



HAL
open science

Complete genome and description of *Corynebacterium incognita* sp. nov.: a new bacterium within the *Corynebacterium* genus

M. Boxberger, A. Antezack, S. Magnien, N. Cassir, B. La Scola

► **To cite this version:**

M. Boxberger, A. Antezack, S. Magnien, N. Cassir, B. La Scola. Complete genome and description of *Corynebacterium incognita* sp. nov.: a new bacterium within the *Corynebacterium* genus. *New Microbes and New Infections*, 2021, 42, pp.100893. 10.1016/j.nmni.2021.100893 . hal-03428391

HAL Id: hal-03428391

<https://amu.hal.science/hal-03428391>

Submitted on 13 Jun 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial 4.0 International License

1 **Complete Genome and Description of *Corynebacterium incognitum* Sp.Nov., A New**
2 **Bacterium within the *Corynebacterium* genus**

3 Manon Boxberger¹⁻², Angéline Antezack¹⁻²⁻³, Sibylle Magnien¹⁻², Nadim Cassir¹⁻², Bernard La
4 Scola^{1-2*}

5 1. Aix Marseille Université, IRD, AP-HM, MEPHI, Marseille, France

6 2. IHU-Méditerranée Infection, Marseille, France

7 3. Faculté des Sciences Médicales et Paramédicales, Ecole de Médecine Dentaire, Aix-
8 Marseille Université, 27 boulevard Jean Moulin, 13385 Marseille, France

9

10 * Corresponding author:

11 E-mail and address:

12 Bernard La Scola,

13 Aix Marseille Université, Marseille,

14 Méditerranée-Infection, 19-21 Boulevard Jean Moulin,

15 13385, Marseille cedex 05, France.

16 E-mail : bernard.la-scola@univ-amu.fr

17

18 **Abstract**

19 In 2020, as part of the diagnosis in IHU-Méditerranée Infection Institute in Marseille
20 (France) we isolated the new bacterial strain Marseille-3630^T from a 7-year-old girl blood
21 specimen (= CSUR: Q3630). Matrix-assisted desorption ionization–time of flight mass
22 spectrometry (MALDI-TOF MS) failed to identify this isolate. Analysis of the 16S rRNA
23 gene and Genome-to-Genome comparison suggested that this taxon belongs to a novel
24 bacterial species within the family *Corynebacteriaceae* in the phylum *Actinobacteria*. We
25 described here its main phenotypic characteristics, genome sequence and annotation of
26 *Corynebacterium incognitum* strain Marseille-3630^T, a new member of the *Corynebacterium*
27 genus, that we propose as type strain.

28 **Keywords: bacteria, *Corynebacterium*, human, genome, species, sp. nov., taxono-**
29 **genomics**

1 **Introduction**

2 The genus *Corynebacterium* (Gr. fem. n. *korynê*, a club; L. neut. n. *bacterium*, a rod, and in
3 biology a bacterium (so called because the first ones observed were rod-shaped); N.L. neut.
4 n. *Corynebacterium*, a club bacterium) belongs to the large family *Corynebacteriaceae* and
5 was first introduced into literature by Lehmann and Neumann in 1896. [1] The genus
6 *Corynebacterium* currently counts 177 species [2], some of them are of medical, veterinary or
7 biotechnological interest [3]. Species within this genus are ubiquitous and are potentially
8 pathogens. As an illustration, toxin production by *C. diphtheriae* is involved in diphtheria,
9 dreadful historical disease in the 19th century and in the first half of the 20th century. This
10 study contributes to the taxonomical and clinical knowledge of this genus by describing a
11 novel species, strain Marseille-Q3630, isolated as part of a microbiological workup of a
12 patient in IHU-Méditerranée Infection Institute in Marseille (France). We aimed at
13 comparing strain Marseille-Q3630 to its closely related phylogenetic neighbors and proposed
14 to establish for this strain the species name *Corynebacterium incognitum* sp. nov.

15 **Material and method**

16 **Strain isolation**

17 *Corynebacterium incognitum* strain Marseille-Q3630^T was isolated after 50µL of liquid
18 aerobic blood culture bottle (BACT/ALERT®, bioMérieux, Marcy l'Etoile, France) was
19 seeded on Columbia Agar with 5% Sheep Blood media (Biomérieux, Marcy l'Etoile, France)
20 and maintained à 37°C for 24 hours. The strain is then routinely cultivated on Columbia Agar
21 with 5% Sheep Blood media ((bioMérieux, Marcy l'Etoile, France)
22 incubated in aerobiosis at 37°C for 24 hours.

23

24 **Strain identification**

25 Matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry
26 (MS protein analysis was carried out using a Microflex spectrometer (Bruker Daltonics,
27 Bremen, Germany) and spectra from strain Marseille-Q3630^T were imported into the MALDI
28 BioTyper software (version 3.0, Bruker, Germny) and analyzed by standard pattern matching
29 (with default parameter settings). As MALDI-TOF analyze failed to identify this organism by
30 analyzing against our database [4] (<https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/urms-data-base/>), the genome was sequenced as described in the
31 following section. BlastN tool from NCBI were performed to compare the 16S best hits
32 sequence from strain Marseille-Q3630 against the 16S database [5]. Phylogenetic trees for the
33 16s RNA and rpoB gene was obtained using the Maximum Likelihood method and Kimura 2-
34 parameter within the MEGA 7 software. [6]

35

36 **Phenotypic tests**

37 Different growth temperatures (20-56°C), atmosphere conditions (anaerobic, aerobic and
38 microaerophilic), using atmosphere generators (CampyGEN, Oxoid, USA) and pH (5,5-8.5)
39 were tested. API ZYM, API Coryne and API 50 CH strips (BioMérieux, Marcy L'Etoile,
40 France) were used to evaluate the biochemical properties of the strain according to the
41 manufacturer's instructions. Morphology was analyzed by scanning electronic
42 microscopy., Briefly, a colony was collected from agar and immersed into a 2.5 %
43 glutaraldehyde fixative solution. The slide was gently washed in water; air dried and
44 examined to evaluate bacterial structure on a TM4000 microscope (Hitachi, Tokyo, Japan).
45 Motility test was performed using the semi solid TCC media [7].

46

47 **Genome sequencing**

49 Genomic DNA (gDNA) of *Corynebacterium incognitum* strain Marseille-Q3630^T was
50 extracted with the EZ1 biorobot (Qiagen) with EZ1 DNA tissues kit after a mechanical and
51 chemical (lysozyme) pretreatment. gDNA was next sequenced on the MiSeq Technology
52 (Illumina Inc, San Diego, CA, USA) with the paired end strategy and was prepared with the
53 Nextera XT DNA sample prep kit (Illumina). Normalized libraries were pooled into a single
54 library for sequencing on the MiSeq. Total information of 6.03 Gb was obtained from a 628
55 K/mm² cluster density with a cluster passing quality control filters of 96.38. The 12 164 746
56 paired end reads were filtered according to the read qualities. In order to improve the genome
57 quality, an Oxford Nanopore approach was performed on 1D gDNA sequencing for the
58 MinIon device using SQK-LSK109 kit. Library was constructed from 1 µg genomic DNA
59 without fragmentation and end repair. 753 active pores were detected for the sequencing and
60 the workflow WIMP was chosen for bioinformatic analysis in live. After 3.5 hours as run time
61 and end life of the flow cell, 61.140 reads as raw data were generated.

62

63 **Genome annotation and genome comparison**

64 Genome assembly was proceed using SPAdes software v3.10 [8]. Genome annotation was
65 obtained through the NCBI Prokaryotic Genome Annotation Pipeline [9]. The TYGS online
66 platform was used to determinate the closely related type strains. Determination of closest
67 type strain genomes was done in two complementary ways: First, the Marseille-Q3630
68 genome was compared against all type strain genomes available in the TYGS database via the
69 MASH algorithm, a fast approximation of intergenomic relatedness [10], and the ten type
70 strains with the smallest MASH distances chosen per user genome. Second, an additional set
71 of ten closely related type strains was determined via the 16S rDNA gene sequences. These
72 were extracted from the user genomes using RNAmmer [11] and each sequence was
73 subsequently BLASTed [5] against the 16S rDNA gene sequence of each of the currently
74 14.130 type strains available in the TYGS database. This was used as a proxy to find the best
75 50 matching type strains (according to the bitscore) for each user genome and to subsequently
76 calculate precise distances using the Genome BLAST Distance Phylogeny approach (GBDP)
77 under the algorithm 'coverage' and distance formula d5 [12]. These distances were finally
78 used to determine the 10 closest type strain genomes for each of the user genomes. The
79 Genome-to Genome Distance Calculator Digital DDH values and confidence intervals were
80 calculated using the recommended settings of the GGDC 2.1 The degree of genomic
81 similarity based on the Ortholog group of genes of *Corynebacterium incognitum* strain

82 Marseille-Q3630 with closely related species was estimated using the OrthoANI software
83 [13].

84

85 **Results**

86 **Strain identification and classification**

87 *Corynebacterium incognitum* strain Marseille-Q3630^T was isolated from a 7-year-old girl that
88 was consulting pediatric service for an acute febrile illness. Blood was collected and analyzed
89 in aerobic blood culture bottle (BACT/ALERT®, bioMérieux, Marcy l’Etoile, France).
90 *Corynebacterium incognitum* strain Marseille-Q3630^T failed to be identified by our
91 systematic MALDI-TOF MS screening, suggesting that the corresponding species was not in
92 the database. **(Figure.1)** Moreover, *Corynebacterium incognitum* strain Marseille-Q3630^T
93 exhibited a 97.16% 16S rRNA sequence similarity with *Corynebacterium*
94 *tuberculostearicum*^T (GenBank accession NR_028975.1), the phylogenetically closest
95 bacterium standing in nomenclature and a 88.03% *rpoB* gene identity with *Corynebacterium*
96 *aurimucosum* ATCC 700975 (extracted from the genome sequence CP001601.1) - shown to
97 be more discriminant for *Corynebacterium* species, validating the <96.6% identity cutoff
98 described by Khamis et al. [14]. **(Figure.2)**. Digital DNA–DNA hybridization analysis
99 between the novel organism and *Corynebacterium diphtheria* subsp. *lausannense*
100 CHUV2995T exhibited value of 25.4%. Furthermore, genomic comparison using the
101 OrthoANI parameter provided a value of 72.06% *Corynebacterium ureicelerivorans* strain
102 IMMIB RIV-2301^T. **(Table.1 and Supplementary file1)**

103

104 **Phenotypic characteristics**

105 Colonies from strain Marseille-Q3630^T showed a white pigmentation and no hemolysis.
106 Bacterial cells were gram-positive, non-motile, rod shaped, with a mean size of 0.5 x 0.9 µm
107 determined by scanning electronic microscopy **(Figure.3)**. Strain Marseille-Q3630^T is
108 facultatively aerobic. Optimal growth medium temperature, pH and NaCl concentration is
109 comprised between 31-37°C, 5.5-8.5 and 10-15g/L respectively. The sporulation test (20
110 minutes at 80°C) is negative. Using API strips, positive reactions were shown for Pyrazine-
111 carboxamide, 2-naphthyl-phosphate, D-glucose, Alkaline phosphatase, Esterase Lipase (C8),
112 Naphthol-AS-BI-phosphohydrolase, D-fructose. All other reactions tested were negative. In
113 addition, this bacterium shows catalase positive and oxidase negative. These results are
114 summarized in **Table.2**

115

116 **Genome properties**

117 The assembly was achieved in a single contig with a coverage value 22.017x. The genome is
118 2.348.605 bp long with a 62.44% G+C content. The genome assembly of this strain was
119 achieved on a single contig with a N₅₀ value of 22.017. Of the 2.178 predicted genes, 2.083
120 were protein-coding genes and 63 were RNAs (3 16S rRNA, 4 5S rRNAs, 3 23S rRNAs, 50
121 tRNAs, and 3 ncRNA). (**Supplementary file 2**). The genome properties and distribution of
122 genes into COGs functional categories are detailed in **Supplementary file.3**. The *in silico*
123 resistome of the strain Marseille-Q3630 shows *erm(X)_4* gene with 94.74% identity
124 percentage, notably involved in erythromycin resistance.

125 **Discussion and conclusion**

126 Using the taxono-genomics concept *i.e.*, the combination of the genomic and phenotypic
127 properties of a putative new taxon [15], we have characterized a new bacterial species
128 representing a new species within the family *Corynebacteriaceae* found in human. Although
129 it was found in a blood culture of a 7-year-old girl, *Corynebacterium* sp are known to be
130 associated with such contaminated samples. It is important to keep in mind that
131 *Corynebacterium incognitum* could also be such skin contaminant.[16] This strain is most
132 closely related to *Corynebacterium tuberculostearicum*^T with a 16S rRNA sequence
133 similarity value of 97.16%. Furthermore, genomic comparison using the OrthoANI parameter
134 provided a value of 72.06% with *Corynebacterium ureicelerivorans*^T and a dDDH value of
135 25.4 % with *Corynebacterium diphtheria* subsp. lausannense CHUV2995T Indeed, although
136 they are not universal cutoff, a value lower than 70% of DDH and 95-96% of ANI are
137 common indicators for a new species discovery, this new strain shows a *rpoB* gene identity
138 with *Corynebacterium aurimucosum* of 88.03%, validating the <96.6% identity cutoff. [14]
139 Taken altogether, these parameters have prompt us to propose *Corynebacterium incognitum*
140 strain Marseille-Q3630^T as a new member of *Corynebacterium* genus. Gr. fem. n. *korynê*, a
141 club; L. neut. n. *bacterium*, a rod, and in biology a bacterium (so called because the first ones
142 observed were rod-shaped); N.L. neut. n. *Corynebacterium*, a club bacterium. *Incognitum*,
143 *lat. incognitus* « *id.* », *der. cognitus*, known. **(Table.3)**

144

145 **Deposit in culture collections and Sequences Database**

146 *Corynebacterium incognitum* strain Marseille-Q3630^T, was deposited in CSUR collections
147 under accession CSUR-Q3630. The 16S rRNA and genome sequences available in GenBank
148 under accession numbers MT772002 and GCA_014217255.1 respectively.

149

150 **Ethics Committee**

151 The study was validated by the ethics committee of the Institut Fédératif de Recherche IFR48.

152

153 **Transparency declaration**

154 None to declare

155

156 **Funding**

157 MB is PhD granted by the collaboration between M&L Laboratories and Aix Marseille
158 University referenced PVM :2018-200. This study was supported by the French State

159 managed by the National Research Agency under the "Investissements d'avenir (Investments
160 for the Future)" program under the reference ANR-10-IAHU-03 (Méditerranée Infection) and
161 by the Région Provence-Alpes-Côte-d'Azur and the European funding FEDER PRIMI.

162

163 **Acknowledgements**

164 We acknowledge Dr Alexandre Toro and the clinical microbiology team of Martigues
165 hospital for sending us the sample to identify this strain. The authors are indebted to Ludivine
166 Brechard for sequencing the genome and the platform of electron microscopy of IHU -MI for
167 the electron micrographs.

168

169 **Reference**

170

171 [1] Lehmann Karl Bernhard, Royal College of Physicians of Edinburgh. Atlas und
172 Grundriss der Bakteriologie und Lehrbuch der speziellen bakteriologischen Diagnostik. vol. 1.
173 Munchen : Lehmann,; 1896.

174 [2] LPSN PAC. List of Prokaryotic names with Standing in Nomenclature (bacterio.net),
175 20 years on. International Journal of Systematic and Evolutionary Microbiology
176 2018;68:1825–9. <https://doi.org/10.1099/ijsem.0.002786>.

177 [3] Oliveira A, Oliveira LC, Aburjaile F, Benevides L, Tiwari S, Jamal SB, et al. Insight
178 of Genus Corynebacterium: Ascertaining the Role of Pathogenic and Non-pathogenic Species.
179 Front Microbiol 2017;8:1937. <https://doi.org/10.3389/fmicb.2017.01937>.

180 [4] Grégory D, Chaudet H, Lagier J-C, Raoult D. How mass spectrometric approaches
181 applied to bacterial identification have revolutionized the study of human gut microbiota.
182 Expert Rev Proteomics 2018;15:217–29. <https://doi.org/10.1080/14789450.2018.1429271>.

183 [5] Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K. BLAST+:
184 architecture and applications. BMC Bioinformatics 2009;10. [https://doi.org/10.1186/1471-](https://doi.org/10.1186/1471-2105-10-421)
185 2105-10-421.

186 [6] Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis
187 Version 7.0 for Bigger Datasets. Mol Biol Evol 2016;33:1870–4.
188 <https://doi.org/10.1093/molbev/msw054>.

189 [7] Tittsler RP, Sandholzer LA. The Use of Semi-solid Agar for the Detection of Bacterial
190 Motility. J Bacteriol 1936;31:575–80.

191 [8] Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, et al.
192 SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell
193 Sequencing. Journal of Computational Biology 2012;19:455–77.
194 <https://doi.org/10.1089/cmb.2012.0021>.

195 [9] Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L.
196 NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res 2016;44:6614–24.
197 <https://doi.org/10.1093/nar/gkw569>.

198 [10] Ondov BD, Treangen TJ, Melsted P, Mallonee AB, Bergman NH, Koren S. Mash: fast
199 genome and metagenome distance estimation using MinHash. Genome Biol 2016;17.
200 <https://doi.org/10.1186/s13059-016-0997-x>.

201 [11] Lagesen K, Hallin P, Rødland EA, Stærfeldt H-H, Rognes T, Ussery DW. RNAmmer:
202 consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Research

203 2007;35:3100–8. <https://doi.org/10.1093/nar/gkm160>.

204 [12] Meier-Kolthoff JP, Auch AF, Klenk H-P, Göker M. Genome sequence-based species
205 delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics*
206 2013;14. <https://doi.org/10.1186/1471-2105-14-60>.

207 [13] Lee I, Ouk Kim Y, Park S-C, Chun J. OrthoANI: An improved algorithm and software
208 for calculating average nucleotide identity. *International Journal of Systematic and*
209 *Evolutionary Microbiology* 2016;66:1100–3. <https://doi.org/10.1099/ijsem.0.000760>.

210 [14] Khamis A, Raoult D, La Scola B. rpoB Gene Sequencing for Identification of
211 *Corynebacterium* Species. *Journal of Clinical Microbiology* 2004;42:3925–31.
212 <https://doi.org/10.1128/JCM.42.9.3925-3931.2004>.

213 [15] Abdallah RA, Beye M, Diop A, Bakour S, Raoult D, Fournier P-E. The impact of
214 culturomics on taxonomy in clinical microbiology. *Antonie van Leeuwenhoek*
215 2017;110:1327–37. <https://doi.org/10.1007/s10482-017-0871-1>.

216 [16] Doern GV, Carroll KC, Diekema DJ, Garey KW, Rupp ME, Weinstein MP, et al.
217 *Practical Guidance for Clinical Microbiology Laboratories: A Comprehensive Update on the*
218 *Problem of Blood Culture Contamination and a Discussion of Methods for Addressing the*
219 *Problem. Clin Microbiol Reviews* 2019;33:CMR.00009-19, e00009-19.
220 <https://doi.org/10.1128/CMR.00009-19>.

221 [17] Grant S JR, P. The CGView Server: a comparative genomics tool for circular
222 genomes. *Nucleic Acids Research* 2008;36:W181-4. <https://doi.org/10.1093/nar/gkn179>.

223

224 **Figure.1** MALDI-TOF MS reference mass spectrum. Spectra from 12 individual colonies of
225 *Corynebacterium incognitum* strain Marseille-Q3630^T were compared and a reference
226 spectrum was generated

227

228 **Figure 2:** A. *16S* rRNA gene (A) and *RpoB* gene (B) based phylogenetic trees highlighting the
229 position of *Corynebacterium incognitum* sp., nov., strain Marseille-Q3630 (red) relative to
230 other closely related bacterial taxa. Best hits of BlastN megablast was added to the relative
231 pointed by the TYGS software. Sequences were aligned using Muscle v3.8.31 with default
232 parameters and phylogenetic relationship inferred using the Maximum Likelihood method,
233 with 1,000 bootstrap replicates, within the MEGA software version 7

234

235 **Figure 3:** Scanning electron microscopy of *Corynebacterium incognitum* sp. nov., strain
236 Marseille-Q3630^T using a Tabletop microscope TM 4000plus (Hitachi, Tokyo, Japan). The
237 scale bar represents 5 μ m

238

239 **Table1:** Orthologous Average Nucleotide Identity from OrthoANI software and Digital
240 DNA–DNA hybridization values obtained by sequence comparison of all studied genomes
241 using TYGS comparison server using the 2nd formula

242

243 **Table.2** Differential characteristics of *Corynebacterium incognitum* strain Marseille- Q3630^T
244 and closest species standing in nomenclature

245

246 **Table.3:** Description of *Corynebacterium incognitum* sp. nov. strain Marseille-Q3630^T

247

248

249 **Table.1:** Digital DNA–DNA hybridization values obtained by sequence comparison of all
 250 studied genomes using TYGS comparison server using the 2nd formula

Subject strain	OrthoANI value (Supplementary Fig.1)	dDDH (in %) with <i>Corynebacterium incognitum</i> strain <i>Marseille-Q3630T</i>	Confidence Interval (in %)	G+C content difference (in %)
<i>Corynebacterium diphtheriae</i> <i>subsp. lausannense</i> <i>CHUV2995</i>	69.3094	25,4	[23.1 - 27.9]	8,49
<i>Corynebacterium rouxii</i> <i>FRC0190 T</i>	69.6315	25,1	[22.8 - 27.6]	9,21
<i>Corynebacterium mustelae</i> <i>DSM 45274</i>	68.4165	24,6	[22.3 - 27.1]	9,86
<i>Corynebacterium diphtheriae</i> <i>NCTC 11397</i>	69.5648	24,5	[22.2 - 27.0]	8,91
<i>Corynebacterium belfantii</i> <i>FRC0043</i>	69.4349	24,1	[21.8 - 26.6]	8,81
<i>Corynebacterium</i> <i>pseudotuberculosis ATCC</i> <i>19410</i>	68.5154	23,8	[21.4 - 26.2]	10,25
<i>Corynebacterium</i> <i>pseudotuberculosis DSM</i> <i>20689</i>	Not found in public database	23,8	[21.4 - 26.2]	10,25
<i>Corynebacterium</i> <i>ureicelerivorans DSM 45051</i>	72.0657	23,6	[21.3 - 26.0]	2,57
<i>Corynebacterium ulcerans</i> <i>NCTC 7910</i>	68.928	23,6	[21.3 - 26.1]	9,12
<i>Corynebacterium jeikeium</i> <i>ATCC 43734</i>	71.0532	23,6	[21.3 - 26.0]	0,8

251

252 **Table.2** Differential characteristics of *Corynebacterium incognitum* strain Marseille- Q3630^T and closest species standing in nomenclature.

	<i>C. incognitum</i>	<i>C. tuberculostearicum</i>	<i>C. tuscaniense</i>	<i>C. macginleyi</i>	<i>C. simulans</i>	<i>C. accolens</i>
Properties	Marseille-Q3630	Medalle X	ISS-5309	JCL-2	DSM 44415	CIP 104783T
Oxygen requirement	Facultative	Facultative	+	Facultative	Facultative	Facultative
Gram Strain	+	+	+	+	+	+
Motility	-	-	-	-	-	-
Endospore formation	-	-	-	na	-	-
Optimum temperature for growth (°C)	31-37°C	na	na	37°C	na	37°C
Production of :						
Alkaline phosphatase	+	+	+	+	+	-
Catalase	+	+	+	+	+	+
Oxidase	-	-	na	-	na	-
α-Glucosidase	-	-	-	-	-	+
β-galactosidase	-	-	-	-	-	-
Acid from:						
N-Acetylglucosamine	-	+	-	-	-	+
L-arabinose	-	na	na	+	-	na
D-ribose	-	+	-	+	+	+
D-mannose	-	+	na	na	+	+
D-mannitol	-	-	-	+	-	-
D-glucose	+	+	+	+	+	+
D-fructose	+	+	na	+	+	+
D-maltose	-	-	+	-	-	-
D-lactose	-	-	-	-	-	-
Genome size	2,348,605	2,453,172	2,263,530	2,419,073	2,598,702	2,465,636

Isolation source

Human healthy skin

Clinical and food samples

Blood cultures of a
patient with
endocarditis

Bacterial flora of
certain human body
sites

Clinical
samples

Clinical and food
samples

254 **Table.3:** Description of *Corynebacterium incognitum* sp. nov. strain Marseille-Q3630^T

Type of description	New description
Species name	<i>incognitum</i>
Genus name	<i>Corynebacterium</i>
Specific epithet	<i>Corynebacterium</i>
Species Status	sp nov
Species etymology	Corynebacterium incognitum strain Marseille-Q3630T. Gr. fem. n. korynê, a club; L. neut. n. bacterium, a rod, and in biology a bacterium (so called because the first ones observed were rod-shaped); N.L. neut. n. Corynebacterium, a club bacterium. Incognitum, lat. incognitus « id. », der. cognitus, known.
Authors	Manon Boxberger, Angéline Antezack, Sibylle Magnien, Nadim Cassir, Bernard La Scola
Designation of the type strain	Marseille Q3630
Strain collection number	CSUR:3630
16S rRNA gene accession number	<u>MT772002</u>
Genome accession number	<u>GCA_014217255.1</u>
Genome status	Whole genome
Genome size	2,348,605-bp
GC%	62.44%

Country of origin	France
Date of isolation	2020
Source of isolation	Human healthy skin
Growth medium, incubation	Columbia Agar with 5% Sheep Blood media (Biomérieux, France), 37°C, Aerobiosis, 1day
Gram stain	Positive
Cell shape	Rod shaped
Cell size	0.9 x 0.5 µm
Motility	-
Sporulation	-
Colony morphology	White
Temperature range	21°C-56°C
Temperature optimum	37°C
Relationship to O₂	Facultative
O₂ for strain testing	Anaerobiosis, microaerophilic, aerobiosis
Oxidase	Negative
Catalase	Positive
