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REVIEW ARTICLE

Characterization of bacteria of the genus *Dietzia*: an updated review

Seyed Mohammad Taghi Gharibzahedi · Seyed Hadi Razavi · Seyed Mohammad Mousavi

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Abstract The aim of this study was to characterize several aspects of species of the genus *Dietzia*, such as current taxonomic placement, morphological and growth characteristics, biochemical reactions, cellular lipid and fatty acid composition, the amino acids and sugars of whole-cell hydrolysates and the respiratory quinone system, and genomic guanine and cytosine (G + C) content. The species chosen for study were *D. aerolata*, *D. alimentaria*, *D. aurantiaca*, *D. cerdiciphylli*, *D. cinnamea*, *D. kunjamensis*, *D. lutea*, *D. maris*, *D. natronolimnaea*, *D. papillomatosis*, *D. psychralcaliphila*, *D. schimae*, and *D. timorensis*. The colony morphology study revealed that the colonies were small, smooth, circular and convex. Nitrate reduction, H_2S production, hydrolysis of urea, starch, and Tween 80, and the Voges–Proskauer and methyl red tests were performed for biochemical differentiation of the various *Dietzia* strains. Optimum growth temperature and pH for the different strains were 25–30 °C and 7–8, respectively. Among the strains studied, *D. timorensis* ID05-A0528^T had the lowest tolerance level to NaCl (7 %). This strain was also able to utilize a wide range of compounds as the sole carbon source. Short-chain mycolic acids were present in these bacteria. The cell wall contained *meso*-diaminopimelic acid, arabinose, and galactose; the glycan moiety of the cell wall contained acetyl residues. The major menaquinone was MK-8 (H_2). The G + C contents of the DNA ranged from 64.7 (*D. alimentaria* 72^T) to 73 mol% (*D. maris* DSM 43672^T). The most important phospholipids in these strains were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol mannoside, phosphatidylinositol, and phosphatidylethanolamine.

S. M. T. Gharibzahedi · S. H. Razavi (✉) · S. M. Mousavi
Bioprocess Engineering Laboratory (BPEL),
Department of Food Science, Engineering & Technology,
Faculty of Agricultural Engineering and Technology,
University of Tehran, P.O. Box 4111, Karaj 31587-77871, Iran
e-mail: srazavi@ut.ac.ir

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Introduction

Dietzia spp. (family *Dietziaceae*, suborder *Corynebacterineae*, order *Actinomycetales*) were originally isolated from various environments (Natarajan et al. 2005). The cells are Gram-positive, aerobic, short rod- and coccoid-like, non-motile, non-endospore-forming, non-acid fast, oxidase-positive, and catalase-positive (Koerner et al. 2009). At the time this article was being written 13 species of this genus had been identified, namely, *D. maris*, *D. natronolimnaea*, *D. psychralcaliphila*, *D. cinnamea*, *D. kunjamensis*, *D. schimae*, *D. cerdiciphylli*, *D. papillomatosis*, *D. lutea*, *D. aerolata*, *D. timorensis*, *D. alimentaria* and *D. aurantiaca*. Sequencing and PCR amplification of 16S ribosomal RNA (rRNA) gene sequences have become the basis for the rapid identification and classification of different *Dietzia* species as a phylogenetic tree (Fig. 1). This phylogenetic tree is a model of the evolutionary relationship between species based on homologous characters (Niwa et al. 2012).

Several strains identified as representing species of the genus *Dietzia* are potential human pathogens in immunocompetent (Pidoux et al. 2001) and immunocompromised (Bemer-Melchior et al. 1999; Yassin et al. 2006) patients. These bacteria also have many applications in a wide range of industries but particularly in the medical, chemical, and food industries. Click and Van Kampen (2010) reported that a number of *Dietzia* strains could be used as potential probiotics to inhibit *Mycobacterium avium* subsp. *paratuberculosis* under in vitro culture conditions. Compared to antimicrobioal drugs used for the same purpose, such *Dietzia* strains are associated with fewer medical complications. Some of the *Dietzia* species described to date have been found to degrade aliphatic hydrocarbons, such as *n*-

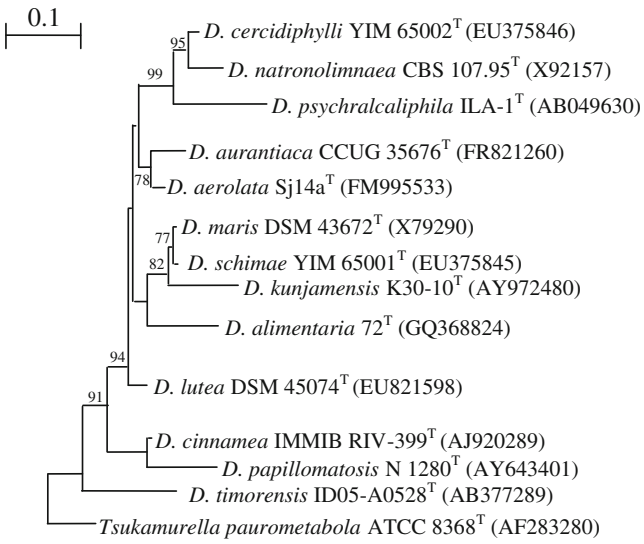

Fig. 1 Phylogenetic analysis of different species of the genus *Dietzia* based on 16S rRNA gene sequence data using the neighbor-joining method (Saitou and Nei 1987). Bootstrap values (expressed as percentages of 1,000 replications) of >50 % are given at the nodes. *Scale bar* represents 0.1 substitutions per nucleotide position. The sequence of *Tsukamurella paurometabola* ATCC 8368^T was used as an outgroup (Kämpfer et al. 2012)

alkanes (Nesterenko et al. 1982; Rainey et al. 1995; Yumoto et al. 2002; Alonso-Gutiérrez et al. 2011; Bihari et al. 2011). There have also been reports on the ability of *Dietzia* strains to degrade aromatic compounds, including benzoate (Maeda et al. 1998), carbazole, quinoline, fluoranthene (Kumar et al. 2011), phenanthrene (Brito et al. 2006; Al-Awadhi et al. 2007), naphthalene, and toluene (von der Weid et al. 2007; Bødtker et al. 2009). Iwaki et al. (2008) found that a *Dietzia* strain isolated from enrichment cultures was able to utilize cyclohexylacetic acid. The production of surface-active compounds related to hydrocarbon degradation has been reported (Nazina et al. 2003). Takeishi et al. (2006) reported the isolation of xylanolytic strains of the genus *Dietzia* from the hindgut and feces of *Trypoxylus dichotomus* larvae. Rashidi et al. (2009), who effectively biotransformed delta9-tetrahydrocannabinol (Δ^9-THC) using *Dietzia* sp. ENZHR1, concluded that alkane oxygenases of *Dietzia* spp. has the potential to play a significant role in the production of novel pharmaceuticals. *Dietzia natronolimnaea* HS-1 and *D. maris* NIT-D are the most promising sources for microbial production of carotenoid pigments, especially canthaxanthin, which are used in different industries, such as nutraceutical, cosmetics, and food and feed industries (Khodaiyan et al. 2007, 2008; Nasri Nasrabadi and Razavi 2010a, b, c; Gharibzahedi et al. 2012a,b, 2013).

Here, we present an overview on the characterization of bacteria of the genus *Dietzia* as a potential source of enzymes for use in the biodegradation, bioremediation, industrial fermentation, and carotenoid pigmentation.

Historical background

The genus *Dietzia* was first proposed by Rainey et al. (1995) to accommodate an actinomycetes previously classified as *Rhodococcus maris* (Nesterenko et al. 1982). *R. maris* was first known as *Flavobactenum maris*, but was subsequently classified as a species of the genus *Rhodococcus* (Rainey et al. 1995) based on the presence of similar morphological and chemotaxonomic characteristics with this genus, such as Gram-positive cells, lack of an aerial mycelium, cell-wall chemotype IV, mycolic acids (MAs) of the *R. eiythropolis* type, MK-8(H_2) as the major isoprenolog, fatty acids that included straight-chain saturated and mono-unsaturated fatty acids and tuberculostearic (10-metyloctadecanoic) acid, and a DNA guanine and cytosine (G + C) content of 73.2 mol% (Harrison 1929; Nesterenko et al. 1982).

This new classification was based on comparisons of 16S ribosomal DNA (rDNA) sequences, as well as on the unusual structure of polar lipids and the presence of short-chain MAs. This strain had been isolated from marine, soil and the skin and intestinal tract of a carp (Nesterenko et al. 1982; Rainey et al. 1995). Bemer-Melchior et al. (1999) were the first to report a case of bacteremia due to *D. maris* infection associated with a catheter in an immunocompromised patient presenting with septic shock and pneumothorax. *D. maris* has also been isolated from a bone biopsy specimen from a hospitalized patient associated with a total hip prosthesis replacement (Pidoux et al. 2001). Duckworth et al. (1998) isolated *D. natronolimnaios* strain 15LN1, as a secondary proposed member of the genus *Dietzia*, from an east African soda lake and compared its characteristics with *D. maris*. Using phenotypic characterization and the results of phylogenetic analyses based on 16S rRNA gene sequences, Yumoto et al. (2002) identified *D. psychralcaliphila* as another species of the genus *Dietzia* that can grow on a chemically defined medium containing *n*-alkanes as the sole carbon source. This facultatively psychrophilic alkaliphile was isolated from a drain of a fish product-processing plant. In 2006, *D. cinnamea* and *D. kunjamensis* were proposed as two additional members of the genus *Dietzia* (Mayilraj et al. 2006; Yassin et al. 2006). These strains were isolated from a perianal swab of a patient with a bone marrow transplant and a soil sample collected from Kunjam Pass (a cold desert of the Indian Himalayas), respectively. Li et al. (2008) studied the diversity of endophytic actinobacteria from important pharmaceutical plants and isolated two novel bacteria of the genus *Dietzia*, namely, *D. schimae* and *D. cercidiphylli*, from the surface-sterilized stems of *Schima* sp. and surface-sterilized roots of *Cercidiphyllum japonicum*, respectively, on tap water–yeast extract agar medium. Jones et al. (2008) also isolated an actinomycete from an immunocompetent patient suffering from confluent and reticulated papillomatosis. Using a polyphasic taxonomic

approach, these authors found that this bacterium (*D. papillomatosis*) is a novel species of the genus *Dietzia*. In 2009, *D. lutea*, which was isolated from a soil sample collected from the eastern desert of Egypt, was introduced as the ninth member of the genus *Dietzia* (Li et al. 2009). During the period 2010–2012, Kämpfer et al. (2010), Yamamura et al. (2010), Kim et al. (2011), and Kämpfer et al. (2012) identified four new species of the *Dietzia* genus, including *D. aerolata*, *D. timorensis*, *D. alimentaria*, and *D. aurantiaca*. These species were isolated from the air of a duck barn, soil, a traditional salt-fermented seafood in Korea, and cerebrospinal fluid from a 24-year-old woman, respectively.

Characterization of the different species of *Dietzia*

Phenotypic characteristics

Morphological characteristics of Dietzia colonies and cells

The colonies of different *Dietzia* strains tested were characterized by their small size, circular shape, and convex form. The surface of the convex portion of the colonies was smooth. However, *D. papillomatosis* N 1280^T and *D. natronolimnaea* CBS 107.95^T had colonies with a shiny surface. The color of *D. aerolata* Sj14a^T, *D. aurantiaca* CCUG 35676^T, and *D. maris* DSM 43672^T colonies was deep orange (Table 1), while those of *D. kunjamensis* K30-10^T, *D. cercidiphylli* YIM 65002^T, *D. papillomatosis* N 1280^T, *D. lutea* DSM 45074^T, *D. timorensis* ID05-A0528^T, and *D. cinnamea* IMMIB RIV-399^T were red, reddish-orange, orange, orange–yellow, orange–yellow and yellow, respectively. The colonies of other *Dietzia* strains also had a different color (Table 1).

Table 1 also shows the cell morphology of the type strains of *Dietzia* species. The cells varied in shape from rods (*D. alimentaria* 72^T, *D. aurantiaca* CCUG 35676^T), short rods (*D. maris* DSM 43672^T, *D. natronolimnaea* CBS 107.95^T), coccoids (*D. aerolata* Sj14a^T, *D. aurantiaca* CCUG 35676^T), and rods and coccoids (*D. kunjamensis* K30-10^T, *D. lutea* DSM 45074^T, *D. timorensis* ID05-A0528^T). The cells of short, rod-shaped cells of *D. cercidiphylli* YIM 65002^T and *D. schimae* YIM 65001^T also exhibited snapping division and produce V-forms. Moreover, *D. papillomatosis* N 1280^T cells showed snapping division and V-forms and a rod–coccus life cycle (Table 1). Generally, the mean cell diameter of the type strains of *Dietzia* species was approximately 1.1–1.5 μm. According to currently available data, the cells of *D. lutea* DSM 45074^T and *D. papillomatosis* N 1280^T were the largest and smallest, respectively, of all *Dietzia* strains (Table 1).

Table 1 Colony morphology and cell morphology characteristics of the type strains of *Dietzia* species

Type strain of *Dietzia* species	Colony morphology			Cell morphology			Reference
	Shape	Surface	Color	Shape	Size (μm)		
D. aerolata Sj14a^T	Circular	ND	Deep orange	Coccoid	1.0–1.5 (diameter)		Kämpfer et al. (2010)
D. alimentaria 72^T	Circular, convex	Smooth	Coral red	Rod	1.0–1.5 (diameter)		Kim et al. (2011)
D. aurantiaca CCUG 35676^T	Circular, convex	ND	Deep orange	Coccoid	1.0–1.5 (diameter)		Kämpfer et al. (2012)
D. cercidiphylli YIM 65002^T	Circular	Smooth	Reddish–orange	Short and rod with snapping division and V-forms	ND		Li et al. (2008)
D. cinnamea IMMIB RIV-399^T	Circular	Smooth	Yellow	Rod	ND		Yassin et al. (2006)
D. kunjamensis K30-10^T	Circular, convex	Smooth	Red	Rod and coccoid	1.0–1.2×1.1–2.0		Mayilraj et al. (2006)
D. lutea DSM 45074^T	Circular, convex	Smooth	Orange–yellow	Short rod and coccoid	1.0–1.2×1.1–2.4		Li et al. (2009)
D. maris DSM 43672^T	Circular	ND	Deep orange	Short-rod	ND		Li et al. (2008)
D. natronolimnaea CBS 107.95^T	Circular, convex	Glistening	Soft pink	Short-rod	ND		Duckworth et al. (1998)
D. papillomatosis N 1280^T	Circular, convex	Shiny	Orange	Rod and coccoid with snapping division and V-forms	1.0–1.4×0.2–0.4		Jones et al. (2008)
D. psychralcaliphila ILA-1^T	Circular, convex	ND	Soft red	Rod with snapping division	0.8–1.0×1.0–2.2		Yumoto et al. (2002)
D. schimae YIM 65001^T	Circular	Smooth	Deep pink	Short and rod with snapping division and V-forms	ND		Li et al. (2008)
D. timorensis ID05-A0528^T	Circular,convex	ND	Orange–yellow	Rod and coccoid	ND		Yamamura et al. (2010)

ND Not determined

Biochemical reactions

Nitrate reduction, H_2S production, hydrolysis of urea, starch, and Tween, and the Voges–Proskauer (VP) and methyl red (MR) tests are the seven main biochemical reactions used to discriminate the different *Dietzia* strains. Li et al. (2009) showed that *D. lutea* DSM 45074^T is negative for all of these phenotypic characteristics. *D. cinnamea* IMMIB RIV-399^T, *D. maris* DSM 43672^T, and *D. papillomatosis* N 1280^T were able to reduce nitrates to nitrogen and hydrolyze urea. In contrast, *D. timorensis* ID05-A0528^T tested negative for nitrate reduction and urea hydrolysis (Table 2). *D. natronolimnaea* CBS 107.95^T and *D. psychralcaliphila* ILA-1^T were positive for H_2S production and hydrolysis of urea, but they could not reduce nitrates to nitrogen. A dissimilar behavior was observed for *D. schimae* YIM 65001^T. *D. cercidiphylli* YIM 65002^T and *D. kunjamensis* K30-10^T also showed two different behaviors in terms of the studied phenotypic properties (Table 2). The tested strains of *D. alimentaria* 72^T, *D. cercidiphylli* YIM 65002^T, *D. kunjamensis* K30-10^T, and *D. lutea* DSM 45074^T were not able to hydrolyze starch. In contrast, *D. cinnamea* IMMIB RIV-399^T, *D. maris* DSM 43672^T, *D. natronolimnaea* CBS 107.95^T, *D. papillomatosis* N 1280^T, and *D. psychralcaliphila* ILA-1^T were able to hydrolyze starch (Table 2). The performed studies on some of the *Dietzia* strains revealed that these bacteria were able to degrade Tween 80. The VP and MR tests were negative for some of the investigated strains, such as *D. cercidiphylli* YIM 65002^T (Li et al. 2008), *D. kunjamensis* K30-10^T (Mayilraj et al. 2006), *D. lutea* DSM 45074^T (Li et al. 2009), *D. psychralcaliphila* ILA-1^T (Yumoto et al. 2002), and *D. schimae* YIM 65001^T (Li et al. 2008).

Growth characteristics

D. schimae YIM 65001^T, *D. kunjamensis* K30-10^T, *D. lutea* DSM 45074^T, and *D. maris* DSM 43672^T had the highest tolerance to NaCl concentration (15 %). *D. timorensis* ID05-A0528^T was the least tolerant to NaCl concentration (tolerant to 7 %) among all of the *Dietzia* strains (Table 3). *D. psychralcaliphila* ILA-1^T, *D. natronolimnaea* CBS 107.95^T, *D. cercidiphylli* YIM 65002^T, and *D. alimentaria* 72^T tolerated up to 10 % NaCl. The maximum NaCl tolerance for the culturing of *D. aurantiaca* CCUG 35676^T, *D. papillomatosis* N 1280^T, and *D. cinnamea* IMMIB RIV-399^T was 12, 8, and 12 %, respectively.

D. cercidiphylli YIM 65002^T, *D. kunjamensis K30-10^T*, *D. natronolimnaea* CBS 107.95^T, *D. papillomatosis* N 1280^T, *D. psychralcaliphila* ILA-1^T, and *D. timorensis* ID05-A0528^T had a similar range in growth temperature—10–37 °C (Table 3). A growth temperature range of 10–45 °C has also been reported for *D. lutea* DSM 45074^T, *D. maris* DSM 43672^T, and *D. schimae* YIM 65001^T (Table 3). These strains had the widest range of temperature for the cell growth. The growth temperature range for *D. aerolata* Sj14a^T, *D. alimentaria* 72^T, *D. aurantiaca* CCUG 35676^T, and *D. cinnamea* IMMIB RIV-399^T was 10–30 °C, 15–37 °C, 4–37 °C, and 22–45 °C, respectively (Table 3). In general, the optimum growth temperature for the various strains was between 25 and 30 °C.

The bacterial growth of *D. aurantiaca* CCUG 35676^T took place at a pH range of5.5–12.5; the approximate optimum was at pH7.0–8.0 (Kämpfer et al. 2012). Of all *Dietzia* strains, *D. aurantiaca* CCUG 35676^T grows in the largest pH range. Therefore, these researchers pointed out that growth at higher pH values of 10 must be interpreted with

Table 2 Some phenotypic properties of type strains of *Dietzia* species

Type strain of *Dietzia* species	Nitrate reduction	H_2S production	Urea hydrolysis	Starch hydrolysis	Reference
D. aerolata Sj14a^T	ND	ND	−	ND	Kämpfer et al. (2010)
D. alimentaria 72^T	+	ND	−	−	Kim et al. (2011)
D. aurantiaca CCUG 35676^T	ND	ND	ND	ND	Kämpfer et al. (2012)
D. cercidiphylli YIM 65002^T	−	−	+	−	Li et al. (2008)
D. cinnamea IMMIB RIV-399^T	+	ND	+	+	Yassin et al. (2006)
D. kunjamensis K30-10^T	+	+	−	−	Mayilraj et al. (2006)
D. lutea DSM 45074^T	−	−	−	−	Li et al. (2009)
D. maris DSM 43672^T	+	−	+	+	Li et al. (2008)
D. natronolimnaea CBS 107.95^T	−	+	+	+	Duckworth et al. (1998)
D. papillomatosis N 1280^T	+	ND	+	+	Jones et al. (2008)
D. psychralcaliphila ILA-1^T	−	+	+	+	Yumoto et al. (2002)
D. schimae YIM 65001^T	+	−	−	ND	Li et al. (2008)
D. timorensis ID05-A0528^T	−	ND	−	ND	Yamamura et al. (2010)

Characteristics were scored as: +, Positive; −, negative

Table 3 Growth conditions of type strains of *Dietzia* species

Type strain of *Dietzia* species	Growth conditions			Reference
	Maximum NaCl tolerance (%, w/v)	Temperature range (°C)	pH range	
D. aerolata Sj14a^T	ND	10–30	ND	Kämpfer et al. (2010)
D. alimentaria 72^T	10	15–37	7–10	Kim et al. (2011)
D. aurantiaca CCUG 35676^T	12	4–37	5.5–12.5	Kämpfer et al. (2012)
D. cercidiphylli YIM 65002^T	10	10–37	6–9	Li et al. (2008)
D. cinnamea IMMIB RIV-399^T	12	22–45	ND	Yassin et al. (2006)
D. kunjamensis K30-10^T	15	10–37	7–10	Mayilraj et al. (2006)
D. lutea DSM 45074^T	15	10–45	5–9	Li et al. (2009)
D. maris DSM 43672^T	15	10–45	ND	Li et al. (2008)
D. natronolimnaea CBS 107.95^T	10	10–37	6–10	Duckworth et al. (1998)
D. papillomatosis N 1280^T	8	10–37	ND	Jones et al. (2008)
D. psychralcaliphila ILA-1^T	10	10–37	7–10	Yumoto et al. (2002)
D. schimae YIM 65001^T	15	10–45	6–9	Li et al. (2008)
D. timorensis ID05-A0528^T	7	10–37	ND	Yamamura et al. (2010)

ND Not determined

care, because even if the medium pH is adjusted to 12.5, CO_2 production will lead to a fairly rapid drop in the pH. Li et al. (2008) reported that two strains of *D. cercidiphylli* YIM 65002^T and *D. schimae* YIM 65001^T had a growth pH range of about 6.0–9.0. *D. alimentaria* 72^T, *D. kunjamensis K30-10*^{T}, and *D. psychralcaliphila* ILA-1^T had a similar pH growth range of 7.0–10.0 (Table 3).

Table 4 also shows sole carbon source utilization profiles of the type strains of *Dietzia* species. Among the strains, only *D. timorensis* ID05-A0528^T was able to utilize all of the mentioned sole carbon sources, including D-adonitol, aesculin, D-arabitol, L-arabinose, arbutin, cellobiose, D-fucose, D-fructose, gentiobiose, D-galactose, D-glucose, glycerol, inositol, inulin, lactose, D-lyxose, maltose, D-mannose, melezitose, melibiose, *N*-acetylglucosamine, raffinose, L-rhamnose, D-ribose, salicin, sucrose, D-tagatose, trehalose, turanose, xylitol, and D-xylose (Yamamura et al. 2010).

Chemotaxonomic characterization

Cellular lipid and fatty acid compositions

The polar lipid profiles present in the type strains of *Dietzia* species are given in Table 5. As shown in this table, diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol mannoside, phosphatidylinositol, and phosphatidylethanolamine (PE) were most important phospholipids in these strains. *Dietzia aerolata* Sj14a^T and *D. lutea* DSM 45074^T contain all of the mentioned polar lipids. *D. alimentaria 72*^{T} and *D. cercidiphylli* YIM 65002^T had all of the phospholipids except PE. In contrast, each recognized *Dietzia* species only contained two or three of these five kinds of phospholipid components (Table 5). The polar lipid profiles of *D. aurantiaca* CCUG 35676^T and *D. alimentaria* 72^T also contained several unidentified glycolipids. Moreover, several unknown aminolipids were detected in *D. aerolata* Sj14a^T and *D. alimentaria* 72^T.

Table 6 shows the gas chromatography (GC) analysis of the cellular fatty acid profiles of the type strains of all *Dietzia* species under the same conditions according to the standard Microbial Identification System (MIDI). Whole-cell fatty acids consist of predominantly straight-chain saturated and unsaturated components. $C_{13:0}$, $C_{13:0}$ 2-OH, $C_{13:0}$ 3-OH, and $C_{14:1}\omega5c$ were only present as cellular fatty acids of *D. schimae*. *D. cercidiphylli* YIM 65002^T also only had iso-$C_{15:1}$ (0.4 %) fatty acid. The highest amounts of $C_{14:0}$, $C_{15:0}$, $C_{16:0}$, $C_{17:0}$, and $C_{18:0}$ fatty acids were in *D. schimae* YIM 65001^T (2.9 %), *D. cinnamea* IMMIB RIV-399^T (8.3 %), *D. timorensis* ID05-A0528^T (48.0 %), *D. aurantiaca* CCUG 35676^T (25.9 %), and *D. psychralcaliphila* ILA-1^T (13.9 %). The highest levels of 10-methyl $C_{16:0}$, 10-methyl $C_{17:0}$, and 10-methyl $C_{18:0}$ were found in *D. cinnamea* IMMIB RIV-399^T (3.2 %), *D. cinnamea* IMMIB RIV-399^T (11.1 %), and *D. natronolimnaea* CBS 107.95^T (30.2 %), respectively (Table 6). However, *D. cinnamea* IMMIB RIV-399^T contained the maximum amount of methyl-saturated fatty acids (43.1 %). Iso-$C_{17:0}$ and anteiso-$C_{17:0}$ fatty acids were present only in *D. cercidiphylli* YIM 65002^T. Also, *D. aerolata* Sj14a^T was only the genus containing iso-$C_{19:0}$, anteiso-$C_{19:0}$, and iso-$C_{20:0}$ fatty acids. The fatty acid profile of all of the strains consisted of $C_{16:1}\omega7c$ except for *D. timorensis* ID05-A0528^T. *D. timorensis* ID05-A0528^T possessed the highest $C_{18:1}\omega9c$ amount (39.0 %). *D. cercidiphylli* YIM 65002^T had the second highest $C_{18:1}\omega9c$ level (27.9 %) followed by *D. kunjamensis* K30-10^T (27.3 %).

Table 4 Sole carbon source utilization profiles of the type strains of *Dietzia* species

Utilization as sole carbon	Type strains of *Dietzia* species[a,b]												
	A	B	C	D	E	F	G	H	I	J	K	L	M
D-Adonitol	−	−	−	−	−	−	−	−	−	+	+	−	+
Aesculin	ND	+	ND	+	−	+	+	+	−	ND	+	+	+
D-Arabitol	−	w	ND	−	ND	−	−	−	−	ND	+	−	+
L-Arabinose	−	−	+	+	−	−	+	−	−	+	−	−	+
Arbutin	−	+	−	+	ND	−	−	−	−	+	−	−	+
Cellobiose	−	−	+	−	−	+	−	−	+	+	+	+	+
D-Fucose	ND	−	ND	−	−	w	−	−	−	ND	+	−	+
D-Fructose	ND	w	ND	+	+	+	+	+	−	ND	+	+	+
Gentiobiose	ND	−	ND	−	−	+	−	−	−	+	+	−	+
D-Galactose	ND	−	ND	−	−	w	+	+	+	ND	−	−	+
D-Glucose	+	+	+	+	+	+	+	+	+	+	−	+	+
Glycerol	ND	−	ND	−	−	−	+	w	+	ND	+	−	+
Inositol	−	w	−	−	−	−	+	−	−	+	+	−	+
Inulin	−	+	−	−	ND	+	−	−	−	ND	−	−	+
Lactose	ND	+	ND	+	−	+	−	−	+	+	+	+	+
D-Lyxose	ND	−	ND	+	−	+	+	−	−	ND	−	−	+
Maltose	−	+	−	+	+	−	−	+	+	+	+	−	+
D-Mannose	+	+	−	+	ND	+	+	−	+	+	+	+	+
Melezitose	ND	−	ND	−	−	w	−	+	+	+	+	−	+
Melibiose	−	−	−	−	ND	+	−	−	+	+	+	−	+
N-Acetylglucosamine	−	+	+	−	ND	−	−	−	+	ND	+	−	+
Raffinose	−	−	ND	−	−	+	−	−	+	+	+	−	+
L-Rhamnose	−	+	−	−	−	+	+	−	−	ND	−	−	+
D-Ribose	ND	−	+	−	w	w	+	+	+	ND	−	w	+
Salicin	−	+	−	−	+	−	ND	−	−	+	−	−	+
Sucrose	−	+	+	+	−	+	−	−	+	+	+	+	+
D-Tagatose	ND	−	ND	+	+	−	−	−	−	+	−	−	+
Trehalose	−	+	−	−	−	+	−	−	+	+	+	−	+
Turanose	ND	−	ND	−	−	+	−	+	−	ND	+	−	+
Xylitol	ND	−	ND	+	−	+	−	w	−	ND	−	+	+
D-Xylose	−	−	−	−	+	−	+	w	−	+	−	−	+
Reference	Kämpfer et al. (2010)	Kim et al. (2011)	Kämpfer et al. (2012)	Li et al. (2008)	Yassin et al. (2006)	Mayilraj et al. (2006)	Li et al. (2009)	Li et al. (2008)	Li et al. (2008)	Jones et al. (2008)	Yumoto et al. (2002)	Li et al. (2008)	Yamamura et al. (2010)

[a] A, *D. aerolata* Sj14a^T; B, *D. alimentaria* 72^T; C, *D. aurantiaca* CCUG 35676^T; D, *D. cercidiphylli* YIM 65002^T; E, *D. cinnamea* IMMIB RIV-399^T; F, *D. kunjamensis* K30-10^T; G, *D. lutea* DSM 45074^T; H, *D. maris* DSM 43672^T; I, *D. natronolimnaea* CBS 107.95^T; J, *D. papillomatosis* N 1280^T; K, *D. psychralcaliphila* ILA-1^T; L, *D. schimae* YIM 65001^T; M, *D. timorensis* ID05-A0528^T

[b] Characteristics were scored as: +, positive; w, weakly positive; −, negative

Table 5 Polar lipids and isoprenoid menaquinone present in the type strains of *Dietzia* species

Type strain of *Dietzia* species	Polar lipids[a,b]					Isoprenoid menaquinones [b]			DNA guanine and cytosine (G+C) content (mol%)	Reference
	DPG	PG	PIM	PI	PE	MK-7(H_2)	MK-8(H_2)	MK-9(H_2)		
D. aerolata Sj14a^T	+	+	+	+	+	+	+ (max)	+ (min)	ND	Kämpfer et al. (2010)
D. alimentaria 72^T	+	+	+	+	−	ND	+ (max)	ND	64.7	Kim et al. (2011)
D. aurantiaca CCUG 35676^T	+	+	−	+	−	+	+ (max)	+ (min)	ND	Kämpfer et al. (2012)
D. cercidiphylli YIM 65002^T	+	+	+	+	−	ND	+ (max)	ND	72.6	Li et al. (2008)
D. cinnamea IMMIB RIV-399^T	+	+	−	−	+	+ (min)	+ (max)	−	72.3	Yassin et al. (2006)
D. kunjamensis K30-10^T	+	+	−	+	−	ND	+ (max)	ND	67.0	Mayilraj et al. (2006)
D. lutea DSM 45074^T	+	+	+	+	+	ND	+ (max)	ND	70.5	Li et al. (2009)
D. maris DSM 43672^T	+	+	−	−	+	ND	+ (max)	ND	73.0	Li et al. (2008)
D. natronolimnaea CBS 107.95^T	+	+	−	−	+	ND	+ (max)	ND	66.1	Duckworth et al. (1998)
D. papillomatosis N 1280^T	+	+	−	−	+	+ (min)	+ (max)	−	ND	Jones et al. (2008)
D. psychralcaliphila ILA-1^T	ND	ND	ND	ND	ND	ND	+ (max)	ND	69.6	Yumoto et al. (2002)
D. schimae YIM 65001^T	+	+	−	+	−	ND	+ (max)	ND	71.9	Li et al. (2008)
D. timorensis ID05-A0528^T	−	+	−	w	−	ND	+ (max)	ND	65.5	Yamamura et al. (2010)

[a] *DPG* Diphosphatidylglycerol, *DPG* phosphatidylglycerol, *PIM* phosphatidylinositol mannoside, *PI* Phosphatidylinositol, *PE* Phosphatidylethanolamine

[b] Characteristics were scored as +, positive; w, weakly positive; −, negative; + (max), maximum positive value; + (min), minimum positive value

MAs are complex hydroxylated branched-chain fatty acids with a long alkyl branch in two positions. Generally, the degree of unsaturation, the average carbon number (ACN), and the structure of the α-alkyl branch can be determined by characterizing the MAs (Nishiuchi et al. 1999). The ACN is calculated by summing the multiplication product of the number of overall carbons (N_c) and the composition (C_c, %) of each molecular species ($ACN = (\sum N_C \times C_c)/100$). A high-resolution procedure [capillary GC/mass spectroscopy (MS)] can be used to analyze MAs from *Dietzia*. Using this procedure, Nishiuchi et al. (1999) separated trimethylsilyl ether derivatives of MA methyl ester based on their number of total carbons and double bonds. These authors found that capillary GC/MS is able to detect minor components of molecular species and to reveal differences of the MA profiles among *Nocardia* species.

Genera with long-carbon-chain MAs, such as all of the *Gordonia* species, usually have an ACN in the upper 50s and 60s, none or only small quantities of saturated fatty acids (SFAs), and large amounts of polyunsaturated acids with up to five double bonds. Each species containing long-carbon-chain MAs also contained a predominant content of di-, tri- or tetraenoic acids, the α-alkyl branches of which varied in size from C_{12} to C_{18}. However, genera containing short-carbon-chain MAs, such as *D. maris* 58001^T and *Rhodococcus* strains, possess an ACN in the 30s and large quantities of SFAs. Also, the main α-alkyl branch of this group is $C_{14:0}$ and $C_{16:0}$ (Nishiuchi et al. 1999, 2000). Thus, short-carbon-chain MAs are present in most *Dietzia* species. For example, the carbon-chain length of MAs for *D. kunjamensis* K30-10^T, *D. psychralcaliphila* ILA-1^T, *D. maris* DSM 43672^T, and *D. natronolimnaea* CBS 107.95^T is 33–40, 34–39, 33–38, and 34–38, respectively (Mayilraj et al. 2006). Therefore, due to the short chain length of their MAs (34–38), *Dietzia* strains can be differentiated readily from *Rhodococcus* (34–52), *Nocardia* (46–60), *Gordonia* (48–66), *Tsukamurella* (64–78), and *Mycobacterium* (60–90) (Nishiuchi et al. 2000; Goodfellow and Maldonado 2006). This short-carbon-chain length of probably indicates that *Dietzia* species possess a novel pathway for fatty acid biosynthesis. However, their carbon chain length is not a very excellent chemotaxonomic index because there is a degree of overlap among the four genera *Rhodococcus*, *Nocardia*, *Dietzia* and *Gordonia*.

The use of rapid identification methods, such as a combination from the morphological and chemotaxonomic characteristics (Koerner et al. 2009), can be applied to separate *Dietzia* from other amycelial MA-containing genera. Niwa et al. (2012) characterized 16 human clinical isolates of *Dietzia* species which had been previously misidentified as *R. equi* using phenotypic methods, including traditional and commercial (API Coryne) biochemical tests, antimicrobial susceptibility testing, and 16S rRNA gene and DNA gyrase β subunit (*gyrB*) gene sequencing. These authors concluded that the hydrolysis of adenine and the Christie–Atkins–Munch–Petersen (CAMP) reaction can suitably discriminate between *Dietzia* isolates and the type strain of *R. equi*. Traditional and commercial phenotypic profiles are inappropriate for identifying *Dietzia* species. Also, in a study by Niwa et al. (2012),

Table 6 Fatty acid profiles of the type strains of *Dietzia* species

Fatty acid (%)	Type strains of *Dietzia* species[a]												
	A	B	C	D	E	F	G	H	I	J	K	L	M
$C_{13:0}$	–	–		–	–	–	–	–	–	–	–	0.2	–
$C_{13:0}$ $^{2-OH}$	–	–		–	–	–	–	–	–	–	–	0.5	–
$C_{13:0}$ $^{3-OH}$	–	–		–	–	–	–	–	–	–	–	0.5	–
$C_{14:0}$	0.5	–	0.9	1.2	0.8	0.5	1.0	0.8	1.0	–	0.8	2.9	–
$C_{14:1}$ $^{\omega5c}$	–	–		–	–	–	–	–	–	–	–	0.2	–
$C_{15:0}$	–	–	2.5	–	8.3	–	3.7	–	–	5.4	–	–	–
Iso-$C_{15:1}$	–	–		0.4	–	–	–	–	–	–	–	–	–
Iso-$C_{15:1}$ ^{G}	–	–		–	–	–	–	–	–	–	0.1	0.9	–
$C_{15:1}$ $^{\omega5c}$	–	–		–	–	–	–	0.4	–	–	–	0.4	–
$C_{15:1}$ $^{\omega8c}$	–	–		–	–	–	–	0.2	–	–	0.2	0.8	–
$C_{16:0}$	22.7	15.5	21.7	18.9	28.9	13.0	15.4	15.3	14.1	21.1	16.9	22.2	48.0
Iso-$C_{16:0}$	–			1.6	–	–	–	–	–	–	–	–	–
$C_{16:1}$ $^{\omega7c}$	5.6	15.1	9.8	18.7	2.8	12.9	6.7	10.6	33.0	3.0	10.1	25.8	–
$C_{16:1}$ $^{\omega9c}$	–	–		0.5	–	–	3.8	–	–	–	0.8	–	–
10-methyl $C_{16:0}$	–	–	0.5	1.1	3.2	–	–	0.6	0.7	–	0.3	0.8	–
$C_{17:0}$	14.0	10.8	25.9	–	11.7	8.8	22.4	13.2	–	6.1	13.8	–	–
Iso-$C_{17:0}$	–	–		0.2	–	–	–	–	–	–	–	–	–
Anteiso-$C_{17:0}$	–	–		0.9	–	–	–	–	–	–	–	–	–
$C_{17:1}$ $^{\omega7c}$	–	4.9	0.4	2.2	5.3	7.6	–	–	–	–	–	19.2	–
$C_{17:1}$ $^{\omega8c}$	5.0	–		3.7	–	8.7	12.2	17.2	–	2.7	7.5	–	–
$C_{17:1}$ $^{anteiso\ B}$	–	–		–	–	–	–	–	–	–	1.7	6.1	–
10-methyl $C_{17:0}$	0.7	–	1.8	0.4	11.1	1.5	2.9	5.3	0.8	–	0.6	2.0	–
$C_{18:0}$	6.9	–	7.9	–	2.3	–	8.0	12.3	–	–	13.9	–	–
$C_{18:1}$ $^{\omega7c}$	–	–		3.5	–	–	1.7		4.5	–	–	–	–
$C_{18:1}$ $^{\omega9c}$	19.7	7.4	17.2	27.9	4.8	27.3	10.2	13.9	15.7	9.0	–	–	39.0
$C_{18:3}$ $^{\omega6c}$		–		1.4	–	–	–		–	–	–	–	
10-methyl $C_{18:0}$	13.2	14.6	18.8	17.9	28.8	19.8	7.8	10.3	30.2	22.1	9.7	13.4	8.0
$C_{19:0}$	8.4	9.1	4.4	–	–	–	2.6	–	–	2.6	9.6	–	–
Iso-$C_{19:0}$	1.1	–		–	–	–	–	–	–	–	–	–	–
Anteiso-$C_{19:0}$	1.7	–		–	–	–	–	–	–	–	–	–	–
$C_{20:0}$	–	–	0.4	0.2	–	–	–	–	–	–	–	–	–
Iso-$C_{20:0}$	0.9	–		–	–	–	–	–	–	–	–	–	–
$C_{20:1}$ $^{\omega9c}$	–	4.5	3.9	–	–	–	–	–	–	–	–	–	–
$C_{20:4}$ $^{\omega6,9,12,15c}$	1.4	–	1.9	–	–	–	–	–	–	–	11.7	–	–

Table 6 (continued)

Fatty acid (%)	Type strains of *Dietzia* species[a]												
	A	B	C	D	E	F	G	H	I	J	K	L	M
Total	101.8	81.9	118.0	100.7	108.0	100.1	98.4	100.1	100.0	72.0	97.7	95.9	95.0
Reference	Kämpfer et al. (2010)	Kim et al. (2011)	Kämpfer et al. (2012)	Li et al. (2008)	Yassin et al. (2006)	Mayilraj et al. (2006)	Li et al. (2009)	Li et al. (2008)	Li et al. (2008)	Jones et al. (2008)	Yumoto et al. (2002)	Li et al. (2008)	Yamamura et al. (2010)

[a] A, *D. aerolata* Sj14a^T; B, *D. alimentaria* 72^T; C, *D. aurantiaca* CCUG 35676^T; D, *D. cercidiphylli* YIM 65002^T; E, *D. cinnamea* IMMIB RIV-399^T; F, *D. kunjamensis* K30-10^T; G, *D. lutea* DSM 45074^T; H, *D. maris* DSM 43672^T; I, *D. natronolimnaea* CBS 107.95^T; J, *D. papillomatosis* N 1280^T; K, *D. psychralcaliphila* ILA-1^T; L, *D. schimae* YIM 65001^T; M, *D. timorensis* ID05-A0528^T

the analysis of 16S rRNA gene and *gyrB* gene sequences were able to differentiate all *Dietzia* strains from the type strain of *R. equi*. Antimicrobial susceptibility testing and carbon utilization assays with the application of easy-to-perform procedures (Biotype-100 strips) also can be an effective approach to identify these microorganisms (Bizet et al. 1997)

The amino acids and sugars of whole-cell hydrolysates

Hydrolysis of the peptidoglycans of whole cells showed that *meso*-diaminopimelic acid as a diamino acid was the major amino acid present in *Dietzia* strains. However, this amino acid has been not reported in two strains of *D. aerolata* Sj14a^T and *D. aurantiaca* CCUG 35676^T. The major cell-wall sugars were arabinose and galactose. The glycan moiety of the cell wall contained *N*-acetyl residues (*N*-acetylmuramic acid) (Duckworth et al. 1998; Yumoto et al. 2002; Mayilraj et al. 2006; Yassin et al. 2006; Jones et al. 2008; Li et al. 2008, 2009; Kämpfer et al. 2010; Yamamura et al. 2010; Kim et al. 2011; Kämpfer et al. 2012).

The respiratory quinone system and the DNA G + C content

The isoprenoid or respiratory quinones are a class of terpenoid lipids with a similar inherent potential in chemotaxonomy. They are constituents of the bacterial plasma membranes and play important roles in electron transport, oxidative phosphorylation, and possibly active transport (Goodfellow and Maldonado 2006). The different *Dietzia* species contained dehydrogenated menaquinones with eight isoprene units [MK-8(H_2)] as the predominant isoprenologue (Table 5). MK-8(H_2) is also the major isopronolog found in the genus *Rhodococcus* (Rainey et al. 1995). A minor amount of MK-7(H_2) was also observed in *D. cinnamea* IMMIB RIV-399^T, *D. papillomatosis* N 1280^T, *D. aerolata* Sj14a^T, and *D. aurantiaca* CCUG 35676^T. Moreover, the quinone system of *D. aerolata* Sj14a^T and *D. aurantiaca* CCUG 35676^T was composed of MK-9(H_2) (Table 5).

DNA base composition, especially guanine + cytosine (G + C) content as a bacterial taxonomic marker, was considered. For example, actinobacteria have a high content of G + C in their genomes, whereas clostridia have low GC-containing genomes. DNA with a high GC content is more stable than DNA with low a GC content (Sueoka 1961). The mol%G + C content of DNA generally applies as part of the description of the type strain of the type species of a new genus. As illustrated in Table 5, among the various *Dietzia* species, the mean G + C content of genomic DNA varied from approximately 64.7 (*D. alimentaria* 72^T) to 73 % (*D. maris* DSM 43672^T). However, the G + C contents of the DNA for different *Dietzia* species are similar to that of *Corynebacterium* (51–67 %), *Mycobactenurn* (70–72 %), *Nocardia* (64–72 %), *Rhodococcus* (63–73 %),

Tsukamurella (67–68 %), and *Gordonia* (63–69 %) which phylogenetically were members of the MA-containing group (Rainey et al. 1995).

Concluding remarks

The present overview presents the results of a taxonomic study on the family *Dietziaceae* since the name *Dietzia* was formally introduced more than half a century ago. Over recent years, there has been a growing interest in species of the genus *Dietzia,* especially in *D. maris*, *D. natronolimnaea*, *D. cinnamea*, *D. psychralcaliphila*, and *D. cerdiciphylli* (Von der Weid et al. 2007; Alonso-Gutiérrez et al. 2011; Nakano et al. 2011; Gharibzahedi et al. 2012b). Apart from the well-established use of *Dietzia* strains in therapeutic biotreatments for adult paratuberculosis animals, the production of carotenoid pigments, and animal feed additives, various applications in biosurfactant and biodemulsifier production, pollutant bioremediation, biodegradation of petroleum hydrocarbons and crude oil, and in the production of extracellular polymeric substances have also been developed. The application of *Dietzia* strains as biotechnological tools could thus be used to improve the optimization and quality assurance of food ingredients and products, the capability of environmental pollution degradation and remediation methods, and the efficiency of bioconversion systems for energy recovery and bioprocessing of value-added products. In order to develop these bacteria for agro-environmental applications, specific and robust methods that are easy to apply, efficient in terms of time and cost, and characterized by a high sensitivity and reproducibility need to be developed to accumulate accurate information on their epidemiology and occurrence, whether in the environment and/or in food. The cellular micro-morphological, biochemical, growth and chemotaxonomic characteristics of a microorganism are frequently applied to isolate and identify that microorganism. However, these strategies are not always adequate for the classification and identification. Phylogenetic analysis using 16S rRNA gene sequences and the neighbor-joining method have been successfully applied as a molecular clock to estimate relationships among these bacteria, but more recently it has also become important as a means to identify an unknown bacterium to the genus or species level. Moreover, *gyrB* gene sequencing could be efficiently used to reliably identify *Dietzia* species. A nested-PCR amplification procedure combined with denaturing gradient gel electrophoresis enabled the detection of *Gordonia* populations from wastewater treatment plant foam samples (Shen et al. 2007); this approach could also improve the identification of *Dietzia* bacteria in different environments. The use of a considerable number of powerful molecular techniques, such as massive parallel sequencing, metagenomics, metatranscriptomics, and metaproteomics, will allow researchers to probe deeper into the characteristics of species of the genus *Dietzia*, providing more comprehensive results than conventional diagnosis and enhancing understanding of their epidemiology and natural history. The future perspective is to use these molecular procedures to overcome certain limitations, generate insights into the biology and molecular processes of *Dietzia* species, and also provide useful quantitative results.

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References

Al-Awadhi H, Sulaiman RHD, Mahmoud HM, Radwan SS (2007) Alkaliphilic and halophilic hydrocarbon-utilizing bacteria from Kuwaiti coasts of the Arabian Gulf. Appl Microbiol Biotechnol 77:183–186

Alonso-Gutiérrez J, Teramoto M, Yamazoe A, Harayama S, Figueras A, Novoa B (2011) Alkane-degrading properties of *Dietzia* sp. H0B, a key player in the Prestige oil spill biodegradation (NW Spain). J Appl Microbiol 111:800–810

Bemer-Melchior P, Haloun A, Riezel P, Drugeon H (1999) Bacteremia due to *Dietzia maris* in an immunocompromised patient. Clin Infect Dis 29:1338–1340

Bihari Z, Szvetnik A, Szabo Z, Blastyak A, Zombori Z, Balazs M, Kiss I (2011) Functional analysis of long-chain *n*-alkane degradation by *Dietzia* spp. FEMS Microbiol Lett 316:100–107

Bizet C, Barreau C, Harmant C, Nowakowski M, Pietfroid A (1997) Identification of *Rhodococcus*, *Gordonia* and *Dietzia* species using carbon source utilization tests ("Biotype-100" strips). Res Microbiol 148:799–809

Bødtker G, Hvidsten IV, Barth T, Torsvik T (2009) Hydrocarbon degradation by *Dietzia* sp. A14101 isolated from an oil reservoir model column. Antonie Van Leeuwenhoek 96:459–469

Brito EM, Guyoneaud R, Goni-Urriza M, Ranchou-Peyruse A, Verbaere A, Crapez MA, Wasserman JC, Duran R (2006) Characterization of hydrocarbonoclastic bacterial communities from mangrove sediments in Guanabara Bay, Brazil. Res Microbiol 157:752–762

Click RE, Van Kampen CL (2010) Assessment of *Dietzia* subsp. *C79793-74* for treatment of cattle with evidence of paratuberculosis. Virulence 1–3:145–155

Duckworth AW, Grant S, Grant WD, Jones BE, Meijer D (1998) *Dietzia natronolimnaios* sp. nov., a new member of the genus *Dietzia* isolated from an east African soda lake. Extremophiles 2:359–366

Gharibzahedi SMT, Razavi SH, Mousavi SM (2012a) Developing an emulsion model system containing canthaxanthin biosynthesized by *Dietzia natronolimnaea* HS-1. Int J Biol Macromol 51:618–626

Gharibzahedi SMT, Razavi SH, Mousavi SM, Moayedi V (2012b) High efficiency canthaxanthin production by a novel mutant isolated from *Dietzia natronolimnaea* HS-1 using central composite design analysis. Ind Crop Prod 40:345–354

Gharibzahedi SMT, Razavi SH, Mousavi SM (2013) Psyllium husk gum: An attractive carbohydrate biopolymer for the production of stable canthaxanthin emulsions. Carbohydr Polym 92:2002–2011

Goodfellow M, Maldonado LA (2006) The families *Dietzieaceae*, *Gordoniaceae*, *Nocardiaceae* and *Tsukamurellaceae*. In: Dworkin M, Falkow S, Schleifer KH, Stackebrandt E (eds) The prokaryotes. Springer, New York, pp 343–388

Harrison FC (1929) The discoloration of halibut. Can J Res 1:214–239
Iwaki H, Nakai E, Nakamura S, Hasegawa Y (2008) Isolation and characterization of new cyclohexylacetic acid-degrading bacteria. Curr Microbiol 57:107–110
Jones AL, Koerner RJ, Natarajan S, Perry JD, Goodfellow M (2008) *Dietzia papillomatosis* sp. nov., a novel actinomycete isolated from the skin of an immunocompetent patient with confluent and reticulated papillomatosis. Int J Syst Evol Microbiol 58:68–72
Kämpfer P, Langer S, Martin E, Jackel U, Busse HJ (2010) *Dietzia aerolata* sp. nov., isolated from the air of a duck barn, and emended description of the genus *Dietzia* Rainey et al. Int J Syst Evol Microbiol 60:393–396
Kämpfer P, Falsen E, Frischmann A (2012) *Dietzia aurantiaca* sp. nov., isolated from a human clinical specimen. Int J Syst Evol Microbiol 62:484–488
Khodaiyan F, Razavi SH, Emam-Djomeh Z, Mousavi SMA, Hejazi MA (2007) Effect of culture conditions on canthaxanthin production by *Dietzia natronolimnaea* HS-1. J Microbiol Biotechnol 17:195–201
Khodaiyan F, Razavi SH, Mousavi SM (2008) Optimization of canthaxanthin production by *Dietzia natronolimnaea* HS-1 from cheese whey using statistical experimental methods. Biochem Eng J 40:415–422
Kim J, Roh SW, Choi JH, Jung MJ, Nam YD, Kim MS, Park EJ, Shin KS, Bae JW (2011) *Dietzia alimentaria* sp. nov., isolated from a traditional Korean food. Int J Syst Evol Microbiol 61:2254–2258
Koerner RJ, Goodfellow M, Jones AL (2009) The genus *Dietzia*: a new home for some known and emerging opportunist pathogens. FEMS Immunol Med Microbiol 55:296–305
Kumar S, Upadhayay SK, Kumari B, Tiwari S, Singh SN, Singh PK (2011) In vitro degradation of fluoranthene by bacteria isolated from petroleum sludge. Bioresour Technol 102:3709–3715
Li J, Zhao GZ, Zhang YQ, Klenk HP, Pukall R, Qin Sh XLH, Li WJ (2008) *Dietzia schimae* sp. nov. and *Dietzia cercidiphylli* sp. nov., from surface-sterilized plant tissues. Int J Syst Evol Microbiol 58:2549–2554
Li J, Chen C, Zhao GZ, Klenk HP, Pukall R, Zhang YQ, Tang SK, Li WJ (2009) Description of *Dietzia lutea* sp. nov., isolated from a desert soil in Egypt. Syst Appl Microbiol 32:118–123
Maeda M, Roberts MS, Ohta Y, Fuji F, Travisano M, Kudo T (1998) Isolation and characterization of a new aromatic compound-degrading alkalitrophic bacteria. J Gen Appl Microbiol 44:101–106
Mayilraj S, Suresh K, Kroppenstedt RM, Saini HS (2006) *Dietzia kunjamensis* sp. nov., isolated from the Indian Himalayas. Int J Syst Evol Microbiol 56:1667–1671
Nakano M, Kihara M, Iehata S, Tanaka R, Maeda H, Yoshikawa T (2011) Wax ester-like compounds as biosurfactants produced by *Dietzia maris* from *n*-alkane as a sole carbon source. J Basic Microbiol 51:490–498
Nasri Nasrabadi MR, Razavi SH (2010a) Enhancement of canthaxanthin production from *Dietzia natronolimnaea* HS-1 in a fed-batch process using trace elements and statistical methods. Braz J Chem Eng 27:517–529
Nasri Nasrabadi MR, Razavi SH (2010b) High levels lycopene accumulation by *Dietzia natronolimnaea* HS-1 using lycopene cyclase inhibitors in a fed-batch process. Food Sci Biotechnol 19:899–906
Nasri Nasrabadi MR, Razavi SH (2010c) Use of response surface methodology in a fed-batch process for optimization of tricarboxylic acid cycle intermediates to achieve high levels of canthaxanthin from *Dietzia natronolimnaea* HS-1. J Biosci Bioeng 109:361–368
Natarajan S, Milne D, Jones AL, Goodfellow M, Perry J, Koerner RJ (2005) *Dietzia* strain X: a newly described Actinomycete isolated from confluent and reticulated papillomatosis. Br J Dermatol 153:825–827
Nazina TN, Sokolova DS, Grigoryan AA, Xue YF, Belyaev SS, Ivanov MV (2003) Production of oil-releasing compounds by microorganisms from the Daqing oil field, China. Microbiology 72:173–178
Nesterenko OA, Nogina TM, Kasumova SA, Kvasnikov EI, Batrakov SG (1982) *Rhodococcus luteus* nom. nov. and *Rhodococcus maris* nom nov. Int J Syst Bacteriol 32:1–14
Nishiuchi Y, Baba T, Hotta H, Yano I (1999) Mycolic acid analysis in *Nocardia* species: the mycolic acid compositions of *Nocardia asteroides*, *N. farcinica*, and *N. nova*. J Microbiol Methods 37:111–122
Nishiuchi Y, Tuneko B, Yano I (2000) Mycolic acids from *Rhodococcus*, *Gordonia* and *Dietzia*. J Microbiol Methods 40:1–9
Niwa H, Lasker BA, Hinrikson HP, Franzen CG, Steigerwalt AG, Whitney AM, Brown JM (2012) Characterization of human clinical isolates of *Dietzia* species previously misidentified as *Rhodococcus equi*. Eur J Clin Microbiol Infect Dis 31:811–820
Pidoux O, Argenson JN, Jacomo V, Drancourt M (2001) Molecular identification of a *Dietzia maris* hip prosthesis infection isolate. J Clin Microbiol 39:2634–2636
Rainey FA, Klatte S, Kroppenstedt RM, Stackebrandt E (1995) *Dietzia*, a new genus including *Dietzia maris* comb. nov., formerly *Rhodococcus maris*. Int J Syst Bacteriol 45:32–36
Rashidi H, Akhtar MT, van der Kooy F, Verpoorte R, Duetz WA (2009) Hydroxylation and further oxidation of delta9-tetrahydrocannabinol by alkane-degrading bacteria. Appl Environ Microbiol 75:7135–7141
Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol 4:406–425
Shen FT, Huang HR, Arun AB, Lu HL, Rekha PD, Young CC (2007) Detection of filamentous genus *Gordonia* in foam samples using genus-specific primers combined with PCR-denaturing gradient gel electrophoresis analysis. Can J Microbiol 53:768–774
Sueoka N (1961) Variation and heterogeneity of base composition of deoxyribonucleic acids: a compilation of old and new data. J Mol Biol 3:31–40
Takeishi H, Anzai H, Urai M (2006) Xylanolytic and alkaliphilic *Dietzia* sp. isolated from larvae of the Japanese horned beetle, *Trypoxylus dichotomus*. Actinomycetologica 20:49–54
von der Weid I, Marques JM, Cunha CD, Lippi RK, Dos Santos SCC, Rosado AS, Lins U, Seldin L (2007) Identification and biodegradation potential of a novel strain of *Dietzia cinnamea* isolated from a petroleum-contaminated tropical soil. Syst Appl Microbiol 30:331–339
Yamamura H, Lisdiyanti P, Ridwan R, Ratnakomala S, Sarawati R, Lestari Y, Triana E, Kartina G, Widyastuti Y, Ando K (2010) *Dietzia timorensis* sp. nov., isolated from soil. Int J Syst Evol Microbiol 60:451–454
Yassin AF, Hupfer H, Schaal KP (2006) *Dietzia cinnamea* sp. nov., a novel species isolated from a perianal swab of a patient with a bone marrow transplant. Int J Syst Evol Microbiol 56:641–645
Yumoto I, Nakamura A, Iwata H, Kojima K, Kusumoto K, Nodasaka Y, Matsuyama H (2002) *Dietzia psychralcaliphila* sp. nov., a novel, facultatively psychrophilic alkaliphile that grows on hydrocarbons. Int J Syst Evol Microbiol 52:85–90