Soybean Genetics Committee Report

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IV. SOYBEAN GENETICS COMMITTEE REPORT

Minutes of the Meeting

The Soybean Genetics Committee met Monday, Feb. 23, 1987, at the Ramada Inn, Memphis, TN. This meeting was held in conjunction with the annual Soybean Breeders Workshop.

Committee members in attendance were R. L. Bernard, W. D. Beversdorf, Y. T. Kiang, J. H. Orf and J. R. Wilcox. Also present were B. A. McBlain, J. Specht and B. D. Rennie. G. R. Bowers and B. A. McBlain have been elected to three-year terms on the Committee, replacing W. D. Beversdorf and J. R. Wilcox. Current Committee members and the expiration date of their terms are as follows:

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Dr. R. I. Buzzell was elected chairman of the Committee for 1987. Manuscripts concerning qualitative genetics interpretation and gene symbols should be sent to him for review.

In order to reduce the time required to review and return manuscripts, the following changes will be made in the procedures used by the Committee:

1. Reviewers of manuscripts will be given a deadline of two weeks to return the reviewed manuscript to the Chairman (who will then get it to the author as soon as possible). If the reviewer has not returned the manuscript by this time (or phoned in their comments), a phone call will be made to remedy the situation.
2. The review will only be for "validity of the genetic interpretation" and "appropriateness of gene symbol." The manuscript will not be reviewed for style except as it influences the clarity of interpretation. Authors may submit unpublished (but comprehensible) manuscripts for review. This should reduce some of the delay that accompanies production of an article.

3. Gene symbols will only be approved in cases where the relevant material is made available to the soybean germplasm collection. The Committee encourages authors not to assign any symbol when they are doing genetic work on material that will not be made available. (Publication of genetic interpretations does not depend on symbols, in most cases). The purpose of assigning a symbol is to ensure constancy when others use the material for subsequent studies. If the material is not made available, a symbol is unnecessary.

Minutes

In discussion, it was agreed that the Committee had been inefficient in dealing with manuscripts in the past. It was moved (Orf/Bernard), and passed, that deadlines should be set to speed up reviews (see above). In addition, a form will be drafted for assisting the reviewers in assessing the manuscripts.

It was agreed (Wilcox/Orf) that no symbols will be assigned if material has not been submitted to, or is not currently available in, the soybean germplasm collection. In the case of materials identified as possessing two or more "new" loci or alleles, lines isolating single loci are preferred.

The committee appointed to review the assigning of symbols for transformed material reported several proposals for symbols. However, the Committee felt that since these sorts of material will not be available in the immediate future, no decision was necessary at this time. The Committee will be monitoring the progress made in tomatoes and other crops that are being transformed to assist it in making a decision.

It was agreed (Orf/Kiang) that the Committee should publish a complete list of approved soybean gene symbols in the Soybean Genetics Newsletter in 1987 and every 5 years thereafter. A cumulative update of new symbols would be published between the full updates.

A discussion occurred on the potential to involve more researchers from other countries in the use of a single set of gene symbols. Submission of manuscripts from distant lands would not be practical, but an attempt will be made to contact a few researchers from each geographic region in order to foster cooperation in this field.

The Committee reaffirmed its stand to retain the original symbol approved for a gene and its alleles. Discussion of dominance and codominance was ruled less important than reducing confusion. It was suggested that authors only use those symbols appearing in the official list. However, if other symbols have appeared in the literature, these could be referred to for clarity.
Guidelines on the Evidence Necessary for the Assignment of Gene Symbols

Researchers are strongly encouraged to send all gene symbols and genetic interpretations to the Soybean Genetics Committee for review prior to publication to avoid duplication and/or confusion.

The following is a set of guidelines prepared by the Soybean Genetics Committee and intended to help researchers undertaking genetic analysis of soybean traits. Of necessity, these procedures will often need to be modified by the researcher to fit the specific situation, but an application of these guidelines should aid in making the correct genetic interpretation.

1. A genetic hypothesis is made on the basis of classification of segregating progeny, usually the F2 generation and here called the hypothesis generation.

2. A second generation is classified to confirm the proposed genetic hypothesis. This second generation may be progeny of the hypothesis generation (usually F3) or progeny of a testcross (F1 x recessive homozygote).

3. Traits that are strongly influenced by nongenetic factors require verification of the classification scheme by evaluation of the progeny from homozygous plants of the hypothesis generation. Testcross data are not suitable for this purpose.

4. For genes controlling a phenotypic expression similar to that of previously published genes, data must be obtained to test for uniqueness and allelism. This will usually require crossing a homozygous line carrying the newly identified gene with the original sources of the previously published genes.

5. Follow the guidelines (Rules for Genetic Symbols) published in the Soybean Genetics Newsletter to assign the symbol.

6. Submit the manuscript to the chair, Soybean Genetics Committee, for review of the genetic interpretation and approval of the gene symbol (see Soybean Genetics Newsletter for name and address).

7. If the line in which the new gene occurs is not already in the USDA Germplasm Collection, send a seed sample of the line to the curator of the Genetic Type Collection for assignment of a T-number and maintenance of the seed (see current Soybean Genetics Newsletter for name and address).

References


Rules for Genetic Symbols

1) Gene Symbols

a) Gene symbols should not be assigned to traits for which no inheritance data are presented.

b) A gene symbol shall consist of a base of one to three letters, to which may be appended subscripts and/or superscripts as described below. Gene symbols may, however, be written on one line.

c) Genes that are allelic shall be symbolized with the same base letter(s) so that each gene locus will be designated by a characteristic symbol base.

d) Gene pairs with the same or similar effects (including duplicate, complementary or polymeric genes) should be designated with the same letter base differentiated by numerical subscripts, assigning 1, 2, 3, 4, etc., consecutively in the order of publication. (Example: Y₁, Y₂, etc.) The numerals may be written on the same line as the base. (Example: Y₁, Y₂, etc.) This shall be the only use of numerals. Letter designations should not be used. The numeral 1 is automatically a part of the first reported gene symbol for each base but may be omitted only until the second symbol is assigned.

e) The first pair of alleles reported for a gene locus shall be differentiated by capitalizing the first letter of the symbol for the dominant or partially dominant allele. (Example: Ab, ab. Ab is allelic and dominant to ab.)

f) If two alleles are equivalent, codominant, or if dominance is not consistent, the capitalized symbol may be assigned at the author's discretion and the alleles may be differentiated by adding one or two uncapitalized letters as superscripts to the base. When more than two alleles exist for a locus, the additional alleles or those symbolized subsequently to the pair first published shall be differentiated by adding one or two uncapitalized letters as a superscript to the base. (Example: R, r, r.) This shall be the only use of superscripts. The letters may be written on the same line as the base if preceded by a hyphen. (For example, Rps₁-b, Rps₁-k, and Ap-a, Ap-b, Ap-c.) The base for the additional alleles is capitalized only when the gene is dominant or equivalent to the allele originally designated with a capitalized symbol. The letters may be an abbreviation of a descriptive term.

If independent mutations with the same or similar phenotype are identified at the same locus, until it is possible genetically to ascertain if they represent identical or separate alleles, the gene symbol should be followed by an identifying designation in parentheses. The identifying designation, which should NOT be in italics or underlined, can be the place where the mutation was found, the cultivar in which it was found, or any other relevant characteristic of the mutation. (Example: msl (Tonica), or msl (Ames 2).) This will ensure that possible subtle differences between the mutations, such as differences in DNA sequence, or unique pleiotropic side effects, are not overlooked by workers using those genes.
g) Base letters may be chosen so as to indicate apparent relationships among traits by using common initial letters for all loci in a related group of traits. Examples are P for pubescence type, R for disease reaction (plus two initials of the pathogen to complete the base), and L for leaf shape.

h) The distinction between traits that are to be symbolized with identical, similar, or with unrelated base letters is necessarily not clear-cut. The decision for intermediate cases is at the discretion of the author, but should be in accordance with previous practices for the particular type of trait.

The following sections concern supplementary symbols that may be used whenever desired as aids to presentation of genetic formulas.

i) An underscore may be used in place of a gene symbol to represent any allele at the indicated locus. The locus represented should be apparent from its position in the formula. (Example: A_ represents both AA and Aa.)

j) A question mark may be used in place of a symbol when the locus or allele is unknown or doubtful. The name of the line in which the gene was identified should be included in the symbol, in parentheses. A hyphen preceding the question mark indicates an unknown allele at a known locus, the absence of a hyphen indicates an unknown locus. (Example: Rps? (Harosoy) an allele in Harosoy at an unknown locus or Ap-? (T160) an unknown allele in T160 at the Ap locus.)

k) Plus symbols may be used in place of the assigned gene symbols of a designated standard homozygous strain when this will facilitate presenting genetic formulas. The standard strain may be any strain selected by the worker, as long as the strain being used and its genetic formula are made explicit.

II) Isoenzyme Symbols and Protein Gene Symbols

The following set of guidelines is to be used when assigning gene symbols to isoenzyme variants. As far as possible, these recommendations are consistent with the existing guidelines for assigning gene symbols in soybeans.

a) A gene symbol (generally three letters) that indicates, as clearly as possible, the name of the enzyme should be used. The example, Adh (alcohol dehydrogenase); Idh (isocitrate dehydrogenase). The appropriate Enzyme Commission name and number should be used in the original article, when appropriate, to designate the specific enzyme activity being investigated.

b) The electrophoretic conditions used to characterize a locus or allele should be specified clearly and in sufficient detail to be repeated by others interested in using the locus in genetic studies. The electrophoretic mobility, or other properties of an allele, should be clearly described by the authors.

c) Publications should include a photograph and/or an interpretive zymogram that allows readers to visualize the variability described by the authors, as well as to ensure that subsequent work corresponds to the original study.
III) Linkage and Chromosome Symbols

a) Linkage groups and the corresponding chromosomes shall be designated with arabic numerals. Linkage shall be indicated in a genetic formula by preceding the linked genes with the linkage group number and listing the gene symbols in the order that they occur on the chromosome.

b) Permanent symbols for chromosomal aberrations shall include a symbol denoting the type of aberration plus the chromosome number(s) involved. Specific aberrations involving the same chromosome(s) shall be differentiated by a letter as follows: The symbol Tran shall denote translocations. Tran 1-2a would represent the first case of reciprocal translocations between chromosomes 1 and 2, Tran 1-2b the second, etc. The symbol Def shall denote deficiencies, Inv inversions, and Tri primary trisomics. The first published deficiency in chromosome 1 shall be symbolized as Def 1a, the second as Def 1b, etc. The first published inversion in chromosome 1 shall be designated with the arabic numeral that corresponds to its respective linkage group number.

c) Temporary symbols for chromosomal aberrations are necessary, as it may be many years before they are located on their respective chromosomes. Tran 1 would represent the first case of a published reciprocal translocation; Tran 2, the second case, etc. The first published deficiency shall be symbolized as Def A, the second as Def B, etc. The first published inversion shall be symbolized as Inv A, and the second as Inv B, etc. The first published trisomic shall be designated as Tri A, the second as Tri B, etc. When appropriate genetic and/or cytological evidence is available, the temporary symbols should be replaced with permanent symbols, with the approval of the Soybean Genetics Committee.

IV) Cytoplasmic Factor Symbols

a) Cytoplasmic factors shall be designated with one or more letters prefixed by cyt-. (Example: cyt-G indicates the cytoplasmic factor for maternal green cotyledons, cyt-Y indicates that for maternal yellow cotyledons.)

V) Priority and Validity of Symbols

a) A symbol shall be considered valid only when published in a recognized scientific journal, or when reported in the Soybean Genetics Newsletter, with conclusions adequately supported by data which establish the existence of the entity being symbolized. Publication should include an adequate description of the phenotype in biological terminology, including quantitative measurements wherever pertinent.

b) In cases where different symbols have been assigned to the same factor, the symbol first published should be the accepted symbol, unless the original interpretation is shown to be incorrect, the symbol is not in accordance with these rules, or additional evidence shows that a change is necessary.

VI) Rule Changes

a) These rules may be revised or amended by a majority vote of the Soybean Genetics Committee.