**Rothia santali** sp. nov., endophytic bacteria isolated from sandalwood (*Santalum album* L.) seedling

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**Abstract**

A novel, mustard yellow-pigmented aerobic bacterial strain designated AR01⁷ was isolated from hypocotyl tissue of a sandalwood seedling from Bangalore, India. The 16S rRNA gene of strain AR01⁷ had the highest 98.97% sequence similarity with *Rothia halotolerans* YIM 90716⁷ (KCTC 19172) followed by *Rothia kristinae* PM 129⁷ (NBRC 15354⁷) (97.31%) and *Rothia koreensis* P31⁷ (JCM 15915) (97.11%), respectively. The strain AR01⁷ was coccoid-shaped, non-motile, non-spore forming, oxidase negative and catalase positive. The strain AR01⁷ has a genome size of 3.31 Mb containing 2993 protein-coding genes including 48 tRNA and 10 rRNAs spread across 84 contigs. The genomic DNA G + C content was 71.77 mol%. The calculated dDDH was 31.10% and the OrthoANI value was 85.27% when compared with its closest related type strain *Rothia halotolerans* YIM 90716⁷. The predominant cellular fatty acids were C₁₆:0 iso, C₁₅:0 anteiso and C₁₇:0 anteiso. The strain AR01⁷ contains major polar lipids including diphosphatidylglycerol and phosphatidylglycerol. The distinct physiological, biochemical characteristics and genotypic relatedness indicated that AR01⁷ represents a novel species of the genus *Rothia*, for which the name *Rothia santali* sp. nov. (Type strain AR01⁷ = MCC 4800⁷ = JCM 35593⁷) is proposed.

**Keywords** Rothia · Kocuria · *Santalum album* · Endophytic bacteria

**Abbreviations** Rothia · Kocuria · *Santalum album* · Endophytic bacteria

**Introduction**

The genus *Rothia* was initially classified as *Nocardia* (Onishi 1949) which was later renamed *Rothia* by (Georg and Brown 1967). In the beginning, *Rothia* was a group under the *Actinomycetaceae* family which was then transferred to
The Micrococcaceae family by Stackebrandt et al. (1997). They have described cells of Rothia are usually cocoid in morphology with raised smooth colonies and gram-stain-positive. The cellular structure is mostly comprising peptidoglycan type A3α and contains alanine, glutamic acid and lysine. Accurate identification of Rothia by the conventional method may be not straight forward because of its high similarity to genus like Kocuria and Nocardia. In such cases, the polyphasic approach of microbial taxonomic characterization is employed for a more reliable and accurate approach for the novel identification of a species. To date, 14 Rothia species have been described: amongst which “Rothia arfidiae” (Ko et al. 2009), “Rothia marina” (Liu et al. 2013) and ”Rothia nasisuis” (Schlattmann et al. 2018) are listed as ‘invalidly published’ species (Parte et al., 2020). The members of the genus Rothia have been mostly isolated from human skin and tooth, plant rhizosphere, saline soil, air, waste and estuarine water and domesticated animals (Pandhi and Hammond 1975; Fotos et al. 1982; Bednář and Mára 1991; Collins et al., 2000; Chou et al. 2008; Fan et al. 2004; Li et al. 2004; Tang et al. 2009; Park et al. 2010; Xiong et al., 2013; Kömpfer et al., 2016; Ananieva et al. 2018; Nougouts et al. 2018). In this study, the strain AR01T was isolated from hypocotyl tissue of 10–15 days old symptomatic sandalwood (Santalum album L.) seedlings which were screened for the presence of pathogenic and commensal microbiome associated with high mortality rate during post-germination period.

Materials and methods

Isolation and culture conditions

The strain AR01T was isolated from hypocotyl tissue of sandalwood seedlings showing symptoms of stunt and abnormal growth collected from insect-free sandalwood nursery at the Indian Wood Science and Technology (IWST) institute located in Bangalore, India. The sandalwood seedling was surface sterilized by washing with sodium dodecyl sulphate (L3771; Sigma Aldrich, Germany) and processed to obtain endophytic microbes. The pre-processed samples were grown on R2A (M1743; HiMedia, India) and TSA (M1968; HiMedia, India) media, respectively. The plates were incubated at 28 °C for 24–48 h and checked for their growth. Morphologically different isolates from the mix, including new strain AR01T, were further sub-cultured on LA (M557; HiMedia, India) medium till pure colonies were obtained. The purified strain AR01T was maintained on LA plates at 4 °C, storage stock was prepared using 20% (v/v) glycerol (MB060; HiMedia, India) and maintained at 80 °C and in liquid nitrogen. The strain AR01T was deposited to National Centre for Microbial Resource (NCMR), National Centre for Cell Science (NCCS), India with accession number MCC 4800 and Japan Collection of Microorganisms (JCM) with accession number JCM 35593.

Morphological, physiological and biochemical characteristics

The Gram staining nature of AR01T was determined by observing the culture smear under a light microscope (Model BX53; Olympus, USA) with the help of a Gram staining kit (K001-KT; HiMedia, India). The size and shape of the cells were determined by scanning electron microscope (Carl Zeiss, EVO 18, Version 6.02). Prior to that the bacterial samples were fixed in 2.5% glutaraldehyde solution (G5882; Merck, Germany) and dehydrated using graded alcohol concentrations of 20%, 30%, 40%, 50%, 60%, 70%, 80% and 90%, one time and twice in 100% for 10 min each (Kannan 2018). The dehydrated samples were coated with gold particles using a sputter coater (model, SC7620; Quorum technologies, UK).

For the media optimization, cells of strain AR01T were grown in a different media plate including R2A, LA, NA and TSA and incubated at 28 °C for 24 h. Optimization of physiological characteristics like temperature, pH and salt tolerance was carried out in LB within a duration of 7 days each, respectively. Cell growth was tested at various temperatures, starting at 5 to 40 °C at an interval of 5 °C on LB medium. The cells’ ability to sustain growth at different pH was checked at pH ranging from pH 4–12 units. Buffer systems were prepared as follows: acetate buffer (pH 4–5), phosphate Buffer (pH 6–7) and bicarbonate–carbonate buffer (pH 8–12). The salt tolerance of the culture was checked by inoculation in LB having the salinity range of 0% to 5% of NaCl with an increment of 0.5%, examined at 28 °C for 7 days.

The ability of AR01T to produce spores was observed by Schaeffer–Fulton staining technique (Schaeffer–Fulton, 1933) with methylene blue as the primary strain and 0.5% saffron as a secondary stain. Cell motility was checked by stubbing the culture in a motility test medium (M260; HiMedia, India). The oxidase and catalase activity of the strain AR01T was checked by oxidase discs (DD018; HiMedia, India) and 3% (v/v) hydrogen peroxide (31,642; Sigma Aldrich, Germany), respectively.

Utilization of carbon sources, assimilation and additional biochemical sensitivity tests were determined by performing API 20 NE (Biomerieux, France) and GEN III MicroPlate (BIOLOG, USA) assays according to standard manufacturer instructions. The enzyme activity against different substrates of strain AR01T was performed using API ZYM (Biomerieux, France). The type strain of R. halotolerans YIM 90716T (KCTC 19172) was used as a reference strain for all the tests mentioned earlier.
Cellular fatty acids of strain AR01<sup>T</sup> were analyzed by Sherlock™ Microbial ID System (MIDI, Version 6.1; USA) using the RTSBA6 library as per the manufacturer’s instructions (Sasser 2001) using the cell mass of strain AR01<sup>T</sup> and R. halotolerans YIM 90716<sup>T</sup> (KCTC 19172) harvested by growing them on TSA media at pH 7.3 ± 0.2 for 48 h. For polar lipid analysis, cell mass was harvested from cultures at the logarithmic phase. Methanol/chloroform/0.3% sodium chloride (2:1:0.8, by vol.) was used for the extraction of polar lipids (Bligh and Dyer 1959) in addition to the modifications of (Card 1973). Two-dimension chromatography was used for separation using chloroform–methanol-water (40:7.5:6:2, by vol.) in the second dimension on silica gel TLC (Kieselgel 60 F254; Merck) (Minnikin et al. 1984). The plates were dried and sprayed with 5% ethanolic phosphomolybdic acid for visualization of total lipids. Further characterization was done by spraying the plates with ninhydrin (for amino groups), molybdenum blue (for phosphates), Dragendorff (for quaternary nitrogen) or α-naphthol (for sugars) (Card 1973).

Chemotaxonomic characterization

Sequencing of the 16S rRNA gene and phylogenetic analysis

Genomic DNA of the strain AR01<sup>T</sup> was extracted using the CTAB DNA extraction protocol (Ausubel, 1989). The quality and quantity were checked using a UV Spectrophotometer Nanodrop One, (Thermo Fisher Scientific, USA) and Qubit fluorometer (Thermo Fisher Scientific, USA). The partial 16S rRNA gene was amplified using the bacterial universal primer 27F and 1492R. The purified PCR products were further sequenced using primers 343R, 704F, 907R and 1028F (Baker et al. 2003). The obtained 16S rRNA gene sequence (OM838448, 1485 bp) of AR01<sup>T</sup> was compared with the closest known sequences with valid names only according to EzBioCloud Database (Yoon et al. 2017). Phylogenetic trees were constructed using Neighbour-joining (NJ), maximum-likelihood (ML) and maximum-parsimony (MP) methods to infer the position of the AR01<sup>T</sup> and its closest known relatives using the MEGA7 (Kumar et al. 2016) software with 1000 replications of bootstrap analysis. The type strain R. halotolerans YIM 90716<sup>T</sup> (KCTC 19172) was which was closest phylogenetic relative, procured from their respective culture collections for comparative polyphasic characterization and maintained on LA media at pH 7 and 28 °C.

Using Illumina MiSeq and Oxford Nanopore Technology (ONT) platform, the genomic DNA of strain AR01<sup>T</sup> was sequenced to obtain its genome sequence. The Illumina MiSeq raw reads were checked for their quality using FastQC v0.10.1 (Brown et al. 2017). The sequenced data obtained from ONT sequencing data were base-called with quality filtering (> Q7) using Guppy v3.5.4. The quality-filtered sequence of Illumina MiSeq and ONT reads were assembled using SPAdes version v3.15.3 (Antipov et al. 2016; Prijibelski et al. 2020) to obtain hybrid genome assembly of the strain AR01<sup>T</sup>. The quality and completeness of the assembled genome were checked using QUAST v5.0.2 (Gurevich et al. 2013) and CheckM v1.1.3 (Parks et al. 2015). The rRNA and tRNA screening was done by running RNAmmer (version 1.2) as described by (Lagesen et al. 2007). The DNA G + C content of strain AR01<sup>T</sup> was calculated. The digital DNA–DNA hybridization (dDDH) values were calculated using the Genome-to-Genome Distance Calculator (GGDC) webserver following the recommended formula 2 and orthoANI calculator for Average nucleotide identity (ANI), respectively (Meier-Kolthoff et al. 2014; Auch et al. 2010; Yoon et al. 2017). Further, the genome of strain AR01<sup>T</sup> was annotated from the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (Zhao et al. 2012). The functional groups of strain AR01<sup>T</sup> were analyzed using Clusters of Orthologous Groups (COG) in eggNOG-mapper v2 (Cantalapiedra et al. 2021) from the PGAP annotated protein sequences. A comparison of orthologous gene clusters amongst the genomes under study was made using OrthoVenn2 (Xu et al. 2019).

To validate and confirm the taxonomic position of the new strain AR01<sup>T</sup>, a phylogenetic tree based on the core genome was constructed using BPGA, version 1.3.0 (Chaudhari et al. 2016) and UBCG, version 3.0 (Na et al. 2018) of 10 type strains phylogenetically related to strain AR01<sup>T</sup>. As described by Edgar 2010, using the integrated USEARCH algorithm the BPGA pipeline generated orthologous protein clusters. The generated protein sequences were further aligned and concatenated. Finally, the phylogenetic tree was reconstructed using the BPGA concatenated sequences by the neighbour-joining method in MEGA 7. A total of 18,883 amino acids position were constructed in the final phylogeny tree. In addition, UBCG identified the bacterial core gene of strain AR01<sup>T</sup> and its closely related species. The identified genes were further concatenated, align and then processed for reconstructing the phylogenetic tree. The length of concatenated alignment was 93,480 bp containing 92 marker genes identified using HMMER (Potter et al. 2018) and predicted using Prodigal search (Hyatt et al. 2010).
Results and discussion

Phylogenetic and genotypic analysis

The 16S rRNA gene of strain AR01T (OM838448, 1485 bp) showed its highest sequence similarity to *R. halotolerans* YIM 90716T (KCTC 19172) (Tang et al. 2009) with 98.97% followed by *R. kristinae* PM 129T (NBRC 15354) (97.31%) (Kloos et al. 1974) and *R. koreensis* P31T (JCM 15915) (Park et al. 2010) with 97.11% similarity. Based on the 16S rRNA gene neighbour-joining phylogenetic tree construction of strain AR01T formed a distinct monophyletic clade with *R. halotolerans* YIM 90716T (KCTC 19172) (Fig. 1).

The genome sequence of strain AR01T generated 3,375,449 reads from the Illumina MiSeq and 3,399,524 reads from the ONT sequencing. Depth coverage of 80 × was obtained with 99.01% complete genome containing 84 scaffolds with the largest contigs of 2,20,631 bp. The DNA G + C contents were 71.77 mol %. The final genome assembly of strain AR01T was deposited in NCBI GenBank bearing accession number JANAFB00000000. The digital DNA–DNA hybridization (dDDH) values for strain AR01T in against *R. halotolerans* YIM 90716T (KCTC 19172) were 31.10% and 85.27% for orthoANI. A phylogenetic tree constructed from the core genome using BPGA and UBCG further supported the phylogeny derived using 16S rRNA gene sequences (Fig. 2).

A total of 2993 protein-coding genes were predicted including 48 tRNA and 10 rRNA. A total of 1670 genes had specific functional distributions according to the COG categories. The functional genes were assigned to 18 functional categories and 1 category (458 genes) with unknown function. The Venn diagram represents 1415 gene clusters shared by AR01T alone with its closely related type strains while 207 gene clusters were shared by all strains (Fig. 3a). The genes responsible for amino acid transport and metabolism (224 genes), transcription (199) and translation, ribosomal structure and biogenesis (154 genes) were the most abundant followed by genes responsible for Inorganic ion transport and metabolism (139 genes), energy production and conversion (136 genes) (Fig. 3b).

Morphological, physiological and biochemical characteristics

Colonies of strain AR01T were a mustard yellow-pigmented colony, smooth surface with an entire margin, it is a non-endospore forming and non-motile. The cells of strain AR01T were gram-positive, coccoid-shaped with 0.8 to 1 µm in diameter as seen in scanning electron micrographs. Strain AR01T showed an optimum growth in LA incubated at 25–30 °C (optimum 28 °C) for 2 days. The cells of AR01T were able to grow in a salinity range of 0.0% to 5.0% at neutral pH of 7.0. However, the new strain was able to grow at a high pH of 10.0 (Table 1). Strain AR01T was found to be catalase-positive and oxidase-negative.
Fig. 2 A combined pan-genome phylogenetic tree of strain AR01T derived from the orthologous protein and gene sequences was constructed using BPGA and UBCG tools using available genome sequences. No genome sequences are available for type strains of “Rothia arfidiae" SMC-2244 T, “Rothia nasisuis" la5R-CH16T and “Rothia marina" JSM 078151 T. The BPGA- and UBCG-based phylogenetic trees were reconstructed in MEGA 7 using the neighbour-joining method and maximum-likelihood methods, respectively, at 1000 bootstrap replicates. The figures at branch points are bootstrap values observed in trees obtained using BPGA and UBCG, respectively. The draft genome sequence of Zhihengliuella flava H85-3 T (JADOTZ000000000) was used as an outgroup. Bar indicates the number of substitutions per site.

Fig. 3 Venn diagram of protein orthologs (a) and the COG functional category distribution of genes (b) shared by Rothia santali AR01T (MCC 4800), Rothia halotolerans YIM90716T (KCTC 19172), Rothia koreensis P31T (JCM 15915) and Rothia kristinae PM 129 T (NBRC 15354). The figures on the bars indicate a number of genes assigned to a particular functional category listed on the right side in the COG functional category distribution.
Based on the API 20 NE test performed, strain AR01T was found negative for nitrate reduction and could not hydrolyze ESCulin (β-glucosidase) whereas strain R. halotolerans YIM 90716T (KCTC 19172) showed positive results. Assimilation of L-arabinose, D-mannose, N-acetyl-glucosamine and potassium gluconate was detected negative in the strain KCTC 19172 but not in AR01T. The APIZYM test performed showed a positive enzyme activity of alkaline phosphatase and α-glucosidase for strain AR01T and negative for KCTC 19172. However, the esterase enzyme activity tested positive for strain KCTC 19172T but not for strain AR01T. In the BIOLOG GEN III microplate assays, strain AR01T and YIM90716T (KCTC 19172) showed utilising various substrates; all related data including the morphological, physiological and biochemical characteristics of strain AR01T and YIM90716T (KCTC 19172) are given in Table 1 and supplementary table S1.

Chemotaxonomic characterization

The cellular major fatty acids contained in the strain AR01T were C16:0 iso (30.04%), C15:0 anteiso (37.42%) and C17:0 anteiso (21.78%) (Supplementary Table S2). The major polar lipids present in strain AR01T mainly comprised phosphatidylglycerol (PG) and diphasphatidylglycerol (DGP) along with unidentified glycolipid (GL), traces of unidentified lipid 1–5 designated as L1, L2, L3, L4, L5, unidentified amino-phospholipid (APL) and unidentified phospholipid lipid (PL). The strain KCTC 19172T contain fatty acid of phosphatidylglycerol (PG) and diphasphatidylglycerol (DGP), unidentified lipid 1, 3, 5, unidentified glycolipid (GL), unidentified phospholipid lipid (PL) (Table 1).

Description of Rothia santali sp. nov.

Rothia santali sp. nov. (san'ta.li. L. gen. n. santali, of Santalum, referring to the host plant sandalwood, Santalum album L., from which the type strain was isolated).

Gram staining positive, coccoid-shaped, 0.8 to 1 μM nm in diameter; non-endospore forming and non-motile; catalase-positive and oxidase-negative; colonies mustard yellow-pigmented, smooth round with convex elevation (2-3 mm in diameter) with the entire margin; grow at a temperature range of 25–30 °C (optimum 28 °C) at pH 7.0–10.0 with optimum pH of 7.0 and a salinity range of 0–5.0% (w/v); alkaline phosphatase and α-glucosidase positive; positive assimilation of sugars like D-maltose, stachyose, D-raffinose, D-melibiose, α-D-glucose, D-galactose, D-fructose-6-PO4, L-arginine, L-glutamic acid, L-serine, lincomycin guanidine HCl, methyl pyruvate and propionic acid; resistant to fusidic acid, D-serine, 1% sodium lactate, rifamycin SV, Vancomycin, Nalidixic Acid, Aztreonam and Sodium Bromate; contains polar lipids phosphatidylglycerol and DPG, PG DPG, PG.
Diphosphatidylglycerol and cellular fatty acids C_{16:0} iso and C_{15:0 anteiso} and C_{17:0 anteiso}. The genomic DNA G+C contents were 71.77 mol %.

The type strain AR01T (= MCC 4800 = JCM 35593) was isolated from hypocotyl tissues of sandalwood (Santalum album L.) seedlings located in Bangalore, India.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s00203-022-03237-6.

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Author contributions NT and GN carried out the morphological, physiological and biochemical characterization; KK performed genome sequencing and partial genome analysis; NT constructed the phylogenetic trees and bioinformatic analysis; SP and PS did the survey of natural habitats of sandalwood, collected the seeds, generated the seedlings and maintained them; VT isolated and identified the bacterial isolates; SS partially supervised the work; SR coordinated forest seedlings and maintained them; NT wrote the first draft of the manuscript; AY conceptualized and coordinated the overall work and finalized the manuscript.

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Declarations

Conflict of interest The authors declare that there are no conflicts of interest.

Ethical statement No human or animal subjects were recruited for this study.

References

Ananieva MM, Nazarchuk OA, Faustova MO et al (2018) Pathogenicity factors of Kocuria kristinae contributing to the development of peri-implant mucositis. Malays J Med Health Sci 14(3):34–38
Antipov D, Korobeynikov A, McLean JS, Pevzner PA (2016) hybridSPAdes: an algorithm for hybrid assembly of short and long reads. Bioinformatics 32:1009–1015. https://doi.org/10.1093/bioinformatics/btw688
Auch AF, Klenk H-P, Göker M (2010) Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. Stand Genom Sci 2:142–148. https://doi.org/10.4056/sigs.541628
Ausubel FM, Brent R, Kingston RE et al (1994) Current protocols in molecular biology. Willey, New York

Baker GC, Smith JJ, Cowan DA (2003) Review and re-analysis of domain-specific 16S primers. J Microbiol Methods 55:541–555. https://doi.org/10.1016/j.mimet.2003.08.009
Bednář M, Mára M (1991) Immunostimulatory effect of Rothia dentocariosa in Mice. Zentralblatt für Bakteriologie 274:527–532. https://doi.org/10.1007/S0933-8840(11)80091-5
Bligh EG, Dyer WJ (1959) A rapid method of total lipid extraction and purification. Can J Biochem Physiol 37:911–917. https://doi.org/10.1139/e59-099
Brown J, Furrung M, McCue LA (2017) FQC Dashboard: integrates FastQC results into a web-based, interactive, and extensible FASTQ quality control tool. Bioinformatics 33:3137–3139. https://doi.org/10.1093/bioinformatics/btx373
Cantalamapeda CP, Hernández-Plaza A, Letunic I et al (2021) eggNOG mapper v2: functional annotation, orthology assignments, and domain prediction at the metagenomic scale. Mol Biol Evol 38:5825–5829. https://doi.org/10.1093/molbev/msab293
Card GL (1973) Metabolism of phosphatidylglycerol, phosphatidyl-ethanolamine, and cardiolipin of Bacillus stearothermophilus. J Bacteriol 114:1125–1137. https://doi.org/10.1128/jb.114.3.1125-1137.1973
Chaudhari NM, Gupta VK, Dutta C (2016) BPGA-an ultra-fast pan-genome analysis pipeline. Sci Rep 6:1–10. https://doi.org/10.1038/srep24373
Chou Y-J, Chou J-H, Lin K-Y et al (2008) Rothia terrae sp. nov. isolated from soil in Taiwan. Int J Syst Evol Microbiol 58:84–88. https://doi.org/10.1099/ijs.0.061005041
Collins MD, Hutson RA, Baverud V, Falsen E (2000) Characterization of a Rothia-like organism from a mouse: description of Rothia nasimurium sp. nov. and reclassification of Stomatococcus mucilaginosus as Rothia mucilaginosa comb. nov. Int J Syst Evol Microbiol 50:1247–1251. https://doi.org/10.1099/00207713-50-3-1247
Edgar R (2010) Usearch. Lawrence Berkeley National Lab. (LBNL). Berkeley, CA (United States). https://doi.org/10.1093/bioinformatics/btq461
Fan Y, Jin Z, Tong J et al (2002) Rothia amarae sp. nov., from sludge of a foul water sewer. Int J Syst Evol Microbiol 52:2257–2260. https://doi.org/10.1099/00207713-52-6-2257
Fotos PG, Gerencser VF, Gerencser MA (1982) Blastogenic response of human lymphocytes to antigens of Rothia dentocariosa. J Dent Res 61:640–644. https://doi.org/10.1177/00220345820610050401
Georg LK, Brown JM (1967) Rothia, gen. nov. an aerobic genus of the family Actinomycetaceae. Int J Syst Bacteriol 17:79–88. https://doi.org/10.1099/00207713-17-1-79
Gurevich A, Saveliev V, Vyahl N, Tesler G (2013) QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086
Hyatt D, Chen G-L, Locascio PF et al (2010) Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinform 11:119. https://doi.org/10.1186/1471-2105-11-119
Kämpfer P, Kleinlagauer T, Busse H-J et al (2016) Rothia aerolata sp. nov., isolated from exhaust air of a pig barn. Int J Syst Evol Microbiol 66:3102–3107. https://doi.org/10.1099/ijs.0.001153
Kannan M (2018) Scanning electron microscopy: Principle, components and applications. A Textb. Fundam Appl Nanotechnol. Berkeley, CA (United States). https://doi.org/10.1093/bioinformatics/btx373
Kloos WE, Tornabene TG, Schleifer KH (1974) Isolation and characterization of micrococcii from human skin, including two new species: Micrococcus lylae and Micrococcus kristinae. Int J Syst Evol Microbiol 24:79–101. https://doi.org/10.1099/00207713-24-1-79
Ko KS, Lee MY, Park YK et al (2009) Molecular identification of clinical Rothia isolates from human patients: Proposal of a novel Rothia Species, Rothia arfidiae sp. nov. J Bacteriol Virol 39:159–164. https://doi.org/10.4167/jbv.2009.39.3.159
