NOTE

DNA–DNA relatedness among *Thermoactinomyces* species: *Thermoactinomyces candidus* as a synonym of *Thermoactinomyces vulgaris* and *Thermoactinomyces thalpophilus* as a synonym of *Thermoactinomyces sacchari*

Jung-Hoon Yoon, Yong Kook Shin and Yong-Ha Park

Author for correspondence: Yong-Ha Park. Tel: +82 42 860 4620. Fax: +82 42 860 4598. e-mail: yhpark@kribb4680.kribb.re.kr

Korea Research Institute of Bioscience and Biotechnology (KIRIBB), PO Box 115, Yusong, Taejon, Korea

DNA–DNA relatedness of all validly described *Thermoactinomyces* species was determined to infer the genetic relationships between them. The levels of DNA–DNA relatedness among the type strains of *Thermoactinomyces* species ranged from 2.5 to 92.8%. Based on DNA relatedness data, the type strains of *Thermoactinomyces intermedius*, *Thermoactinomyces putidus*, *Thermoactinomyces dichotomicus* and *Thermoactinomyces peptonophilus* were considered to be distinct species of the genus *Thermoactinomyces*. However, the relationship between the type strains of *Thermoactinomyces vulgaris* and *Thermoactinomyces candidus* and the relationship between the type strains of *Thermoactinomyces sacchari* and *Thermoactinomyces thalpophilus* were re-evaluated from levels of DNA–DNA relatedness. The independent DNA relatedness values between *Thermoactinomyces vulgaris* KCTC 9076T and *Thermoactinomyces candidus* KCTC 9557T were 90.8 and 92.8%. *Thermoactinomyces thalpophilus* KCTC 9789T and *Thermoactinomyces sacchari* KCTC 9790T exhibited independent values of 85.6 and 87.3%. Accordingly, on the basis of DNA–DNA relatedness data together with 16S rDNA sequence data determined recently, it is proposed that *Thermoactinomyces candidus* should be considered as a synonym of *Thermoactinomyces vulgaris* and *Thermoactinomyces thalpophilus* be considered as a synonym of *Thermoactinomyces sacchari*.

Keywords: *Thermoactinomyces* species, DNA–DNA relatedness, taxonomic re-evaluation

*Thermoactinomyces* species are taxonomically very interesting taxa. Morphological properties of forming aerial and substrate mycelia led *Thermoactinomyces* species to be classified in actinomycetes. However, taxonomic data, such as the ability to produce dipicolinic-acid-containing endospores (Cross et al., 1968; Lacey & Vince, 1971), low G + C content (Lacey & Cross, 1989), menaquinone profiles (Collins et al., 1982; Tseng et al., 1990) and 5S rRNA (Park et al., 1993) and 16S rRNA oligonucleotide sequences (Stackebrandt & Wöese, 1981), suggested that *Thermoactinomyces* species should no longer be classified within the order *Actinomycetales* and should be placed within the family *Bacillaceae*. Recently, our phylogenetic inference based on 16S rDNA sequences showed clearly that *Thermoactinomyces* species are phylogenetically related to the family *Bacillaceae* (Yoon & Park, 2000). There are currently eight validly described *Thermoactinomyces* species, namely, *Thermoactinomyces candidus* (Kurup et al., 1975), *Thermoactinomyces dichotomicus* (Krasil’nikov & Agre, 1964; Cross & Goodfellow, 1973), *Thermoactinomyces intermedius* (Kurup et al., 1980), *Thermoactinomyces peptonophilus* (Nonomura & Ohara, 1971), *Thermoactinomyces putidus* (Lacey & Cross, 1989), *Thermoactinomyces sacchari* (Lacey, 1971), *Thermoactinomyces thalpophilus* (Waksman & Corke, 1953; Lacey & Cross, 1989) and *Thermoactinomyces*
vulgaris (Tsiklinsky, 1899), the type species of the genus. However, these species have mainly been differentiated by morphological and physiological characteristics (Lacey & Cross, 1989). The 16S rDNA sequence analysis showed that some Thermoactinomyces species are phylogenetically closely related and may have to be taxonomically re-evaluated (Yoon & Park, 2000). In particular, Thermoactinomyces vulgaris KCTC 9076\textsuperscript{T} and Thermoactinomyces candidus KCTC 9557\textsuperscript{T} shared identical 16S rDNA sequences. Thermoactinomyces intermedius KCTC 9646\textsuperscript{T} also exhibited relatively high 16S rDNA similarity values of 99.4\% with Thermoactinomyces vulgaris KCTC 9076\textsuperscript{T} and Thermoactinomyces candidus KCTC 9557\textsuperscript{T}. Thermoactinomyces sacchari KCTC 9790\textsuperscript{T} and Thermoactinomyces thalphotophilus KCTC 9789\textsuperscript{T} had the same 16S rDNA sequences, except position corresponding to one ambiguous nucleotide (C or T) of 16S rDNA sequences, except position corresponding to one ambiguous nucleotide (C or T) of Thermoactinomyces sacchari KCTC 9790\textsuperscript{T}.

In current bacterial systematics, DNA–DNA relatedness data are now recognized as being the most important for inferring the relationships between species belonging to a genus (Wayne et al., 1987), together with phylogenetic inference based on 16S rDNA sequence comparison. The current phylogenetic definition of a species states that strains having approximately 70\% or greater DNA similarity are members of the same species; thus, there is general agreement that a level of DNA–DNA relatedness of 70\% is the threshold value for defining species (Wayne et al., 1987). Therefore, the aims of this study were to determine the levels of DNA–DNA relatedness among validly described Thermoactinomyces species and to investigate with the result of DNA–DNA relatedness, together with the result of 16S rDNA sequence analysis, whether current taxonomic status of Thermoactinomyces species is correct or not.

The following type strains of the eight validly described Thermoactinomyces species were used for this study: Thermoactinomyces candidus KCTC 9557\textsuperscript{T}, Thermoactinomyces dichotomicus KCTC 3667\textsuperscript{T}, Thermoactinomyces intermedius KCTC 9646\textsuperscript{T}, Thermoactinomyces peptonophilus KCTC 9740\textsuperscript{T}, Thermoactinomyces putidus KCTC 3666\textsuperscript{T}, Thermoactinomyces sacchari KCTC 9790\textsuperscript{T}, Thermoactinomyces thalphotophilus KCTC 9789\textsuperscript{T} and Thermoactinomyces vulgaris KCTC 9076\textsuperscript{T}. Chromosomal DNAs were isolated as described previously (Yoon et al., 1996), with the exception that ribonuclease T1 was used together with ribonuclease A. DNA–DNA hybridization to determine genomic relatedness was performed fluorometrically by the method of Ezaki et al. (1989) using photobiotin-labelled DNA probes and microdilution wells. Brief procedure is as follows: each 25 µl of purified DNA samples (200 µg ml\textsuperscript{-1}) was denatured by boiling for 5 min and then diluted to 10 µg ml\textsuperscript{-1} with cold PBS containing 0.1 M MgCl\textsubscript{2}. Each diluted DNA suspension was distributed to 5 wells in microplate (Nunc) at 100 µl per well and the plate incubated for 8 h at 30 °C. Excess DNA suspensions were discarded and the plate was dried for 30 min at 45 °C. The plate was prehybridized with 1 x SSC and 100 µl streptavidin-o-galactosidase (Gibco-BRL) (1000-fold diluted with 0.5 \% BSA-PBS) was added to each well. The plate was incubated at 37 °C for 30 min and washed three times with 1 x SSC. Finally, 100 µl of 4-methylumbelliferyl-β-D-galacto-pyranoside (substrate 10 mg dimethylformamide ml\textsuperscript{-1} diluted 100-fold with PBS) was added to the wells and the plate was incubated at 37 °C for 30 min. The fluorescence intensities were read with a Labsystems fluoroskan II at a wavelength of 360 nm for excitation and 450 nm for emission. The highest and lowest values in each sample were excluded and the remaining three values were used for calculation of similarity value. DNA relatedness values are the mean of three values.

The genus Thermoactinomyces has had a very confusing taxonomic history; it consists currently of eight validly described species. Thermoactinomyces vulgaris was the first proposed species of the genus Thermoactinomyces (Tsiklinsky, 1899), and prior to 1964, six Thermoactinomyces species had been described. Among them, three species, ‘Thermoactinomyces glaucus’ (Henssen 1957), ‘Thermoactinomyces thermodus’ (Waksman 1961) and ‘Thermoactinomyces monosporus’ (Waksman and Corke 1953), are nomina dubia. One species, Thermoactinomyces viridis (Schuurmans et al., 1956), was reclassified in a new genus, Saccharomonospora, as Saccharomonospora viridis by Nonomura & Ohara (1971). Two other species, Thermoactinomyces vulgaris and Thermoactinomyces thalphotophilus, were placed as synonyms by Küster & Locci (1964). There were only two species, Thermoactinomyces vulgaris and Thermoactinomyces sacchari, listed in 8th edition of Bergey’s Manual of Determinative Bacteriology (Küster, 1974). Since then, there were many changes in the genus Thermoactinomyces including the transfer of Actinobifida dichotoma to Thermoactinomyces dichotomicus (Cross & Goodfellow, 1975), the description of Thermoactinomyces candidus (Kurup et al., 1975), Thermoactinomyces intermedius (Kurup et al., 1980), Thermoactinomyces peptonophilus (Nonomura & Ohara, 1971) and Thermoactinomyces putidus (Lacey & Cross, 1989) as new species and the revival of Thermoactinomyces thalphotophilus (Lacey & Cross, 1989). The inclusion of additional strains led to Thermoactinomyces vulgaris becoming a variable species (Flockton & Cross, 1975). This species acquired some characters that were not present in the original description of Tsiklinsky (1899). For example, the ability to utilize starch, which was previously not observed, is found in the description of Thermoactinomyces vulgaris of the 8th edition of the Manual (Küster, 1974). Kurup et al. (1975) classified the isolates lacking amylase as Thermoactinomyces candidus and the isolates producing amylase as Thermo-
The currently available type strain of *Thermoactinomyces vulgaris* was that isolated by Erikson (1953) as *Micromonospora vulgaris* strain D, which is listed as strain KCC A-0162 in the Approved Lists of Bacterial Names (Skerman et al., 1980). This strain corresponded to the original concept of *Thermoactinomyces vulgaris* by Tsiklinsky (1899) and the concept of *Thermoactinomyces candidus*. The two species were hence regarded as synonyms by Lacey & Cross (1989), but this thought has not been accepted. Revival of *Thermoactinomyces thalpophilus* was with the isolates named as *Thermoactinomyces vulgaris* by Kurup et al. (1975). In addition, ‘*Thermoactinomyces antibioticus*’ and ‘*Thermoactinomyces albus*’ had been known, but they were described to be synonyms of *Thermoactinomyces thalpophilus* and *Thermoactinomyces vulgaris*, respectively (Lacey & Cross, 1989). It is described in the 1st edition of Berger’s *Manual of Systematic Bacteriology* that the taxonomic status of *Thermoactinomyces vulgaris*, *Thermoactinomyces candidus* and *Thermoactinomyces thalpophilus* is confused and there can be little doubt that the three species are closely related (Lacey & Cross, 1989). However, recent 16S rDNA sequence analysis showed a little different results (Yoon & Park, 2000). The type strain of *Thermoactinomyces candidus* was shown to be phylogenetically closely related to the type strain of *Thermoactinomyces vulgaris*, but *Thermoactinomyces thalpophilus* KCTC 9789T is more closely related to *Thermoactinomyces sacchari* KCTC 9790T than *Thermoactinomyces vulgaris* KCTC 9076T.

The type strains of all validly described *Thermoactinomyces* species used in this study exhibited levels of DNA–DNA relatedness ranging from 2–5 to 92.8% (Table 1). On the basis of DNA–DNA relatedness values between *Thermoactinomyces* species obtained, the taxonomic status of *Thermoactinomyces* species was elucidated. As shown in Table 1, DNA–DNA relatedness between other *Thermoactinomyces* species, except for the relationships between *Thermoactinomyces vulgaris* and *Thermoactinomyces candidus* and between *Thermoactinomyces thalpophilus* and *Thermoactinomyces sacchari*, exhibited such values confirming their status as distinct species. It was proven from DNA–DNA relatedness values that *Thermoactinomyces intermedius* is the species distinct from other *Thermoactinomyces* species as well as *Thermoactinomyces vulgaris* and *Thermoactinomyces candidus* that exhibit relatively high 16S rDNA similarities. Also, *Thermoactinomyces putidus* KCTC 3666T exhibited DNA relatedness values below 13.5% to other *Thermoactinomyces* species, *Thermoactinomyces dichotomicus* KCTC 3667T below 5.6% to other *Thermoactinomyces* species and *Thermoactinomyces peptonophilus* KCTC 9740T below 4.5% to other *Thermoactinomyces* species (Table 1). *Thermoactinomyces metamorphus* KCTC 3666T, *Thermoactinomyces peptonophilus* KCTC 9740T have already been found to exhibit such low levels of 16S rDNA similarity that they can be considered as distinct species of the genus *Thermoactinomyces* (Yoon & Park, 2000).

**Table 1. Levels of DNA–DNA relatedness among the type strains of *Thermoactinomyces* species**

<table>
<thead>
<tr>
<th>Species</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. <em>T. vulgaris</em> KCTC 9076T</td>
<td>100</td>
<td>92.8</td>
<td>48.7</td>
<td>64</td>
<td>6.3</td>
<td>5.0</td>
<td>5.6</td>
<td>3.0</td>
</tr>
<tr>
<td>2. <em>T. candidus</em> KCTC 9557T</td>
<td>90.8</td>
<td>100</td>
<td>49.5</td>
<td>43</td>
<td>5.1</td>
<td>3.7</td>
<td>5.0</td>
<td>2.8</td>
</tr>
<tr>
<td>3. <em>T. intermedius</em> KCTC 9646T</td>
<td>47.4</td>
<td>51.2</td>
<td>100</td>
<td>3.9</td>
<td>4.4</td>
<td>3.8</td>
<td>4.8</td>
<td>2.5</td>
</tr>
<tr>
<td>4. <em>T. sacchari</em> KCTC 9790T</td>
<td>3.4</td>
<td>3.7</td>
<td>4.2</td>
<td>100</td>
<td>85.6</td>
<td>7.7</td>
<td>4.4</td>
<td>2.7</td>
</tr>
<tr>
<td>5. <em>T. thalpophilus</em> KCTC 9789T</td>
<td>4.6</td>
<td>40</td>
<td>4.7</td>
<td>87.3</td>
<td>100</td>
<td>13.5</td>
<td>40</td>
<td>2.8</td>
</tr>
<tr>
<td>6. <em>T. putidus</em> KCTC 3666T</td>
<td>40</td>
<td>3.7</td>
<td>4.8</td>
<td>11.9</td>
<td>10.5</td>
<td>100</td>
<td>5.0</td>
<td>2.5</td>
</tr>
<tr>
<td>7. <em>T. dichotomicus</em> KCTC 3667T</td>
<td>4.8</td>
<td>40</td>
<td>4.2</td>
<td>3.7</td>
<td>3.4</td>
<td>4.3</td>
<td>100</td>
<td>4.5</td>
</tr>
<tr>
<td>8. <em>T. peptonophilus</em> KCTC 9740T</td>
<td>3.2</td>
<td>2.7</td>
<td>3.0</td>
<td>28</td>
<td>2.5</td>
<td>3.1</td>
<td>48</td>
<td>100</td>
</tr>
</tbody>
</table>
16S rDNA similarities of 100% respectively. Accordingly, on the basis of DNA-DNA relatedness and the results of 16S rDNA sequence analysis, it is correct that *Thermoactinomyces vulgaris* and *Thermoactinomyces candidus* should be unified as one species and *Thermoactinomyces thalpophilus* and *Thermoactinomyces sacchari* as one species. According to international rule in which the oldest legitimate epithet has the priority, we propose that *Thermoactinomyces candidus* should be considered as a synonym of *Thermoactinomyces vulgaris* and *Thermoactinomyces thalpophilus* be considered as a synonym of *Thermoactinomyces sacchari*.

**Acknowledgements**

This work was supported by grant HS2321 from the Ministry of Science and Technology (MOST) of the Republic of Korea. We are grateful to Dr Akio Seino for providing *Thermoactinomyces peptonophilus* and to CCRC (Culture Collection and Research Center, Taiwan), IFO (Institute for Fermentation, Osaka) and JCM (Japan Collection of Microorganisms) for providing strains used in this study.

**References**


