Editorial

Toward a Sensible Taxonomy of Bacterial Plant Pathogens

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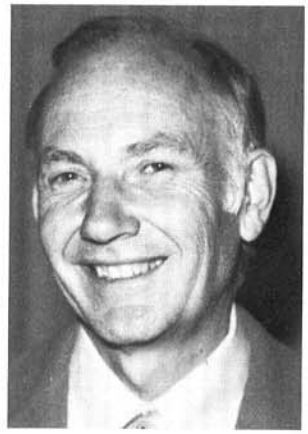

Dr. Hildebrand

The current pathovar system adopted for the majority of bacterial phytopathogens is unsatisfactory and should be replaced. The pathovar system was necessary to conserve the names of many pathogens that would not have been accepted by the Judicial Committee of the ICSB (International Committee on Systematic Bacteriology) charged with forming the 1980 Approved Lists of Bacterial Names. The committee accepted only species or subspecies whose names had been validly published and were represented by authentic, extant types or neotype cultures with modern descriptions to enable their ready differentiation from other species or subspecies using practical, laboratory diagnostic methods. D. W. Dye deserves special credit for his role in the development and adoption of the pathovar system.

Since there was not time either to assemble all the available data to make a case for conserving a name or to make the necessary studies to enable the retention of many species of bacterial phytopathogens, the present pathovar system is an expediency. Taxonomic knowledge should be directed toward defining what organisms are as well as their evolutionary and genetic relationships. The identification of organisms should be provided, and it is helpful if their names convey something of their nature. The pathovar system fails to do this. Plant pathologists were castigated years ago for basing their nomenclature on pathogenicity, the new host–new species syndrome, as noted by M. P. Starr. The pathovar system appears to be a step back to those days. Pathogenicity is of important practical value but of limited taxonomic value. Pathogenicity varies among strains, may be readily lost in culture, and is a relative and nonunitary characteristic that differs with the selection and variation in the host. Often there is a gradation of virulence ranging from virulent to avirulent. Furthermore, host specificity is seldom absolute and pathogenicity is seldom tested in large and varied groups of plant hosts. Thus, a given pathovar found on a host other than the "normal" one might well be identified as a new pathovar, since there is no easy way to identify it or relate it back to its "normal" host.

The hazard of using pathogenicity as a primary taxonomic character is exemplified by crown gall and vascular necrosis and rot of sugar beet caused by *Agrobacterium* spp. and *Erwinia* sp., respectively. With crown gall, tumors may be caused by clusters of strains that physiologically and genetically belong to groups sufficiently different to be recognized as separate species (Holmes and Roberts, J. Appl. Bacteriol. 50:443-467). Similarly, the same disease symptoms on a sugar beet can be caused by different physiological groups of *Erwinia* strains (*E. carotovora* subsp. *betavasculorum* and M. E. Stanghellini's *Erwinia* strains from the Willcox, Arizona, area). Thus, the pathovar system conveys little about the ecology, physiology, and genetics of the organisms that obviously are very different. It also is misleading by implying a closer relationship than exists.

The lumping of large numbers of bacterial phytopathogens into such species as *Pseudomonas syringae* and *Xanthomonas campestris* serves little purpose and cannot be rationalized on a molecular-genetic basis. Many of the bacteria lumped into the *P. syringae* group have a DNA-DNA hybridization value of only 60%, which is below the level usually considered to represent a species. Organisms with this level of homology vary greatly in pathogenic, physiological, and ecological properties because of their substantial genomic differences. A number of phenotypic differences are already known, and a concerted effort should distinguish many more. Within the saprophytic *Pseudomonas* group, the two species *P. chlororaphis* and *P. aureofaciens* are 85% related, the same level of homology shared by *P. syringae* pv. *glycinea* and *P. syringae* pv. *phaseolicola*, the two most closely related pathogens known at this time within the *P. syringae* group. Furthermore, *P. chlororaphis* shows a 57% relationship to *P. stutzeri*, the same general level of homology shown by *P. syringae* pv. *syringae* and *P. syringae* subsp. *savastanoi* pv. *savastanoi* (for name, see Janse, Int. J. Syst. Bacteriol. 32:166-169). Also, *P. chlororaphis* has a homology of 41% with *P. syringae* pv. *phaseolicola*, which is close to the 43% homology shown by *P. syringae* pv. *phaseolicola* and *P. syringae* pv. *coronafaciens*. Thus, the rationale to retain the great majority of fluorescent *Pseudomonas* phytopathogens in *P. syringae* seems illogical and inconsistent.

Taxonomy is an arbitrary science because there are no acceptable criteria for defining boundaries of genetically related groups or species of asexually reproducing organisms. There appears to be an infinite number of species in nature because of a continuous spectrum of intermediate types. How should organisms be categorized, knowing that any system is artificial? We proposed a taxonomic scheme based on two concepts: the three-dimensional nucleic acid homology matrix and the nonrandom variation in the distribution of phenotypic characters within this matrix (Annu. Rev. Phytopathol. 20:235-256). With the nucleic acid homology matrix concept, the relationship of any bacterial strain to any other strain can be precisely determined with homology measurements (DNA-DNA for closely related strains and RNA-DNA for distantly related strains), using a minimum of four common reference strains. With the nonrandom variation concept, whereby a phenotypic property occurs only in adjacent strains within the DNA matrix and is not scattered throughout the matrix, a strain within the DNA matrix can be located solely on the basis of phenotypic characterization.

Our concept of a species is that it represents a given area of a DNA homology matrix. The type strain occupies a precise fixed point within a DNA homology matrix and becomes the reference point within the matrix for the species. The phenotypic properties of this strain would be determined and mapped on the surrounding points in the DNA matrix. By definition, a species would consist of those strains occurring within a given distance of the location of the type strain or sharing the phenotypic properties of the type strain. Any strains falling between two areas of the matrix could be given hyphenated names to indicate their intermediate nature until making them a species was considered appropriate.

Perhaps the greatest problem in the development of a rational taxonomic scheme for phytopathogens and related saprophytes is neglect, largely because of the absence of funds and the seemingly low prioritization of systematics and microbial repositories. Few scientists today specialize in this field. Bacterial plant pathogens are important, and understanding their systematics would provide a foundation for the investigation of their ecology, physiology, and genetics.