Reinterpretation of the Taxonomic Position of *Xanthomonas maltophilia* and Taxonomic Criteria in This Genus

Request for an Opinion

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The inclusion of “*Pseudomonas maltophilia*” Hugh 1981 in the genus *Xanthomonas* as *Xanthomonas maltophilia* (Hugh 1981) Swings et al. 1983 is questioned in view of the significant differences between these two taxa. This reclassification is not acceptable if practical means of differentiation in this genus are considered. The proposed alteration of the description of the genus *Xanthomonas* is also questionable because of the implications for everyday phytobacteriology. In view of the natural similarities, as well as the profound differences, between *X. maltophilia* and the genus *Xanthomonas*, we propose that a new genus should be created for *X. maltophilia*, which could be placed together with the genus *Xanthomonas* in a separate natural group.

The taxonomic position of *Xanthomonas maltophilia* (Hugh 1981) Swings et al. 1983 has been the subject of much debate (1, 7, 16, 18, 25, 26, 28, 35, 37, 38). Initially isolated from pleural fluid in 1943 and named “*Bacterium bookerii*,” this ubiquitous bacterium was reclassified as “*Pseudomonas maltophilia*” by Hugh and Ryschenkow in 1961 (15). As “*P. maltophilia*” and species of the genus *Xanthomonas* exhibit substantial levels of rRNA homology (28), it appeared to be appropriate to assign this species to the genus *Xanthomonas* (26). A number of arguments in the literature also support this view, and consequently Swings et al. (37) proposed the transfer of *P. maltophilia* Hugh 1981 to the genus *Xanthomonas* as *Xanthomonas maltophilia* (Hugh 1981) comb. nov.

In view of the significant differences between these two taxa, this reclassification remains questionable (27), partly because of the redefinition of the genus *Xanthomonas* that would be required to accommodate *X. maltophilia* (1, 26).

As our own results (39) also argue against inclusion of *X. maltophilia* in the genus *Xanthomonas*, the purposes of this paper are to question some of the assumptions made by Swings et al. (37), to summarize the latest information on this subject, and to request an opinion.

The arguments below proceed from the reclassification proposed by Swings et al. (37) and should be considered together with their corresponding discussions.

DNA-rRNA hybridization. The taxonomic value and reliability of DNA-rRNA hybridization for classifying bacteria on generic and suprageneric levels have been demonstrated by several workers (4–8, 12, 22). However, the data discussed below from the reclassification proposed by Swings et al. (37) are confusing. Although Swings et al. (37) referred to an extensive DNA-rRNA hybridization study of the genus *Pseudomonas* by De Vos and De Ley (in press at that time), different melting temperature [$T_{m(e)}$] ranges were reported by these authors for exactly the same *Xanthomonas* strains. Swings et al. (37) reported a range of 78.8 to 81.5°C, while De Vos and De Ley (7) found a range of 80.0 to 81.5°C for the same 27 *Xanthomonas* strains when they used identical

conditions and the same *Xanthomonas campestris* NCPPB 528^T (T = type strain) reference rRNA. Therefore, the range determined for *X. maltophilia* by Swings et al. (37) (76.5 to 78.0°C) (7, 37) almost overlapped the range for the genus *Xanthomonas*, whereas De Vos and De Ley (7) found that *X. maltophilia* was removed from the genus *Xanthomonas* at a $T_{m(e)}$ of 3°C under the conditions used. This placed the *X. maltophilia* cluster close to the genus *Xanthomonas*, but still not in the genus. This finding was confirmed by Van den Mooter and Swings (38), who found an *X. maltophilia* $T_{m(e)}$ range of 77 to 78°C, while the $T_{m(e)}$ values for the rest of the *Xanthomonas* species ranged from 79 to 82°C. Also, when reference rRNAs from three *Pseudomonas* spp. type strains were used, *X. maltophilia* was located close to the genus *Xanthomonas*, but was never included in the same similarity cluster (7).

As the level of hybrid formation depends not only on the actual sequence homology, but also on the size of the genome, its state of replication, and the number of rRNA cistrons per genome, rRNA similarity should be expressed by two parameters, percentages of rRNA binding and melting points [$T_{m(e)}$ values] of DNA-rRNA hybrids (19, 32). Swings et al. (37) did not mention the percentage of rRNA binding in their study. Although the percentage of rRNA binding might not be a direct measure of rRNA cistron homology, it is a useful parameter for separating taxa with the same $T_{m(e)}$ value (8); in this case percentage of rRNA binding removed *X. maltophilia* even further from the extremely tight *Xanthomonas* cluster when the values were plotted on a similarity map (7).

As DNA-rRNA hybridization data were the first indicators that “*P. maltophilia*” might be transferred to the genus *Xanthomonas* (28), it is interesting to note the opinions concerning the DNA-rRNA approach described below. According to Woese et al. (44), the DNA-rRNA approach offers no advantage over DNA-DNA hybridization (which revealed low levels of DNA similarity among *Pseudomonas* species [18]) when it comes to groupings at the generic level and has the disadvantage that it samples only one or two genes. According to Sneath (32), the reliability of the DNA-rRNA approach has not yet received critical study with a sound theoretical basis. Some fundamental questions have

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also arisen because many groups based on rRNA analysis are not easily definable in terms of phenotypic similarities, raising doubt about the practicality of a phylogenetic classification based on rRNA analysis (22).

DNA-DNA homology. At present, DNA-DNA homology is widely accepted as an expression of genetic relatedness (16). However, membrane competition experiments have revealed very low levels of DNA similarity among *Pseudomonas* species belonging to the five different rRNA subgroups (18). Interspecies similarity values are in the 5 to 20% range, and the average DNA similarity values between species belonging to different rRNA similarity clusters are even lower (not more than 1 to 2%) (18). For *X. maltophilia* the percentages of similarity with labeled DNAs from *X. campestris* strains range from 22 to 37% (16) or from 1 to 16% when the S1 nuclease method is used (18). Such low values are at the border of or below the sensitivity of this method (37) and are very difficult to interpret. According to Johnson (17), values in the lower homology range (20 to 60% DNA homology) indicate species which are often quite distinct phenotypically from the species with which they are compared, although they may be regarded as closely related. Unfortunately, there is currently no satisfactory phylogenetic definition of a genus (42).

The low levels of DNA similarity between *Pseudomonas* species have far-reaching implications for taxonomy and phylogenetic relationships in this group, when it is considered that the DNA-DNA approach actually represents (an average of) the entire genome and not merely a few genes in the genome (44). For classification purposes it is now also considered necessary to calibrate techniques for the differentiation of strains against DNA-DNA hybridization, the conventional method used for the delineation of species (40). Furthermore, it is suggested that minimal standards for the genus *Xanthomonas* should include tests for generic identity (45). However, it is possible that DNA-DNA homology analyses may not reveal the elements of a genome which are taxonomically significant (21). This again accentuates the importance of a polyphasic approach that also incorporates phenotypic properties (22, 45).

DNA-DNA hybridization data divided *Pseudomonas* rRNA group V strains into two subgroups, an *X. maltophilia* subgroup and an *X. campestris* subgroup, with substantial heterogeneity among the strains in each subgroup (18). Ikemoto et al. (16) also observed heterogeneity among *X. maltophilia* strains and delineated five clusters on the basis of DNA-DNA homology data. There was also a difference between methionine-requiring and methionine-nonrequiring strains of *X. maltophilia* with respect to DNA-DNA homology (16).

G+C contents. The guanine-plus-cytosine (G+C) range determined for *X. maltophilia* (63 to 67.5 mol%) fits well into the *Xanthomonas* range (63 to 71 mol%) (1), and although it also fits into the *Pseudomonas* range (58 to 70 mol%) (26), these values are not inconsistent with inclusion of *X. maltophilia* in the genus *Xanthomonas*. However, it is also important to bear in mind that although these G+C values are very similar for related organisms, the reverse is not true; two organisms with similar G+C contents are not necessarily related, as the G+C values do not take into account the linear arrangement of the nucleotides in the DNAs (3, 17).

Comparative enzymology. According to Swings et al. (37), "both '*P. maltophilia*' and *Xanthomonas* are unusual in that they lack NADP-linked dehydrogenases and possess NAD-specific prephenate and arogenate dehydrogenases for tyrosine biosynthesis." Referring to the original article on this

topic (2), we learned that rRNA homology groups I, IV, and V of the genus *Pseudomonas* all lack activity for arogenate-NADP dehydrogenase, while groups I and V also lack prephenate-NADP dehydrogenase activity. As both groups I and V also possess NAD-specific prephenate and arogenate dehydrogenases for tyrosine biosynthesis (2), *X. maltophilia* and the genus *Xanthomonas* are not so unusual in this regard. Groups I and V are separated by comparing the relative allosteric sensitivities of NAD-dependent dehydrogenases (2). Unfortunately, results for *X. maltophilia* were not included in the comparison of the sensitivities of the NAD-dependent dehydrogenases to tyrosine inhibition, and only one *Pseudomonas* species (*Pseudomonas gardneri*) was grouped with all of the *Xanthomonas* species studied (2).

The control pattern for the enzyme 3-deoxy-D-arabinoheptulosonate-7-phosphate synthetase is a useful indicator of taxonomic relationships at about the level of genera (43). The occurrence of this unique control mechanism in *X. maltophilia*, as well as in species of the genus *Xanthomonas*, indeed supports a close taxonomic relationship between these two taxa (37, 43), but it has to be remembered that the comparative allostery of 3-deoxy-D-arabinoheptulosonate-7-phosphate synthetase alone does not unambiguously establish group placement (43).

Ubiquinones. Swings et al. (37) state that both *X. maltophilia* and the genus *Xanthomonas* contain ubiquinones with eight isoprene units (Q-8), whereas all other *Pseudomonas* strains tested generally contain ubiquinones with nine isoprene units (Q-9) as major components. In our opinion this does not reflect the true situation correctly. Oyaizu and Komagata (24) examined the quinone systems of 75 *Pseudomonas* strains and divided them into nine groups according to this characteristic, as well as fatty acid composition. Of the nine groups determined, only group I (corresponding to rRNA homology group I) species contain a Q-9 system, while five groups of named pseudomonads contain Q-8 quinone systems. These groups include a *Pseudomonas solanacearum* group (rRNA group II), a "*Pseudomonas acidovorans*" group (rRNA group III), *X. maltophilia* (rRNA group V), *Pseudomonas avenae*, and *Pseudomonas palleronii* (rRNA group III). The three other groups contain Q-10 systems (24).

On the basis of ubiquinone content, the *X. maltophilia*-*Xanthomonas* group is not as unusual as implied by Swings et al. (37).

Cellular fatty acid composition. Quantitative differences in fatty acids were found between the *X. maltophilia* strains that do not require methionine and the methionine-requiring strains of this species, although both groups have almost the same kinds of fatty acids (16). On the basis of cellular fatty acid compositions, a similarity value of 82% was calculated for the two groups (16). From the data of Ikemoto et al. (16), it is interesting to note that *X. maltophilia* strains which do not require methionine also share relatively high mean percentages of i-C_{16:0} and C_{17:0} fatty acids with two of the three *Xanthomonas* strains studied and have values that are considerably higher than the percentages determined for methionine-requiring strains of *X. maltophilia*. On the other hand, *Xanthomonas oryzae* has a fatty acid composition quite different from that of *X. maltophilia* (16).

Phage typing. Phage typing studies provided evidence for a relationship between *X. maltophilia* and the genus *Xanthomonas* (37). However, this technique is not very successful as a taxonomic tool in the genus *Xanthomonas*, mainly because of a lack of specificity (1, 10).

In addition, temperate phages have been found in *X. maltophilia* (26), while nothing of this nature has been reported for the genus *Xanthomonas*.

Growth and pigments. The colonies of *Xanthomonas* species are distinctively yellow, and this pigmentation is very important in the presumptive identification of these organisms (35, 45). It has been suggested that these pigments (xanthomonadins) might serve as adequate chemotaxonomic markers for the genus *Xanthomonas* (35). *X. maltophilia* cultures do not exhibit the yellow mucoid growth typical of the genus *Xanthomonas*, and its pigments are not xanthomonadins or closely related to the xanthomonadins that have been studied (26, 35, 37).

Nonpigmented *Xanthomonas* strains do exist, but evidence in the literature indicates that pigmented forms exist for all of the nonpigmented *Xanthomonas* species which occur naturally (29–31, 36).

Swings et al. (37) reported that some *X. maltophilia* strains characteristically form brownish grey water-soluble pigments, which have also been observed in six pathovars of *X. campestris*. Gilardi (11) believes that the brown coloration of the culture medium that is associated with *X. maltophilia* and has been previously described as a pigment is probably due to a secondary chemical reaction among extracellular products which react to form the brown color.

When grown on media containing usable carbohydrates, most *Xanthomonas* strains produce characteristic extracellular polysaccharides or xanthan gums, resulting in very mucoid colonies (1, 37). The growth of *X. maltophilia* is shiny, but not mucoid (37). This presents a practical problem, as slime formation has some value in screening *Xanthomonas* cultures (9). Except for *Xanthomonas albilineans*, 99% of the *X. campestris* strains and 100% of the strains of five other *Xanthomonas* phena tested by Van den Mooter and Swings (38) produced mucoid colonies. Only 14% of the *X. maltophilia* strains were mucoid (38).

Niches. All species currently included in the genus *Xanthomonas* are highly specialized plant pathogens (1), while at present nothing is known about the phytopathogenic capacity of *X. maltophilia* strains (37). Most *X. maltophilia* strains have been isolated from clinical specimens; *X. maltophilia* is the second most frequently isolated *Pseudomonas* species in clinical laboratories (26). Strains of this species appear to be opportunistic human pathogens (26). There is currently no evidence of any *Xanthomonas* species associated with human infections.

X. maltophilia strains are also found in frozen food, milk, and water, while *X. maltophilia* predominates over other pseudomonads in the rhizospheres of several cultivated plants, probably because of the excretion of S-containing amino acids by the roots (26). However, for *Xanthomonas* species the minimum growth temperature is above 5°C (1). *Xanthomonads* have occasionally been detected in runoff water and ditches around fields of infected plants, but data indicate that survival in this situation is short (1). Saprophytic survival in soil is also unusual for *Xanthomonas* species (1). However, two pathovars of *X. campestris* are known to spend the interseasonal time epiphytically (1).

Other morphological, physiological, and biochemical characteristics. From the literature we know that *X. maltophilia* and the genus *Xanthomonas* share a number of morphological, physiological, and biochemical characteristics (37). Swings et al. (37) calculated a simple matching similarity coefficient (S_{SM}) of approximately 75% between these two taxa from the available phenotypic data.

Despite the high similarity value (S_{SM}) of 79% calculated

for *X. maltophilia* NCPPB 1974 in a phenotypic study in which 53 standard phenotypic tests were used and with data agreeing well with the data available in the literature, *X. maltophilia* NCPPB 1974 was less closely related to the *Xanthomonas* group than the majority of *Pseudomonas* strains studied were (39). This finding was confirmed by the results of a numerical analysis of the electrophoretic protein patterns of the same strains, in which a correlation value of $r = 0.65$ was determined between *X. maltophilia* NCPPB 1974 and the larger *Pseudomonas*-*Xanthomonas* cluster (39).

In an extensive phenotypic study of *Xanthomonas* strains, Van den Mooter and Swings (38) placed *X. maltophilia* in phenon 1 of their dendrogram; *Pseudomonas pictorum* and unidentified strain LMG 949 were the only other strains included in this phenon as remote neighbors. Strain LMG 949 deviates in several characteristics from the new generic description of the genus *Xanthomonas* given in the same paper (38). An S_{SM} value of 65% was reported between phenon 1 and four other *Xanthomonas* phena (namely, *Xanthomonas fragariae*, *X. albilineans*, *Xanthomonas axonopodis*, and *Xanthomonas populi*) (38). However, *X. maltophilia* was phenotypically less closely related to the four *Xanthomonas* phena mentioned above than to *Xylophilus ampelinus*, which is not a member of the genus *Xanthomonas* at all (38).

The number of polar flagella is an important taxonomic characteristic (26). The presence of a single polar flagellum is an important characteristic of the genus *Xanthomonas*. Very rarely cells with two polar flagella occur (1). On the other hand, *X. maltophilia* is multitrichous (26, 37).

At present no pili or fimbriae have been described for the genus *Xanthomonas* (1), while polarly inserted pili or fimbriae have been described for *X. maltophilia* (26).

According to the present generic definition of the genus *Xanthomonas*, no nitrate reduction occurs (1). *X. maltophilia* strains reduce nitrates to nitrites (20, 37).

According to Swings et al. (37), some of the characteristics shared by *X. maltophilia* and the genus *Xanthomonas* are acid production from (among other compounds) lactose, fructose, and maltose, as well as hydrolysis of esculin. According to Bradbury (1), he actually found variation in these reactions. For acid production from lactose and maltose three *Xanthomonas* species gave negative reactions, while 11 to 89% of the *X. campestris* strains were positive; for acid production from fructose, two *Xanthomonas* species gave negative reactions, while three species were positive. Tests for hydrolysis of esculin also resulted in varied reactions; three *Xanthomonas* species were positive, and one *Xanthomonas* species was negative (1).

Other differences between *X. maltophilia* and the genus *Xanthomonas* include the production of lysine decarboxylase, starch hydrolysis, resistance to antibiotics (especially streptomycin, kanamycin, tetracycline, and chloramphenicol), dyes, and metals, and tolerance to 4% NaCl (37, 38). According to the generic definition, *Xanthomonas* growth is inhibited by 0.1% triphenyltetrazolium chloride (1). All of the *X. maltophilia* strains tested by Van den Mooter and Swings (38) grew on 0.1% triphenyltetrazolium chloride.

From the data discussed above it is clear that there are profound differences between *X. maltophilia* and the genus *Xanthomonas*, differences which are not without substantial practical implications for the already complex taxonomic structure and identification system in the genus *Xanthomonas*.

Additional remarks. Since the publication of the proposal for the transfer of "*P. maltophilia*" to the genus *Xanthomo-*

nas (37), the considerations discussed below have appeared in favor of or as arguments against this inclusion.

(i) **Oligonucleotide cataloging of 16S rRNA.** S_{AB} analysis of oligonucleotide cataloging has shown that *X. maltophilia* and "its close relatives (i.e., the xanthomonads)" cluster peripherally with the fluorescent pseudomonas group (*Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Pseudomonas syringae*, etc.) in particular (44). However, catalogs of members of the *X. maltophilia* group also show that these organisms have a remarkable number of oligonucleotides in common with group II species (*Comamonas acidovorans*, *Pseudomonas testosteroni*, *Pseudomonas cepacia*, etc.) (44).

(ii) **Respiratory chain.** Difference spectra at the liquid air temperature have shown that there is a slight shoulder for the genus *Xanthomonas* at 549 nm, suggesting that these organisms have a very small cytochrome *c* content. The difference spectra for *P. syringae* and *X. maltophilia* are very similar, but do not have any noticeable peak or shoulder at or near 549 nm (1).

(iii) **Growth factor requirement.** Many *Xanthomonas* strains require growth factors, usually amino acids such as methionine and/or glutamic acid. Nicotinic acid is occasionally required (1). *X. maltophilia* has a requirement for methionine, although strains of *X. maltophilia* which do not require methionine have been described (16). These methionine-requiring and methionine-nonrequiring strains of *X. maltophilia* differ from each other with respect to phenotypic characteristics, cellular fatty acid composition, DNA base composition, and DNA-DNA hybridization and can be separated into two clusters on the basis of methionine requirement and some other properties (16). It is also noteworthy that the requirement for methionine depends upon the carbon compounds used (16). Although it is likely that the genus *Pseudomonas* will be reserved in the future for species that do not require growth factors, there are also a few *Pseudomonas* species that require the addition of organic growth factors. For example, *Pseudomonas diminuta* also needs methionine, while growth factor-requiring strains of *Pseudomonas caryophylli* and *P. syringae* are occasionally encountered in nature (26).

(iv) **Metabolism of aromatic compounds.** On the basis of the dehydratases of the two pathways to phenylalanine, five rRNA-DNA hybridization groups have been distinguished. *X. maltophilia* was assigned to group V together with other *Xanthomonas* strains. However, group V could not be distinguished from group Ib by using these enzymes (1).

(v) **Glycoside hydrolases.** Hayward (13) demonstrated the presence of α -glucosidase, β -glucosidase, β -galactosidase, and β -xylosidase activities in most of the 39 *Xanthomonas* strains which he examined, as well as in *X. maltophilia* ("*P. maltophilia*") alone among the *Pseudomonas* species.

(vi) **Cell walls.** Both *X. maltophilia* and members of the genus *Xanthomonas* have a high rhamnose content, a low 2-keto-3-deoxyoctonate content, D-galacturonic acid, and no heptoses in their cell walls. However, all of the *Xanthomonas* strains examined so far for these characteristics are members of one species, *X. campestris* (1). An interesting feature of the lipopolysaccharide of *X. maltophilia* is the presence of a pentose derivative that has been identified as 3-O-methyl-L-xylose, which thus far has not been found in other bacteria except *Rhodopseudomonas viridis* (26).

(vii) **Exoproductions.** High degrees of similarity (>90%) among the electropherograms of the exoproductions of 31 *Pseudomonas* strains, including (among others) *X. malto-*

philia, *P. aeruginosa*, *P. fluorescens*, *P. alcaligenes*, etc., have been shown by polyacrylamide gel electrophoresis (41).

(viii) **Asparagine.** Starr (34) and Dye (9) have reported that asparagine is inadequate as a sole source of carbon and nitrogen for xanthomonads. Bradbury (1) included this property in the definition of the genus *Xanthomonas*, and this characteristic is presently used as a diagnostic test for the genus *Xanthomonas*, since yellow members of the *Enterobacteriaceae* and many *Pseudomonas* species grow with asparagine as a sole source of both carbon and nitrogen (1). In a previous study (39) we found that *X. maltophilia* NCPPB 1974 and *Pseudomonas hibiscicola* NCPPB 1683 are capable of growing with 0.2% asparagine as a sole source of C and N. Using a totally different medium and 0.1% asparagine, Van den Mooter and Swings (38) recorded a negative reaction for this test.

To summarize, at present the characteristic determinative tests for the genus *Xanthomonas* are as follows: Gram reaction, cell morphology, flagellar insertion (single, polar), oxygen requirement, absence of nitrate reductase, no denitrification, triphenyltetrazolium chloride sensitivity, inability to use asparagine as a sole source of carbon and nitrogen, requirement for specific growth factors, and production of a distinctive pigment by a majority of the strains (45). Bradbury (1) also added plant pathogenicity. In addition, according to Young et al. (45), "unless these criteria are always met, further confusion can be expected, particularly between the genera *Xanthomonas* and *Pseudomonas*, as the number of species described increase."

On the other hand, *X. maltophilia* is multitrichous and reduces nitrates, and its growth is not inhibited by 0.1% triphenyltetrazolium chloride. It may be able to grow with asparagine as a sole source of carbon and nitrogen, while there are strains that do not require methionine as a growth factor. The pigments of *X. maltophilia* are not xanthomonadins. At present this organism is not regarded as a plant pathogen; on the contrary, it is associated with human infections, survives saprophytically in several niches, and occurs free living in nature. It does not produce the characteristic xanthan gums, and its colonies differ from those of most other *Xanthomonas* species by their umbonate form (38). Pili or fimbriae are present. A low level of correlation in electrophoretic protein patterns has been demonstrated. DNA-DNA and DNA-rRNA hybridization results can be interpreted in various ways, but to us these data also points to inclusion of the two taxa in a natural group as close relatives, rather than inclusion in the same genus. Unlike other xanthomonads, *X. maltophilia* grows at 37°C, tolerates 4% NaCl, and is resistant to several antibiotics, dyes, and metals. Oxidase activity was present in 71% of the *X. maltophilia* strains studied by Van den Mooter and Swings (38), while except for 19% of the *X. campestris* strains, oxidase activity was absent in all other *Xanthomonas* phenotypes (38). As discussed above, several properties are also shared with *Pseudomonas* species.

Swings et al. (37) proposed an improved definition of the genus *Xanthomonas*, namely, that "all *Xanthomonas* strains tested fall in the $T_{m(e)}$ range from 76 to 81°C when their DNAs are hybridized with labeled rRNA from type strain *X. campestris* pv. *campestris* NCPPB 528." However, it is not clear to what extent this $T_{m(e)}$ range was lowered mainly to include *X. maltophilia*.

In our view the question of the reclassification of *X. maltophilia* is closely linked to the taxonomic situation in the genus *Xanthomonas* and confirms the need for minimal standards for this genus (45). At present, there are many

arguments in favor of a more phylogenetically based system of classification rather than a determinative system. However, it will be a major setback for everyday phytobacteriology, in which speed, cost effectiveness, and the availability of sophisticated apparatus are often issues, if an improved definition of the genus *Xanthomonas* is based upon characteristics of phylogenetic value which cannot be readily determined or repeated by workers in less well-equipped laboratories. For example, Vauterin et al. (40) are of the opinion that in a general taxonomic environment there is no reason to assign crucial importance to a single phenotypic feature, such as plant pathogenicity. However, plant pathogenicity and host specificity play a very important role in the presumptive identification of xanthomonads by plant pathologists, and provision must be made for this feature, as well as several other practical means of differentiation, in the proposed improved definition and the promulgation of minimal standards for the genus *Xanthomonas*. Although modern bacterial systematists cannot be expected to work with an artificial type of classification for practical purposes only, a natural classification without practical implications is also not acceptable (40). A classification that is of little use to microbiologists, no matter how fine a scheme or who devised it, will soon be ignored or significantly modified (36). It is completely impracticable to define genera solely on the basis of phylogenetic data. Genera need to be characterized by using phenotypic properties, even if the choice of phenotypic markers might change with the development of better tests (23). Furthermore, published descriptions of taxa should preserve the ability to identify strains to species level in laboratories that rely mainly on phenotypic properties (45).

The same argument applies to *X. maltophilia*. Although evidence of a more phylogenetic nature suggests that there is a close relationship between *X. maltophilia* and the genus *Xanthomonas*, the inclusion of this species in the genus *Xanthomonas* is not acceptable on practical grounds. With an improved description of the genus *Xanthomonas* (38), *X. maltophilia* is so often the exception to the rule that its inclusion in the genus *Xanthomonas* does not promote taxonomic stability in this genus. Instead, and contradictory to the aims of taxonomy, it leads to confusion, complicating the task of classifying and identifying field isolates of this species.

In order to provide for the natural similarities, as well as the significant differences discussed here, we propose that a separate genus should be created for *X. maltophilia*, which could be placed with the genus *Xanthomonas* in the same natural group.

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