Cronobacter gen. nov., a new genus to accommodate the biogroups of *Enterobacter sakazakii*, and proposal of *Cronobacter sakazakii* gen. nov., comb. nov., *Cronobacter malonaticus* sp. nov., *Cronobacter turicensis* sp. nov., *Cronobacter muytjensii* sp. nov., *Cronobacter dublinensis* sp. nov., *Cronobacter* genomospecies 1, and of three subspecies, *Cronobacter dublinensis* subsp. *dublinensis* subsp. nov., *Cronobacter dublinensis* subsp. *lausannensis* subsp. nov. and *Cronobacter dublinensis* subsp. *lactaridi* subsp. nov.

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[*Enterobacter*] *sakazakii* is an opportunistic pathogen that can cause infections in neonates. This study further clarifies the taxonomy of isolates described as [*E.*] *sakazakii* and completes the formal description of the proposed reclassification of these organisms as novel species and subspecies within a proposed novel genus, *Cronobacter* gen. nov. [*E.*] *sakazakii* was first defined in 1980, however recent polyphasic taxonomic analysis has determined that this group of organisms consists of several genomospecies. In this study, the phenotypic descriptions of the proposed novel species are expanded using Biotype 100 and Biolog Phenotype MicroArray data. Further DNA–DNA hybridization experiments showed that malonate-positive strains within the [*E.*] *sakazakii* genomospecies represent a distinct species, not a subspecies. DNA–DNA hybridizations also determined that phenotypically different strains within the proposed species, *Cronobacter dublinensis* sp. nov., belong to the same species and can be considered as novel subspecies. Based on these analyses, the following alternative classifications are proposed: *Cronobacter sakazakii* gen. nov., comb. nov. [type strain ATCC 29544^T (=NCTC 11467^T)]; *Cronobacter malonaticus* sp. nov. [type strain CDC 1058-77^T (=LMG 23826^T=DSM 18702^T)]; *Cronobacter turicensis* sp. nov. [type strain z3032^T (=LMG 23827^T=DSM 18703^T)]; *Cronobacter muytjensii* sp. nov. [type strain ATCC 51329^T (=CIP 103581^T)]; *Cronobacter*

Abbreviation: f-AFLP, fluorescent-amplified fragment length polymorphism.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of the members of the genus *Cromobacter* gen. nov. described in this paper are the following: *Cronobacter sakazakii* gen. nov., comb. nov. ATCC 29544^T, EF059843; *Cronobacter malonaticus* sp. nov. CDC 1058-77^T, EF059881; *Cronobacter turicensis* sp. nov. z3032^T, EF059891; *Cronobacter muytjensii* sp. nov. ATCC 51329^T, EF059845; *Cronobacter dublinensis* sp. nov. DES187^T, EF059892; *Cronobacter dublinensis* subsp. *lausannensis* subsp. nov. E515^T, EF059841; *Cronobacter dublinensis* subsp. *lactaridi* subsp. nov. E464^T, EF059838, and *Cronobacter* genomospecies 1 strain NCTC 9529, EF059877.

dublinensis sp. nov. [type strain DES187^T (=LMG 23823^T=DSM 18705^T)]; *Cronobacter dublinensis* subsp. *dublinensis* subsp. nov. [type strain DES187^T (=LMG 23823^T=DSM 18705^T)]; *Cronobacter dublinensis* subsp. *lausannensis* subsp. nov. [type strain E515^T (=LMG 23824=DSM 18706^T)], and *Cronobacter dublinensis* subsp. *lactaridi* subsp. nov. [type strain E464^T (=LMG 23825^T=DSM 18707^T)].

[*Enterobacter*] *sakazakii* was defined as a novel species by Farmer *et al.* (1980), however the existence of divergent biogroups suggested that these organisms represented multiple species. Recently, a study using a polyphasic taxonomic approach was undertaken utilizing full-length 16S rRNA gene sequencing, ribotyping, fluorescent-amplified fragment length polymorphism (f-AFLP) and DNA–DNA hybridization, which showed that these organisms comprise at least five genomospecies (Iversen *et al.*, 2007). It was also proposed that these species should be moved to a novel genus, *Cronobacter* gen. nov., but this new genus name and those proposed for the novel species were not validly published. This reclassification will facilitate the continued recognition of all these organisms in current identification schemes, the proposed genus *Cronobacter* being contaxic with [*Enterobacter*] *sakazakii*.

The division of species is for the most part equated to particular previously described biogroups. Farmer's original biogroups identified as 1–4, 7, 8, 11 and 13 are proposed as *Cronobacter sakazakii* gen. nov., comb. nov. and biogroups 5, 9 and 14 as *Cronobacter malonaticus* sp. nov. (Farmer *et al.*, 1980; Iversen *et al.*, 2007). Farmer's biogroup 15 is proposed as *Cronobacter muytjensii* sp. nov. and the recently described biogroup 16 (Iversen *et al.*, 2006) is proposed as *Cronobacter turicensis* sp. nov., with the exception of two strains that appear to be a separate genomospecies and which are designated at this time as *Cronobacter* genomospecies 1 (Iversen *et al.*, 2007). Farmer's biogroups 6, 10 and 12 are proposed as *Cronobacter dublinensis* sp. nov., with biogroup 12 proposed as *Cronobacter dublinensis* subsp. *dublinensis* subsp. nov., biogroup 10 as *Cronobacter dublinensis* subsp. *lausannensis* subsp. nov., and biogroup 6 as *Cronobacter dublinensis* subsp. *lactaridi* subsp. nov.

Bacterial strains were sourced as described previously (Iversen *et al.*, 2007). DNA–DNA hybridizations were carried out spectrophotometrically in 2×SSC+5% formamide by the DSMZ, Braunschweig, Germany, using the method described by De Ley *et al.* (1970) at 70 °C, with consideration of the modifications described by Huß *et al.* (1983). The DNA–DNA relatedness values for the proposed species are given in Table 1. Biochemical tests were performed using the Biotype 100 system (bioMérieux) with Biotype Medium 1. Positive tests were scored after observation of turbidity or colour change following growth in single carbon sources according to the manufacturer's instructions. For the Biolog Phenotype MicroArray (Biolog), cell suspensions were prepared from 24 h cultures grown on blood agar at 37 °C and suspended in either IF-0 or IF-10 medium (Biolog) to the appropriate density. Metabolic panels PM1 and PM2A (Biolog) were inoculated with 200 µl per well from an inoculum comprising 15 ml

Table 1. DNA–DNA relatedness of *Cronobacter* strains

Taxa: 1, *C. sakazakii* ATCC 29544^T; 2, *C. sakazakii* ATCC 12868; 3, *C. turicensis* z3032^T; 4, *C. muytjensii* ATCC 51329^T; 5, *C. malonaticus* CDC 1058-77^T; 6, *C. dublinensis* NCTC 9844. Similarity values are means of duplicate measurements and standard deviations are given in parentheses (values can be reproduced in a range of about 10%).

Strains	DNA–DNA relatedness (%) with *Cronobacter* strains (in 2×SSC+5% formamide at 70 °C)					
	1	2	3	4	5	6
C. sakazakii ATCC 12868 (biogroup 1)	70.0 (2.4)					
C. turicensis z3032^T (=LMG 23827^T) (biogroup 16)	51.8 (2.8)	51.9 (2.6)				
C. turicensis E609 (biogroup 16)	61.7 (3.6)	52.7 (1.8)	86.1 (1.3)			
C. muytjensii ATCC 51329^T (biogroup 15)	53.3 (3.0)	42.0 (4.0)	56.0 (4.2)			
C. muytjensii CDC 3523-75 (biogroup 15)	37.7 (1.8)	31.3 (6.2)		91.9 (4.9)		
C. malonaticus CDC 1058-77^T (biogroup 9)	54.7 (6.1)	54.1 (0.9)	54.0 (8.1)	54.3 (0.3)		
C. malonaticus E265 (biogroup 5)	55.6 (5.5)	60.1 (6.4)			95.6 (7.2)	
C. dublinensis subsp. *lausannensis* NCTC 9844 (biogroup 10)	16.7 (7.6)	43.0 (9.8)	36.8 (2.2)	54.5 (4.7)	46.4 (1.3)	
C. dublinensis subsp. *lactaridi* CDC 5960-70 (biogroup 6)	37.3 (0.0)	54.8 (2.1)				77.4 (7.5)
C. dublinensis subsp. *dublinensis* DES187^T (=LMG 23823^T) (biogroup 12)	54.1 (5.1)	52.0 (6.7)				95.2 (7.9)
Cronobacter genomospecies 1 NCTC 9529 (biogroup 16)	55.5 (1.0)	54.4 (3.9)	55.0 (3.3)	53.1 (6.6)	60.1 (1.3)	45.9 (2.0)

of 1.2 × IF-0 medium and 0.225 ml dye mix D (Biolog), 3.45 ml sterile distilled water and 0.375 ml cell suspension in IF-0 corresponding to 42 % transmittance. Metabolic panels PM9 and PM10 (Biolog) were inoculated with 200 µl per well from an inoculum comprising 20.8 ml 1.2 × IF-10 medium and 0.25 ml dye mix D, 3.8 ml sterile distilled water and 0.125 ml cell suspension in IF-10 corresponding to 85 % transmittance. All of the plates were incubated for 48 h at 37 °C and the data recorded using an Omnilog instrument (Biolog). The areas under the growth curves were analysed and a value of greater than 15 000 tetrazolium dye reduction units was used to designate a positive result for individual tests. This cut-off value was determined by comparing quantitative plate counts with tetrazolium dye reduction units over a 48 h incubation period for the type strain of *Cronobacter sakazakii* gen. nov., comb. nov. ATCC 29544^T, grown in IF-0 medium supplemented with sodium succinate as the carbon source plus a 1 : 5 dilution of IF-10 medium. The utilization of malonate was also determined using malonate phenylalanine broth (Fluka 63286; Sigma-Aldrich), with a colour change in the broth from green to blue indicating a positive result. Indole production was determined by adding Kovac's reagent to cultures grown in tryptone. A negative designation for a particular trait denotes consistent negative results for isolates across all methods. A positive designation denotes a positive result using one or more methods, the test methods that distinguish the species and subspecies are indicated in Table 2.

The DNA–DNA hybridization results in Table 1 include data for at least two strains from each proposed novel species. As described previously, results for *C. sakazakii* gen. nov., comb. nov., *C. turicensis* sp. nov. and *C. muytjensii* sp. nov. intra-species pairs were at or above a relatedness value of 70 %, while the inter-species hybridization results were below 70 % (Iversen *et al.*, 2007). Previously 16S rRNA gene sequencing and ribotyping indicated that biogroups 5, 9 and 14 formed a subgroup within the *C. sakazakii* genomospecies (Iversen *et al.*, 2007). However, DNA–DNA hybridization showed that the DNA relatedness of strain CDC 1058-77^T (biogroup 9) with strain E265 (biogroup 5) was 95.6 % and the DNA–DNA relatedness to the type strains of other species of *Cronobacter* gen. nov. was less than 70 %. Therefore these strains represent a distinct species, not a subspecies, and it is proposed that they are classified as *Cronobacter malonaticus* sp. nov. The proposed species *Cronobacter dublinensis* sp. nov. comprises strains identified previously as biogroups 6, 10 and 12 (Farmer *et al.*, 1980). DNA–DNA hybridization of strain CDC 5960-70 (biogroup 6) and strain NCTC 9844 (biogroup 10) showed 77.4 % DNA–DNA relatedness, while DNA–DNA hybridization of strain NCTC 9844 with strain DES187^T (biogroup 12) showed 95.2 % relatedness. The DNA relatedness to *C. sakazakii* gen. nov, comb. nov. strains ATCC 29544^T and ATCC 12868 (both biogroup 1 strains) was less than 55 % for all strains of *C. dublinensis* sp. nov. Also, the DNA–DNA relatedness values for *C. dublinensis* sp. nov. strain NCTC 9844 with *C. turicensis* sp. nov. strain z3032^T, with *C. muytjensii* sp. nov. strain ATCC 51329^T and with *C. malonaticus* sp. nov. strain CDC 1058-77^T were less than 55 %. These results support the conclusion that the strains of *C. dublinensis* sp. nov. belong to the same species, which is distinct from other proposed species of the genus *Cronobacter* gen. nov.

Table 2. Biochemical tests for the differentiation of species and subspecies of the genus *Cronobacter* gen. nov.

Taxa: 1, *C. sakazakii*; 2, *C. malonaticus*; 3, *C. turicensis*; 4, *Cronobacter* genomospecies 1; 5, *C. muytjensii*; 6, *C. dublinensis* subsp. *dublinensis*; 7, *C. dublinensis* subsp. *lactaridi*; 8, *C. dublinensis* subsp. *lausannensis*. +, >90 % Positive; v, 20–80 % positive; −, <10 % positive. All results are from Biotype 100 unless otherwise indicated.

Characteristic	1	2	3	4	5	6	7	8
Indole production*	−	−	−	−	+	+	+	v
Carbon source utilization:								
Dulcitol†	−	−	+	+	+	−	−	−
Lactulose	+	+	+	+	+	+	+	−
Malonate‡	−	+	+	v	+	+	−	−
Maltitol	+	+	+	+	−	+	+	−
Palatinose	+	+	+	+	v	+	+	+
Putrescine	+	v	+	v	+	+	+	v
Melezitose	−	−	+	−	−	+	−	−
Turanose	+	+	+	v	v	+	v	−
myo-Inositol†	v	v	+	+	+	+	+	−
cis-Aconitate	+	+	+	+	v	+	+	+
trans-Aconitate	−	+	−	+	v	+	+	+
1-0-Methyl α-D-glucopyranoside	+	+	+	+	−	+	+	+
4-Aminobutyrate	+	+	+	v	+	+	+	+

*Using Kovac's reagent after growth in tryptone.
†Additional data from Biolog Phenotype MicroArray.
‡Using malonate phenylalanine broth.

The phenotypic profiles determined the presence of fourteen variable biochemical characteristics that differentiated the proposed novel species and subspecies within *Cronobacter* gen. nov. These were, utilization of dulcitol, lactulose, maltitol, palatinose, putrescine, melezitose, turanose, *myo*-inositol, *trans*-aconitate, *cis*-aconitate, 1-0-methyl α-D-glucopyranoside and 4-aminobutyrate as sole carbon sources; utilization of malonate as indicated by increase in pH in malonate phenylalanine broth, and production of indole as revealed on addition of Kovac's reagent to cultures grown in tryptone. Moreover, phenotypic analysis, with the Biotype 100 and Biolog Phenotype MicroArray, of at least two strains from each of the proposed novel species and subspecies within the proposed novel genus *Cronobacter* enabled further description of the proposed reclassification of [*Enterobacter*] *sakazakii*.

As only two strains exist in the DNA–DNA hybridization group described as *Cronobacter* genomospecies 1, at the present time it is proposed that a novel genomospecies is

designated, represented by strain NCTC 9529. This strain was originally isolated from water and deposited at the NCTC, London, UK, in 1954. It has previously been described as biogroup 16, subgroup c, within the 16S rRNA gene cluster group 2 by Iversen *et al.* (2006). *Cronobacter* genomospecies 1 strains are positive for the utilization of dulcitol, *myo*-inositol, *trans*-aconitate, *cis*-aconitate, maltitol, lactulose, palatinose and 1-0-methyl α-D-glucopyranoside. The utilization of turanose, putrescine, malonate and 4-aminobutyrate is variable.

Description of *Cronobacter* gen. nov.

Cronobacter [Cro.no.bac′ter. Gr. n. *Cronos* one of the Titans of mythology who swallowed each of his children as soon as they were born (Graves, 1992); N.L. masc. n. *bacter* a rod; N.L. masc. n. *Cronobacter* a rod that can cause infection in neonates].

Comprises oxidase-negative, catalase-positive, facultatively anaerobic, peritrichous, Gram-negative rods that are approximately 3 μm × 1 μm in size. Generally motile, reduce nitrate, utilize citrate, hydrolyse aesculin and arginine and test positive for L-ornithine decarboxylation. Acid is produced from D-glucose, sucrose, raffinose, melibiose, cellobiose, D-mannitol, D-mannose, L-rhamnose, L-arabinose, D-xylose, trehalose, galacturonate and maltose. Generally positive for acetoin production (Voges–Proskauer test) and negative for the methyl red test, indicating 2,3-butanediol rather than mixed acid fermentation. Growth occurs between 6 and 45 °C in brain heart infusion broth (CM1032; Oxoid). Growth also occurs between pH 5 and 10, inclusive, as measured by the Biolog Phenotype MicroArray, with no growth for any strain below pH 4.5. Growth also consistently occurs in concentrations of sodium chloride up to 7 % (w/v) and no isolates are able to grow in 10 % sodium chloride. Growth is possible in concentrations up to 100 mM of ammonium sulphate, sodium nitrate and sodium nitrite, in 200 mM sodium phosphate, in 5 % sodium sulphate and in 20 % ethylene glycol. Growth does not occur above a concentration of 20 mM sodium benzoate. The following compounds are utilized as sole carbon sources: α-D-glucose, β-D-fructose, D-galactose, trehalose, D-mannose, α-melibiose, sucrose, raffinose, maltotriose, maltose, α-lactose, 1-0-methyl α/β-galactopyranoside, cellobiose, β-gentiobiose, 1-0-methyl β-D-glucopyranoside, aesculin, L-arabinose, D-xylose, glycerol, D-mannitol, L-malate, D-glucuronate, D-galacturonate, 2-keto-D-gluconate, *N*-acetyl-D-glucosamine, arbutin, DL-α-glycerol-phosphate, dihydroxyacetone, D-ribose, L-lyxose, pyruvic acid, D-gluconate, DL-lactate, succinate, fumarate, DL-glycerate, D-glucosamine, L-aspartate, L-glutamate, L-proline, D-alanine, L-alanine and L-serine. Metabolize the substrates 5-bromo-4-chloro-3-indolyl-α-D-glucopyranoside, 4-methylumbelliferyl-α-D-glucopyranoside, 4-nitrophenyl-α/β-D-glucopyranoside and 4-nitrophenyl-α/β-D-galactopyranoside. The following compounds are not hydrolysed: 4-nitrophenyl-β-D-glucuronide, L-aspartic acid 4-nitroanilide. Negative reactions include hydrogen sulphide production, urea hydrolysis, lysine decarboxylation and β-D-glucuronidase activity. The following compounds are not utilized as sole sources of carbon: L-sorbose, α-L-fucose, D-arabitol, L-arabitol, xylitol, D-tagatose, D-sorbitol, adonitol, hydroxyquinoline-β-glucuronide, *i*-erythritol, 3-0-methyl D-glucopyranose, D-saccharate, mucate, L-tartrate, D-tartrate, *meso*-tartrate, tricarballylate, 5-keto-D-gluconate, L-tryptophan, phenylacetate, protocatechuate, 4-hydroxybenzoate, quinate, gentisate, 3-hydroxybenzoate, benzoate, 3-phenylpropionate, *m*-coumarate, trigonelline, betaine, histamine, caprate, caprylate, L-histidine, glutarate, 5-aminovalerate, ethanolamine, tryptamine, itaconate, 3-hydroxybutyrate, propionate, L-tyrosine, α-ketoglutarate, sodium pyruvate, amygdalin, D-serine, D-threonine, inulin, L-alaninamide, laminarin, L-glucose, L-homoserine, L-isoleucine, L-leucine, L-lysine, L-methionine, L-phenylalanine, L-valine, mannan, tyramine, glucose 1-phosphate and glucose 6-phosphate (Farmer *et al.*, 1980; Farmer, 1999; Iversen *et al.*, 2006, 2007; and this study). The utilization of melezitose, malonate, dulcitol, *myo*-inositol, turanose, *trans*-aconitate, *cis*-aconitate, maltitol, putrescine, lactulose, 1-0-methyl α-D-glucopyranoside, palatinose, adenosine, D-arabinose, D-psicose, formate, inosine, L-asparagine, L-glutamine, L-rhamnose, salicin, stachyose, thymidine, uridine and 4-aminobutyrate, and the production of indole are variable. The type species is *Cronobacter sakazakii*.

Description of *Cronobacter sakazakii* comb. nov.

Cronobacter sakazakii (sa.ka.za′ki.i. N.L. gen. n. *sakazakii* of Sakazaki, in honour of the Japanese microbiologist Riichi Sakazaki).

Basonym: *Enterobacter sakazakii* Farmer *et al.* 1980.

Comprises biogroups 1–4, 7, 8, 11 and 13 as previously described (Farmer *et al.*, 1980) and gives a positive result in tests for the utilization of putrescine, turanose, maltitol, lactulose, 1-0-methyl α-D-glucopyranoside, palatinose, *cis*-aconitate and 4-aminobutyrate. The utilization of *myo*-inositol is variable and a small number of strains (less than 5 %) utilize malonate. The type strain is positive for utilization of *myo*-inositol and negative for utilization of malonate.

The type strain, ATCC 29544^T (=NCTC 11467^T), was originally isolated from a child's throat (Farmer *et al.*, 1980). Previously, DNA G+C ratios of 57 and 56.7 mol% have been reported for strains of [*Enterobacter*] *sakazakii* (Farmer *et al.*, 1980; http://genome.wustl.edu/pub/organism/Microbes/Enteric_Bacteria/Enterobacter_sakazakii/assembly/draft/Enterobacter_sakazakii-4.0/ASSEMBLY).

Description of *Cronobacter malonaticus* sp. nov.

Cronobacter malonaticus (mal.on.at.i′cus. N.L. n. *malonas* -*atis* malonate; L. suff. -*icus* suffix used with the sense of belonging to; N.L. masc. adj. *malonaticus* pertaining to the utilization of malonate).

This species comprises biogroups 5, 9 and 14 as previously described (Farmer *et al.*, 1980). Positive for utilization of malonate, lactulose, 4-aminobutyrate, maltitol, 1-0-methyl α-D-glucopyranoside, turanose, *trans*-aconitate, *cis*-aconitate and palatinose. Utilization of putrescine and *myo*-inositol is variable. The type strain is positive for utilization of putrescine and negative for *myo*-inositol.

The type strain, CDC 1058-77^T (=LMG 23826^T=DSM 18702^T), was originally isolated from a breast abscess.

Description of *Cronobacter turicensis* sp. nov.

Cronobacter turicensis (tu.ri.cen′sis. L. masc. adj. *turicensis* pertaining to Turicum, the Latin name of Zurich, as the type strain was isolated in Zurich, Switzerland).

This species is derived from biogroup 16 as described by Iversen *et al.* (2006). Strains are positive for utilization of melezitose, dulcitol, *myo*-inositol, turanose, *cis*-aconitate, maltitol, putrescine, lactulose, 1-0-methyl α-D-glucopyranoside, palatinose, malonate and 4-aminobutyrate.

The type strain, z3032^T (=LMG 23827^T=DSM 18703^T), was isolated from a blood culture during a case of neonatal meningitis occurring in Zurich in 2005 (Essers *et al.*, 2006).

Description of *Cronobacter muytjensii* sp. nov.

Cronobacter muytjensii (muy.tjen.si.i. N.L. gen. n. *muytjensii* of Muytjens, named in honour of the Dutch microbiologist Harry Muytjens, who performed much of the early work on [*Enterobacter*] *sakazakii*).

Comprises biogroup 15 as previously described (Farmer *et al.*, 1980). Positive for indole production and utilization of malonate, dulcitol, *myo*-inositol, putrescine, lactulose and 4-aminobutyrate. Utilization of turanose, *trans*-aconitate, *cis*-aconitate and palatinose is variable. The type strain is positive for utilization of turanose and palatinose but negative for utilization of *trans*- and *cis*-aconitate.

The type strain, ATCC 51329^T (=CIP 103581^T), was originally deposited in both collections by bioMérieux, La Balme-les-Grottes, France.

Description of *Cronobacter dublinensis* sp. nov.

Cronobacter dublinensis (dub.lin.en′sis. N.L. masc. adj. *dublinensis* pertaining to Dublin, Ireland, the origin of the type strain).

Comprises biogroups 6, 10 and 12 as previously described (Farmer *et al.*, 1980). Generally positive for utilization of *trans*-aconitate, *cis*-aconitate, 1-0-methyl α-D-glucopyranoside, palatinose and 4-aminobutyrate. The utilization of melezitose, malonate, *myo*-inositol, turanose, maltitol, putrescine, lactulose, and the production of indole are variable. The type strain gives a positive result for all of these tests.

The type strain, DES187^T (=LMG 23823^T=DSM 18705^T), was isolated from an environmental sample obtained from a milk powder manufacturing facility in 2004. The strain has also been referred to as strain CFS237.

Description of *Cronobacter dublinensis* subsp. *dublinensis* subsp. nov.

Cronobacter dublinensis subsp. *dublinensis* (dub.lin.en′sis. N.L. masc. adj. *dublinensis* pertaining to Dublin, Ireland, the origin of the type strain).

This subspecies corresponds to Farmer's biogroup 12 (Farmer *et al.*, 1980) and is positive for production of indole and for utilization of melezitose, malonate, *myo*-inositol, turanose, *trans*-aconitate, *cis*-aconitate, maltitol, putrescine, lactulose, 1-0-methyl α-D-glucopyranoside, palatinose and 4-aminobutyrate.

The type strain is DES187^T (=LMG 23823^T=DSM 18705^T).

Description of *Cronobacter dublinensis* subsp. *lausannensis* subsp. nov.

Cronobacter dublinensis subsp. *lausannensis* (lau.sann.en′sis. L. masc. adj. *lausannensis* pertaining to Lausanne, Switzerland, the origin of the type strain for this subspecies).

This subspecies corresponds to Farmer's biogroup 10 (Farmer *et al.*, 1980). Positive for utilization of *trans*-aconitate, *cis*-aconitate, 1-0-methyl α-D-glucopyranoside, palatinose and 4-aminobutyrate. The production of indole and utilization of putrescine are variable, however the type strain is positive for these tests.

The type strain, E515^T (=LMG 23824^T=DSM 18706^T), was originally isolated from the basin of a water fountain in 2004.

Description of *Cronobacter dublinensis* subsp. *lactaridi* subsp. nov.

Cronobacter dublinensis subsp. *lactaridi* (lact.ar′id.i. L. n. *lac lactis* milk; L. adj. *aridus* dried; N.L. gen. n. *lactaridi* of dried milk).

This subspecies corresponds to Farmer's biogroup 6 (Farmer *et al.*, 1980). Positive for production of indole and for utilization of *myo*-inositol, maltitol, *trans*-aconitate, *cis*-aconitate, 1-0-methyl α-D-glucopyranoside, putrescine, lactulose, 4-aminobutyrate and palatinose. Utilization of turanose is variable and the type strain is positive for this test.

The type strain of this subspecies, E464^T (=LMG 23825^T=DSM 18707^T), was originally isolated from a dried milk production facility in 2003.

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