Taxonomic Note: Implementation of the Provisional Status
*Candidatus* for Incompletely Described Procaryotes

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The International Committee on Systematic Bacteriology recommended that the category *Candidatus*,
recently proposed by Murray and Schleifer (Int. J. Syst. Bacteriol. 44:174-176, 1994) to record the properties
of putative taxa of procaryotes, should be implemented. This category should be used for describing procaryotic
taxa for which more than a mere sequence is available but for which characteristics required for description
according to the International Code of Nomenclature of Bacteria are lacking. In addition to genomic information,
such as sequences apt to determine the phylogenetic position of the organism, all information, including
structural, metabolic, and reproductive features, should be included in the description of a provisional taxon,
together with the natural environment in which the organism can be identified by in situ hybridization or other
similar techniques for cell identification.

The International Committee on Systematic Bacteriology discussed the proposal of Murray and Schleifer (9) for a new
procaryotic category, *Candidatus*, during their meeting in Prague, Czech Republic, in July 1994 (7). The members of this
committee agreed that such a category would be useful and timely because of the increasing involvement of sequencing
technology in the characterization of procaryotes that are difficult to cultivate and can only be described in limited terms.
The International Committee on Systematic Bacteriology has stated previously that “the integrated use of phylogenetic and
phenotypic characteristics, or polyphasic taxonomy, is necessary for the delineation of taxa at all levels from kingdom to
genus” (8). We should be reminded in this context that the *International Code of Nomenclature of Bacteria* (12) permits the
naming of taxa even for organisms that cannot be maintained in laboratories as pure cultures, provided that a description,
preserved specimen, or illustration is provided as a type (rule 16a). Examples of this are *Prochloron didemni*, *Planctomyces
bekefii*, and *Pasteuria penetrans*, as well as *Buchnera* and *Holospora* species.

Although the *International Code of Nomenclature of Bacteria* allows systematists to include in a description taxonomic
features that can be recognized only in situ, at the present time microbiologists are not encouraged to base a taxonomic
description solely on a phylogenetic placement inferred from a comparison of nucleotide sequences. We feel that decisions
concerning the roles of DNA and RNA data in taxonomy are important with respect to the evolution of taxonomic rules in
response to progress in methods and increases in knowledge. We expect that some of what we know about the interactions
and activities of bacteria will come from biota that have not been cultivated yet and in situ observations, and this information
needs to be recorded. But it is cultivation that has allowed assessment and comparison among species of actual and
potential capacities and has allowed us to understand what it is that evolution has brought about. After cultivation, more
precise descriptions and a nomenclature that allows effective communication become effective. In the meantime, as molec-
ular biology settles into the fabric of bacteriology, various attitudes concerning the changes will be expressed (2, 5, 6).

Current wisdom suggests that a description of a potential new procaryotic genus and species would be inadequate for formal
naming under the following circumstances: (i) when information comes exclusively from an analysis of clones,
generated from DNA that has been isolated directly from a natural sample; (ii) when the authenticity of the genetic
material is verified in the environment by reamplification of DNA with sequence-specific PCR primers, but the presence
of cells containing that DNA is not confirmed by microscopy or isolation; (iii) when the origin of genetic material from living
cells is detected in a natural sample, but the authenticity of the bacterial cells in the host is not proven by in situ hybridization,
as in the case of the agent of bacillary angiomatosis (*10*) and Whipple’s disease bacillus (*11*); and (iv) when the origin of
the genetic material from living cells is detected in a natural sample by in situ hybridization, but information concerning
properties other than phylogenetic position and morphology is lacking. The essence of this strategy, with a cloning step
omitted, has been used in naming obligate intracellular symbionts, which are often small in number and size. An unambiguous sequence is most likely obtained only in the absence of large numbers of contaminating cells, a single
readable sequence may be indicative of the presence of a dominating population (3, 4).

The status *Candidatus* has been discussed as a possible taxonomic status for uncultured procaryotic cells for which
relatedness has been determined (e.g., relatedness to the nearest neighbor) and authenticity has been verified by in situ
probing or a similar technique for cell identification (additional studies will be necessary to investigate whether reamplifica-
tion of a sequence determined with sequence-specific primers is sufficient proof of authenticity). In addition, it is mandatory
that information concerning phenotypic properties, such as structural peculiarities and certain metabolic and physiological
features, is made available as a starting point for further investigation and eventual description and naming. It is obvi-
ous that at the present time it is mainly symbionts and parasites of eucaryotic cells, as well as cultures obtained from special
enrichment preparations, that are candidates for this provisional status because such organisms can be recognized by
their molecular structures but cannot be assigned to a known

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The number of such organisms is small, as the list below attests, should include a reprint to back it up.

but a status that is not formally recognized in the Candidatus the International Journal of Systematic Bacteriology when they identification of a morphotype with a specific probe (probe identification). Undoubtedly, contentious discussion will focus on whether amplification of DNA or RNA with oligonucleotide sequence complementary to unique region of 16S rRNA 5'-GTCCTGAGGCTCCCCGAAAGGCACCTC TTAATC-3'; S (Sus, ileum); M). Gebhart et al., Int. J. Syst. Bacteriol. 43:533, 1993.

"Candidatus magnetobacterium" ([new subcell of Proebacteria or new lineage) NC; G--; R; NAS (EMBL number X71838), oligonucleotide sequence complementary to unique region of 16S rRNA 5'-GGCATCCTCGTTACT-3'; FL (freshwater lake sediment); microer., magnetosomes, sulfur inclusions; M). Spring et al., Appl. Environ. Microbiol. 59:2397, 1993.

"Candidatus Liberobacter asiaticum" ([a-Proteobacteria) NC; G--; F; NAS (GenBank number L22532), oligonucleotide sequence complementary to unique region of 16S rRNA 5'-GCCTATGCAATACGCGCCA-3'; S (Citrus, phloem; Diaphorina citri (Psyllidae), hemolymph, salivary glands); M). Jagoueix et al., Int. J. Syst. Bacteriol. 44:386, 1994.

"Candidatus Liberobacter africanum" ([a-Proteobacteria) NC; G--; F; NAS (GenBank number L22533), oligonucleotide sequence complementary to unique region of 16S rRNA 5'-GGCGCATTTTACGGCGCA-3'; S (Citrus, phloem; Triozia erytreae (Psyllidae), hemolymph, salivary glands); M). Jagoueix et al., Int. J. Syst. Bacteriol. 44:386, 1994.

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REFERENCES

is intended to record discoveries and to provide a basis for recognizing putative taxa that are equivalent to genus or higher rank.

We thank K. H. Schleifer for helpful discussions.

REFERENCES


### TABLE 1. Items for inclusion in the codified record of a provisional taxon

<table>
<thead>
<tr>
<th>Order of mention</th>
<th>Example responses</th>
</tr>
</thead>
<tbody>
<tr>
<td>Status............</td>
<td><em>Candidatus</em></td>
</tr>
<tr>
<td>Vernacular epithet</td>
<td>&quot;another&quot;</td>
</tr>
<tr>
<td>Phylogenetic lineage or possible genus</td>
<td>e.g., <em>b-Proteobacteria</em>, possible (probable) <em>Desulfovibrio</em></td>
</tr>
<tr>
<td>Cultivation</td>
<td>Cultivated or Not Cultivated</td>
</tr>
<tr>
<td>Gram reaction</td>
<td>G+, G-, Variable, or Not Applicable</td>
</tr>
<tr>
<td>Morphology</td>
<td>Rod, Coccus, Filamentous, Mycolial, Other, Unknown</td>
</tr>
<tr>
<td>Basis of assignment</td>
<td>Nucleic Acid Sequence (data bank #), Morphology, etc.</td>
</tr>
<tr>
<td>Specific identification of morphotype</td>
<td>Probe identity</td>
</tr>
<tr>
<td>Habitat, association, or host</td>
<td>Symbiotic (name host and tissue), Free-Living (sea, etc.), etc.</td>
</tr>
<tr>
<td>Metabolism and unusual features</td>
<td>Aer., Anaer., Microaer., etc.</td>
</tr>
<tr>
<td>Growth temperature</td>
<td>Mesophile, Psychrophile, Thermophile</td>
</tr>
<tr>
<td>Source</td>
<td>From leaf cells of pigs</td>
</tr>
<tr>
<td>Author(s)</td>
<td>Essential reference</td>
</tr>
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</table>

* Modified from reference 9.