III. SOYBEAN GENETICS COMMITTEE REPORT

Minutes of the Meeting

The Soybean Genetics Committee met Feb. 25, 1985, at the Ramada Inn - Executive Plaza, Memphis, TN. This meeting was held in conjunction with the Annual Soybean Breeders Workshop.

Committee members in attendance were W. D. Beversdorf, R. L. Bernard, H. R. Boerma, X. Delannay, T. C. Kilen, J. H. Orf, R. G. Palmer, and J. R. Wilcox. Also present were J. Griffin, B. Hedges, T. Hymowitz and Y. T. Kiang. R. I. Buzzell and X. Delannay have been elected to new three-year terms on the committee replacing Kilen and Orf, whose terms expired at the close of the meeting. Present committee members and the expiration of their terms are as follows:

R. L. Bernard, Ex officio
(Curator of soybean genetics collection)
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W. D. Beversdorf, Chairman (1987)
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H. R. Boerma (1986)
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R. I. Buzzell (1988)
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T. E. Devine (1986)
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R. G. Palmer, Ex officio
(Editor of Soybean Genetics Newsletter)
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J. R. Wilcox (1987)
Department of Agronomy
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West Lafayette, IN 47907

X. Delannay (1988)
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W. D. Beversdorf was elected chairman of the committee for 1985, so manuscripts concerning qualitative genetic interpretation and gene symbols should be sent to him for review.

The number of manuscripts received for review by the committee increased from 18 to 20. Persons who are not members of the committee may be asked to review manuscripts when their area of expertise is needed and/or to spread the workload.

A number of changes in the rules for genetic symbols were approved by the Committee. The major changes were revisions to accommodate the optional use of gene symbols on one line (the use of subscripts and superscripts is still permitted) and amendments dealing with isoenzyme and protein gene symbols. These amendments were made since several recent articles, both in the Soybean Genetics Newsletter and elsewhere, have reported on the inheritance of isoenzyme variants in soybeans. Some of these publications have assigned gene symbols to the loci responsible for these variants. There is a lack of consistency in the nomenclature used by the various research groups responsible for this work. In order to avoid confusion in the future, the committee decided it was necessary to agree on a common system of gene symbol nomenclature.

The changes in the gene symbol rules approved by the committee are underlined in the rules published this year.

The committee discussed the type and amount of data needed for the assignment of gene symbols. The requirements will be published in the Soybean Genetics Newsletter so that those researchers submitting articles with the assignment of new gene symbols will know what data are expected before the committee will consider assigning a gene symbol.

A committee consisting of W. Beversdorf, X. Delannay, Y. T. Kiang and T. Hymowitz was appointed to consider rules for gene symbols introduced into soybeans from other organisms via such methods as gene transfer, transformation, and other genetic engineering techniques and also to consider rules for assigning gene symbols to genes in the perennial species of the subgenus *Glycine*. A report and/or proposal will be made at the 1986 committee meeting.

The committee also discussed the use of provisional gene symbols and the reassignment of gene symbols. After some discussion, it was agreed that T-numbers instead of provisional symbols would be appropriate until the genetics of a new genotype were completed. The committee also agreed not to change the $\underline{Sp_1}$ gene symbol (the symbol for beta-amylase).

The committee urges researchers who report lines carrying new genes to submit a seed sample to R. L. Bernard so a genetic type collection designation (T-number) can be assigned. Dr. Bernard will maintain the seed and have it available on request.

Rules for Genetic Symbols

I) 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: Y_1, Y_2, 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.

3) 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^m, 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.

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) A dash 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 gene is unknown or doubtful, or it may be used as a superscript or on the base line if preceded by a hyphen. (Example: $a^{?}$ or a-? indicates that the latter is an unknown allele at the A 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. For 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 confirm 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 denoted as Inv 1a, etc. The first published primary trisomic 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 second as Inv B. 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.

It is recommended that all gene symbols and genetic interpretation be reviewed by the Soybean Genetics Committee prior to publication to avoid duplication and/or confusion.