TAXONOGENOMICS: GENOME OF A NEW ORGANISM

High-quality genome sequencing and description of Dermabacter indicis sp. nov.

C. I. Lo¹, S. A. Sankar¹, C. B. Ehounoud¹, O. Mediannikov¹, N. Labas¹, A. Caputo¹, D. Raoult¹², P.-E. Fournier¹ and F. Fenollar¹
¹) Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes, UM 63, CNRS 7278, IRD 198, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Aix-Marseille Université, Marseille, France and ²) Infectious Agents Unit, King Fahd Medical Research Center, King Abdulaziz University, Jeddah, Saudi Arabia

Abstract

Strain FF11T was isolated from the wound on a researcher’s finger who had been bitten by a fish (Protopterus annectens) in Senegal. Analysis by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry did not provide any identification, but the 16S rRNA sequence exhibited 97.9% identity with Dermabacter hominis. Phenotypic and genomic analyses demonstrated that strain FF11T is Gram-positive, facultatively anaerobic, nonmotile and non–spore forming; it exhibited a genome of 2222902 bp encoding 2074 protein-coding and 50 RNA genes, with a 63.2% G+C content. We consequently proposed the creation of Dermabacter indicis strain FF11T.

Introduction

The Dermabacter genus is considered a common colonizer of human skin [1]. Currently this genus includes only one validly published species named Dermabacter hominis [2], which was formerly known as the coryneform bacteria of the Centers for Disease Control groups 3 and 5 [3,4]. Members of this genus are Gram-positive, non–spore forming, non–acid fast, nonmotile, short rods, facultatively anaerobic, catalase positive and oxidase negative [1]. Dermabacter hominis is involved in bacteraemia as a rare pathogen [5]. D. hominis has also been detected in clinical samples such as wound swabs, bronchial washings, abscesses and ear smears [3–6].

Keywords: Bacteria, culturomics, Dermabacter indicis, genome, taxonogenomics

Original Submission: 22 December 2015; Revised Submission: 8 February 2016; Accepted: 16 February 2016

Article published online: 23 February 2016

Corresponding author: F. Fenollar, URMITE, UMR CNRS 7278, IRD 198, INSERM U1095, Faculté de médecine, Aix-Marseille Université, 27 Boulevard Jean Moulin, 13385 Marseille Cedex 5, France
E-mail: florence.fenollar@univ-amu.fr
C.I. Lo and S.A. Sankar contributed equally to this article, and both should be considered first author.

Recently, high-throughput genome sequencing and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF) analyses of bacteria have given unprecedented access to an abundance of genetic and proteomic information [7,8]. Thus, a polyphasic approach is currently proposed in our laboratory to describe new bacterial taxa, including their genome sequence, MALDI-TOF spectrum, and major phenotypic characteristics such as Gram staining, culture conditions, metabolic characteristics, habitat and, if applicable, pathogenicity [9].

Here we present a summary classification and a set of features for Dermabacter indicis sp. nov., together with a description of the complete genome sequencing and annotation. These characteristics support the circumscription of the Dermabacter indicis species.

Classification and features

Strain isolation and identification

In May 2014, while working at Dakar, the index finger of a researcher was bitten by a fish. Strain FF11T (Table 1) was isolated from this wound by culture on 5% sheep’s blood–enriched Columbia agar (bioMérieux, Marcy l’Etoile, France). In order to
TABLE 1. Classification and general features of Dermabacter indicis strain FF11T

| MIGS ID | Property | Term | Evidence codea |
|---------|----------|------|---------------|
|         | Current classification | Domain: Bacteria | TAS [10] |
|         |           | Phylum: Actinobacteria | TAS [11] |
|         |           | Class: Actinobacteria | TAS [12,13] |
|         |           | Order: Micrococcales | TAS [13,14] |
|         |           | Family: Dermabacteraceae | TAS [13,14] |
|         |           | Genus: Dermabacter | TAS [1] |
|         |           | Species: Dermabacter indicis | IDA |
|         | Type strain: FF11T | IDA |
|         | Gram stain | Positive | IDA |
|         | Cell shape | Rods | IDA |
|         | Motility | Nonmotile | IDA |
|         | Sporulation | Non-sporing | IDA |
|         | Temperature range | 30–37°C | IDA |
|         | Optimum temperature | 37°C | IDA |
|         | pH range; optimum | 7.4–7.2; 7.6 | IDA |
|         | Carbon source | Unknown | IDA |
| MIGS-6  | Habitat | Human wound | IDA |
| MIGS-6.3| Salinity | Unknown | IDA |
| MIGS-22 | Oxygen requirement | Facultatively anaerobic | IDA |
| MIGS-15 | Biotic relationship | Free-living | IDA |
| MIGS-14 | Pathogenicity | Unknown | IDA |
| MIGS-4  | Geographic location | Senegal | IDA |
| MIGS-5  | Sample collection | June 2014 | IDA |
| MIGS-4.1| Latitude | 14.6937000 | IDA |
| MIGS-4.4| Longitude | −17.4440600 | IDA |
| MIGS-4.4| Altitude | 12 m above sea level | IDA |

MIGS, minimum information about a genome sequence.

aEvidence codes are as follows: IDA, inferred from direct assay; TAS, traceable author statement (i.e. a direct report exists in the literature); NAS, nontraceable author statement (i.e. not directly observed for the living, isolated sample, but based on a generally accepted property for the species or anecdotal evidence). These evidence codes are from the Gene Ontology project (http://www.geneontology.org/GO.evidence.shtml) [16]. If the evidence code is IDA, then the property should have been directly observed, for the purpose of this specific publication, for a live isolate by one of the authors, or by an expert or reputable institution mentioned in the acknowledgements.

identify the strain FF11T, MALDI-TOF protein analysis was performed using a Microflex LT (Bruker Daltonics, Leipzig, Germany), as previously reported [17,18]. The scores previously established by Bruker to identify or validate species compared to the instrument’s database were applied. In short, a score of ≥2.000 with a species with a validly published name allows identification at the species level; scores of ≥1.700 and <2.000 allow identification at the genus level; and a score of <1.700 does not allow any identification to be made. We performed 12 distinct deposits from 12 isolated colonies of strain FF11T. They were then imported into MALDI Biotyper software (version 2.0, Bruker) and analysed by standard pattern matching (with default parameter settings) against the main spectra. Scores ranging from 1.315 to 1.511 were obtained for FF11T, suggesting that this strain was not a member of any known species. The reference mass spectrum from strain FF11T was incremented in our database (Fig. 1).

Moreover, strain FF11T exhibited 97.9% 16S rRNA sequence similarity with Dermabacter hominis [1] (GenBank accession no. X91034), the phylogenetically closest bacterial species with standing in the nomenclature (Fig. 2). This value was lower than 98.7% 16S rRNA sequence identity threshold recommended by Meier-Kolthoff et al. [19] in 2013 to delineate a new species within the Firmicutes phylum without carrying out DNA-DNA hybridization.

Phenotypic and biochemical features

Different growth temperatures (25, 28, 37, 45 and 56°C) were tested. Growth was obtained at 37°C only. Growth of the strain was also tested under anaerobic and microaerophilic conditions using GENbag anaer and GENbag microaer systems (bioMérieux), respectively, and under aerobic conditions, with or without 5% CO2. Optimal growth was observed under aerobic and microaerophilic conditions, but weak growth was observed under anaerobic conditions at 37°C. Strain FF11T shows white convex colonies measuring approximately 1 mm in diameter on 5% sheep’s blood–enriched Columbia agar (bioMérieux). Cells are Gram-positive, nonmotile, non–spore forming short rods (Fig. 3). The negative staining of the cells and observation under transmission electron microscopy (FEI Company, Hillsboro, Oregon, USA) displays cells lacking flagella (Fig. 4).

Dermabacter indicis is catalase positive and oxidase negative. Using an API 50CH strip (bioMérieux), fermentation was observed for D-galactose, D-glucose, N-acetyl-D-glucosamine, D-lactose, D-saccharose, D-trehalose, D-melezitose, D-raffinose, starch and D-turanose. Using the API Coryne strip (bioMérieux), positive reactions were also observed for pyrazincarboxamide, pyroglutamic acid-β-naphthalamide, esculin ferric citrate, urea and D-maltose. Negative reactions were noted for potassium nitrate (reduction of nitrates), β-glucuronidase, gelatin, D-ribose, D-xyllose, D-mannitol and glycojen. Using the API ZYM strip (bioMérieux), enzymatic reactions were observed for esterase, esterase−lipase, lipase, acid phosphatase, alkaline phosphatase, naphthol-AS-BI-phosphohydrolase, cystine arylamidase, trypsin, α-glucosidase, β-galactosidase, α-mannosidase, α-fucosidase and N-acetyl-β-glucosaminidase. Negative reactions were observed for
leucine arylamidase, valine arylamidase, β-glucosidase, α-galactosidase and β-glucuronidase.

Strain FF11T is susceptible to ciprofloxacin, amoxicillin/clavulanic acid, ticarcillin, ceftriaxone, imipenem, doxycycline, gentamicin and cefalotin, but it is resistant to colistin, trimethoprim/sulfamethoxazole, erythromycin and nitrofurantoin. A comparison of phenotypic characteristics with Dermabacter hominis [1], Brachybacterium faecium [20], Brachybacterium muris [21], and Helcobacillus massiliensis [22] is summarized in Table 2.

Genome sequencing information

Genome project history

The organism was selected for sequencing on the basis of its phylogenetic position, 16S rRNA similarity and phenotypic differences with other members of the Dermabacteraceae family. Here we present the first Dermabacter indicis sp. nov. genome. The EMBL/EBI accession number is CYUG00000000. Table 3 shows the project information and its association with MIGS (minimum information about a genome sequence) version 2.0 compliance [23].

Growth conditions and DNA isolation

Dermabacter indicis strain FF11T (= CSUR P1488 = DSM 100283) was grown on 5% sheep’s blood–enriched Columbia agar (bioMérieux) at 37°C. Bacteria grown on four petri dishes were resuspended in 5 × 100 μL of Tris-EDTA buffer and 150 μL of this suspension was diluted in: 350 μL Tris-EDTA buffer 10×, 25 μL proteinase K and 50 μL sodium dodecyl sulfate for lysis treatment. This preparation was incubated overnight at 56°C. Extracted DNA was then purified using three successive phenol–chloroform extractions and ethanol precipitations at −20°C overnight. After centrifugation, DNA was suspended in 65 μL of EB buffer. The genomic DNA concentration was measured at 69.3 ng/μL using the Qubit assay with the high sensitivity kit (Life Technologies, Carlsbad, CA, USA).

Genome sequencing and assembly

Genomic DNA (gDNA) of Dermabacter indicis FF11T was sequenced on the MiSeq Technology (Illumina, San Diego, CA, USA) with the mate pair strategy. The gDNA was barcoded in order to be mixed with 11 other projects with the Nextera Mate Pair Sample Prep Kit (Illumina). The mate pair library was prepared with 1.5 μg of gDNA using the Nextera Mate Pair Prep Kit.
Illumina guide. The gDNA sample was simultaneously fragmented and tagged with a mate pair junction adapter. The pattern of the fragmentation was validated on an Agilent 2100 BioAnalyzer (Agilent Technologies, Santa Clara, CA, USA) with Brachybacterium paraconglomeratum (EU660359), Brachybacterium conglomeratum (AB537169), Brachybacterium saurushtrense (EU937750), Brachybacterium faecium (NR 074655), Brachybacterium alimentarium (X91031), Brachybacterium tyrofermentans (X91657), Brachybacterium sacelli (AJ415381), Brachybacterium fresconis (AJ415379), Brachybacterium zhongshanense (EF125186), Brachybacterium nesterenkovii (NR 026270), Brachybacterium muris (AJ537574), Brachybacterium squillarum (NR 117297), Brachybacterium rhamnosum (AJ415376), Helcobacillus massiliensis (NR 044506), Dermabacter hominis (NR 026271), and Micrococcus luteus (AJ536198).

**FIG. 2.** Phylogenetic tree highlighting position of Dermabacter indicis sp. nov. strain FF11T relative to other type strains within Dermabacteraceae family. Sequences were aligned using Clustal W, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA6. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 1000 times to generate majority consensus tree. Micrococcus luteus strain was used as outgroup. Scale bar = 10% nucleotide sequence divergence.

**FIG. 3.** Gram staining of Dermabacter indicis sp. nov. strain FF11T.

**FIG. 4.** Transmission electron microscopy of Dermabacter indicis strain FF11T. Cells were observed on Tecnai G2 transmission electron microscope operated at 200 keV. Scale bar = 500 nm.
a DNA 7500 LabChip. The DNA fragments are ranged in size from 1.5 to 11 kb with an optimal size at 6.730 kb. No size selection was performed, and 636 ng of tagmented fragments were circularized. The circularized DNA was mechanically sheared into small fragments with an optimum at 653 bp on the Covaris device S2 in T6 tubes (Covaris, Woburn, MA, USA). The library profile was visualized on a High Sensitivity Bioanalyzer LabChip (Agilent), and the final concentration library was measured at 59.1 nmol/L.

The libraries were normalized at 2 nM and pooled. After a denaturation step and dilution at 15 pM, the pool of libraries was loaded onto the reagent cartridge and then onto the instrument along with the flow cell. Automated cluster generation and sequencing runs were performed in a single 39-hour run at a 2 × 251 bp read length.

Total information of 5.9 GB was obtained from a 624K/mm² cluster density with cluster passing quality control filters of 96.33% (12 040 000 clusters). Within this run, the index representation for Dermabacter indicis FF11T was determined at 16.54%. The 1 918 640 paired reads were filtered according to the read qualities. These reads were trimmed and then assembled using the CLC genomics WB4 software.

**Genome annotation**

Open reading frames (ORFs) were predicted using Prodigal [24] with default parameters, but the predicted ORFs were excluded if they spanned a sequencing gap region. The predicted bacterial genes, while ribosomal RNAs were found using RNAmmer [27].

**TABLE 2. Differential characteristics of Dermabacter indicis strain FF11T with Dermabacter hominis [1], Brachybacterium faecium [20], Brachybacterium muris [21] and Helcococcus massiliensis [22]**

| Character              | D. indicis | D. hominis | B. faecium | B. muris | H. massiliensis |
|------------------------|------------|------------|------------|----------|----------------|
| Gram stain             | +          | +          | +          | +        | +              |
| Motility               | −          | −          | −          | −        | −              |
| Endosporule formation  | −          | −          | −          | −        | −              |
| Production of:         |            |            |            |          |                |
| Alkaline phosphatase   | +          | NA         | −          | NA       | −              |
| Acid phosphatase       | +          | NA         | −          | NA       | −              |
| Catalase               | −          | −          | −          | −        | −              |
| Oxidase                | −          | −          | −          | −        | −              |
| B-Hemolysis            | −          | −          | −          | −        | −              |
| Nitrate reductase      | −          | −          | −          | −        | −              |
| α-Galactosidase        | −          | −          | −          | −        | −              |
| β-Galactosidase        | +          | NA         | −          | NA       | −              |
| α-Glucosidase (PNPG)   | +          | NA         | −          | NA       | −              |
| β-Glucosidase          | −          | NA         | −          | NA       | −              |
| Esterase               | −          | NA         | −          | NA       | −              |
| Esterase Igase         | −          | NA         | −          | NA       | −              |
| N-Acetyl-β-glucosaminidase | − | NA | − | NA | − |
| Utilization of:        |            |            |            |          |                |
| α-Fructose             | −          | NA         | −          | +        | +              |
| α-Mannose              | −          | −          | −          | +        | +              |
| α-Xylose               | −          | −          | −          | −        | −              |
| α-Glucose              | +          | +          | +          | +        | +              |
| Habitat                | Human wound| Human skin | Faeces     | Mouse    | Human skin     |

+ , positive result; −, negative result; NA, data not available.

**TABLE 3. Project information**

| MIGS ID | Property                  | Term                                |
|---------|---------------------------|-------------------------------------|
| MIGS-31 | Finishing quality         | High-quality draft                  |
| MIGS-28 | Libraries used            | Mate-par library                    |
| MIGS-29 | Sequencing platforms      | Illumina MiSeq                      |
| MIGS-30 | Assemblers                | CLC GENOMICS WB4                    |
| MIGS-32 | Gene calling method       | Prodigal                            |
|         | BioProject ID             | PJEB10992                           |
|         | GenBank accession numbers | CYUG01000001/CYUG01000017           |
|         | GenBank Date of Release   | 25 September 2015                   |
|         | Project relevance         | MALDI-TOF implementation in Dakar   |

MALDI-TOF, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry; MIGS, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry.

and BLASTn against the GenBank database. Transmembrane topology and signal peptide predictors were provided using the Phobius server [28]. ORFans were identified if their BLASTP E value was lower than 1e-03 for an alignment length greater than 80 aa. If alignment lengths were smaller than 80 aa, we used an E value of 1e-05. Such parameter thresholds have been used in previous works to define ORFans. Artemis [29] was used for data management and DNA Plotter [30] for the visualization of genomic features. The Mauve alignment tool (version 2.3.1) was used for multiple genomic sequence alignment [31]. Briefly, this software combines the Proteinortho software [32] for detecting orthologous proteins in pairwise genomic comparisons, then retrieves the corresponding genes and determines the mean percentage of nucleotide sequence identity among orthologous ORFs using the Needleman-Wunch global alignment algorithm. Annotation and comparison processes were performed in the Multi-Agent Software System DAGOBH [33], including Figenix [34] libraries that provide pipeline analyses. Genome-to-Genome Distance Calculator (GGDC) analysis was also performed using the GGDC web server as previously reported [35,36]. Here, the genome of
Dermabacter indicis strain FF11\textsuperscript{T} (EMBL/EBI accession no. CYUG00000000) is compared to those of Dermabacter hominis strain 1368 (JDRS00000000), Brachybacterium faecium strain DSM 4810\textsuperscript{T} (CP001643), Brachybacterium paraconglomeratum strain LC44 (AGSO00000000), Brachybacterium squillarum strain M-6-3\textsuperscript{T} (AGBX00000000) and Brachybacterium muris strain UCD-AY4 (AORC00000000).

**Genome properties**

The EMBL/EBI BioProject number is PRJEB10922 and consists of 248 large contigs. Finally, the draft genome of D. indicis FF11\textsuperscript{T} generated a 2 222 902 bp long genome with a 63.2\% G+C content (Fig. 5). Of the 2124 predicted genes, 2074 were protein-coding genes and 50 were RNAs (three 5S rRNA genes).}

**TABLE 4. Nucleotide content and gene count levels of genome**

| Attribute                        | Genome (total) | Value   | % of total\(^a\) |
|----------------------------------|----------------|---------|------------------|
| Size (bp)                        |                | 2 222 902| 100              |
| G+C content (bp)                 |                | 1 400 428| 63.2             |
| Coding region (bp)               |                | 2 019 684| 90.85            |
| Total genes                      |                | 2 124   | 100              |
| RNA genes                        |                | 50      | 2.35             |
| Protein-coding genes             |                | 2 074   | 97.64            |
| Genes with function prediction   |                | 1 557   | 73.30            |
| Genes assigned to COGs           |                | 1 422   | 66.94            |
| Genes with peptide signals       |                | 110     | 5.17             |
| Genes with transmembrane helices |                | 435     | 20.48            |

COGs, Clusters of Orthologous Groups database.
\(^a\)Total is based on either the size of the genome in base pairs or the total number of protein-coding genes in the annotated genome.
genes, one 16S rRNA gene, one 23S rRNA gene and 45 tRNA genes). A total of 59 genes (2.77%) were identified as ORFans. The remaining genes were annotated as hypothetical proteins. The properties and statistics of the genome are summarized in Table 4. The distribution of genes into COGs functional categories is presented in Table 5.

Genomic comparison with other Dermabacteraceae species

The draft genome of D. indicis is smaller than D. hominis, B. faecium, B. paraconglomeratum, B. squillarum and B. muris (2.22, 2.51, 3.61, 3.78, 3.19 and 3.26 Mb respectively). The G+C content of D. indicis is higher than that of D. hominis (63.2 and 62.7%, respectively) but lower than that of B. faecium, B. paraconglomeratum, B. squillarum and B. muris (72.0, 72.4, 72.8 and 70.0% respectively). The gene content of D. indicis is smaller than that of D. hominis, B. faecium, B. paraconglomeratum, B. squillarum and B. muris (2124, 2302, 3191, 3432, 2869 and 2914 respectively). However, the distribution of genes into COGs categories was similar in all the genomes compared (Fig. 6). In addition, D. indicis shared 2074, 2226, 3068, 3341, 2765 and 2806 orthologous genes with D. hominis, B. faecium, B. paraconglomeratum, B. squillarum and B. muris (Fig. 6). The genomic similarity between strain FF11T and the closely related Brachybacterium species was also estimated using GGDC (Table 6).

Conclusion

The results of phenotypic, phylogenetic and genomic analyses allow us to propose the creation of *Dermabacter indicis* sp. nov., which contains strain FF11T. The strain was isolated from a human wound in Dakar, Senegal.

**TABLE 5. Number of genes associated with 25 general COGs functional categories**

| Code | Value | % value | Description |
|------|-------|---------|-------------|
| J    | 151   | 7.28    | Translation |
| A    | 0.04  |         | RNA processing and modification |
| K    | 124   | 5.97    | Transcription |
| L    | 135   | 6.50    | Replication, recombination and repair |
| B    | 0     | 0.00    | Chromatin structure and dynamics |
| D    | 21    | 1.01    | Cell cycle control, mitosis and meiosis |
| Y    | 0     | 0.00    | Nuclear structure |
| V    | 43    | 2.07    | Defense mechanisms |
| T    | 63    | 3.03    | Signal transduction mechanisms |
| M    | 82    | 3.95    | Cell wall/membrane biogenesis |
| N    | 1     | 0.04    | Cell motility |
| Z    | 0     | 0.00    | Cytoskeleton |
| W    | 0     | 0.00    | Extracellular structures |
| U    | 22    | 1.06    | Intracellular trafficking and secretion |
| Q    | 69    | 3.32    | Posttranslational modification, protein turnover, chaperones |
| C    | 93    | 4.48    | Energy production and conversion |
| G    | 179   | 8.63    | Carbohydrate transport and metabolism |
| E    | 144   | 6.94    | Amino acid transport and metabolism |
| F    | 64    | 3.08    | Nucleotide transport and metabolism |
| H    | 72    | 3.47    | Coenzyme transport and metabolism |
| I    | 42    | 2.02    | Lipo transport and metabolism |
| P    | 106   | 5.11    | Inorganic ion transport and metabolism |
| Q    | 22    | 1.06    | Secondary metabolites biosynthesis, transport and catabolism |
| R    | 198   | 9.54    | General function prediction only |
| S    | 105   | 5.16    | Function unknown |
| —    | 1183  | 35.23   | Not in COGs |

COGs, Clusters of Orthologous Groups database. *Total is based on total number of protein-coding genes in annotated genome.*

**FIG. 6.** Distribution of functional classes of predicted genes in genomes of indicated chromosomes according to clusters of orthologous groups of proteins. BF, *Brachybacterium faecium*; BM, *Brachybacterium muris*; BP, *Brachybacterium paraconglomeratum*; BS, *Brachybacterium squillarum*; DH, *Dermabacter hominis*; DI, *Dermabacter indicis*. New Microbes and New Infections © 2016 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases. NMNI, 11, 59–67. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/)
TABLE 6. Pairwise comparisons of Dermabacter species and Brachybacterium species using GGDC formula 2 (DDH estimates based on identities/HSP length)*

|        | DI | DH | BF | BM | BP | BS |
|--------|----|----|----|----|----|----|
| DI     | 100.00% | 26.9% ± 3.0S | 20.7% ± 2.57 | 20.7% ± 2.57 | 20.7% ± 2.58 | 20.3% ± 2.58 |
| DH     | 100.00% | 20.7% ± 2.57 | 21.1% ± 2.56 | 20.1% ± 2.58 | 20.7% ± 2.57 |
| BF     | 100.00% | 21.7% ± 2.93 | 25.1% ± 3.11 | 21.9% ± 2.97 |
| BM     | 100.00% | 22.2% ± 2.95 | 22.2% ± 2.97 |
| BP     | 100.00% | 22.2% ± 2.97 |
| BS     | 100.00% |

*The confidence intervals indicate the inherent uncertainty in estimating DDH values from intergenomic distances based on models derived from empirical test data sets (which are always limited in size); details are provided elsewhere [19]. The distance formulas are explained elsewhere [23]; formula 2 is recommended, particularly for draft genomes.

**Taxonomic and nomenclatural proposals**

**Description of Dermabacter indicis strain FF11T sp. nov.**

*Dermabacter indicis* (in.dii.cis, L. gen. neutr. n. indicis, pertaining to the Latin name of the index finger, from which the type strain was isolated).

Strain FF11T is a Gram-positive bacterium, facultatively anaerobic, with small (1 mm) and white colonies on 5% sheep blood–enriched Columbia agar. Strain FF11T is nonmotile, non–spore forming, oxidase negative and catalase positive. Strain FF11T grows at 37°C. Strain FF11T presents positive reactions for D-galactose, D-glucose, D-trehalose, D-melezitose, D-raffinose, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyrazinecarboxamide, pyroglutamic acid–fi-nase, starch, D-turanose, esterase, esterase-lipase, pyra

**Acknowledgements**

The authors thank the Xegen Company (http://www.xegen.fr/) for automating the genomic annotation process. This study was funded by the Fondation Méditerranée Infection. We also thank C. Andrieu for administrative assistance.

**Conflict of interest**

None declared.

**References**

[1] Jones D, Collins MD. Taxonomic studies on some human cutaneous coryneform bacteria: description of *Dermabacter hominis* gen. nov., sp. nov. *FEMS Microbiol Lett.* 1988;51:15–5.

[2] Parte AC. LPSN—list of prokaryotic names with standing in nomenclature. *Nucleic Acids Res* 2014;42:D613–6.

[3] Fernández-Natal I, Sáez-Nieto JA, Medina-Pascual MJ, Albersmeier A, Valdezate S, Guerra-Laso JM, et al. *Dermabacter hominis*: a usually daptomycin-resistant Gram-positive organism infrequently isolated from human clinical samples. *New Microbes New Infect* 2013;1:35–40.

[4] Funk G, Stubbs S, Pfyffer GE, Marchiani M, Collins MD. Characteristics of CDC group 3 and group 5 coryneform bacteria isolated from clinical specimens and assignment to the genus *Dermabacter*. *J Clin Microbiol* 1994;32:1223–8.

[5] Gómez-Garcés JL, Oteo J, García C, Aracil B, Alós JL, Funke G. *Bacteria* by *Dermabacter hominis*, a rare pathogen. *J Clin Microbiol* 2001;39:2356–7.

[6] Siméon D, Le Costumier A, Gariot P, Riegel P. *Dermabacter hominis*: revive des données bactériologiques et cliniques. À propos d’un cas d’infection chez un patient diabétique. *Med Maladies Infect* 1999;29: 739–48.

[7] Ramasamy D, Mishra AK, Lagier JC, Padhmanabhan R, Rossi-Tamisier M, Sentausa E, et al. A polyphasic strategy incorporating genomic data for the taxonomic description of new bacterial species. *Int J Syst Evol Microbiol* 2014;64:384–431.

[8] Fournier PE, Drancourt M. *New Microbes New Infections* promotes modern prokaryotic taxonomy: a new section ‘TaxonoGenomics: new genomes of microorganisms in humans’. *New Microbes New Infect* 2015;7:48–9.

[9] Sankar SA, Lo CI, Fall B, Sambe-Ba B, Mediannikov O, Diallo I, et al. *Dermabacter hominis*, a rare pathogen. *J Clin Microbiol* 2001;39:2356–7.

[10] Woese CR, Kandler O, Wheels ML. Towards a natural system of organisms: proposal for the domains Archaea, Bacteria, and Eukarya. *Proc Natl Acad Sci U S A* 1990;87:4576–9.

[11] Garrity GM, Holt JG. The road map to the manual. In: Garrity GM, Boone DR, Castenholz RW, editors. *Bergey’s manual of systematic bacteriology*. 2nd ed., vol. 1. New York: Springer; 2001. p. 119

[12] Ezubey JP, Tindall BJ. Nomenclatural type of orders: corrections necessary according to Rules 15 and 21a of the Bacteriological Code (1990 Revision) and designation of appropriate nomenclatural types of classes and subclasses. Request for an opinion. *Int J Syst Evol Microbiol* 2001;51:725–7.

[13] Zhi XY, Li WJ, Stackebrandt E. An update of the structure and 16S rRNA gene sequence-based definition of higher ranks of the class Actinobacteria, with the proposal of two new suborders and four new families and emended descriptions of the existing higher taxa. *Int J Syst Evol Microbiol* 2009;59:589–608.

[14] Lo CI, Padhmanabhan R, Mediannikov O, Keita AK, Michelle C, Terras J, et al. Noncontiguous finished genome sequence and
description of Diaminobutyricimonas massiliensis strain FF²\textsuperscript{T} sp. nov. New Microbes New Infections 2015;8:31–40.

[15] Stackebrandt E, Rainey FA. Proposal for a new hierarchical classification system, Actinobacteria clavis nov. Int J Syst Bacteriol 1997;47:479–91.

[16] Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, et al. Gene ontology: tool for the unification of biology. The Ontology Consortium. Nat Genet 2000;25:25–9.

[17] Fall B, Lo Cl, Samb- Ba B, Perrot N, Diawara S, Gueye MW, et al. The ongoing revolution of MALDI-TOF mass spectrometry for microbiology reaches tropical Africa. Am J Trop Med Hyg 2015;92:641–7.

[18] Lo CI, Padhamanabhan R, Fall B, Sambe-Ba B, Mediannikov O, Nguyen TT, et al. Noncontiguous finished genome sequence and description of Necropsobacter massiliensis sp. nov. New Microbes New Infections 2015;8:41–50.

[19] Meier-Kolthoff JP, Góker M, Spröer C, Klenk HP. When should a DDH experiment be mandatory in microbial taxonomy? Arch Microbiol 2013;195:413–8.

[20] Collins MD, Brown J, Jones D. Brachybacterium faecium gen. nov., sp. nov., a Coryneform bacterium from poultry deep litter. Int J Syst Bacteriol 1988;38:45–8.

[21] Buczolits S, Schumann P, Weidler G, Radax C, Busse HJ. Brachybacterium murni sp. nov., isolated from the liver of a laboratory mouse strain. Int J Syst Evol Microbiol 2003;53:1955–60.

[22] Renvoise A, Aldrovandi N, Raoult D, Roux V. Helcococcus massiliensis gen. nov., sp. nov., a novel representative of the family Dermabacteraceae isolated from a patient with a cutaneous discharge. Int J Syst Evol Microbiol 2009;59:2346–51.

[23] Field D, Garrity G, Gray T, Morrison N, Selengut J, Sterk P, et al. The minimum information about a genome sequence (MIGS) specification. Nat Biotechnol 2008;26:541–7.

[24] Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ. Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics 2010;11:119.

[25] Benson DA, Karsch-Mizrachi I, Clark K, Lipman DJ, Ostell J, Sayers EW. GenBank. Nucleic Acids Res 2012;40:48–53.

[26] Lowe TM, Eddy SR. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res 1997;25:955–64.

[27] Lagesen K, Hallin P, Rodland EA, Staerfeldt HH, Rognes T, Ussery DW. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucl Acids Res 2007;35:3100–8.

[28] Kall L, Krogh A, Sonnhammer ELL. A combined transmembrane topology and signal peptide prediction method. J Mol Biol 2004:338:1027–36.

[29] Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, et al. Artemis: sequence visualization and annotation. Bioinformatics 2000;16:944–5.

[30] Carver T, Thomson N, Bleasby A, Bertram M, Parkhill J. DNAPlotter: circular and linear interactive genome visualization. Bioinformatics 2009;25:119–20.

[31] Darling AC, Mau B, Blatzer FR, Perna NT. Mauve: multiple alignment of conserved genomic sequence with rearrangements. Genome Res 2004;14:1394–403.

[32] Lechner M, Findeln S, Steiner L, Marz M, Stadler PF, Prohaska SJ. Proteinortho: detection of (co-)orthologs in large-scale analysis. BMC Bioinformatics 2011;12:124.

[33] Gouret P, Paganini j, Dainat J, Louati D, Darbo E, Pontarotti P, et al. Integration of evolutionary biology concepts for functional annotation and automation of complex research in evolution: the multi-agent software system DAGOBAH. In: Pontarotti P, editor. Evolutionary biology—concepts, biodiversity, macroevolution and genome evolution. Berlin: Springer; 2011. p. 71–87.

[34] Gouret P, Vitiello V, Balandaud A, Gilles A, Pontarotti P, Danchin EJ. FIGENIX: intelligent automation of genomic annotation: expertise integration in a new software platform. BMC Bioinformatics 2005:6:198.

[35] Auch AF, Klenk HP, Góker M. Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. Stand Genomic Sci 2010;2:142–8.

[36] Meier-Kolthoff JP, Auch AF, Klenk HP, Góker M. Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinformatics 2013;14:60.