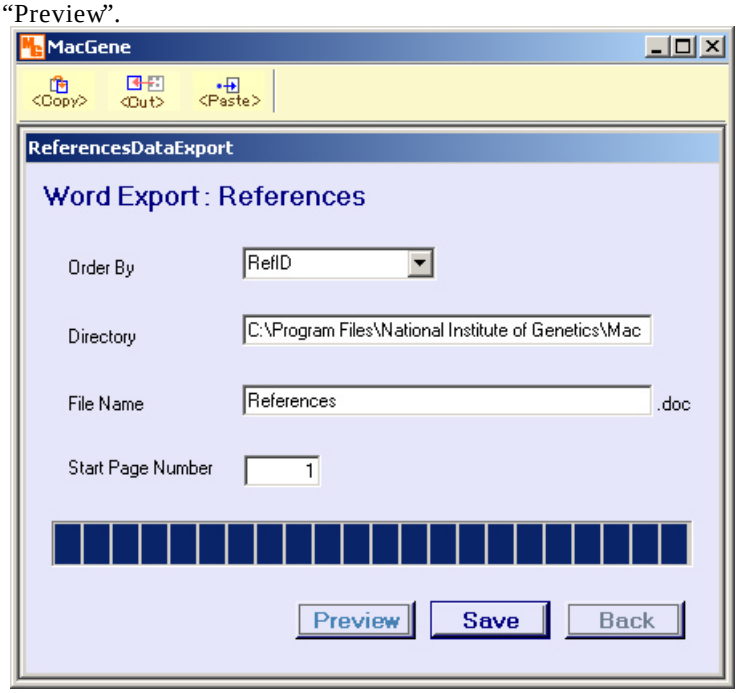
Click "Word Export" on the main page.

3.5. Word Export Options.



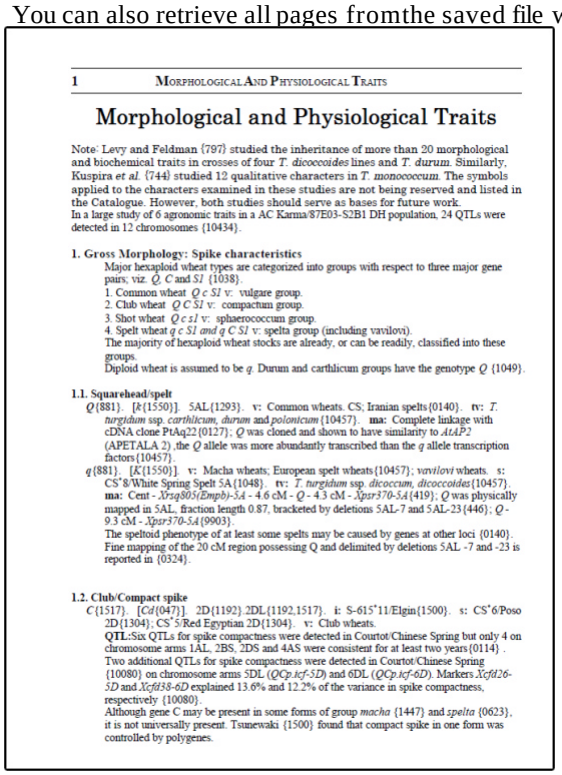
You can choose the relevant option.

3.6. After you click "Save", "Preview" appears on the next screen. 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

Morphological and Physiological Traits

Note: Levy and Feldman {797} studied the inheritance of more than 20 morphological and biochemical traits in crosses of four *T. dicoccoides* lines and *T. durum*. Similarly, Kuspira *et al.* {744} studied 12 qualitative characters in *T. monococcum*. 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/87E03-S2B1 DH population, 24 QTLs were detected in 12 chromosomes {10434}.

1. Gross Morphology: Spike characteristics

Major hexaploid wheat types are categorized into groups with respect to three major gene pairs; viz. *Q*, *C* and *S1* {1038}.
1. Common wheat *Q c S1* v: vulgare group.
2. Club wheat *Q C S1* v: compactum group.
3. Shot wheat *Q c s1* v: sphaerococcum group.
4. Spelt wheat *q c S1 and q C S1* v: spelta group (including vavilovi).
The majority of hexaploid wheat stocks are already, or can be readily, classified into these groups.
Diploid wheat is assumed to be *q*. Durum and carthlicum groups have the genotype *Q* {1049}.

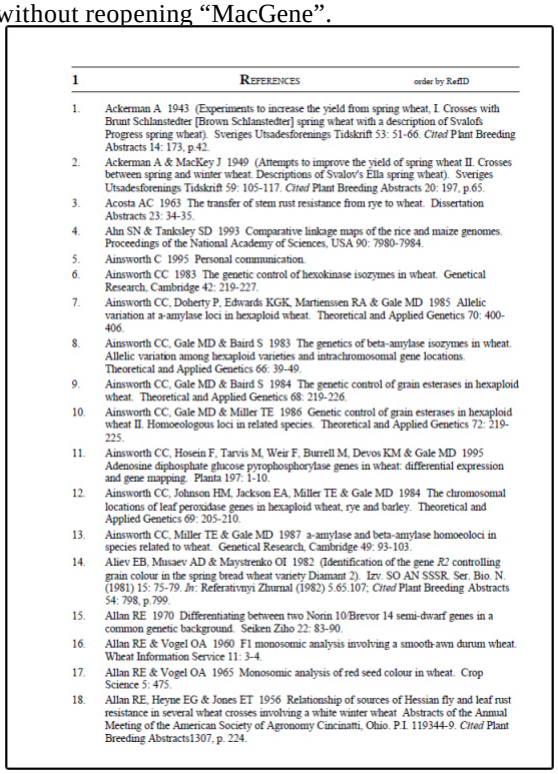
1.1. Squarehead/spelt

Q {881}. [*k*{1550}]. 5AL{1293}. **v:** Common wheats. CS; Iranian spelts{0140}. **tv:** *T. turgidum* ssp. *carthlicum, durum* and *polonicum* {10457}. **ma:** Complete linkage with cDNA clone PtAq22{0127}; *Q* was cloned and shown to have similarity to *AtAP2* (APETALA 2) ,the *Q* allele was more abundantly transcribed than the *q* allele transcription factors{10457}.
q {881}. [*K*{1550}]. **v:** Macha wheats; European spelt wheats{10457}; *vavilovi* wheats. **s:** CS*8/White Spring Spelt 5A{1048}. **tv:** *T. turgidum* ssp. *dicoccum, dicoccoides*{10457}. **ma:** Cent - *Xrsq805(Empb)-5A* - 4.6 cM - *Q* - 4.3 cM - *Xpsr370-5A*{419}; *Q* was physically mapped in 5AL, fraction length 0.87, bracketed by deletions 5AL-7 and 5AL-23{446}; *Q* - 9.3 cM - *Xpsr370-5A*{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 Q and delimited by deletions 5AL -7 and -23 is reported in {0324}.

1.2. Club/Compact spike

C{1517}. [*Cd*{047}]. 2D{1192}.2DL{1192,1517}. **i:** S-615*11/Elgin{1500}. **s:** CS*6/Poso 2D{1304}; CS*5/Red Egyptian 2D{1304}. **v:** Club wheats.
QTL: Six 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 (*QCp.icf-5D*) and 6DL (*QCp.icf-6D*). Markers *Xcfd26-5D* and *Xcfd38-6D* explained 13.6% and 12.2% of the variance in spike compactness, respectively {10080}.
Although gene C may be present in some forms of group *macha* {1447} and *spelta* {0623}, it is not universally present. Tsunewaki {1500} found that compact spike in one form was controlled by polygenes.

Genes



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Reference