A SUGGESTION FOR THE NOMENCLATURE OF ISOZYME LOCI

Weeden, N. F'. NYS Agricultural Experiment Station
Geneva, NY 14456 USA

Genes coding enzymatically active proteins have become important genetic markers because of their relative abundance, codominant expression, and freedom from epistatic interactions. Many laboratories are now studying isozymes by means of electrophoretic techniques; yet isozyme terminology often differs markedly among these laboratories. A standardized system of nomenclature for isozymes would facilitate the communication of results and avoid considerable confusion concerning the biochemical reaction being assayed.

Although there is *no* a_ priori reason for the selection of one laboratory's terminology over that used in another, there is a obvious reason for disregarding the system used by most of tiiese laboratories. The correct identification of enzymes is of greatest concern to protein biochemists, not geneticists, breeders, or population biologists. We should therefore refer to the biochemical literature for appropriate terminology. Indeed, a standard nomenclature for enzymes has been published by the International Union of Biochemists (2). I propose that the acronyms used for gene symbols of pea isozyme loci be based on the recommended name given in the current Enzyme Nomenclature (2).

When more than one activity band is observed after electrophoresis, the different forms may be isozymes (coded by different loci), allozymes (coded by different alleles of a single locus), or products of the same allele which have undergone different post-trans1ationa1 modifications. Different isozymes are generally distinguished by a numerical suffix to the acronym identifying the enzyme system (e.g. ADH-1, ADH-2). Isozymes are numbered sequentially based on their -nobility relative to the anode, with the most anodal being number 1. The isozyme acronym is all in capital letters in order to distinguish it from the locus designation which is underlined and has only the first letter capitalized (e.g. Adh-1).

In certain enzyme systems, such as leucine aminopeptidase, esterase, acid phosphatase, peroxidase, and diaphorase, the generally accepted terminology is based on the assay used to visualize the isozymes rather than on the actual in vivo reaction catalyzed by the enzyme. For reasons of practicality and uniformity, I recommend that in most of these cases the isozymes and loci be named according to the generalized assay rather than attempt to determine the physiological substrate and name each isozyme on that basis.

For several enzyme systems, particularly aspartate aminotransferase, glucosephosphate isomerase, phosphoglucorautase, 6-phosphogluconate dehydrogenase, and triosephosphate isomerase, the number of isozymes and their subcellular distribution are highly conserved among plant taxa, whereas their respective mobilities are not. In order to facilitate the recognition of homologous loci in different species, as well as increase the information value of the locus designation, it has been suggested (3) that a letter suffix, reflecting the subcellular compartmentation of the isozyme, be used in the locus designation instead of a number. Thus, the cytosolic isozyme of phosphoglucorautase (PGM-1) is coded by the locus Pgm-c. Similarly,

the cytosolic, plastid, mitochondrial, and microbody isozymes of aspartate aminotransferase are coded by the loci Aat-c, Aat-p, Aat-m, and Aat-mb, respectively (3). In all cases examined to date, organelle specific isozymes are specified by genes located on nuclear DNA.

Two additional provisions are required for naming isozyme loci. First, a suffix is not required on the locus designation when only one gene product is observed after electrophoresis. Second, if there are two isozymes in the same compartment for an enzyme system with isozymes in several compartments, the respective loci for the former two isozymes are distinguished by a number immediately following the letter designating the localization (e.g. Pgm-c1, Pgm-c2). Cases in which this latter provision would apply are rare and usually indicate a gene duplication event (1). It has not been necessary to use the additional numerical suffix in any enzyme system so far examined in Pisum.

The naming of allelic variants at isozyme loci is relatively simple. The allozymes are identified by a lower case letter designation after the acronym or acronym-number combination (e.g. ADH-la). The letters are assigned in alphabetical order, starting with the most anodal allozyme and continuing in sequence cathodally. If an additional allozyme is discovered later, it receives the letter next in sequence regardless of the mobility of the allozyme. In many cases only two allozymic forms have been identified, and these have been designated "fast" and "slow" or "F" and "S". It is recommended that this terminology be dropped, for it will ultimately lead to confusion when new variants are resolved. Similarly, the practice of designation allozymes by their mobility, either relative to the front or to another internal marker, (e.g. ADH-.51) is discouraged because it is usually difficult to reproduce the exact mobility in another laboratory despite the use of identical conditions or the same internal standard. The alleles at a locus can be best designated by a superscript corresponding to the letter identifying the allozyme. For instance, in pea the allele coding the fastest variant of the plastid specific aspartate aminotransferase, AAT-2a, would be designated Aat-p . Null alleles could be identified by an "n" or "null" term.

The approach to naming loci outlined here is what the author considers the most reasonable compromise between the various systems currently being used. It can be extended to proteins in general by identifying the source (e.g. seed protein=SP) or the type (e.g. legumin=LG) and the relative position on the gel (e.g. SP-1, SP-2, etc.). For proteins the locus designation should be as specific as possible (i.e. Lg-1 would be preferable to Sp-2) because of the very large number of gene products that can be identified).

1. Gottlieb, L. D. 1982. Science 216:373-380.
2. International Union of Biochemistry Nomenclature Committee. 1984. Enzyme Nomenclature. Academic Press, New York.
3. Weeden, N.F. and G. A. Marx. 1984. J. Hered. 75:365-370.

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