Towards a standardized format for the description of a novel species (of an established genus): *Ochrobactrum gallinifaecis* sp. nov.

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A format for the description of single novel species is proposed, which should facilitate the reviewing process by assisting the provision of data in a standardized form. The abstract must be short and concise, highlighting phylogenetic position, morphology and chemotaxonomy for genus affiliation, the genotypic and phenotypic basis for species differentiation, and the name and deposition numbers from two public culture collections in different countries for the type strain: A Gram-negative, rod-shaped, non-spore-forming bacterium (Iso 196 T ) was isolated from chicken faeces. On the basis of 16S rRNA gene sequence similarity, strain Iso 196 T was shown to belong to the α-2 subclass of the Proteobacteria related to *Ochrobactrum tritici* (95 ± 6 %), *Ochrobactrum grignonense* (95 ± 0 %) and *Ochrobactrum anthropi* (94 ± 6 %), and the phylogenetic distance from any validly described species within the genus *Brucella* was less than 95 %. Chemotaxonomic data (major ubiquinone – Q-10; major polyamines – spermidine and putrescine; major polar lipids – phosphatidylethanolamine, phosphatidylglycerol and phosphatidylcholine; major fatty acids – C18:1ω7c and C19:0 cyclo ω8c) supported the affiliation of strain Iso 196 T to the genus *Ochrobactrum*. The results of DNA–DNA hybridization and physiological and biochemical tests allowed genotypic and phenotypic differentiation of strain Iso 196 T from the four validly published *Ochrobactrum* species. Iso 196 T therefore represents a new species, for which the name *Ochrobactrum gallinifaecis* sp. nov. is proposed, with the type strain Iso 196 T (= DSM 15295 T = CIP 107753 T ).

In an editorial article, the Managing Editor of IJSEM reiterated the policy of the Editors and the Editorial Office to strengthen the conversion of full papers to the Note format, especially for the description of a single new species (Parte, 2002). This policy has been introduced not only for economic reasons, but also to allow a higher throughput of high-quality descriptions that combine the publication of taxa as printed material, as required by Rule 25a of the *Bacteriological Code* (1990 Revision) (Lapage et al., 1992), with the option of online access to supplementary data. Although the Note format has been well received, the Editors of IJSEM agreed that the provision of an even more standardized format would facilitate the efforts of both authors and referees. On the other hand, it has been made very clear that any format should not be seen purely from an economic point of view, and that some degree of flexibility should be granted at the discretion of the Editors, depending on the availability of salient characters that cannot be defined as supplementary data. It is unlikely that a single format will be appropriate for the description of all prokaryotic taxa, as the information needed to describe, for example, a chemolithoautotrophic organism, differs significantly from the description of an actinobacterium. Thus, Supplementary fatty acid and phylogenetic trees are available in IJSEM Online.

Published online ahead of print on 21 February 2003 as DOI 10.1099/ ijs.0.02710-0.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain Iso 196 T is AJ519939.

Supplementary fatty acid and phylogenetic trees are available in IJSEM Online.
several formats may need to be developed to cover the taxon species of the domains *Archaea* and *Bacteria*.

The following format is written for a heterotrophic, Gram-negative member of the *Proteobacteria*, a category to which a large number of recent newly described taxa belong. The following points highlight the most important features of the standardized format, but the authors are also asked to follow the Instructions for Authors. It should be stressed that the description should meet all the requirements of the Minimal Standards, if available. Presentation of results must be accompanied with the confirmation that the analyses carried out conformed to tests recommended in the minimal standards. Authors should also consult the report on the re-evaluation of the species definition in bacteriology (Stackebrandt et al., 2002).

**Introduction:** *this section can be omitted in most descriptions; refrain from history of the genus, only listing references of already described species, listing of species names and ecological role. In most cases, it is not important to state the reasons why strains of the new taxon have been isolated.*

The genus *Ochrobactrum* was first described by Holmes et al. (1988), and at present the genus comprises the four species, *Ochrobactrum anthropi* (Holmes et al., 1988), *Ochrobactrum intermedium* (Velasco et al., 1998), *Ochrobactrum tritici* and *Ochrobactrum grignonense* (Lebuhn et al., 2000).

All sections describing isolation and determination of characteristics should allow repetition of the work. Recent surveys on individual subsections have indicated rather extensive coverage of molecular methods and phylogenetic analysis. In many cases, citations can replace detailed descriptions of the procedures. Variations of the rRNA gene sequence and phylogenetic analysis, and analysis of chemical constituents only necessary for genus affiliation, should be described in comparison with published data as concisely as possible. Phylogenetic analyses should be done at least with the neighbour-joining algorithm and maximum-parsimony algorithm with bootstrap values to provide evidence for the robustness of the analysis. Phylogenetic dendrograms should only be shown if the position of the novel species changes significantly the intrageneric structure of previously published dendrograms. Large datasets should go into the supplementary data system in IJSEM Online.

During the characterization of organisms isolated from chicken faeces, strain Iso 196$^T$ was recovered on MacConkey agar (Oxoid) at 37 °C, showing a beige-coloured colony on nutrient agar. Subcultivation was done on tryptone soy agar (TSA) at 28 °C for 48 h. On this agar, Iso 196$^T$ was able to grow at 10–37 °C, but not at 4 or 45 °C. Growth at 37 °C was also observed on nutrient agar and R2A agar, but not on SS agar (all from Oxoid).

Gram-staining was performed as described by Gerhardt et al. (1994). Cell morphology was observed under a Zeiss light microscope at ×1000, with cells grown for 3 days at 28 °C on TSA. The 16S rRNA gene was analysed as described by Kämpfer et al. (2003). Phylogenetic analysis was performed using the software packages *ARB* (Strunk et al., 2000) and *MEGA* (Molecular Evolutionary Genetics Analysis) version 2.1 (Kumar et al., 2001) after multiple alignment of data by *CLUSTALX* (Thompson et al., 1997). Distances (distance options according to the Kimura two-parameter model) and clustering with the neighbour-joining and maximum-parsimony methods were determined by using bootstrap values based on 1000 replications (results are available as supplementary data in IJSEM Online). The 16S rRNA sequence of strain Iso 196$^T$ was a continuous stretch of 1415 bp. Sequence similarity calculations after a neighbour-joining analysis indicated that the closest relatives of strain Iso 196$^T$ were *O. tritici* (95-6 %), *O. grignonense* (95-0 %) and *O. anthropi* (94-6 %). Lower sequence similarities (<95-0 %) were found with all validly described species of the genus *Brucella*.

Results of chemotaxonomic analyses are given in the species description. The following analytical procedures were performed as described: respiratory quinones (Tindall, 1990; Altenburger et al., 1996); polyamines (Busse & Auling, 1988; Busse et al., 1997); polar lipids (Ventosa et al., 1993); fatty acids (Kämpfer & Kroppenstedt, 1996). The quinone system supports affiliation of Iso 196$^T$ to the *z-Proteobacteria*, where the majority of species (including *O. anthropi*) have Q-10 as the major quinone (Lechner et al., 1995; Yokota et al., 1992). The polyamine pattern is in excellent agreement with the patterns reported previously for two strains, including the type strain, of *O. anthropi* (Lechner et al., 1995; Hamana & Takeuchi, 1998) and is distinct from the polyamine patterns of members of the genera *Rhizobium*, *Mesorhizobium*, *Sinosrhizobium*, *Aminobacter*, *Pseudaminobacter*, *Phyllobacterium* and *Mycoplana*, which were shown to contain sym-homospermidine in at least minor amounts (Busse & Auling, 1988; Hamana & Takeuchi, 1998; Kämpfer et al., 1999). The polar lipid profile of Iso 196$^T$ (available as supplementary data in IJSEM Online) is similar to those reported for species of the related genera *Aminobacter*, *Pseudaminobacter* (Kämpfer et al., 1999), *Sinosrhizobium* (Geiger et al., 1999) and *Mesorhizobium* (Choma & Komaniecka, 2002). The presence of the unknown aminolipid (AL) distinguishes Iso 196$^T$ and *O. anthropi* LMG 7991 from both *Aminobacter* and *Pseudaminobacter*, but it may correspond to the phosphorus-free ornithine lipid detected in species of the genera *Mesorhizobium* and *Sinosrhizobium*. The fatty acid profile of strain Iso 196$^T$ (available as supplementary data in IJSEM Online) was composed of C$_{19:0}$ cyclo _08c_ (47-2 %), C$_{18:1}$ω7c (28-8 %), C$_{16:0}$ (8-9 %), C$_{18:0}$ (3-7 %), summed feature 3 = C$_{16:1}$ω7c5C$_{15:0}$ 2-OH (3-7 %), C$_{18:1}$ω2-OH (1-5 %), C$_{17:0}$ cyclo (2-9 %) and 11-methyl-C$_{18:1}$ω7t (1-1 %). No significant differences in the fatty acid profiles were found for the other *Ochrobactrum* species, except that *O. tritici* produced significantly lower amounts of C$_{19:0}$ cyclo _08c_ (data not shown).
Phenotypic (here physiological) and genotypic properties for species differentiation within a genus should only be shown in comparison to phylogenetically related species (if possible all species of the genus) in table format (or in the text, if possible) and the species description should refer to this table. Only discriminatory reactions (on the basis of comparable methods, which has to be proven) should be shown in the body of the table, while identical reactions should be given in the legend.

Results of the physiological characterization are given in the species description, with methods as described previously (Kämpfer et al., 1991). DNA–DNA hybridization experiments were performed with Iso 196\(^T\) and type strains of all Ochrobactrum species using the method described by Ziemke et al. (1998), except that for nick translation, 2 μg DNA was labelled during a 3 h incubation at 15 °C. Strain Iso 196\(^T\) showed relatively low DNA–DNA similarity to the type strains of O. anthropi CIP 14970\(^T\) (34%), O. intermedium LMG 3301\(^T\) (14%), O. tritici LMG 18957\(^T\) (33.5%) and O. grignonense DSM 13338\(^T\) (18.8%). Pooled standard deviations of all hybridization experiments were between 2.0 and 11.6%.

Species description: if necessary give emended description of the genus.

Description of Ochrobactrum gallinifaecis sp. nov.

Ochrobactrum gallinifaecis (gal.li.ni.fa’ e’cis. L. fem. n. gallina hen; L. n. faex feces; N.L. gen. n. gallinifaecis of the feces of a hen).

Cells are non-motile, non-spore-forming rods (approx. 2 μm in length). Gram-negative, oxidase-positive, showing an oxidative metabolism. Good growth occurs on R2A agar, TSA, nutrient agar and MacConkey agar at 25–30 °C; beige, translucent and shiny colonies with entire edges form within 24 h, with a diameter of approximately 2 mm. Quinone system of strain Iso 196\(^T\) consists of Q-10 (89.9%), Q-9

Table 1. Physiological characteristics of the type strains of Ochrobactrum species

<table>
<thead>
<tr>
<th>Test</th>
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<tr>
<td>Hydrolysis of:</td>
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<tr>
<td>pNP-Phenyl-phosphonate</td>
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<tr>
<td>1-L-Glutamate-γ-3-carboxy-pNA</td>
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<td>1-L-Proline-pNA†</td>
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<tr>
<td>Assimilation of:</td>
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<tr>
<td>D-Fructose, L-inositol*, L-rhamnose*, D-sorbitol*</td>
<td>−</td>
<td>+</td>
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<td>+</td>
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<td>cis-aconitate, citrate†, DL-3-hydroxybutyrate*</td>
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<td>4-Amino butyrate, β-alanine*</td>
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<tr>
<td>D-Maltose†, adonitol†, N-acetyl-D-glucosamine*</td>
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<td>+</td>
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<td>trans-Aconitate†</td>
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<td>(+)</td>
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<td>D-Celllobiose†</td>
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<tr>
<td>N-Acetyl-D-galactosamine</td>
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<td>Suberate†</td>
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<tr>
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<tr>
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<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>(+)</td>
</tr>
</tbody>
</table>

*Test (based on a different method) was also performed by Holmes et al. (1988) with O. anthropi and gave congruent results.
†Test (based on a different method) was also performed by Velasco et al. (1998) with O. intermedium and gave congruent results.
‡Test (based on a different method) was also performed by Lebuhn et al. (2000) with type strains of all four previously described species and gave congruent results.
(9-7 %) and Q-8 (0-4 %). Polyamine pattern consists of the major compounds spermidine [11-9 μmol (g dry wt)\(^{-1}\)] and putrescine [6-5 μmol (g dry wt)\(^{-1}\)]. Predominant polar lipids are phosphatidylethanolamine (PE), phosphatidylglycerol (PG) and phosphatidylcholine (PC). Additionally, moderate amounts of phosphatidylmonomethylethanolamine (PME), phosphatidylmethylethanolamine (PDE), diphosphatidylglycerol (DPG) and an unidentified phosphorus-free aminolipid (AL); small amounts of two unknown phospholipids (PL1, PL2) and three unknown lipids (L1, L2, L3) are detected. Fatty acid profile was largely composed of C\(_{16:0}\) (28.8 %) and C\(_{19:0}\) cyclo (47-2 %). In addition, C\(_{18:1}\) 2-OH (1-5 %) was detected. Carbon source utilization and hydrolysis of chromogenic substrates (including differentiating characters for all *Ochrobactrum* species) are indicated in Table 1.

Isolated from chicken faeces in Marburg, Germany. Type strain is Iso 196\(^{2}\) (= DSM 15295\(^{2}\) = CIP 107753\(^{2}\)).

**Acknowledgements**

We are grateful to Anton Hartmann for providing reference strains, to Udo Jackel for help with the phylogenetic analyses, to Aidan Parte and Natalie Wilder for critical reading of the manuscript, to two colleagues from the Editorial Board for refereeing the manuscript, and to Jean Euzéby for support with the nomenclature.

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