Proposal of the genus *Thermoactinomyces* *sensu stricto* and three new genera, *Laceyella*, *Thermoflavimicrobium* and *Seinonella*, on the basis of phenotypic, phylogenetic and chemotaxonomic analyses

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Phylogenetic analysis based on 16S rRNA gene sequences revealed that *Thermoactinomyces* species with validly published names can be assigned to four clusters or lineages. The type strains of *Thermoactinomyces sacchari* and *Thermoactinomyces putidus* were differentiated from the type strains of *Thermoactinomyces vulgaris* and *Thermoactinomyces intermedius* by the predominant menaquinone and fatty acid profiles. The type strains of *Thermoactinomyces dichotomicus* and *Thermoactinomyces peptonophilus* formed lines of descent distinct from other *Thermoactinomyces* species. *Thermoactinomyces dichotomicus* KCTC 3667^T was distinguishable from the type strains of *Thermoactinomyces vulgaris* and *Thermoactinomyces intermedius* by the contents of two fatty acids, iso-C_{16:0} and iso-C_{17:0}. *Thermoactinomyces dichotomicus* could be distinguished from other *Thermoactinomyces* species by DNA G + C content and some phenotypic properties, particularly its property of forming a yellow colour. The type strain of *Thermoactinomyces peptonophilus* was distinguishable from other *Thermoactinomyces* species by differences in menaquinone profile, major fatty acids, DNA G + C content and some physiological properties including optimal growth temperature. On the basis of these data, the creation of three new genera, *Laceyella*, *Thermoflavimicrobium* and *Seinonella*, is proposed in addition to the genus *Thermoactinomyces sensu stricto*. The genus *Laceyella* gen. nov. is proposed to accommodate *Thermoactinomyces sacchari* and *Thermoactinomyces putidus* as *Laceyella sacchari* comb. nov. and *Laceyella putida* comb. nov., the genus *Thermoflavimicrobium* gen. nov. is proposed for *Thermoactinomyces dichotomicus* as *Thermoflavimicrobium dichotomicum* comb. nov. and the genus *Seinonella* gen. nov. is proposed for *Thermoactinomyces peptonophilus* as *Seinonella peptonophila* comb. nov.

The genus *Thermoactinomyces* was proposed by Tsilinsky (1899) with the single species *Thermoactinomyces vulgaris*. Additional *Thermoactinomyces* species have since been described: *Thermoactinomyces sacchari* (Lacey, 1971), *Thermoactinomyces peptonophilus* (Nonomura & Ohara, 1971), *Thermoactinomyces candidus* (Kurup *et al.*, 1975), *Thermoactinomyces intermedius* (Kurup *et al.*, 1980), *Thermoactinomyces thalpophilus* (Unsworth & Cross, 1980) and *Thermoactinomyces putidus* (Lacey & Cross, 1989).

Thermoactinomyces dichotomicus was proposed for ‘*Actinobifida dichotomica*’, described previously by Krasil’nikov & Agre (1964) (Cross & Goodfellow, 1973). More recently, *Thermoactinomyces candidus* was reclassified as a synonym of *Thermoactinomyces vulgaris* and *Thermoactinomyces thalpophilus* as a synonym of *Thermoactinomyces sacchari* (Yoon *et al.*, 2000). *Thermoactinomyces* species were long recognized as actinomycetes because of their morphological characteristics, forming aerial and substrate mycelia. On the basis of endospore formation, DNA G + C content and phylogenetic data, the genus *Thermoactinomyces* has now been placed within the family *Bacillaceae*, not the order *Actinomycetales* (Cross *et al.*, 1971; Lacey & Vince, 1971; Stackebrandt & Woese, 1981; Lacey & Cross, 1989; Park *et al.*, 1993; Yoon & Park, 2000).

Thermoactinomyces species are aerobic, Gram-positive and

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Abbreviations: DAP, diaminopimelic acid; FAME, fatty acid methyl ester.

thermophilic, with the exception of one mesophilic species, *Thermoactinomyces peptonophilus* (Nonomura & Ohara, 1971). The genus *Thermoactinomyces* contains meso-diaminopimelic acid (meso-DAP) but no diagnostic sugars in the cell wall (Lacey & Cross, 1989), indicating that the wall chemotype is type III (Lechevalier & Lechevalier, 1970). On the basis of differences in some phenotypic properties and predominant menaquinone profiles, together with the result of phylogenetic analysis, it was suggested that the genus *Thermoactinomyces* might be a heterogeneous group containing more than one genus (Yoon & Park, 2000). In particular, *Thermoactinomyces* species were found to have different predominant menaquinone profiles (Collins *et al.*, 1982; Tseng *et al.*, 1990). Accordingly, the aim of the present study was to elucidate the exact taxonomic status of the genus *Thermoactinomyces* by a comparative chemotaxonomic analysis using newly determined menaquinone and fatty acid profiles together with phenotypic comparisons and phylogenetic analysis based on 16S rRNA gene sequences.

Thermoactinomyces vulgaris KCTC 9076^T, *Thermoactinomyces vulgaris* KCTC 9557 (previously the type strain of *Thermoactinomyces candidus*), *Thermoactinomyces intermedius* KCTC 9646^T, *Thermoactinomyces sacchari* KCTC 9790^T, *Thermoactinomyces sacchari* KCTC 9789 (previously the type strain of *Thermoactinomyces thalophilus*), *Thermoactinomyces putidus* KCTC 3666^T, *Thermoactinomyces dichotomicus* KCTC 3667^T and *Thermoactinomyces peptonophilus* KCTC 9740^T were used in this study. Cell biomass for analyses of isoprenoid quinones and fatty acid methyl esters (FAMES) was obtained from cultivation in liquid SY medium which contained (l⁻¹ tap water) 15 g starch, 10 g yeast extract and 0.5 g MgSO₄. Since the SY medium showed good growth for all *Thermoactinomyces* species, it was used in this study for experimental standardization. All strains, except *Thermoactinomyces peptonophilus*, were cultivated at appropriate temperatures between 45 and 55 °C; *Thermoactinomyces peptonophilus* was cultivated at 35 °C. Hydrolysis of hypoxanthine, tyrosine and xanthine for *Thermoactinomyces peptonophilus* KCTC 9740^T was tested on solid SY medium using the substrate concentrations described by Cowan & Steel (1965). Isoprenoid quinones were analysed as described by Komagata & Suzuki (1987) using reversed-phase HPLC. For quantitative analysis of cellular fatty acid composition, freeze-dried cells

(approx. 7 mg) were used and FAMES were extracted and prepared according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). Chromosomal DNA was isolated and purified according to the method described previously (Yoon *et al.*, 1996), with the exception that RNase T1 was used together with RNase A. The DNA G + C content was determined by the method of Tamaoka & Komagata (1984) with the modification that DNA was hydrolysed and the resultant nucleotides were analysed by reversed-phase HPLC. Phylogenetic analyses based on 16S rRNA gene sequences were performed with the sequences of *Thermoactinomyces* species determined by Yoon & Park (2000). Alignment of 16S rRNA gene sequences was carried out using CLUSTAL W software (Thompson *et al.*, 1994). Evolutionary distance matrices were calculated using the algorithm of Jukes & Cantor (1969) with the program DNADIST within the PHYLIP package (Felsenstein, 1993). The phylogenetic tree was constructed by using the neighbour-joining method (Saitou & Nei, 1987) with the program NEIGHBOR of the same package. The stability of relationships was assessed by a bootstrap analysis of 1000 datasets by using the programs SEQBOOT, DNADIST, NEIGHBOR and CONSENSE of the PHYLIP package.

In the neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, *Thermoactinomyces* species have been found to form differential clusters or independent lineages (Fig. 1; Yoon & Park, 2000). *Thermoactinomyces vulgaris* KCTC 9076^T, *Thermoactinomyces vulgaris* KCTC 9557 and *Thermoactinomyces intermedius* KCTC 9646^T formed one coherent cluster and *Thermoactinomyces sacchari* KCTC 9790^T, *Thermoactinomyces sacchari* KCTC 9789 and *Thermoactinomyces putidus* KCTC 3666^T formed a second coherent cluster (Fig. 1; Yoon & Park, 2000). *Thermoactinomyces dichotomicus* KCTC 3667^T and *Thermoactinomyces peptonophilus* KCTC 9740^T formed separate phylogenetic lineages independent of the clusters comprising other *Thermoactinomyces* species (Fig. 1). The same tree topology was also found in trees generated with the maximum-likelihood and maximum-parsimony algorithms (Fig. 1). *Thermoactinomyces dichotomicus* KCTC 3667^T and *Thermoactinomyces peptonophilus* KCTC 9740^T exhibited relatively low 16S rRNA gene similarity levels, of 90.1–94.2 % and 90.1–91.6 %, respectively, to the type strains of the other *Thermoactinomyces* species.

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationships of *Thermoactinomyces* species. Scale bar, 0.01 substitutions per nucleotide position. Bootstrap values (expressed as percentages of 1000 replications) greater than 50 % are shown at branch points. *Escherichia coli* was used as the outgroup. Dots indicate nodes that were also recovered in maximum-likelihood and maximum-parsimony trees.

This phylogenetic differentiation correlated with differences in predominant menaquinones and cellular fatty acids and physiological properties. In the study of Tseng *et al.* (1990), the type strains of *Thermoactinomyces vulgaris* (89 % MK-7), *Thermoactinomyces candidus* (89 % MK-7) and *Thermoactinomyces intermedius* (90 % MK-7) were reported to have MK-7 as the predominant menaquinone, whereas the type strains of *Thermoactinomyces sacchari* (75 % MK-9) and *Thermoactinomyces thalophilus* (75 % MK-9) had MK-9 as the predominant menaquinone. The type strain of *Thermoactinomyces putidus* and *Thermoactinomyces putidus* JCM 3213 were found to have MK-9 as the predominant menaquinone (Collins *et al.*, 1982; Tseng *et al.*, 1990). The same results have been obtained from our study. *Thermoactinomyces vulgaris* KCTC 9076^T, *Thermoactinomyces vulgaris* KCTC 9557 (previously the type strain of *Thermoactinomyces candidus*) and *Thermoactinomyces intermedius* KCTC 9646^T contained MK-7 as the predominant menaquinone, at peak area ratios of approximately 74–83 %. *Thermoactinomyces sacchari* KCTC 9790^T, *Thermoactinomyces sacchari* KCTC 9789 (previously the type strain of *Thermoactinomyces thalophilus*) and *Thermoactinomyces putidus* KCTC 3666^T contained MK-9 as the predominant menaquinone, at peak area ratios of approximately 60–75 %. *Thermoactinomyces sacchari* KCTC 9790^T, *Thermoactinomyces sacchari* KCTC 9789 and *Thermoactinomyces putidus* KCTC 3666^T could also be distinguished from *Thermoactinomyces vulgaris* KCTC 9076^T, *Thermoactinomyces vulgaris* KCTC 9557 and *Thermoactinomyces intermedius* KCTC 9646^T by differences in the contents of some fatty acids, particularly anteiso-C_{15:0} and iso-C_{17:0} (Table 1). Accordingly, *Thermoactinomyces sacchari* and *Thermoactinomyces putidus* can be differentiated from *Thermoactinomyces vulgaris* and *Thermoactinomyces intermedius* on the basis of menaquinone and fatty acid profiles as well as phylogenetic distinctiveness, although their morphological properties are similar (Tables 1 and 2).

Thermoactinomyces dichotomicus KCTC 3667^T was found to have MK-7 (85 %) as the predominant menaquinone. This result is consistent with those of Collins *et al.* (1982) and Tseng *et al.* (1990). Although *Thermoactinomyces dichotomicus* KCTC 3667^T showed a fatty acid profile similar to those of *Thermoactinomyces vulgaris* KCTC 9076^T, *Thermoactinomyces vulgaris* KCTC 9557 and *Thermoactinomyces intermedius* KCTC 9646^T, it showed some differences from these three strains in the contents of two fatty acids, iso-C_{16:0} and iso-C_{17:0} (Table 1). *Thermoactinomyces dichotomicus* can be distinguished from other *Thermoactinomyces* species by differences in some phenotypic properties, including its morphological property of forming a yellow colour (Lacey & Cross, 1989) (Table 2).

Thermoactinomyces peptonophilus KCTC 9740^T formed a phylogenetic lineage distinct from other *Thermoactinomyces* species and exhibited low 16S rRNA gene sequence similarity (90.1–91.6 %) to the type strains of other *Thermoactinomyces* species with validly published names.

Table 1. Percentage cellular fatty acid compositions of *Thermoactinomyces* species on SY medium

Strains: 1, *T. vulgaris* KCTC 9076^T; 2, *T. vulgaris* KCTC 9557; 3, *T. intermedius* KCTC 9646^T; 4, *T. sacchari* KCTC 9790^T; 5, *T. sacchari* KCTC 9789; 6, *T. putidus* KCTC 3666^T; 7, *T. dichotomicus* KCTC 3667^T; 8, *T. peptonophilus* KCTC 9740^T. Fatty acids representing 1 % of the total fatty acids of at least one of the strains are shown. —, Not detected.

Fatty acid	1	2	3	4	5	6	7	8
Straight-chain								
C _{14:0}	0.5	0.8	1.2	2.8	6.2	2.6	5.8	1.9
C _{15:0}	0.2	0.3	0.2	0.5	0.7	0.7	1.8	0.4
C _{16:0}	2.1	2.8	3.5	3.8	8.1	7.2	6.7	9.2
Unsaturated								
C _{16:1} ω7c alcohol	—	—	—	—	—	—	—	2.0
C _{16:1} ω11c	—	—	—	—	—	—	—	7.0
C _{18:1} ω9c	—	0.4	0.7	0.4	0.3	—	—	1.1
Branched-chain								
iso-C _{11:0}	1.0	0.4	0.4	—	—	—	—	—
iso-C _{13:0}	1.9	1.7	1.8	0.5	0.5	0.3	1.2	0.1
iso-C _{14:0}	0.9	1.0	0.8	2.3	3.2	2.4	5.8	26.9
iso-C _{15:0}	54.3	51.8	55.1	47.5	42.3	31.7	46.7	3.1
anteiso-C _{15:0}	10.2	13.4	11.4	28.0	24.8	28.4	12.7	26.5
iso-C _{16:0}	4.2	4.3	3.0	5.2	6.4	7.6	10.3	15.7
iso-C _{17:0}	18.6	15.5	16.3	5.0	4.2	9.2	7.0	1.7
anteiso-C _{17:0}	5.4	6.2	3.9	3.5	2.8	8.3	1.3	1.6

Thermoactinomyces peptonophilus differed from other *Thermoactinomyces* species in some physiological properties, including lack of resistance to novobiocin, requirement for a high peptone concentration for growth, optimal temperature of 35 °C and others (Nonomura & Ohara, 1971; Lacey & Cross, 1989). *Thermoactinomyces peptonophilus* KCTC 9740^T contained MK-7 (59 %) as the predominant menaquinone, and significant amounts of MK-9 (17 %), MK-10 (14 %) and MK-8 (10 %) were also present. The cellular fatty acid profile of *Thermoactinomyces peptonophilus* KCTC 9740^T showed clear difference from those of the type strains of other *Thermoactinomyces* species (Table 1). While fatty acid iso-C_{14:0} and unsaturated fatty acids were major components in *Thermoactinomyces peptonophilus* KCTC 9740^T, they were minor components in the type strains of other *Thermoactinomyces* species (Table 1). The fatty acid iso-C_{15:0} was a major component in the type strains of other *Thermoactinomyces* species, whereas it was a minor component in *Thermoactinomyces peptonophilus* KCTC 9740^T (Table 1). The DNA G+C contents of *Thermoactinomyces dichotomicus* KCTC 3667^T and *Thermoactinomyces peptonophilus* KCTC 9740^T were lower than those of the type strains of other *Thermoactinomyces* species: *Thermoactinomyces dichotomicus* KCTC 3667^T and *Thermoactinomyces peptonophilus* KCTC 9740^T had respective DNA G+C contents of 43 and 40 mol%, whereas the type strains of other *Thermoactinomyces* species had DNA G+C contents of 48–49 mol%.

Table 2. Differential phenotypic characteristics of the emended genus *Thermoactinomyces* and newly proposed genera

Data from Nonomura & Ohara (1971), Lacey & Cross (1989) and this study. +, Positive; –, negative; ND, not detected.

Characteristic	<i>Thermoactinomyces</i>	<i>Laceyella</i>	<i>Thermoflavimicrobium</i>	<i>Seinonella</i>
Colour of aerial mycelium	White	White	Yellow	White
Sessile spores on dichotomously branched sporophores	–	–	+	–
Growth on 25 µg novobiocin ml ⁻¹	+	+	+	–
Degradation of:				
Casein	+	+	+	–
Gelatin	+	+	+	–
Starch	–	+	–	–
Hypoxanthine	–	–	+	–
Xanthine	–	–	+	–
Optimal temperature for growth (°C)	50–55	48–55	55	35
Predominant menaquinone	MK-7	MK-9	MK-7	MK-7
Major menaquinone(s)*	MK-8 or MK-9	MK-7 or MK-8 or MK-10	ND	MK-8, MK-9, MK-10
Major fatty acids	iso-C _{15:0} ; iso-C _{17:0} ; anteiso-C _{15:0}	iso-C _{15:0} ; anteiso-C _{15:0}	iso-C _{15:0} ; anteiso-C _{15:0} ; iso-C _{16:0}	iso-C _{14:0} ; anteiso-C _{15:0} ; iso-C _{16:0}
DNA G + C content (mol%)	48	48–49	43	40

*Other components making up >10 % peak area ratio are shown.

On the basis of the phylogenetic and phenotypic characteristics presented, it appears to be more appropriate that *Thermoactinomyces* species are divided into four different genera, including the genus *Thermoactinomyces sensu stricto*. In conclusion, we propose that *Thermoactinomyces sacchari* and *Thermoactinomyces putidus* are reclassified in a new genus *Laceyella* gen. nov. as *Laceyella sacchari* comb. nov. and *Laceyella putida* comb. nov., respectively, *Thermoactinomyces dichotomicus* be reclassified in a new genus *Thermoflavimicrobium* gen. nov. as *Thermoflavimicrobium dichotomicum* comb. nov. and *Thermoactinomyces peptonophilus* be reclassified in a new genus *Seinonella* gen. nov. as *Seinonella peptonophila* comb. nov.

Emended description of the genus *Thermoactinomyces* Tsilinsky 1899

Cells are aerobic, Gram-positive, non-acid-fast and chemo-organotrophic. Aerial mycelium is abundant and white. Well-developed, branched and septate substrate mycelium is formed. Endospores are sessile and formed singly on aerial and substrate hyphae or on unbranched short sporophores. Thermophilic. Growth occurs at 55 °C but not at 30 °C. Further descriptive information is given by Lacey & Cross (1989). Additional characters found in this study are as follows. Predominant menaquinone is MK-7. Major fatty acid is iso-C_{15:0}, and significant amounts of iso-C_{17:0} are present. Two species are assigned to the emended genus *Thermoactinomyces*: *Thermoactinomyces vulgaris* and *Thermoactinomyces intermedius*. The DNA G+C content of the type strains of *Thermoactinomyces vulgaris* and *Thermoactinomyces intermedius* is 48 mol%

(determined by HPLC in this study). The type species is *Thermoactinomyces vulgaris* Tsilinsky 1899.

Description of *Laceyella* gen. nov.

Laceyella (La.cec.el'la. N.L. dim. fem. n. *Laceyella* named to honour Dr John Lacey, an English microbiologist, for his contribution to the taxonomy of the genus *Thermoactinomyces* and actinomycetes).

Cells are aerobic, Gram-positive, non-acid-fast and chemo-organotrophic. Aerial and substrate mycelia are formed. Aerial mycelium is white. Yellow–brown or greyish-yellow soluble pigment may be produced. Sessile endospores may be produced on sporophores. Thermophilic. The cell-wall peptidoglycan contains *meso*-DAP but no characteristic sugars. Additional characters found in this study are as follows. Predominant menaquinone is MK-9. Major fatty acids are iso-C_{15:0} and anteiso-C_{15:0}. DNA G + C content of the type strains of two species is 48–49 mol% (determined by HPLC in this study). The type species is *Laceyella sacchari* (Lacey 1971).

Description of *Laceyella sacchari* (Lacey 1971) comb. nov.

Basonym: *Thermoactinomyces sacchari* Lacey 1971.

The description is the same as that given by Lacey & Cross (1989). Some additional characteristics are as follows. A sparse, transient, tufted aerial mycelium, rapidly autolysing and depositing endospores in a thick layer, is produced on the surface of yeast malt or nutrient agar supplemented with

1 % (w/v) glucose. Growth on nutrient agar is poor, restricted and thin with no aerial mycelium and few spores. Endospores are produced on sporophores up to 3 µm long. Yellow–brown soluble pigment may be produced. Growth occurs at 55 °C. Growth at 30 °C is variable. Water-soluble melanin is produced or not on CYC agar with 0.5 % (w/v) L-tyrosine. Elastin, DNA, RNA and Tweens 20, 40, 60 and 80 are degraded. Adenine, cellulose, guanine and keratin are not degraded. Degradation of aesculin, arbutin, chitin and tyrosine is variable. D-Glucose, D-fructose and D-mannitol are utilized as carbon sources. Cellulose, *meso*-inositol, D-raffinose, L-rhamnose and D-xylose are not utilized. Utilization of L-arabinose, D-mannose and sucrose is variable. No growth occurs in the presence of 5 % (w/v) NaCl; growth in the presence of 1 % (w/v) NaCl is variable. Further descriptive information is given by Lacey & Cross (1989) or is shown in Table 1. The DNA G+C content of the type strain is 48 mol% (determined by HPLC in this study). Isolated from sugar cane, self-heated sugar cane bagasse, filter press muds, sugar mills and soil.

The type strain is ATCC 27375^T (= KCTC 9790^T = DSM 43356^T = NCIMB 10486^T).

Description of *Laceyella putida* (Lacey and Cross 1989) comb. nov.

Basonym: *Thermoactinomyces putidus* Lacey and Cross 1989.

The description is the same as that given by Lacey & Cross (1989). Some additional characteristics are as follows. Colonies are often very wrinkled and puckered with endospores formed on short and unbranched sporophores. Aerial mycelium white, but may appear cream, pale yellow or yellowish-brown due to yellowish-brown substrate mycelium. Sporing hyphae lyse quickly, leaving spores on the surface of agar. Greyish-yellow soluble pigment may be produced. Brown, water-soluble melanin pigment is produced on CYC agar supplemented with 0.5 % (w/v) L-tyrosine. Sensitive to 1 % (w/v) NaCl. Growth at 55 and 30 °C is variable. Degradation of aesculin, arbutin and chitin is variable. Tyrosine is degraded, but DNA is not. D-Glucose and sucrose are utilized as carbon sources. D-Fructose, glycerol, D-mannitol, D-mannose, D-ribose and D-trehalose are not utilized. Further descriptive information is given by Lacey & Cross (1989) or is shown in Table 1. The DNA G+C content of the type strain is 49 mol% (determined by HPLC in this study). Isolated from soil, deep mud cores and a lung biopsy of a patient with farmer's lung.

The type strain is NCIMB 12324^T (= ATCC 49853^T = KCTC 3666^T = DSM 44608^T).

Description of *Thermoflavimicrobium* gen. nov.

Thermoflavimicrobium (Ther' mo. fla. vi. mi. cro' bi. um. Gr. adj. *thermos* hot; L. adj. *flavus* yellow; Gr. adj. *mikros* small; Gr. n. *bios* life; N.L. neut. n. *Thermoflavimicrobium* a thermophilic yellow-coloured microbe).

Cells are aerobic, Gram-positive, non-acid-fast and chemo-organotrophic. Aerial and substrate mycelia are formed. Aerial mycelium is yellow and abundant. Sessile endospores are produced on dichotomously branched sporophores. Thermophilic. The cell-wall peptidoglycan contains *meso*-DAP but no characteristic sugars. Additional characters found in this study are as follows. Predominant menaquinone is MK-7. Major fatty acids are iso-C_{15:0}, anteiso-C_{15:0} and iso-C_{16:0}. The DNA G+C content of the type strain of the type species is 43 mol% (determined by HPLC in this study). The type species is *Thermoflavimicrobium dichotomicum* (Cross and Goodfellow 1973).

Description of *Thermoflavimicrobium dichotomicum* (Cross and Goodfellow 1973) comb. nov.

Basonym: *Thermoactinomyces dichotomicus* (ex Krasil'nikov and Agre 1964) Cross and Goodfellow 1973.

The description is the same as that given by Lacey & Cross (1989). Some additional characteristics are as follows. Colonies are yellow to orange, distinctively fast-growing with dichotomously branched mycelium and sporophores on nutrient agar and CYC agar at 55 °C. Growth occurs at 55 °C, but not at 30 °C. Margins of colonies are entire on CYC agar. Exosporium surrounding the spores is present. Elastin, DNA, guanine, RNA and Tweens 20, 40, 60 and 80 are degraded. Aesculin, adenine, arbutin, cellulose, hippurate, keratin and tyrosine are not degraded. Growth occurs in the presence of 0.5 % (w/v) NaCl, but not in the presence of 1.0 % (w/v) NaCl. L-Arabinose, D-galactose, D-glucose, glycerol, lactose, maltose, mannitol, *meso*-inositol, D-raffinose, L-rhamnose, D-sorbitol, starch, sucrose and D-xylose are utilized as carbon sources. Further descriptive information is given by Lacey & Cross (1989) or is shown in Table 1. The DNA G+C content of the type strain is 43 mol% (determined by HPLC in this study). Isolated from soil and mushroom compost.

The type strain is KCTC 3667^T (= ATCC 49854^T = JCM 9688^T = DSM 44778^T).

Description of *Seinonella* gen. nov.

Seinonella (Sei.no.nel'la. N.L. dim. fem. n. *Seinonella* named to honour Dr Akio Seino, a Japanese microbiologist, for his contribution to the taxonomy of the genus *Thermoactinomyces* and actinomycetes).

Aerial mycelium is white and substrate mycelium is white to yellowish brown. Endospores are sessile on flexuous branches of the aerial mycelium and on the substrate mycelium. Mesophilic. The cell-wall peptidoglycan contains *meso*-DAP. Additional characters found in this study are as follows. Predominant menaquinone is MK-7 and significant amounts of MK-8, MK-9 and MK-10 are present. The major fatty acids are iso-C_{14:0} and anteiso-C_{15:0}. The type species is *Seinonella peptonophila* (Nonomura and Ohara 1971).

Description of *Seinonella peptonophila* (Nonomura and Ohara 1971) comb. nov.

Basonym: *Thermoactinomyces peptonophilus* Nonomura and Ohara 1971. Note: Rule 61 of the Bacteriological Code prevents the correction of the epithet to '*peptoniphila*'.

The description is the same as that given by Nonomura & Ohara (1971) and Lacey & Cross (1989). High concentrations of peptone or yeast extract (3 % w/v) in addition to B vitamins are essential for good growth. A low concentration of glycerol or glucose (0.2 % w/v) is favourable for aerial mycelium production. No distinct soluble pigments are produced. Optimal growth temperature is 35 °C; poor growth at 25 °C and no growth at 45 °C. Optimal pH for growth is 7.0–8.0; no growth at pH 5.0. Nitrate reduction is negative. Tyrosine is not hydrolysed. Further descriptive information is given by Nonomura & Ohara (1971) and Lacey & Cross (1989) or is shown in Table 1. The DNA G+C content of the type strain is 40 mol% (determined by HPLC in this study). Isolated from soil.

The type strain is KCTC 9740^T (=ATCC 27302^T=JCM 10113^T=DSM 44666^T).

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