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## Evaluation of Proposed Amended Names of Several Pseudomonads and Xanthomonads and Recommendations

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### ABSTRACT

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In 1980, over 90% of all plant-pathogenic pseudomonads and xanthomonads were lumped into *Pseudomonas syringae* and *Xanthomonas campestris*, respectively, as pathovars. The term "pathovar" was created to preserve the name of plant pathogens, but has no official standing in nomenclature. Proposals to elevate and rename several pathovars of the genera *Pseudomonas* and *Xanthomonas* to the rank of species has caused great confusion in the literature. We believe the following changes have merit and expect to adopt them for publication in a future American Phytopathological Society *Laboratory Guide for Identification of Plant Pathogenic Bacteria*. Upon review of published data and the Rules of The International Code of Nomenclature of Bacteria, we make the following recommendations. We reject the proposal to change the name of *P. sy-*

*ringae* pvs. *phaseolicola* and *glycinea* to *P. savastanoi* pvs. *phaseolicola* and *glycinea*, respectively, because both pathogens are easily differentiated phenotypically from pv. *savastanoi* and convincing genetic data to support such a change are lacking. We accept the elevation of *P. syringae* pv. *savastanoi* to the rank of species. We accept the reinstatement of *X. oryzae* to the rank of species with the inclusion of *X. oryzicola* as a pathovar of *X. oryzae* and we accept the species *X. populi*. We agree with the elevation of the pvs. *cassavae*, *cucurbitae*, *hyacinthi*, *pisi*, and *translucens* to the rank of species but not pvs. *melonis*, *theicola*, and *vesicatoria* type B. We recommend that all type A *X. vesicatoria* be retained as *X. campestris* pv. *vesicatoria* and all type B *X. vesicatoria* be named *X. exitiosa*. We reject the newly proposed epithets *arboricola*, *bromi*, *codiae* (*poinsettiicola* type B), *hortorum*, *sacchari*, and *vasicola* and the transfer of many pathovars of *X. campestris* to *X. axonopodis*. The proposed pathovars of *X. axonopodis* should be retained as pathovars of *X. campestris*.

Due to a general misconception among plant pathologists about acceptance of proposals to change the nomenclature of bacteria, we provide an analysis of several recently proposed names supported by The American Phytopathological Society (APS) Bacteriology Committee. Major changes in nomenclature began in 1973, when the Judicial Commission of the International Committee on Systematic Bacteriology (ICSB) proposed a revision in the nomenclature of bacteria (17) and appointed an Ad Hoc Committee to prepare a list of currently valid names of plant-pathogenic bacteria that were adequately described. This list of names was compiled and published in 1980 (4) by members of the Bacteriology Taxonomy Committee of The International Society of Plant Pathology and included in the Approved Lists of Bacterial Names (22). Discussing the validation of new names in the preface to the Approved Lists of Bacterial Names, V. B. D. Skerman states that "New names are not approved by the ICSB. They are validated as new names as a result of conformity with the Rules of Nomenclature. The ICSB did not approve the names in the approved list. The ICSB simply approved of the listing of the names in lists with a new starting date for the operation of the rule of priority of naming." A list of all names of plant-pathogenic bacteria that have been validly published from 1864 to 1995 is available (40). Because there is no process whereby newly proposed names of bacteria are "approved" or accepted for universal use by the scientific community, it is the purpose of this paper, with the support of the

APS Bacteriology Committee, to clarify the various different names being used for several pseudomonads and xanthomonads.

Because few plant-pathogenic species of bacteria could be differentiated by classical techniques and biochemical tests when the Approved List of Bacterial Names was published (22), most species were lumped together under an infrasubspecific subdivision as pathovars (a temporary name with no taxonomic rank and no nomenclatural standing) under a very few species (4). This was done as a compromise according to the International Code of Nomenclature in order to preserve the name of economically important plant pathogens (38,39). The organisms were to be automatically elevated to their original proper species rank once appropriate phenotypic and genetic data were obtained and validly published. Previously, most species of plant-pathogenic bacteria were named on the basis of the host of origin and, in many cases, included very little genetic and phenotypic data. Designations of infrasubspecific names are not covered by the Rules of the Code of Nomenclature (17,23). Of the fluorescent group of plant-pathogenic pseudomonads, only *Pseudomonas aeruginosa*, *P. agaricae*, *P. asplenii*, *P. cichorii*, *P. (Burkholderia) glumae*, *P. marginalis*, *P. tolaasii*, *P. viridiflava*, *P. woodsii*, and *P. syringae* were retained (4,22). Of these, only *P. syringae* and *B. glumae* are considered major pathogens. Over 90% of all plant-pathogenic *Pseudomonas* species were lumped into *P. syringae* as pathovars. The only species of *Xanthomonas* included on the 1980 list were *X. albilineans*, *X. ampelina* (since reclassified as *Xylophilus ampelinus* [36]), *X. axonopodis*, *X. campestris*, and *X. fragariae* (4,22). The majority of xanthomonads were grouped with the type species *X. campestris*.

Although considerable data have accumulated on numerical analyses (29,34), serology (2,19,28), membrane protein profiles (28, 32,33), and DNA analyses (1,7,8,9,12,13,14,18,20) of *Xanthomonas*

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and *Pseudomonas* spp. since 1980, there have been few pathovars that have been elevated to the rank of species. However, recent proposals to place several pseudomonads into new genera, elevate several pathovars of the genera *Pseudomonas* and *Xanthomonas* to the rank of species, and rename several of them have been published (7,30). We believe the accumulated data warrant elevation and acceptance of most of these taxa, but not some newly proposed epithets and especially not some well-described, historically significant pathogens. We remind colleagues that proposals are simply proposals; they are not mandated by any international rule. Discussions and analyses are needed before proposed names become accepted and universally used. Many scientists believe that once a taxonomic proposal is published in the *International Journal of Systematic Bacteriology* (now published by The Society for General Microbiology in England) the name(s) must be accepted and used. This is not, as stated by V. B. D. Skerman, the case (22). Names of plant pathogens are extremely important to national and international trade, scientists and others who ship cultures, and even funding agencies and organizations. The recent use of the proposed names *X. axonopodis* pv. *phaseoli* (for *X. campestris* pv. *phaseoli* or *X. phaseoli*) and *P. savastanoi* pv. *phaseolicola* (for *P. syringae* pv. *phaseolicola*) in some journal papers and in kits developed by some plant disease diagnostic companies (Viz. D-Genos kits distributed by AES Laboratories, Combourg, France) illustrates the type of confusion this problem is causing in use and in recognition of pathogen names.

**Pseudomonads.** Gardan et al. (7) proposed to change the name of *P. syringae* pv. *phaseolicola*, causal agent of halo blight of bean, and *P. syringae* pv. *glycinea*, causal agent of bacterial blight of soybeans, to *P. savastanoi* pv. *phaseolicola* and *P. savastanoi* pv. *glycinea*, respectively. Based on DNA similarity data and numerical analysis, these authors (7) proposed that *P. syringae* pv. *savastanoi* be elevated to the rank of species and that the other two highly regulated and widely known pathogens be renamed as pathovars of *P. savastanoi*, the causal agent of olive knot. Their conclusions were, however, based upon single strains of *P. syringae* pvs. *phaseolicola* and *glycinea*. In contrast, the authors (7) included over 100 strains of pv. *savastanoi*. We do not believe that such major taxonomic changes should be made from data derived from analysis of single strains. Furthermore, no data for reciprocal DNA similarities were included, experiments were not repeated, and only limited phenotypic tests were included. Other studies using large numbers of strains of these two pathogens show that the organisms are easily differentiated from pv. *savastanoi* on the basis of several additional phenotypic tests (15) and serology (19). Whereas *P. syringae* pv. *phaseolicola* produces levan; utilizes trigonelline,  $\beta$ -hydroxybutyrate, malonate, and quinate; and produces a toxin, *P. syringae* pv. *savastanoi* does not. In contrast, *P. syringae* pv. *savastanoi* utilizes mannitol, inositol, sorbitol, DL-glycerate, and L-lactate and produces indoleacetic acid, whereas *P. syringae* pv. *phaseolicola* does not. Similar differences occur between pvs. *glycinea* and *savastanoi* (15). Ovod et al. (19) showed that the lipopolysaccharide O-chains of 25 strains of *P. syringae* pv. *phaseolicola* were serologically identical and very distinct from 12 strains of *P. syringae* pv. *savastanoi*. These collective chemotaxonomic and phenotypic data show the two organisms to be easily differentiated independent of host reaction. These results, together with the use of limited and preliminary DNA similarity data (7), form the basis upon which we reject the transfer of pvs. *phaseolicola* and *glycinea* to the species *P. savastanoi* (Table 1). The expanded DNA similarity data of Gardan et al. (8) supports the earlier proposed elevation of *P. syringae* pv. *savastanoi* to the rank of species (7). They reported a mean relative DNA similarity of 81.1% ( $\pm 9.9\%$ ) of 10 strains of *P. syringae* pv. *syringae* to a strain of *P. syringae* pv. *syringae*, but only 50.5% ( $\pm 4.5\%$ ) of 20 strains of *P. syringae* pv. *savastanoi* to the same strain of *P. syringae* pv. *syringae*. Reciprocal results using labeled DNA of *P. syringae* pv. *savastanoi* showed a mean similarity of 81.2% with *P. syringae*

pv. *savastanoi* and only 49.0% with *P. syringae* pv. *syringae*. The authors (8) did not include *P. syringae* pv. *phaseolicola* or pv. *glycinea* in these studies. With major phenotypic (15) and genetic (8) differences between pv. *savastanoi* and *P. syringae*, we concur with elevating pv. *savastanoi* to the rank of species (7). However, we believe that adequate differentiation exists (discussed above) between pvs. *savastanoi* and *phaseolicola* and pv. *glycinea* to exclude them as pathovars of *P. savastanoi*. We, therefore, propose they be retained as pathovars of *P. syringae* until adequate data are available for their proper elevation to the rank of species. A recent proposal (9) to name *P. syringae* pvs. *phaseolicola* and *glycinea* as well as 14 other pathovars of *P. syringae* as pathovars of *P. amygdali* causes additional confusion in plant pathology literature and should not be accepted, because the appropriate number of strains were not examined with pairwise DNA similarity assays.

**Xanthomonads.** Several new taxonomic studies have been made of xanthomonads and two major reclassification schemes suggested (30,31). We acknowledge and appreciate the effort of Vauterin et al. (30,31) to provide and assemble the necessary data for proposing the elevation of several pathovars to the rank of species. The strength of the two proposals is that they include DNA similarity data on over 180 xanthomonad strains. However, interpretation of the DNA similarity data is difficult because details in the methods are lacking. Most importantly, it is not clear what strains were labeled to obtain the DNA binding values (%), which method was used for the assays (spectrophotometric or labeled DNA), which similarity assays were performed by the authors or which were compiled from literature, and no reciprocal tests were included. In either event, this required considerable effort. The results presented by Vauterin et al. (30) are generally in agreement with previous results (14) showing that the type species, *X. campestris* pv. *campestris*, has DNA similarity values of only 26% or less with over 20 named pathovars including *vesicatoria*, *phaseoli*, *glycines*, *vignicola*, *poinsetticola*, *begoniae*, *manihotis*, *oryzicola*, *juglandis*, *carotae*, and *pelargonii*. Furthermore, Hildebrand et al. (14) reported that these pathovars showed DNA similarities to each other of less than 70%, except for pvs. *glycines*, *phaseoli*, and *vignicola*, which were 77 to 93% related. These results are different from those showing pvs. *glycines*, *vignicola*, and *phaseoli* to be indistinguishable from pv. *begoniae* by DNA similarities (30). For DNA similarity assays, a species is generally defined as having 70% or greater relatedness (35); therefore, any strain with a relatedness of less than 70% would be accepted as a different species. In contrast, Vauterin et al. (30) chose to use a relatedness of only 60% as their definition of a species. We prefer the widely accepted 70% value. Pathovars *vesicatoria*, *malvacearum*, *manihotis*, *oryzae*, *oryzicola*, *phaseoli*, *sojensis*, *translucens*, and *begoniae* were shown earlier to be differentiated quite easily from each other and from *X. campestris* pv. *campestris* on the basis of serology and membrane proteins (28). Within the work by Thavechai and Schaad (28), the legends for their Figures 5 and 6 showing clear differences between these pathovars, including *X. campestris* pv. *phaseoli*, were mistakenly reversed by the typesetter. This error is easily overlooked by the casual reader.

We accept the reinstatement of pv. *oryzae* to the rank of species with the inclusion of *X. oryzicola* as a pathovar of *X. oryzae* (27). The proposed *X. populi* (21) is accepted. Vauterin et al. (30) designated 20 DNA similarity groups among the xanthomonads and proposed that each group serve as a species. Several new epithets were proposed. However, the DNA similarity values of pathovars within several of the proposed species do not meet the definition of a species (24,35). We enthusiastically support the formal proposal to restore several pathovars to the rank of species including *X. cassavae* and *X. translucens* (Table 2). We see no reason to list pvs. *aberrans*, *armoraciae*, *campestris*, *barbareae*, *incanae*, and *raphani* as pathovars of *X. campestris*, because they already exist (4, 38,40). Similarly, we do not agree with the transfer of the remaining pathovars of *X. campestris* to the species *X. axonopodis* (30).

In contrast to the slow growth of *X. axonopodis* on nutrient agar, these pathovars grow normally compared with *X. campestris*. These should remain in the type species *X. campestris* until adequate data are available as proposed in 1980 (4,38,39), or they should be placed into a new “repository” species, as discussed below. The temporary placement of these pathovars in another existing species epithet such as *X. axonopodis* only creates additional confusion.

We accept the elevation of *X. campestris* pv. *vesicatoria* type B strains to the rank of species (30). The type B strains clearly represent a separate taxon (25,30). However, the epithet *vesicatoria* should be retained for the type A strains, which represent those first described by Doidge in 1920 (3), following Rule 24b (23). Since the same epithet cannot be used for two different organisms (pathovar and species), according to Rule 12b (23), we suggest that the type B strains represented by those described as *exitiosa* by Gardner and Kendrick in 1921 (10), be named *X. exitiosa* and the A strains be retained as *X. campestris* pv. *vesicatoria* until additional data are available.

Some other pathovars Vauterin et al. (30) proposed to elevate to the rank of species should not be elevated, as discussed below. To avoid unnecessary changing of names and resulting confusion, we concur, as suggested previously (4,38,39), that all pathovars of *X. campestris* be retained as pathovars until adequate data are available to elevate a particular pathovar to the rank of species or subspecies. We would prefer to remove all other pathovars from *X. campestris* as proposed by Vauterin et al. (30) and put them into another “holding” or “repository” species. (The artificial taxon, *X. phyllovora*, is discussed below.) However, changing names while waiting for appropriate data is premature and will cause additional confusion. Therefore, we recommend that any pathovar included in the 1980 List of Names (4) be retained until data are available to elevate it to the rank of species. When a pathovar is to be elevated, based upon appropriate data, the name of the oldest recognized pathovar included in the 1980 list of names (4) should be retained according to Rule 24b (23).

Based on DNA similarities determined by the S1 nuclease digestion technique (16), we agree with Vauterin et al. (30) in the elevation of pvs. *cassavae*, *cucurbitae*, *psi*, *vesicatoria* (type B or *exitiosa* group only, as discussed above), *hyacinthi*, and *translucens* (including pvs. and f. spp. *translucens*, *undulosa*, *secalis*, *hordei*, *phleipratensis*, and *cerealis*) to the rank of species. However, the proposed *X. translucens* is a very heterogeneous species. For example, based on an experimental error of 11% (30), 10 of 23 strains tested had DNA similarity values of less than 67% to *X. translucens*.

DNA similarity values ranged from lows of 58% for pv. *translucens* strain LMG 5259, 61% for the single strain of pv. *phleipratensis*, and 66% for pv. *cerealis* strain LMG 679 and *undulosa* strain LMG 892 to a high of 87% for pv. *undulosa* strain LMG 885. Furthermore, other DNA similarity data (G. H. Lacy, unpublished data) show that strains of pvs. *phlei*, *arrhenatheri*, and *poae* have less than 65% similarity to *X. translucens*. These could represent separate subspecies; however, until additional strains are studied, they should, as stated above, remain as pathovars of *X. campestris*. Similarly, the proposed species *X. melonis* and *X. theicola* (30) have not been well studied and should remain as pathovars of *X. campestris* until appropriate data are available. The new species epithets *bromi* and *sacchari* proposed (30) for two strains each of *X. campestris* pv. *graminis* and *X. albilineans*, respectively, should not be accepted until additional strains and data are included.

More problematic are the de novo epithets proposed by Vauterin et al. (30) to encompass strains related at the species level including *X. arboricola*, *X. codiae* (*poinsettiicola* type B), *X. hortorum*, and *X. vasicola*. We believe this to be a premature decision. The primary intent of the pathovar proposal presented by Young et al. (39) at the International Conference on Plant Pathogenic Bacteria in Angers, France, was to save the epithets of plant-pathogenic bacteria that had not been adequately described phenotypically and, therefore, destined to be left off the 1980 List of Names (4). Acceptance of this temporary infrasubspecific epithet meant that the species name was saved from further use. Furthermore, this meant the name could be easily revived once data became available rather than having to propose a new specific epithet, which could result in further confusion. J. M. Young stated at the 1978 Congress that “At present, use of the term pathovar is informal and not governed by the Code. Nonuniform use by pathologists could lead to extensive synonymy if different names were applied to one pathogen....” For groups of pathovars found to be related at the species level, the consolidated species epithet reasonably should be derived by elevation of the earliest legitimately published pathovar epithet (4), according to Rule 24b (International Code of Nomenclature [23]). Further, creation of new names for long-standing pathogens of great economic importance will cause considerable uncertainty among government regulatory officials, seed companies, and scientists. With regard to the deposition of the epithets in the 1980 Approved List of Names, the following is stated (page 230 in literature citation 22): “The International Society for Plant Pathology is publishing, in the Review of Plant Pathology, a list of pathovars of species which appear in the Approved List of Names. Taxonomists

TABLE 1. Summary of rejected and retained or suggested names

Rejected names	Retained or suggested names <sup>a</sup>
<i>Pseudomonas savastanoi</i> pvs. <i>savastanoi</i> , <i>phaseolicola</i> , and <i>glycinea</i> (Garden et al., 1997)	Retain as <i>P. savastanoi</i> and <i>P. syringae</i> pvs. <i>phaseolicola</i> and <i>glycinea</i>
<i>Xanthomonas arboricola</i> (Vauterin et al., 1995), with pvs. <i>corylina</i> , <i>juglandis</i> , <i>pruni</i> , and <i>poinsettiicola</i> type C	Replace with <i>X. juglandis</i> pvs. <i>juglandis</i> , <i>corylina</i> , and <i>pruni</i>
<i>X. axonopodis</i> (Starr and Garces, 1950), Vauterin et al., 1995, all proposed pathovars <sup>b</sup>	Retain <i>X. axonopodis</i> , but not the proposed pathovars
<i>X. bromi</i> (Vauterin et al., 1995)	Retain as pathovar of <i>X. campestris</i>
<i>X. codiae</i> (Vauterin et al., 1995)	Retain as <i>X. campestris</i> pv. <i>poinsettiicola</i> type B
<i>X. hortorum</i> (Vauterin et al., 1995), with pvs. <i>hortorum</i> , <i>hederae</i> , <i>pelargonii</i> , and <i>vitians</i> type B	Replace with <i>X. hederae</i> pvs. <i>hederae</i> and <i>pelargonii</i> and retain <i>vitians</i> type B as <i>X. campestris</i> pathovar
<i>X. melonis</i> (Neto et al., 1984), Vauterin et al., 1995	Retain as <i>X. campestris</i> pv. <i>melonis</i>
<i>X. sacchari</i> (Vauterin et al., 1995)	<i>X. albilineans</i>
<i>X. theicola</i> (Uehara et al., 1980), Vauterin et al., 1995	Retain as <i>X. campestris</i> pv. <i>theicola</i>
<i>X. translucens</i> pvs. <i>arrhenatheri</i> , <i>graminis</i> , <i>phlei</i> , <i>phleipratensis</i> , and <i>poae</i> (Vauterin et al., 1995)	Retain as pathovars of <i>X. campestris</i>
<i>X. vasicola</i> (Vauterin et al., 1995), with pvs. <i>holcicola</i> and <i>vasculorum</i> type B	Retain as <i>X. campestris</i> pvs. <i>holcicola</i> and <i>vasculorum</i>
<i>X. vesicatoria</i> type B (ex Doidge, 1920), Vauterin et al., 1995	Retain <i>X. campestris</i> pv. <i>vesicatoria</i> for type A strains; we suggest the epithet <i>exitiosa</i> be considered for type B strains <sup>c</sup>

<sup>a</sup> Suggested names are in underlined.

<sup>b</sup> The following proposed pathovars of *X. axonopodis* (30) should be retained as pathovars of *X. campestris* until sufficient data are available: *alfalfae*, *bauhiniae*, *begoniae*, *cajani*, *cassavae* (type B), *cassiae*, *citri*, *clitoriae*, *coracanae*, *cyamopsidis*, *desmodii*, *desmodiigangetici*, *desmodiilaxiflori*, *desmodiitrotundifolii*, *dieffenbachiae*, *erythrinae*, *glycines*, *lespedezae*, *malvacearum*, *manihotis*, *patelii*, *phaseoli*, *phyllanthi*, *poinsettiicola* (type A), *rhynchosiae*, *ricini*, *sesbaniae*, *tamarindi*, *vasculorum* (type A), *vesicatoria* (type A), *vignaeradiatae*, *vignicola*, and *vitians* (type A).

<sup>c</sup> All type A strains of pv. *vesicatoria*, including the type strain, should be retained in *X. campestris*.

are urged to consult this list before proposing new species within the relevant genera.” Referring to rejected names, P. H. A. Sneath stated (page XXXIX in literature citation 23) “...but clearly the smooth operation of the provisions for revived names requires the cooperation of bacteriologists in observing recommendations such as those made by pathologists.” Plant bacteriologists attending the Angers meeting clearly were concerned that long-used names for pathogens of economic importance might be lost and never revived. The acceptance of the “pathovar” proposal meant that the names of a large number of economically important pathogens would be saved and that, when appropriate data became available, the organism would be reelevated to the rank of species. In cases in which two or more pathovars were shown to be related at the species level, the oldest epithet would be used for the species name according to the Rules of Nomenclature (23). The International Code of Nomenclature of Bacteria and the Approved List of Bacterial Names emphasized the need for cooperation between taxonomists and plant pathologists in the whole process. Creating new species epithets for highly regulated pathogens such as *X. citri* and *X. phaseoli* could cause serious disruption of international trade. The International Code specifically urges restraint in name changes to minimize confusion (23). Several additional proposed species (30) are discussed below.

We cannot recommend use of the proposed name of *X. hortorum* for regrouping pvs. *pelargonii*, *hederae*, and *vitians* type B (described in 1923, 1920, and 1918, respectively), because the name is not derived from the earliest legitimate pathovar epithet and the usage of the pathovar epithet *vitians* in more than one taxonomic position is confusing.

Similarly, *X. arboricola* (30), a newly proposed epithet to encompass *X. arboricola* for pvs. *corylina* and *juglandis* and some strains of pv. *pruni* (described in 1940, 1901, and 1903, respectively), is rejected because the name, not derived from the earliest legitimate epithet, causes confusion. We accept the elevation of these pathovars to the rank of species. However, we instead recommend use of the name *X. juglandis* for these pathovars, since it was the first of the three taxa described (Rule 24a of the Code [23]).

Elevation of pvs. *vasculorum* type B and *holcicola* to a single species, *X. vasicola*, is rejected because the epithet *X. vasicola* is not derived from the pathovars making it up. Also, these pathovars apparently lack enough common DNA similarity (70%) to belong in the same taxon (G. H. Lacy, unpublished data). These organisms should be retained as pathovars of *X. campestris* until appropriate data are available.

The proposal for the new species epithet *X. codiae* (30), conceived in a manner more consistent with pathology literature, to include strains of pv. *poinsettiicola* type B strains causing disease on crotons (*Codiaeum variegatum*) is more difficult to interpret. *X. campestris* pv. *poinsettiicola* likely includes xanthomonads with similar host reactions but diverse phylogenetic origins similar to the *X. vasculorum* types A and B discussed above. Unpublished DNA similarity assays (G. H. Lacy, unpublished data) support Vauterin et al.’s (30) observation of an intermediate level relatedness of the type strain of pv. *poinsettiicola* (ATCC 11643), presumably type A, to pv. *axonopodis* (Fig. 1, *X. codiae*, in literature citation 30). However, comparing metabolic activities (2 strains versus 99 strains; Table 2 in literature citation 30), only two reactions (with alpha-D-lactose and beta-methyl-D-glucosidase) were different between the two groups representing pv. *poinsettiicola* types A and B. Therefore, while sympathetic to the concept that pv. *poinsettiicola* type B strains may constitute a phylogenetic taxon, we believe that more data, including results of reciprocal and pairwise DNA similarity assays, are needed to establish a new species. It would also be helpful to know if the host ranges of types A and B overlap or are separate. Therefore, in the interim, we recommend that strains representing pv. *poinsettiicola* types A and B remain as pathovars of *X. campestris*.

We cannot accept the reclassification proposal of Vauterin et al. (30) to use *X. axonopodis*, originally described in 1950 (26), as repository of some 35 pathovars including *begoniae*, *citri*, *dieffenbachiae*, *malvacearum*, *phaseoli*, *pruni*, and *vasculorum* (described in 1934, 1915, 1938, 1901, 1897, 1903, and 1893, respectively). Vauterin et al. (30) reported a range of 62 to 92% in DNA similarities with a standard error of 15% (47 to 77%) within this axonopodis group. Of the two strains of pv. *axonopodis* tested, the type strain had a mean DNA similarity value of only 66% ( $\pm 15$ ) to others in the group. Pathovar *axonopodis* only shares DNA similarity of about 37% (G. H. Lacy, unpublished data) with the pathovars currently listed in the axonopodis group. In fact, by DNA similarities (G. H. Lacy, unpublished data), this large interrelated group may contain at least five species-level groups centered on pvs. *begoniae*, *dieffenbachiae*, *malvacearum*, *pruni*, and *vasculorum* type A. The type strain for *X. axonopodis* (ATCC 19312) shares more than 80% DNA similarity (G. H. Lacy, unpublished data) with the type strain of *X. vasculorum* (ATCC 35938, similar to type A strains of Vauterin et al. [30]). Both bacteria cause disease in sugarcane and *Panicum* spp., but they do not share all hosts. According to Rule 24a and b of the International Code of Nomen-

TABLE 2. Summary of accepted names

Accepted names <sup>a</sup>	Comments
<i>Xanthomonas albilineans</i> (Ashby, 1929)	
<i>X. axonopodis</i> (Starr and Garces, 1950)	
<i>X. campestris</i> (Pammel, 1895), Dowson, 1939	Pathovars listed below <sup>b</sup>
<i>X. cassavae</i> (ex Wiehe and Dowson, 1953), Vauterin et al., 1995	Type A strains only
<i>X. cucurbitae</i> (ex Bryon, 1926), Vauterin et al., 1995	
<i>X. exitiosa</i> (Gardner and Kendrick, 1921), this paper	Includes pv. <i>vesicatoria</i> type B strains <sup>c</sup>
<i>X. fragariae</i> (Kennedy and King, 1962)	
<i>X. hederae</i> (Arnaud, 1920), this paper	Includes pvs. <i>hederae</i> and <i>pelargonii</i>
<i>X. hyacinthi</i> (Wakker, 1883), Vauterin et al., 1995	
<i>X. juglandis</i> (Pierce, 1901), this paper	Including pvs. <i>juglandis</i> , <i>corylina</i> , and <i>pruni</i>
<i>X. oryzae</i> (Ishiyama, 1921), Swings et al., 1991, with pvs. <i>oryzae</i> and <i>oryzicola</i>	
<i>X. pisi</i> (ex Goto and Okabe, 1958), Vauterin et al., 1995	
<i>X. populi</i> (Rid�e and Rid�e, 1992)	
<i>X. translucens</i> (ex Jones et al., 1917), Vauterin et al., 1995	Including proposed pvs. <i>translucens</i> , <i>cerealis</i> , <i>hordei</i> , <i>secalis</i> , and <i>undulosa</i> <sup>d</sup>

<sup>a</sup> Original species reference in the work by Young et al. (40).

<sup>b</sup> Including pvs. *alfalfae*, *arrhenatheri*, *bauhiniae*, *begoniae*, *cajani*, *carotae*, *cassavae* (type B), *cassiae*, *citri*, *clitoriae*, *coracanae*, *cyamopsidis*, *desmodii*, *desmodiigangetici*, *desmodiilaxiflori*, *desmodiitrotundifolii*, *dieffenbachiae*, *erythrinae*, *glycines*, *graminis*, *holcicola*, *lespedezae*, *malvacearum*, *manihotis*, *melonis*, *nigromaculans*, *patelii*, *phaseoli*, *phlei*, *phleipratensis*, *phyllanthi*, *poae*, *poinsettiicola* (types A and B), *rhynchosiae*, *ricini*, *sesbaniae*, *tamarindi*, *taraxaci*, *vasculorum* (types A and B), *vesicatoria* (type A), *vignaeradiatae*, *vignicola*, and *vitians*. Additional pathovars in the work by Young et al. (40).

<sup>c</sup> Because the epithet *vesicatoria* must be maintained for the earlier described type A strains (3), it can not be used for the type B strains. The epithet *exitiosa*, as used in 1921 (10), is proposed. The type A strains are maintained as *X. campestris* pv. *vesicatoria*.

<sup>d</sup> Not enough data available to recognize as distinct species.

clature of Bacteria (23), the oldest legitimate epithet should be retained when two or more taxa of the same rank are united. Because *X. vasculorum* was published first (1893), we suggest that these two bacteria be renamed as pathovars of *X. vasculorum* (i.e., *X. vasculorum* pvs. *vasculorum* and *axonopodis*). However, since the epithet *vasculorum* is maintained for type B strains of *X. campestris*, it cannot be used as a species epithet (type A strains) according to Rule 12b. Therefore, we recommend that both type A and B strains of *X. vasculorum* be retained as pathovars of *X. campestris* until their taxonomy is clarified. We reject the axonopodis group as constituted (30) and, to avoid confusion in the literature, we recommend retaining the other 33 pathovars as pathovars of *X. campestris* until additional phylogenetic information has been published clarifying their interrelationships or to place them into a new “repository” species.

Because of their economic and regulatory importance, special mention must be made of *X. campestris* pvs. *citri* and *phaseoli*. We reject, for the reasons stated above, inclusion of these bacteria as pathovars of *X. axonopodis* (30). However, we must consider carefully the possibility that these pathovars deserve reinstatement to the species level based upon the information currently available (6,11,12,33). Van der Mooter and Swings (29) and Vauterin et al. (33) have provided additional phenotypic data since Young et al. (37) rejected the proposal of Gabriel et al. (6) to reinstate these pathovars as species. The phenotypic data of Van der Mooter and Swings (29) did not discriminate between pvs. *citri* and *phaseoli*, grouping both pathovars into a single phenon including *X. campestris*. Analyses of fatty acids and sodium dodecyl sulfate-polyacrylamide gel electrophoresis protein profiles showed clear differences among groups of xanthomonads causing citrus disease but did not indicate the position of the citrus pathogens in relation to other xanthomonads including pv. *phaseoli* (33). Genomic fingerprinting (11), restriction fragment length polymorphism analyses (12), and DNA similarity studies (33) of citrus pathogens also supported differences among citrus pathogens but, likewise, did not address relatedness to other xanthomonads or pv. *phaseoli*. Gabriel et al. (6), using nonpairwise hybridizations of plasmid probes to electrophoresed restriction endonuclease digests of genomic DNA, detected only about 20% similarity between pv. *citri* and pvs. *campestris*, *malvacearum*, or *phaseoli*. However, Egel et al. (5) showed by pairwise DNA similarity assays that while pv. *citri* shares less than 50% similarity with pv. *phaseoli*, it has over 90% DNA similarity with pv. *malvacearum*. The results of Egel et al. (5) are confirmed in the unpublished data of G. H. Lacy. Although significant new knowledge about pvs. *citri* and *phaseoli* have been obtained, lack of similar information about closely related groups makes it possible that premature reinstatement may lead to later confusion should high levels of DNA similarity be discovered with other xanthomonads, especially those with precedence in the literature (i.e., pv. *malvacearum*). Therefore, following the accepted species definition based on DNA similarity analyses (24,35) and Rule 24 of the International Code of Nomenclature of Bacteria (23), we propose that pvs. *citri* and *phaseoli* remain temporarily as pathovars of *X. campestris* until more DNA similarity information is available concerning their relationship to *X. campestris* and other xanthomonads.

**Xanthomonads of uncertain classification.** Confusion on a large scale may potentially be caused by renaming xanthomonads to more accurately approximate their phylogenetic relationships. This confusion results when some xanthomonads are renamed on the basis of new information, while others are left behind in their current classifications, usually as pathovars of *X. campestris*, due to insufficient information. The result is that pathovars of *X. campestris*, rather than reflecting actual phylogenetic relationships also include xanthomonads placed in that group only because of lack of information. One suggestion is to correct this problem for pathologists by creating an artificial neutral taxon as a repository for all pathovars that are inadequately described. This taxon should

be reserved for current and future xanthomonads whose descriptions are inadequate for further classification but cause important plant diseases. Possibly, a name such as *X. phyllovora*, carrying no indication of host specificity, may be useful for this “temporary” file. An artificial taxon may be useful for several to many years, until enough information has been gathered that all the current pathovars of *X. campestris* are moved into phylogenetically acceptable taxons. Such epithets may also have long-term usefulness for newly discovered xanthomonads that have not yet been described adequately for more precise identification. While the former suggestion is interesting, we seek comment from other pathologists on the concept. If acceptable, a brief description of *X. phyllovora* could be published in the *International Journal of Systematic Bacteriology*.

**Summary.** A summary of the names that we propose be rejected and accepted is presented in Tables 1 and 2, respectively. We point out that the newly suggested names such as *X. exitiosa*, *X. hederea*, and *X. juglandis* are suggestions and not formal proposals. A formal proposal must be published in the *International Journal of Systematic Bacteriology*. These recommendations have been discussed and approved by the Bacteriology Committee of APS. We, therefore, recommend to the editors of *Phytopathology*, *Plant Disease*, *Molecular Plant-Microbe Interactions*, and APS Press that authors be advised to follow these recommendations, until further data are forthcoming and evaluated. These choices are generally based upon the date of the original description following Rules 23a, 24a and b, and 26a of Section 5 (Priority and Publication of Names) of the International Code of Nomenclature (23).

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