The Revision of Lipomycetaceae

Yuzo Yamada,1,4,5 Huong Thi Lan Vu,2 Pattaraporn Yukphan,1 Somboon Tanasupawat,3

1Microbial Diversity and Utilization Team, Thailand Bioresource Research Center (TBRC), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Phutthamonthon 12120, Thailand
2Department of Microbiology, Faculty of Biology and Biotechnology, University of Science, Vietnam National University-HCM City, 227 Nguyen Van Cu Street, Ward 4, District 5, Hochiminh City, Vietnam
3Department of Biochemistry and Microbiology, Faculty of Pharmaceutical Sciences, Chulalongkorn University, 254 Phayathai Road, Wangmai, Pathumwan, Bangkok 10330, Thailand
4JICA Senior Overseas Volunteer, Japan International Cooperation Agency, Shibuya-ku, Tokyo 151-8559, Japan
5Laboratory of Applied Microbiology (Professor Emeritus), Department of Agricultural Chemistry, Faculty of Agriculture, Shizuoka University, 836 Ohya, Suruga-ku, Shizuoka 422-8529, Japan

DOI: https://doi.org/10.5281/zenodo.10057492
Published Date: 28-October-2023

Abstract: In the family Lipomycetaceae, the seven genera Waltomyces, Zygozyma, Babjevia, Smithiozyma, Kawasakia, Limtongia and Kockiozyma were introduced. However, all of them were neither accepted nor recognized. This paper described the historical surveys in the systematics of the Lipomycetaceous yeasts and confirmed the total of ten genera within the family Lipomycetaceae, i.e., the genus Lipomyces sensu stricto (the type genus), the above-mentioned seven genera, the monotypic genus Dipodascopsis and the new genus Neoaidaea from the phylogenetic and the phenotypic points of view.

Keywords: Lipomyces sensu stricto; Waltomyces; Zygozyma; Babjevia; Smithiozyma; Limtongia; Kockiozyma; Dipodascopsis; Neoaidaea gen. nov.

Supplementary Abstract

The family Lipomycetaceae Novak et Zetl Genus
1. Lipomyces Loderer et Kriger-van Rij (1952) sensu stricto
2. Dipodascopsis Hata et Mitsuha (1978)
3. Waltomyces Yamada et Nakane (1985)
4. Zygozyma van der Walt et van Am (1987)
5. Babjevia van der Walt et Smith (1995)
10. Neoaidaea Vu, Yukphan, Tanasupawat et Yamada gen. nov.

Species
D. uncinata
W. liyoghi
D. oligophaga
N. anomala (the type species), N. hypniformisforme, N. hypnosa
K. arcu
L. smithiae
K. yamanashiensis, K. geyrophila Es., K. sirzei Es., K. yamanashianensis Es.
N. tchit

The family Lipomycetaceae Novak et Zetl Genus
1. Lipomyces Loderer et Kriger-van Rij (1952) sensu Kurzman, Albertyn et Barcshar-Powens (2007)

Species
D. oligophaga, L. japonica, L. arcu, L. smithiae, L. yamanashiensis
D. uncinata (the type species), D. liyoghi, D. anomala
In the family Lipomycetaceae Novak et Zsolt, the seven genera Waltomyces, Zygozyma, Babjevia, Smithiozyma, Kawasakia, Limtongia and Kockiozyma were once introduced (Yamada and Nakase 1985; van der Walt et al. 1987; Smith et al. 1995; Kock et al. 1995; Yamada and Nagawa 1995b; Jindamorakot et al. 2011, 2012). All of them were respectively taxonomic-homogeneous natured, i.e., morphologically, physiologically, chemotaxonomically, genetically and phylogenetically. However, Kurtzman et al. (2007) divided the family into two, i.e., the monophyletic genus Lipomyces sensu and the paraphyletic genus Dipodascopsis emend. instead (Smith and de Hoog 2011; Smith and Kurtzman 2011).

This paper describes the historical surveys in the systematics of the Lipomycetaceous yeasts and recovers the seven genera mentioned above as taxonomic criteria, in addition to the genus Lipomyces sensu stricto, the monotypic genus Dipodascopsis (Jindamorakot et al. 2011, 2012) and the new genus Neoaidaea from the phylogenetic and the phenotypic points of view. Accordingly, the family is comprised of ten genera in total as follows.

**Genus I. Lipomyces** Lodder et Kreger van-Rij sensu stricto
The type species is Lipomyces starkeyi Lodder et Kreger van-Rij.
Ten genera are included.

1. Lipomyces starkeyi Lodder et Kreger-van Rij (1952)
4. Lipomyces mesembrius Botha, van der Walt et Smith (1997)
5. Lipomyces spencermartinsiae (van der Walt et Smith) van der Walt et Smith (1997)
   Basionym: Lipomyces kononenkoae Nieuwdorp, Bos et Slooff subsp. spencermartinsiae van der Walt et Smith (1995)
6. Lipomyces doorenjorgii van der Walt et Smith (1999)
7. Lipomyces kockii Smith et van der Walt (1999)
8. Lipomyces yamadae van der Walt et Smith (1999)
11. Lipomyces chichibuensis Yamazaki et Kawasaki (2014)
12. Lipomyces kalimantanensis Kanti, Yamazaki et Kawasaki (2017)

The species classified in the genus Lipomyces sensu stricto were tightly coupled with one another in all the three phylogenetic trees based on the concatenated four-gene sequences of 18S rRNA, 26S rRNA, mitochondrial small subunit rRNA and EF1-alpha derived from the neighbour-joining, the maximum parsimony and the maximum likelihood methods (Jindamorakot et al. 2012). On the other hand, the phylogenetic positions of the Lipomyces species newly designated by Kurtzman et al. (2007) were quite changeable in the monophyletic genus Lipomyces sensu (Jindamorakot et al. 2012). In fact, the resulting genus has an extremely wide range of DNA G+C contents (14.2 mol%, from 41.5 - 55.7 mol% G+C; Jindamorakot et al. 2012) and three kinds of ubiquinone isoprenologues (Q-8, Q-9 and Q-10: Yamada 1986; Yamada et al. 1986). According to Nakase and Komagata (1970) and Yamada et al. (1973), such a genus was a taxonomic heterogeneous-natured taxon, just as found in the genus Pichia Hansen once designated.

**Genus II. Dipodascopsis** Batra et Millner
Dipodascopsis uninucleata (Biggs) Batra et Millner (1978)
Basionym: Dipodascus uninucleatus Biggs (1937).
Two varieties are described.

1. *Dipodascopsis uninucleata* var. *uninucleata*


When the phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences was constructed by the neighbour-joining method, the paraphyletic genus *Dipodascopsis* emend. Kurtzman et al. (2007) was split into two and produced a monotypic genus (Fig. 1), as reported previously (Jindamorakot et al. 2011, 2012), indicating that *D. uninucleata*, *D. tothii* and *D. anomala* were not tightly coupled within the genus *Dipodascopsis* emend.

Such a phylogenetic data was also given by Kurtzman (2011), i.e., the phylogenetic tree based on the concatenated three-gene sequences of 26S rRNA, 18S rRNA and EF1-alpha derived from the neighbour-joining method represented that *D. uninucleata* was connected first to *L. starkeyi* but not to *D. anomala* (= *B. anomala*) and then the resulting cluster was done to *D. anomala*. In fact, the calculated sequence similarity (95.7%) between *D. uninucleata* and *L. starkeyi* was much higher than that (90.4%) between *D. uninucleata* and *B. anomala* (Table 1).

Genus III. *Waltomyces* Yamada et Nakase (MB 25779)

*Waltomyces lipofer* (Lodder et Kreger-van Rij ex Slooff) Yamada et Nakase (1985) (MB 103899)


The three partial base sequencings in positions 468-622, 155 bases (designated as region a) and in positions 1611-1835, 225 bases (designated as region b) of 26S rRNA and in positions 1451-1618, 168 bases (designated as region c) of 18S rRNA showed that the Q10-equipped species, *W. lipofer* had 88% maximum homology in region a, along with *B. anomala* (= *D. anomala*), to *L. starkeyi*, *L. tetrasporus* and *L. kononenkoae* in the genus *Lipomyces* sensu stricto (Yamada and Nagawa 1995a). In contrast, the above-mentioned three *Lipomyces* species constituted a cluster with 97% or more maximum homologies within the genus, indicating that the species is accommodated to a different genus from the genus *Lipomyces* sensu stricto (Table 1). Such similar experimental data were shown, since the species was used as outgroup in the phylogenetic trees concerned (Kurtzman et al. 2007; Yamazaki and Kawasaki 2014).

Genus IV. *Zygozyma* van der Walt et von Arx (MB 25149)

*Zygozyma oligophaga* van der Walt et von Arx (1987) (MB 131108)


Four *Zygozyma* species were reported (van der Walt et al. 1987, 1989b, 1990; Smith et al. 1989). However, the four were not tightly coupled with one another in the phylogenetic trees based on the concatenated four-gene sequences derived from the three methods, i.e., the neighbour-joining, the maximum parsimony and the maximum likelihood methods (Jindamorakot et al. 2012) and chemotaxonomically grouped into two based on the ubiquinone isoprenologues, i.e., Q-8 and Q-9 (Fig. 1) (Yamada and Nagawa 1995a; Jindamorakot et al. 2011, 2012). Especially, the Q8-equipped species, *Z. oligophaga* had extremely long branches (Fig. 1) (Jindamorakot et al. 2012) and quite low sequence similarities (81.6 - 86.6%) (Table 1).

Genus V. *Babjevia* van der Walt et Smith (MB 27435)

The type species is *Babjevia anomalata* (Babjeva et Gorin) van der Walt et Smith.

Three species are included.


Kurtzman et al. (2007) accommodated *B. anomalata* to the paraphyletic genus *Dipodascopsis* emend. as *D. anomalata*. However, Jindamorakot et al. (2012) insisted that the species, *D. anomalata* should be transferred again to the genus *Babjevia* as *B. anomalata*, since the species was not tightly coupled with the type species, *D. uninucleata* (Fig. 1). In fact, Yamazaki et
al. (2020) did not classify two new species to the genus *Dipodascopsis* emend. but the genus *Babjevia* as already suggested by Jindamorakot et al. (2012), indicating that the generic concept of Kurtzman et al. (2007) completely lost its validity.

In the phylogenetic tree based on the concatenated four-gene sequences derived from the maximum likelihood method (Yamazaki et al. 2020), *L. lipofer, L. smithiae, Zygozyma arxii (= L. arxii), L. japonicus, L. oligophaga* [sic] and *Zygozyma suomiensis* (= *L. suomiensis*) were preferable to be improved to Walmomyces *lipofer, Limtongia smithiae*, Kawasakia *arxii, Smithiozyma japonica*, *Zygozyma oligophaga* and Kockiozyma *suomiensis* (Jindamorakot et al. 2011, 2012).

Genus VI. *Smithiozyma* Kock, van der Walt et Yamada (MB 27638)


**Synonym:** *Smithiozyma japonica* van der Walt, Smith et Yamada (1989).

In the three partial base sequencings mentioned above, the Q9-equipped species, *S. japonica* (= *L. japonicus*; van der Walt et al. 1989a) represented 89% maximum homology in region a, two base differences in region b and five base differences in region c to *L. starkeyi, L. tetrasporus* and *L. kononenkoae* in the genus *Lipomyces* sensu stricto. In contrast, the above-mentioned three *Lipomyces* species constituted clusters with 97% or more maximum homologies (region a) and no base differences (regions b and c) within the genus (Yamada and Nogawa 1995a), indicating that the species is accommodated taxonomically to a different genus from the genus *Lipomyces* sensu stricto (Table 1).

In the phylogenetic trees based on the concatenated four-gene sequences, *S. japonica* was not tightly coupled, i.e., the species was connected to the cluster comprised of the Q9-equipped species including *L. starkeyi, D. uninucleata* and so on, when constructed by the neighbour-joining method, but to the cluster of Q8-equipped species including *Z. oligophaga* and *Kockiozyma suomiensis*, when constructed by the maximum parsimony method (Jindamorakot et al. 2012).

Genus VII. *Kawasakia* Yamada et Nogawa (MB 27831)


**Synonym:** *Lipomyces arxii* van der Walt, Smith et Yamada (1989).

The Q9-equipped species, *Kawasakia arxii* was very unique in representing considerably large base differences (six) from the above-mentioned three *Lipomyces* species in the partial base sequencing of 18S rRNA (region c), in contrast to *W. lipofer*, which had only one base difference in the same region (Yamada and Nogawa 1995a, b). In the remaining regions a and b, the maximum homology and the base differences of the species were 93% and only one. The calculated 26S rRNA gene D1/D2 domain sequence similarities of *Kawasakia arxii* were 85.7 - 97.5% (Table 1). In the phylogenetic trees based on the concatenated four-gene sequences, the phylogenetic positions of *Kawasakia arxii* were considerably changeable, indicating that the species was not tightly coupled to any of other species (Jindamorakot et al. 2012).

Genus VIII. *Limtongia* Jindamorakot, Am-in, Yukphan et Yamada (MB 582716)


In the three partial base sequencings mentioned above, the Q9-equipped species, *Limtongia smithiae* represented 89% maximum homology, four base differences and three base differences respectively to *L. starkeyi, L. tetrasporus* and *L. kononenkoae* in the genus *Lipomyces* sensu stricto (Yamada and Nogawa 1995a). The calculated 26S rRNA gene D1/D2 domain sequence similarities of the species were 82.9 - 92.4%, indicating that the species is accommodated to an independent genus (Table 1).

Genus IX. *Kockiozyma* Jindamorakot, Yukphan et Yamada (MB 587737)


**Synonym:** *Lipomyces suomiensis* Smith, van der Walt et Yamada (1990).
2. *Kockiozyma geophila* f.a. (van der Walt, Yamada et Nakase) comb. nov.


The type strain is CBS 7219 = NRRL Y-17252.

3. *Kockiozyma sirexii* f.a. (Spaaij et Weber) comb. nov.


The type strain is UOFS Y-2054 = NRRL Y-27626


The type strain is NBRC 110621 = CBS 14748.

In the three partial base sequencings mentioned above, the Q8-equipped species, *Kockiozyma suomiensis* represented 83% maximum homology in region a, 12 base differences in region b, and four base differences in region c respectively to *L. starkeyi*, *L. tetrasporus*, and *L. kononenkoei* in the genus *Lipomyces* sensu stricto (Yamada and Nogawa, 1995a). The calculated 26S rRNA gene D1/D2 domain sequence similarities of the species were 85.9 - 90.6%, indicating that the species is accommodated to an independent genus (Table 1). On the other hand, *Myxozyma geophila*, the Q8-equipped anamorphic species showed 92% maximum homologyn, and one and one base difference to *Kockiozyma suomiensis* in the three partial base sequencings (Yamada and Nogawa, 1995a).

In addition, the sequence similarity between *Kockiozyma suomiensis* and *Myxozyma geophila* was 98.0%, the value of which was almost identical with that (98.1%) between *Octosporomyces octosporus* and *Octosporomyces osmophilus* (Malimas et al. 2023). From the results obtained above, the generic name of *Kockiozyma* was able to be given to the anamorphic species as *Kockiozyma geophila* f.a. (Lachance 2012) as well as *Kockiozyma melibiosi* f.a., *Kockiozyma mucilagina* f.a., *Kockiozyma sirexii* f.a., *Kockiozyma neotropica* f.a., *Kockiozyma vanderwaltii* f.a. and *Kockiozyma neglecta* f.a. (Vu et al. 2022).

*Dipodascopsis tothii* and *B. anomala* (= *D. anomala*) were tightly coupled in the three phylogenetic trees (Jindamorakot et al. 2012), so that the two species appeared to be classified in a single genus (Fig. 1). Due to the priority of *B. anomala*, the single genus was to be named *Babjevia*. However, the distance between the two species, *D. tothii* and *B. anomala* was not so short, when compared with *Kluyveromyces polysporus* (= *Vanderwaltozyma polyspora*; Kurtzman 2003) and *Saccharomyces cerevisiae* (Jindamorakot et al. 2012). In fact, the calculated pair-wise sequence similarity (95.6%) between the two species was interestingly almost the same as that (95.7%) between *D. uninucleata* and *L. starkeyi* and that (95.2%) between *W. lipofer* and *L. starkeyi*, and not so high to accommodate the two species to the single genus *Babjevia* (Table 1), indicating that an additional genus can be phylogenetically introduced for *D. tothii*. Phenotypically, the species was quite different from *B. anomala*, e.g., in the morphology of asci and ascospores and the mode of asexual reproduction (Smith and de Hoog 2011).

Yamazaki et al. (2017a, b) constructed the phylogenetic trees based on the translation elongation factor 1-alpha (EF1-alpha) gene sequences derived from the neighbour-joining method. In the phylogenetic trees, it is of interest that *D. tothii* was found inside and distantly separated from *B. anomala* as well as *D. uninucleata*. In contrast, the cluster including *L. starkeyi* and its relatives and the cluster including *Kockiozyma suomiensis* and its related *Myxozyma* species were tightly coupled without any exception. In this respect, *D. tothii* was quite different phylogenetically from the remaining two species of the paraphyletic genus *Dipodascopsis* emend. Kurtzman et al. (2007), and thus the introduction of a separate new genus was confirmed.

Genus *Neoaidaea* Vu, Yukphan, Tanasupawat et Yamada gen. nov.

*Neoaidaea* (Ne.o.a.i.’d’a.e.a. N. L. fem. n. *Neoaidaea*, new Aida, in honour of Dr. Ko Aida, Professor Emeritus, The Institute of Applied Microbiology, The University of Tokyo, Tokyo, Japan, who introduced the isoprenoid quinone analyses into the microbial systematics.

The colonies are cream-coloured, moist and creamy after 10 d (Smith and de Hoog 2011). Budding cells are absent. Hyphae
are firm with inflated cells and intensely amyloid. Arthroconidia are absent. Gametangia are formed laterally on hyphae as curved branches. Asci arise after fusion of a terminal cell with its penultimate cell. Asci are acicular, 50 - 100 μm long and contain 30 - 100 ascospores. Asci open by rupturing at the apex. Ascospores are subhyaline to hyaline, broadly ellipsoidal, occasionally bean-shaped, 1 x 1.5 - 2 μm and without slime. Fermentation is absent. Grows on glucose, inulin, sucrose, raffinose, galactose, lactose, trehalose, maltose, methyl-β-glucoside, starch, cellobiose, salicin, L-sorbose, xylose, arabinose, L-arabinose, ethanol, glycerol, ribitol, mannotol, glucitol, myo-inositol, succinate (w) and gluconate (v), but not on melibiose, L-rhamnose, ribose, methanol, erythritol, galactitol and D,L-lactate. No growth on vitamin-free medium (Smith and de Hoog 2011).

Ubiquinone-9 (Q-9) is present (Cottrell and Kock 1989).

Mycobank number is 846280.

Neoaidaea tothii (Zolt) Vu, Yukphan, Tanasupawat et Yamada comb. nov.


The characteristics of the species are the same as those described in the genus (Smith and de Hoog 2011).

The holotype is CBS 759.85T = NBRC 10813T.

MycoBank number is 846281.

For the detailed characteristics of the taxa mentioned above and the type strains concerned, refer to the related monographs and/or articles.

Kurtzman (2003) introduced ‘clade’ or ‘phylogenetic circumscribed genus’ as generic concept. However, it was not yet perfect to get the taxonomic homogeneous-natured taxon for the genus. Namely, the branch lengths should be additionally considered in the phylogenetic trees.

In the seven ranks used for the systematics of plants and animals, the homogeneous-natured taxa can be available only when the lower-ranked two taxa, i.e., species and genus are dealt with taxonomically. Therefore, the present authors naturally selected the homogeneous-natured taxon in the generic designation, since the longer the phylogenetic distances are the more taxonomic heterogeneities will be increased.

Thus, the monophyletic genus Lipomyces Lodder et Kreger-van Rij sensu Kurtzman et al. (2007) included the phylogenetic-distant and the phenotypic-different species, i.e., L. lipofer, L. oligophagus, L. japonicus, L. arxii, L. smithiae and L. suomiensis, all of which were re-classified as Waltomyces lipofer, Zygozyma oligophaga, Smithiozyma japonica, Kawasakiia arxii, Limtongia smithiae and Kockiozyma suomiensis respectively, in addition to L. starkeyi, the type species and its closely related Lipomyces species that constituted the genus Lipomyces sensu stricto (Jindamorakot et al. 2011, 2012), and so corresponded taxonomically to the so-called family.

On the other hand, the paraphyletic genus Dipodascopsis Batra et Millner emend. Kurtzman et al. (2007) was a monotypic genus, which included only D. unimacula (Jindamorakot et al. 2012). For the remaining two species, one was transferred again to the genus Babjevia as B. anomala (Jindamorakot et al. 2012; Yamazaki et al. 2020) and the other was classified in the new genus Neoaidaea as Neoaidaea tothii gen. nov., comb. nov.

ACKNOWLEDGEMENTS

The present authors express their sincere thanks for citing a number of articles for detailed discussions.

Funding information

The authors received no specific grant from any funding agency.

Conflicts of interest

The authors declare that there are no conflicts of interest.

Author contributions

Y.Y., H.T.L.V., P.Y. and S.T. designed the study. H.T.L.V. performed the main experiments. P.Y. instructed how to make the experiments. Y.Y. prepared the manuscript. The detailed discussion was made among Y.Y., H.T.L.V., P.Y. and S.T.
REFERENCES


This article is dedicated to Professor Dr. Johannes Petrus van der Walt, South Africa for his excellent taxonomic study on the Lipomycetaceous yeasts, especially in the findings of the Q8-equipped *Zygozya oligophaga* and its related species.

Preliminary reports were opened [19, 27]

Corresponding: Yuzo Yamada [0000-0002-2799-7045], yamada-yuzo@nifty.com

Table 1. The pair-wise 26S rRNA gene D1/D2 domain sequence similarity.

<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>
<th>9</th>
<th>10</th>
<th>11</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. <em>Lipomyces starkeyi</em></td>
<td>95.2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2. <em>Waltonmyces lipofer</em></td>
<td>85.5</td>
<td>83.0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3. <em>Zygozya oligophaga</em></td>
<td>91.7</td>
<td>91.0</td>
<td>81.6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4. <em>Babjevia anomal</em></td>
<td>96.4</td>
<td>93.6</td>
<td>85.5</td>
<td>89.9</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5. <em>Smithiozyma japonica</em></td>
<td>97.5</td>
<td>94.1</td>
<td>85.7</td>
<td>92.2</td>
<td>95.7</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6. <em>Kawasakiia arxii</em></td>
<td>92.4</td>
<td>89.9</td>
<td>82.9</td>
<td>86.8</td>
<td>90.6</td>
<td>91.0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7. <em>Lionothrix smithiae</em></td>
<td>90.6</td>
<td>88.9</td>
<td>85.9</td>
<td>86.2</td>
<td>90.3</td>
<td>90.6</td>
<td>86.4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8. <em>Koviozyma suomiensis</em></td>
<td>90.4</td>
<td>89.0</td>
<td>86.6</td>
<td>85.9</td>
<td>90.4</td>
<td>90.3</td>
<td>85.7</td>
<td>98.0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9. <em>Myxozya geophila</em></td>
<td>95.7</td>
<td>94.0</td>
<td>85.5</td>
<td>90.4</td>
<td>95.0</td>
<td>95.4</td>
<td>91.2</td>
<td>90.2</td>
<td>90.2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10. <em>D. unimicula var. unimicula</em></td>
<td>98.0</td>
<td>89.9</td>
<td>84.1</td>
<td>90.9</td>
<td>94.3</td>
<td>95.2</td>
<td>90.1</td>
<td>90.1</td>
<td>90.1</td>
<td>99.8</td>
<td></td>
</tr>
<tr>
<td>11. <em>D. unimicula var. wickerhamii</em></td>
<td>95.6</td>
<td>93.8</td>
<td>85.4</td>
<td>90.3</td>
<td>94.9</td>
<td>95.2</td>
<td>91.0</td>
<td>90.1</td>
<td>90.1</td>
<td>99.8</td>
<td></td>
</tr>
<tr>
<td>12. <em>Neunaidewa thiti</em></td>
<td>92.6</td>
<td>90.5</td>
<td>83.4</td>
<td>95.6</td>
<td>90.1</td>
<td>95.2</td>
<td>87.8</td>
<td>87.8</td>
<td>86.7</td>
<td>90.6</td>
<td>90.5</td>
</tr>
</tbody>
</table>

*D. unimicula*: *Dipodascopris unimicula*: The type strains were used of the respective species. The pair-wise 26S rRNA gene D1/D2 domain sequence similarities were calculated for 555-568 bases with the program BioEdit (version 7.2.5) (Hall, *GEBF Bull Bioci* 2011; 2: 60.).
Fig. 1. The phylogenetic relationships of the Lipomycetaceous yeast species. The phylogenetic trees based on the 26S rRNA gene D1/D2 domain sequences (526 bases) were constructed for the Lipomycetaceous yeast species by the neighbour-joining method (A) and by the maximum parsimony method (B). *Saccharomyces cerevisiae* was used as reference standards. *Schizosaccharomyces pombe* was used as outgroup. The evolutionary distances were computed using the Kimura 2-parameter method (Kimura, *J Mol Evol* 1980; 16: 111). The numerals at the nodes of the respective branches indicate bootstrap values (%) deduced from 1000 replications (Felsenstein, *Evolution* 1985; 39: 783). The bootstrap values below 50% were deleted. For the additional phylogenetic trees based on the concatenated four-gene sequences, i.e., 18S rRNA, 26S rRNA, mitochondrial small subunit rRNA, and EF1-alpha, derived from the three methods, refer to Jindamorakot et al. (2012). According to the theory of Kurtzman et al. (2007), the Lipomycetaceous yeast species are designated as *L. starkeyi* and its relatives, *Lipomyces lipofer*, *L. oligophagus*, *L. japonicus*, *L. smithiae*, *L. arxii*, *L. suomiensis*, *Dipodascopsis uninucleata*, *D. anomala* and *D. tothii* instead.