Genetic Nomenclature and Practice for Plant Pathogenic Fungi

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A system for genetic nomenclature that is uniform and descriptive, yet simple and clear, can greatly facilitate any area of genetic research. Sound practices in naming strains, genes, and mutations enhance communication between laboratories and, more importantly, foster clear thinking and good design of genetic experiments. Thus, the objective of this proposal is to recommend a collection of well-established practices to those who are studying the genetics of plant pathogenic fungi. The need for a uniform system of genetic nomenclature in fungal plant pathology is especially acute because of the diversity of systems under study in the field. Moreover, as the methods of molecular genetics are brought to bear on the problems of plant pathology, standard nomenclature will encourage the essential flow of ideas and information between those who are investigating the basic genetics of yeasts and saprophytic filamentous fungi and those who are investigating fungi that cause diseases of plants.

The Genetics Committee of the American Phytopathological Society has recognized the need for standardizing the genetic terminology and nomenclature in use among geneticists studying plant pathogenic fungi, and it has commissioned the authors to prepare this proposal. Each member of the Committee has reviewed the proposal, as have selected fungal geneticists who have dealt with the problems of genetic nomenclature.

While none of the recommendations that follow can be binding on individual workers, we hope that our discussion, at the least, will stimulate those studying plant pathogenic fungi to establish and adopt a standardized code. In considering genetic nomenclature, we encourage fungal pathologists to review the rules that have been accepted by geneticists who work with well developed models such as *Escherichia coli* (7), *Saccharomyces cerevisiae* (14), *Neurospora crassa* (1,13), *Aspergillus nidulans* (4), and *Zea mays* (5). A summary of gene symbols used for various fungi has been prepared (2). We have adopted elements from several of these systems, but our proposal is derived primarily from the conventions accepted for yeast (14) because yeast has emerged as the predominant model for eukaryotic genetics and molecular biology and because yeast nomenclature is simple, internally consistent, and relatively informative.

We wish to emphasize that no set of rules can anticipate all possible situations. Therefore, our proposal can be regarded as a guideline to be used as the basis for a system of standard genetic nomenclature and practice. Where there are gaps or inadequacies with respect to certain fungi, we encourage the use of common sense.

In the next section, standard definitions are suggested for genetic terms commonly used for fungal pathogens. Then a series of recommendations follows concerning standard practices for naming strains and maintaining stock collections, naming loci and alleles, representing dominance relationships, distinguishing genotype from phenotype, and designating linkage groups. Special considerations concerning the preservation of germplasm and the use of Latin binomials are also discussed.

Definitions. Plant pathogenic fungi can be wild-type or mutant cultures either taken directly from the field or generated by laboratory manipulations. They may be referred to as strains or races. To distinguish clearly among these designations, the following definitions are suggested:

Strain: A term generally used to distinguish a group of clonally related individuals or cells from other similar, but not identical, groups. Since plant pathologists often deal with fungi that have had little or no genetic characterization, we suggest that all cultures be regarded as different strains unless they are known to be identical.

Race: A more comprehensive term than strain, which could include pathotypes (defined by host specificity), ecological biotypes, etc., of the same species.

Field isolate: Any strain collected directly from nature and genetically unaltered by laboratory manipulation.

Laboratory strain: A strain derived from one or more field isolates by mutation or as the progeny of a cross.

Wild type: An arbitrary designation for one or more strains chosen deliberately as genetic standards. Plant pathogenic fungi often exist in nature as populations of mixed genotypes, any of which may be considered a wild type. However, "wild type" is not synonymous with "a strain from the wild" and frequently wild-type standards are chosen from among laboratory strains, which can be expected to differ from field isolates.

Mutant: A strain that differs from a wild type by an induced mutation of at least one genetic locus. The terms wild type and mutant can be used not only to designate strains, but alleles and chromosomes as well. Naturally occurring differences found among strains in nature or under propagation should not be called mutants; a different term, perhaps "variant," should be used.

Strain designation, description, and storage. Each strain acquired and put in stock should be given a unique stock number or accession number that is simple and short. A convenient way to do this is to assign a serial number, starting the series with 1, prefixed by two letters to indicate the laboratory of origin; the letters could be the initials of the laboratory director. Use of superscripts, subscripts, Greek letters, and dashes should be minimized for simplicity. Indications of genotype or phenotype should not be included as part of a strain's designation. When a strain is received from another laboratory, its original name may or may not be retained. However, every publication should include the original designation, genotype, phenotype, and source of each strain that enters into the investigation.

Each laboratory should maintain a permanent strain collection, giving special attention to the preservation of strains that have been described in publications. The records maintained for this collection should always include a full description of each strain's genotype and phenotype, the genetic operations by which it was

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produced, and the parental strain or strains from which it was derived. It is especially important to record the allele numbers (see below) assigned to all mutations carried by a strain, as different alleles of the same locus can have quite different genetic properties. Any isolate that has undergone, or is suspected of having undergone, any alteration of genotype should receive a new designation.

The importance of maintaining a permanent collection of all wild-type and mutant strains cannot be overemphasized. The storage method of choice for many fungi is maintenance in 15–50% glycerol solution at −80 C; if available, −135 C is even better. This method was developed for the storage of bacteria, but the published procedures of Davis et al (6) and Maniatis et al (11) are known to work well with yeasts and have been adapted for use with filamentous fungi. The advantages of the glycerol method include both easy preparation of stocks and easy recovery of stored material. Furthermore, the storage medium is aqueous, which is gentle on the fungus and obviates the need to maintain dry storage compartments. Thus, there is no loss of stored strains due to the accidental accumulation of moisture. For fungi that don't tolerate freezing in glycerol, there is the silica gel method of Perkins (12), which is known to preserve stocks of *Neurospora* for at least 15 yr (3), and other more specialized methods such as storage on dried filter papers or in dried plant materials. Stocks should not be maintained by continual subculturing or stored in any state where metabolism can occur, such as in an aqueous medium in a refrigerator.

Progeny of sexual crosses may be maintained temporarily in a separate collection because it is unlikely that all of them will become part of the permanent stocks. Some laboratories find it convenient in the short term to assign each spore a unique number indicating the cross in question and the particular spore at hand. For example, 268-12-3 would indicate spore 3 from tetrad 12 of cross 268. The code would be modified for randomly isolated spores, e.g., by substituting an R for the tetrad number. If a progeny joins the permanent culture collection, it should be regarded as a new strain and assigned a serial isolation number as indicated above.

Genotype designation. Each locus, after it has been defined genetically, should be assigned a unique three-letter italicized symbol that recalls the phenotype associated with the mutant allele (*Met* for methionine auxotrophy). The symbol for the locus itself should have the first letter capitalized and the other two lowercase. A dominant allele is indicated by three uppercase letters (*MET*) and a recessive allele by three lowercase letters (*met*). If dominance relationships are unknown, the first letter of the three-letter italicized gene symbol should be capitalized for all alleles; the wild-type allele can be identified by a plus sign following the locus number and a mutant allele by a minus sign.

In many cases, mutations at different loci lead to similar phenotypes; each such locus should be identified by a number unique to that locus. Locus-identifying numbers will usually be assigned in the order in which loci are discovered; the number should immediately follow the three-letter symbol, without a space or hyphen (*Met1* or *Met2*).

Each new mutant allele should be assigned a unique isolation number immediately upon discovery. This could include a letter (e.g., derived from the investigator's name) followed by a serial number (e.g., F36). If a mutant is found to be an auxotroph requiring methionine, it could be called *met*F36, and, if it was the first methionine-requiring mutant recovered, it could be called *met1*F36 to designate a new locus. In written or oral communications, when the allele number is understood and unambiguous, it could be temporarily dropped for brevity in notation. Allelism tests would assign subsequently discovered *met* mutants, each with its unique isolation number, to either *Met1* or another *Met* locus.

Symbols for mutant genes that determine drug resistance are sometimes confusing because such genes can be either dominant, recessive, or semidominant. Furthermore, in different systems, alleles for both sensitivity and resistance encode active gene products and it is often the wild-type allele that confers "no growth" on a selective medium. Given these sources of confusion, it may clarify communication if the letters *R* and *S* following the gene symbol are used to indicate resistance or sensitivity associated with a particular allele. For example, alleles at a locus controlling resistance or sensitivity to cycloheximide could be designated *Cyh1S* (to indicate the allele at locus 1 that confers sensitivity) and *Cyh1R* (to indicate an allele at this locus that confers resistance). Dominance relationships should be indicated in the usual manner (see above).

Since our focus is on plant pathogens, we have considered whether or not genes controlling pathogenicity or virulence should be assigned special symbols. Our recommendation is no. The reasons are: first, that it would be difficult or impossible to devise notations suitable for all systems and anticipatory of all circumstances, and second, that at present there is no reason to suspect fundamental differences between pathogenicity or virulence genes and other genes in the organism; the products of the fungal virulence genes cloned to date are ordinary enzymes (17,18). Thus, we suggest that designations for pathogenicity and virulence genes follow the three-letter format described above, with modifications where necessary to accommodate special cases. The investigator who first identifies a gene has the responsibility to name it, and there may be several reasonable alternative symbols to choose from. For example, there is a gene for race-specificity in *Cochliobolus carbonum* that interacts with a dominant resistance gene (*Hm*) in the host plant, corn (19). The race-specificity gene also controls production of a host-specific toxin, HC-toxin. Although no official name has yet been assigned to this fungal gene, it could justifiably be called either *Tox* (to indicate the toxin-producing phenotype), or *Shm* (to indicate specificity of the gene for the host *Hm* locus), or some other suitable name. The most important consideration is that the name is consistent with designations for other genes in the host/parasite system under study and that all investigators working on the system agree to use the generally accepted symbols (16).

Phenotype designation. To describe the phenotype of a strain, the three-letter symbol of the gene controlling that phenotype should be used. The symbol should appear in Roman type (the first letter uppercase, the second and third lowercase) followed by a plus or a minus sign, preferably on the same line. A plus sign should be used to indicate the wild-type phenotype, and a minus sign should be used to indicate a mutant phenotype. For example, Met+ would designate methionine-independent growth, while Met− would specify methionine auxotrophy. Designations of phenotype and genotype should be clearly distinguished, especially in studies involving genes that interact to produce a phenotype.

To further illustrate our recommendation for phenotype and genotype symbols, we refer to the *S. cerevisiae* example on page 541 in Bennett and Lasure (2).

Non-Mendelian genes. It is most convenient to follow the precedent established in yeast genetics of assigning regular gene symbols to cytoplasmically-inherited genes (8). These symbols should be enclosed in brackets when it is necessary to distinguish them from genes carried on the nuclear chromosomes. When this distinction is clear without the use of brackets, the rules for describing nuclear genes should be observed (see above).

Suppressor loci. The nomenclature for suppressor loci described by Sherman (15) should be observed. It is important to note that the mutant allele is active in suppression and that the wild-type allele is inactive.

Mating-type designation. The two mating types of diallelic mating systems have in the past most often been designated as "*A*" and "*a*." By usual genetic conventions, this usage suggests that one allele is dominant to the other, which is untrue in this situation. The designations "*A*" and "*a*" are also clumsy and confusing in conversation. In yeast genetics, the locus that controls mating type is called *MAT*, and the two alleles are denoted by "*a*" and "α," which offer less opportunity for confusion than "*A*" and "*a*", but are still inconsistent with the convention used for naming alleles at other loci. We suggest a uniform designation for mating-type alleles: the single locus found in many pathogenic fungi should be called *MAT1*, and the two known alleles at that locus would then formally become *MAT1-1* and *MAT1-2* (all letters in the locus

symbol of both alleles are uppercase since both are needed for activity). The letter component of the unique allele serial number, recommended above, could be optional in the case of mating types, e.g., there would be no need for a letter in cases where it is likely that only two alleles exist in nature. In conversation and informally in written material, the mating-type notation could be abbreviated to *MAT-1* and *MAT-2*. If additional loci controlling mating type were discovered, they could be called *MAT2*, *MAT3*, and so forth, with alleles at each locus either numbered serially or assigned a specific isolation number as described above. Bipolar multiple allelic and tetrapolar multiple allelic or mixed diallelic/multiple allelic mating systems could follow the same convention.

To facilitate the transition from one mating type notation to another, we suggest that workers studying a particular organism consult before a change is made. For example, it may be agreed that "*A*" will become *MAT1-1* and that "*a*" will become *MAT1-2*.

Linkage groups. As genetic analysis reveals the arrangement of genes in linkage groups, these should be identified by the use of Roman numerals (for example, "linkage group I" or "linkage group V"). Numerals should be assigned to linkage groups in the order in which they are recognized. Linked genes can be indicated by writing their symbols without punctuation between them, in the order that they appear on the map. Unlinked genes can be separated by a semicolon.

Latin binomials. Unfortunately, species of plant pathogenic fungi are often identified by more than one Latin binomial, which can cause massive confusion in both written and oral communication. Several factors contribute to this multiplicity of names; one of these is that fungi isolated from diseased plant tissues are frequently in their vegetative (asexual) state. Special conditions may be required for the sexual cycle to occur, and these may go undiscovered for long periods. In the meantime, conidial and hyphal morphologies are used as bases for assigning Latin binomials, which are considered provisional pending the discovery of the sexual state (10). When the sexual structures are subsequently identified, a new binomial is constructed to designate them. Since "the rules of botanical nomenclature specify that sexual names should have precedence over the asexual" (9), it has been recommended that the asexual name be inserted into the classification of the sexual state once the proper connection has been made (10). For clarity, and to be consistent with the classification of other groups of organisms, we recommend that the binomial of the sexual stage be used as the primary name in all cases where it is known. For example, *Cochliobolus heterostrophus*, replaces the variety of asexual designations (e.g., *Helminthosporium maydis*, *Bipolaris maydis*, and *Drechslera maydis*) that have been used for the fungus causing southern corn leaf blight. We realize that in some instances the adoption of this convention will cause an inconvenience for the short term, but without it the present confusing situation will deteriorate. To facilitate communication, we suggest that texts (and perhaps titles and abstracts) of published papers include binomials of asexual as well as sexual stages so that relationships between species with and without known sexual states will not be overlooked.

Implementation. To standardize genetic nomenclature and practice for plant pathogenic fungi, we suggest that all workers dealing with a particular fungus agree among themselves on a suitable system that meets the needs in their case and that conforms as closely as possible to the guidelines presented here. All subsequent genetic investigations and publications resulting from them would then be expected to use the agreed upon practice and nomenclature. This would not only result in improved clarity in the literature on genetics of plant pathogenic fungi, but may also promote communication among those studying genetics of fungal pathogens, and could even facilitate collaboration among individuals working on similar host/pathogen combinations.

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