**Cronobacter condimenti** sp. nov., isolated from spiced meat, and **Cronobacter universalis** sp. nov., a species designation for **Cronobacter** sp. genospecies 1, recovered from a leg infection, water and food ingredients

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A re-evaluation of the taxonomic position of five strains, one assigned to **Cronobacter sakazakii** (strain 1330T, isolated from spiced meat purchased in Slovakia), two previously assigned to **Cronobacter** genospecies 1 (strains NCTC 9529T and 731, isolated from water and a leg infection, respectively) and two previously assigned to **Cronobacter turicensis** (strains 96 and 1435, isolated from onion powder and rye flour, respectively) was carried out. The analysis included phenotypic characterization, 16S rRNA gene sequencing and multilocus sequence analysis (MLSA) of seven housekeeping genes (\textit{atpD}, \textit{fusA}, \textit{glnS}, \textit{gltB}, \textit{gyrB}, \textit{infB}, \textit{ppsA}; 3036 bp). 16S rRNA gene sequence analysis and MLSA showed that strain 1330T formed an independent phylogenetic lineage in the MLSA, with **Cronobacter dublinensis** LMG 23823 T as the closest neighbour. DNA–DNA reassociation and phenotypic analysis revealed that strain 1330 T represented a novel species, for which the name **Cronobacter condimenti** sp. nov. is proposed (type strain 1330T = CECT 7863 T = LMG 26250 T). Strains NCTC 9529 T, 731, 96 and 1435 clustered together within an independent phylogenetic lineage, with **C. turicensis** LMG 23827 T as the closest neighbour in the MLSA. DNA–DNA reassociation and phenotypic analysis confirmed that these strains represent a novel species, for which the name **Cronobacter universalis** sp. nov. is proposed (type strain NCTC 9529 T = CECT 7864 T = LMG 26249 T).

The genus **Cronobacter** was created by the reclassification of the species **Enterobacter sakazakii** (Iversen \textit{et al.}, 2007) and belongs to the family **Enterobacteriaceae** of the class **Gammaproteobacteria**. It includes facultatively anaerobic, Gram-negative, oxidase-negative, catalase-positive, non-spor-forming rods that, in general, are motile, able to reduce nitrate to nitrite and to produce acetoin (Voges–Proskauer test), and negative for the methyl red test (Iversen \& Forsythe, 2004; Forsythe, 2005; Osaili \& Forsythe, 2009). The genus includes five species, which were differentiated according to the 16 \textit{E. sakazakii} biogroups, each biogroup being defined by their phenotype based on 10 tests (Farmer \textit{et al.}, 1980; Iversen \textit{et al.}, 2006b): **Cronobacter sakazakii** (biogroups 1–4, 7, 8, 11 and 13), **Cronobacter malonaticus** (biogroups 5, 9 and 14), **Cronobacter turicensis** (biogroups 16, 16a and 16b), **Cronobacter muytjensii** (biogroup 15) and **Cronobacter dublinensis** (biogroups 6, 7, 10)

**Abbreviations:** MLSA, multilocus sequence analysis; MLST, multilocus sequence typing.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains 1330 T, NCTC 9529 T, 1435, 731 and 96 are FNS39031, EF059877 and JN205049–JN205051, respectively, and for the \textit{atpD}, \textit{fusA}, \textit{glnS}, \textit{gltB}, \textit{gyrB}, \textit{infB} and \textit{ppsA} sequences of C. sakazakii ATCC 29544 T, C. malonaticus LMG 23826 T, C. muytjensii ATCC 51329 T, C. dublinensis LMG 23823 T, C. turicensis LMG 23827 T, strain NCTC 9529 T, strain 1330 T and Citrobacter koseri ATCC BAA–895 are JF268258–JF268313; they can also be accessed from the Cronobacter multilocus sequence typing website (http://pubmlst.org/cronobacter).
The taxonomy of the genus Cronobacter is complex due to the high interspecies similarity of the 16S rRNA gene sequences, which ranges from 97.8 to 99.7 %, the overlap of biochemical profiles and a poor correlation between genotypic and phenotypic analyses (Duaga & Breuwer, 2008; Kucerova et al., 2010). Furthermore, confusions with other members of the Enterobacteriaceaeae have been described: a number of Enterobacter cloacae and Enterobacter hormaechei strains isolated from human infections were assigned to the genus Cronobacter using phenotypic tests (Caubilla-Barron et al., 2007; Townsend et al., 2008). The existence of microheterogeneities in the 16S rRNA gene sequence is another factor that can generate misidentifications, as has been reported for certain strains of C. sakazakii and C. malonaticus that could not be differentiated (Iversen et al., 2007). Multilocus sequence analysis (MLSA) based on the sequences of housekeeping genes has proven to be a useful tool for the Enterobacteriaceaeae (Lacher et al., 2007; Ibarz Pavón & Maiden, 2009). Baldwin et al. (2009) applied MLSA based on seven housekeeping genes (atpD, fusA, gltS, gltB, gyrB, infB and ppsA) to C. sakazakii and C. malonaticus and demonstrated a robust phylogenetic analysis that separated the two species. The latter study also showed that some previous confusion between the two species may have been due to incorrect species identification of some biotype index strains (Baldwin et al., 2009). Further MLSA revealed a clear differentiation of all members of the genus Cronobacter and the association of C. sakazakii sequence type 4 with neonatal meningitis (Joseph & Forsythe, 2011; Kucerova et al., 2011). The scheme has open access at the Cronobacter multilocus sequence typing (MLST) website (http://pubmlst.org/ cronobacter). The present investigation determined the taxonomic position of five Cronobacter strains recovered from a leg infection, spiced meat, water and two food ingredients (onion powder and rye flour).

10 and 12) (Iversen et al., 2007, 2008). However, not all E. sakazakii strains were accommodated in the genus Cronobacter. Strain NCTC 9529T, the sole member of biogroup 16c, was suspected to represent another species of the genus Cronobacter, but insufficient strains and biochemical tests were available to define the species and consequently strain NCTC 9529T was assigned to Cronobacter genomospecies 1 (Iversen et al., 2007).

NCTC 9529T was previously assigned to E. sakazakii biogroup 16c as defined by Iversen et al. (2006b) on the basis of non-motility, acid production from inositol and dulcitol and utilization of malonate. The strain was later assigned to Cronobacter genomospecies 1 (Iversen et al., 2007). The remaining strains within biogroup 16 were defined as C. turicensis based on typing, DNA–DNA hybridization and amplified fragment length polymorphism (Iversen et al., 2007).

Strain 731 was isolated in 2005 from a post-operative mixed infection of a 9-year-old boy with humeral fracture treated by osteosynthesis using intra-medullar nailing. The strain was phenotypically identified as E. sakazakii and not further characterized. Staphylococcus aureus was also isolated from the infected site (M.-F. Prère, personal communication).

Strain 96 was isolated from onion powder purchased in the UK using Enterobacteriaceaeae enrichment broth and E. sakazakii chromogenic agar, as described by Iversen & Forsythe (2004). The strain was phenotypically identified as a member of E. sakazakii and assigned to biogroup 16 on the basis of motility, acid production from inositol and dulcitol, and utilization of malonate and ornithine (Iversen et al., 2006b). It was assigned to E. sakazakii cluster 2 according to its partial 16S rRNA gene sequence (528 bp) (accession no. AY579172) and hisp60 sequence (accession no. AY579197) by Iversen et al. (2004). Cluster 2 was later renamed without further analysis of strain 96 as C. turicensis in the taxonomic revision of E. sakazakii (Iversen et al., 2007).

Strain 1435 was isolated from rye flour purchased in Turkey using Enterobacteriaceaeae enrichment broth and Cronobacter chromogenic agar. The strain was phenotypically identified as a member of the genus Cronobacter in our laboratory.

The phenotypic tests used to evaluate strains 1330T, NCTC 9529T, 731, 96 and 1435 in the present study were selected from Iversen et al. (2006a, b, 2007, 2008): catalase and oxidase activity, nitrate reduction, acid production from sugars, malonate utilization, production of indole from tryptophan, motility, gas from D-glucose, Voges–Proskauer, methyl red, α-glucosidase activity, pigment production on tryptone soy agar (TSA; 21 and 37 °C), aerobic and anaerobic growth on TSA (37 °C), growth on MacConkey agar and hydrolysis of DNA. Acid production from carbohydrates was determined in nutrient broth supplemented with phenol red and the following substrates (1 %, w/v); sucrose, L-arabinose, cellobiose, lactose, raffinose, L-rhamnose, inositol, D-mannitol, D-sorbitol, N-acetylglucosamine and salicin. These tests were performed at least twice using conventional methods and, additionally, some tests (production of indole and hydrogen sulphide, Voges–Proskauer test, α-glucosidase and β-galactosidase, ornithine...
Two novel Cronobacter species
decarboxylase, hydrolysis of gelatin and urea and acid pro-
duction from D-mannitol, D-sorbitol, L-rhamnose, myo-
inositol, sucrose and L-arabinose) were performed in parallel
using the API 20 E and ID 32 E systems (bioMérieux).
Fermentation/oxidation of 49 carbohydrates was tested
using the API 50 CH system (bioMérieux), according to
the manufacturer’s instructions. Appropriate positive and
negative controls were included. All tests were performed at
37 °C and evaluated for 48 h. Type strains belonging to all
species of the genus Cronobacter were evaluated under
selected differential tests included in Table 1. Between three and 12 of these tests were able to
distinguish the test strains from other members of the genus Cronobacter.

Strains 1330T, NCTC 9529T, 731, 96 and 1435 were Gram-
negative, oxidase-negative, catalase-positive, facultatively
anaerobic rods that were positive for acetoin production
(Voges–Proskauer) and yellow pigmentation on TSA at 21 °C
after 48 h and negative for the methyl red test. They fer-
memented glucose, sucrose, cellobiose, arabinose, mannitol,
amygdalin and galacturonic acid, reduced nitrate, utilized
citrate, malonate and ornithine, and exhibited delayed DNase
activity. They did not hydrolyse urea or produce acid from
sorbitol, 5-ketogluconate or adonitol. These traits are com-
mon in the genus Cronobacter (Iversen et al., 2007, 2008).

Strain 1330T was found to be biochemically different from
all other members of the genus Cronobacter by at least six
different characters (Table 1). This strain was classified as
a member of C. sakazakii (biogroup 1) using criteria of
Farmer et al. (1980), but on the basis of the present results it
could be differentiated from this biogroup because it was not
motile, was able to produce indole from tryptophan and
and utilize malonate, and was not able to produce acid
from turanose, inositol, lactulose, putrescine, cis-aconit-
ate, 4-aminobutyrate, maltitol or palatinose. Strain 1330T
was relatively similar to strains NCTC 9529T, 731, 96 and
1435 but could be differentiated from them by several
characters, i.e. indole production and no acid production
from dulcitol, melezitose, inositol, lactulose and maltitol
(Table 1).

Strains NCTC 9529T, 731, 96, and 1435 were found to be
biochemically similar and different from all other members of
the genus Cronobacter by at least three characters (Table 1).
They could be differentiated from C. turicensis (biogroups
16, 16a and 16b) because they did not produce acid from
turanose, putrescine or 4-aminobutyrate.

The susceptibility of strains 1330T, NCTC 9529T, 731, 96
and 1435 to 17 antibiotics was assessed according to the
standards and procedures of the British Society for Anti-
microbial Chemotherapy (2010). The strains were classified
as susceptible, intermediate or resistant. Discs (Mast
Diagnostics) containing the following antibiotics were used
(µg per disc): amikacin (30), ampicillin (10), amoxicillin/
clavulanic acid (30), cefotaxime (30), cefuroxime (30),
cefpodoxime (10), ceftazidime (30), chloramphenicol (30),
ciprofloxacin (1), doxycycline (30), gentamicin (10), im-
ipenem (10), piperacillin/tazobactam (75/10), trimetho-
prim (2.5), ceftazidime/clavulanic acid (30/10), cefotaxime/
clavulanic acid (30/10) and cefpodoxime/clavulanic acid
(10/1) were tested.

Table 1. Phenotypic characters differentiating Cronobacter condimenti sp. nov., Cronobacter universalis sp. nov. and other members of the genus Cronobacter

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<td>Motility</td>
<td>-</td>
<td>V (-)</td>
<td>+ (+)</td>
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<td>+ (+)</td>
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<td>+ (+)</td>
<td>+ (+)</td>
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<td>Carbon utilization:</td>
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<tr>
<td>Dulcitol</td>
<td>-</td>
<td>+ (+)</td>
<td>- (-)</td>
<td>- (-)</td>
<td>+ (+)</td>
<td>+ (+)</td>
<td>- (-)</td>
<td>- (-)</td>
<td>- (-)</td>
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<tr>
<td>Indole</td>
<td>-</td>
<td>+ (-)</td>
<td>- (-)</td>
<td>- (-)</td>
<td>- (-)</td>
<td>+ (+)</td>
<td>+ (+)</td>
<td>+ (+)</td>
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<td>Malonate</td>
<td>+</td>
<td>+ (+)</td>
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<td>+ (+)</td>
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<td>10-Methyl x-D-glucopyranoside</td>
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<td>Melezitose</td>
<td>-</td>
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<td>Turanose</td>
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<td>+ (+)</td>
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<td>+ (+)</td>
<td>+ (+)</td>
<td>V (+)</td>
<td>+ (+)</td>
<td>V +</td>
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<tr>
<td>Inositol</td>
<td>-</td>
<td>+ (+)</td>
<td>V (+)</td>
<td>V (-)</td>
<td>+ (+)</td>
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<td>Lactulose</td>
<td>-</td>
<td>+ (+)</td>
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<td>Putrescine</td>
<td>-</td>
<td>+ (+)</td>
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<td>cis-Aconitate</td>
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<td>+ (+)</td>
<td>+ (+)</td>
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<td>+ (+)</td>
<td>+ (+)</td>
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<td>trans-Aconitate</td>
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<td>+ (+)</td>
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<td>+ (+)</td>
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<td>4-Aminobutyrate</td>
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<td>+ (+)</td>
<td>+ (+)</td>
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<tr>
<td>Maltitolar</td>
<td>-</td>
<td>+ (+)</td>
<td>+ (+)</td>
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<tr>
<td>Palatinose</td>
<td>-</td>
<td>V (-)</td>
<td>+ (+)</td>
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<td>+ (+)</td>
<td>V (+)</td>
<td>+ (+)</td>
<td>+ (+)</td>
<td>+ +</td>
</tr>
</tbody>
</table>

Taxa: 1, Cronobacter condimenti sp. nov. 1330T; 2, Cronobacter universalis sp. nov. (n=4); 3, C. sakazakii ATCC 29544T; 4, C. malonicus LMG 23826T; 5, C. turicensis LMG 23827T; 6, C. muytjensii ATCC 51329T; 7, C. dublinensis subsp. dublinensis LMG 23823T; 8, C. dublinensis subsp. lactaridi; 9, C. dublinensis subsp. lausannensis. Data in columns 1 and 2 and in parentheses (i.e. results for type strains) were obtained in this study and data in columns 3–9 were from Iversen et al. (2007, 2008). +, Positive; v, 20–80% variable; –, negative.
For phylogenetic studies of the 16S rRNA gene and seven housekeeping genes (MLSA), strains were cultured on TSA at 37 °C. DNA was extracted from a single colony by using a GenElute Bacterial Genomic DNA kit (Sigma-Aldrich), according to the manufacturer’s instructions. The primers and conditions for amplification and sequencing of the 16S rRNA gene (1361 bp), *atpD* (390 bp), *fusA* (438 bp), *ghsS* (363 bp), *gltB* (507 bp), *gyrB* (402 bp), *infB* (441 bp) and *ppsA* (495 bp) genes have been described elsewhere (Iversen et al., 2007; Baldwin et al., 2009). Amplification products were sequenced with an ABI sequencer (Applied Biosystems). 16S rRNA gene sequences (1361 bp) for the type strains of all members of the genus *Cronobacter* were sequenced with an ABI sequencer (Applied Biosystems). 16S rRNA gene sequences (1361 bp) for the type strains of all members of the genus *Cronobacter* were obtained from GenBank and available housekeeping gene sequences (Baldwin et al., 2009) were obtained from the MLST database. Sequences were independently aligned using CLUSTAL W version 2 (Larkin et al., 2007) and MEGA version 4 (Tamura et al., 2007). Genetic distances and clustering were determined by using Kimura’s two-parameter model (Kimura, 1980) and evolutionary trees were reconstructed using the neighbour-joining method (Saitou & Nei, 1987). The stability of the relationships was assessed using the bootstrap method with 1000 replicates. The 16S rRNA gene sequence similarities (1361 bp) were determined using EzTaxon server (Chun et al., 2007).

The 16S rRNA gene phylogenetic tree of the genus *Cronobacter* (Fig. 1.) showed that strain 1330T formed one independent lineage and that strains NCTC 9529T, 731, 96 and 1435T formed another independent lineage within the cluster containing *C. dublinensis* DES187T and *C. turicensis* z3032T. 16S rRNA gene sequence similarities between strains 1330T and NCTC 9529T and the other recognized members of the genus *Cronobacter* were 99.7–98.2 %, which corresponds to 4–24 bp difference. The highest sequence similarities were obtained between strain NCTC 9529T and *C. turicensis* z3032T (99.7 %; 4 bp difference) and between strain 1330T and *C. turicensis* z3032T (98.6 %; 19 bp difference). Sequence similarities between strain NCTC 9529T and strains 731, 96 and 1435 were 99.4, 99.6 and 99.7 % (8, 5 and 4 bp difference), respectively.

MLSA showed that strains 1330T, NCTC 9529T, 731, 96 and 1435 belonged to the genus *Cronobacter*, but represented two independent branches (Fig. 2). The MLSA phylogenetic tree revealed that the closest phylogenetic neighbour to strain 1330T was *C. dublinensis* LMG 23823T, despite strain 1330T having highest 16S rRNA gene sequence similarity with *C. turicensis* z3032T. However, *C. turicensis* LMG 23827T was the closest neighbour of strains NCTC 9529T, 731, 96 and 1435, as also shown by 16S rRNA gene sequence analysis.

DNA–DNA hybridization (direct and reciprocal) experiments were performed between strains 1330T and NCTC 9529T and between these two strains and the type strains of the currently accepted species of the genus *Cronobacter*. DNA was extracted according to Marmur (1961) and DNA–DNA hybridization was conducted according to Urdiain et al. (2008) under optimal conditions at 68 °C. Single- and double-stranded DNA was separated with hydroxyapatite. Colour development was measured at 405 nm using a Bio Whittaker Kinetic-QCL microplate reader. DNA–DNA reassociation values were determined at least three times. All results were below the 70 % limit for species definition (Table 2) (Wayne et al., 1987; Stackebrandt & Goebel, 1994). Although DNA–DNA relatedness is considered to give information on the similarity of entire bacterial genomes, it has been criticized because of the high number of experimental errors, the lack of reproducibility and the failure to generate collective databases (Rossello-Mora, 2006). Moreover, DNA–DNA relatedness does not provide any information concerning phylogenetic relationships (Harayama & Kasai, 2006), in contrast to the phylogenetic reconstruction with MLSA (Baldwin et al., 2009).

16S rRNA gene sequencing, MLSA, DNA–DNA relatedness and phenotypic characterization clearly differentiated strains 1330T, NCTC 9529T, 731, 96 and 1435 from existing species of the genus *Cronobacter* and showed that they constituted
two independent lineages within the genus. Therefore, two novel species are proposed to accommodate these strains: *Cronobacter condimenti* sp. nov. (strain 1330<sup>T</sup>) and *Cronobacter universalis* sp. nov. (strains NCTC 9529<sup>T</sup>, 731, 96 and 1435).

**Description of Cronobacter condimenti** sp. nov.

*Cronobacter condimenti* (condi.mi.ti. L. gen. n. condimenti of spice, seasoning).

Cells are straight, Gram-negative, non-motile, non-spore-forming rods. Colonies on TSA incubated at 37 °C for 24 h are 2–3 mm in diameter, opaque, circular and yellow. Grows on MacConkey agar. In TSB, grows at 45 °C (optimum 37 °C), but not at 5 °C. No haemolysis is observed on sheep blood agar at 37 °C. Produces catalase, α-glucosidase, β-galactosidase and DNase, but not oxidase. Produces acetoin (Voges–Proskauer positive) and indole from tryptophan, but not hydrogen sulphide. Hydrolyses gelatin, but not urea. Reduces nitrate. Does not produce gas from glucose. Utilizes ornithine, citrate and malonate. Produces acid from 10-methyl α-D-glucopyranoside, glycerol, L-arabinose, ribose, D-xylene, galactose, D-glucose, D-fructose, D-mannose, L-rhamnose, D-mannitol, N-acetylglucosamine, arbutin, aesculin, salicin, cellobose, maltose, lactose, melibiose, sucrose, trehalose, myo-inositol, raffinose, β-gentiobiose, D-fucose, D-fucose and galacturonic acid, but not from dulcitol, inositol, melezitose, turanose, lactulose, putrescine, cis- or trans-aconitate, 4-amino butyrate, maltitol, palatinose, D-erythritol, D-arabinose, adonitol, methyl β-D-xylidine, L-sorbose, dulcitol, sorbitol, methyl α-D-glucoside, inulin, glycogen, xylitol, D-lyxose, D-tagatose, D-arabitol, L-arabitol, gluconate, 2-ketogluconate or 5-ketogluconate. Resistant to doxycycline; susceptible to the other antimicrobials tested. The API 20 E and ID 32 E profiles of the type strain are 3367373 and 342137610030, respectively. The type strain is 1330<sup>T</sup> (CECT 7863<sup>T</sup> LMG 26250<sup>T</sup>), isolated from spiced meat purchased in Slovakia.

**Table 2.** DNA–DNA relatedness between *Cronobacter condimenti* sp. nov. and *Cronobacter universalis* sp. nov. with other members of the genus *Cronobacter*

Data in column 1 were taken from this study and in column 2 from Iversen *et al.* (2008).

<table>
<thead>
<tr>
<th>Strain</th>
<th>Hybridization (mean ± SD; %) with labelled DNA from:</th>
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<tr>
<td></td>
<td><em>C. condimenti</em> 1330&lt;sup&gt;T&lt;/sup&gt;</td>
</tr>
<tr>
<td><em>C. sakazakii</em> ATCC 29544&lt;sup&gt;T&lt;/sup&gt;</td>
<td>40.3 ± 7.7</td>
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<tr>
<td><em>C. malonaticus</em> CDC 1058-77&lt;sup&gt;T&lt;/sup&gt;</td>
<td>53.0 ± 14.4</td>
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<tr>
<td><em>C. muytjensii</em> ATCC 51329&lt;sup&gt;T&lt;/sup&gt;</td>
<td>42.0 ± 9.3</td>
</tr>
<tr>
<td><em>C. dublinensis</em> LMG 23823&lt;sup&gt;T&lt;/sup&gt;</td>
<td>54.2 ± 8.7</td>
</tr>
<tr>
<td><em>C. turicensis</em> LMG 23827&lt;sup&gt;T&lt;/sup&gt;</td>
<td>47.9 ± 5.9</td>
</tr>
<tr>
<td><em>C. universalis</em> NCTC 9529&lt;sup&gt;T&lt;/sup&gt;</td>
<td>50.7 ± 7.6</td>
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</table>

![Fig. 2. Neighbour-joining phylogenetic tree based on concatenated atpD, fusA, glnS, gltB, gyrB, infB and ppsA sequences (http://pubmlst.org/cronobacter), showing the position of strains 1330<sup>T</sup>, NCTC 9529<sup>T</sup>, 96, 731 and 1435 within the genus *Cronobacter*. Bootstrap values (>70%) based on 1000 replications are shown at branch nodes. Bar, 1 substitution per 100 nucleotide positions.](http://ijs.sgmjournals.org)
The species description is based on four strains. Cells are straight, Gram-negative, non-spore-forming rods with variable motility (the type strain is non-motile). Colonies on TSA incubated at 37 °C for 24 h are 2–3 mm in diameter, opaque, circular and yellow. Grows on MacConkey agar. In TSB, grows at 45 °C (optimum 37 °C), but not at 5 °C. No haemolysis is observed on sheep blood agar at 37 °C. Produces catalase, α-glucosidase, β-galactosidase and DNase, but not oxidase. Produces acetoin (Voges–Proskauer positive), but not indole from tryptophan or hydrogen sulphide. Does not hydrolyse gelatin or urea. Reduces nitrate. Utilizes malonate, ornithine and citrate. Produces acid from glucose, 10-methyl α-D-glucopyranoside, dulcitol, inositol, melezitose, lactulose, sucrose, L-arabinose, cellobiose, lactose, myo-inositol, L-rihamnose, D-mannitol, N-acetylglucosamine, salicin, maltitol, D-fucose, amygdalin and galacturonic acid, but not from turanose, D-sorbitol, putrescine, trans-aconitate, L-fucose, adonitol, 5-ketogluconate or 4-aminobutyrate. Variable results are obtained for acid production from cis-aconitate and palatinose and production of gas from glucose (the type strain is negative). Resistant to doxycycline; susceptible to the other antimicrobials tested. The API 20 E and ID 32 E profiles of the type strain are 3205373 and 2427677051, respectively. The type strain is NCTC 9529T (≡CECT 7864T=LMG 26249T), isolated from fresh water and deposited at the NCTC (London) in 1954.

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References


