

# The Subdivision of the Genus *Kazachstania* Zubkova (1971) sensu Kurtzman (2003) (Sacchromycetaceae)

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**Abstract:** The genus *Kazachstania* Zubkova sensu Kurtzman (2003) was first introduced as a monotypic genus including *Kazachstania viticola* Zubkova (1971). Later, a large number of species were accommodated to the genus. However, the phylogenetic analyses indicated that the genus was extremely diverse, since the species concerned showed very long branches in the phylogenetic trees. The calculated pair-wise sequence similarities of *K. viticola* were quite low (88.8 - 95.2%) to the remaining 30 species. The phylogenetic data obtained indicated that the genus formed the so-called *Kazachstania* complex, which was subdivided into 10 taxa at the generic level, as found in the genus *Wickerhamomyces* Kurtzman et al. (2008) as well as the genus *Schizosaccharomyces* Lindner (1893) sensu Kurtzman et Robnett (1991).

**Keywords:** *Kazachstania viticola*; *Vanderwaltomyces africanus*; *Arxiozyma telluris*; *Pachytichospora transvaalensis*; *Sinensiomycetes sinensis*; *Baiomyces aquaticus*; *Mikataea zonata*; *Neoyamazakia rossinii*; *Capriottia servatii*; *Neovaughania barnettii*.

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## 1. INTRODUCTION

The genus *Kazachstania* Zubkova sensu Kurtzman was first introduced as a monotypic genus with *Kazachstania viticola* Zubkova (1971). Later, a large number of species were additionally accommodated to the genus (Kurtzman 2003). However, most of them represented very long phylogenetic branches, along with the type species, *K. viticola* (Kurtzman 2003; Vaughan-Martini et al. 2011; Goulianova and Dimitrov 2020). Such a phenomenon suggested that the genus was quite diverse phylogenetically and taxonomic heterogeneous-natured (Yamada 2023; Yamada et al. 2022; Malimas et al. 2023a, f).

In a previous paper, the present authors newly constructed the phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences for the representative species and showed that one of the several species constituted the new genus *Vanderwaltomyces* with *Vanderwaltomyces africanus*, the new combination (Malimas et al. 2023c).

This paper deals with the presently available sequence data and gives the different conclusion that the genus *Kazachstania* Zubkova sensu Kurtzman (2003) was subdivided into 10 groups at the generic level.

## 2. BODY OF ARTICLE

The phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences was constructed by the neighbour-joining method for 31 species of the genus *Kazachstania* sensu Kurtzman (Fig. 1). For example, the type species, *K. viticola* produced a long branch along with *Kazachstania kunashirensis*. The pair-wise sequence similarity was 95.2% between the two *Kazachstania* species (Table 1), the value of which was almost similar to that (94.1%) between *Vanderwaltozyma polyspora* and *Saccharomyces cerevisiae* used as reference standards (Malimas et al. 2023c). In the additional phylogenetic tree derived from the maximum parsimony method (Fig. 2), *K. kunashirensis* was located at a different position independently apart from the type species, *K. viticola* and connected to the clusters of *Capriottia* species, as reported previously in the relationship between *Dipodascopsis uninucleata* and *Neoaidaea tothii* (= *Dipodascopsis tothii*) (Lipomyetaceae) (Yamada et al. 2022; Jindamorakot et al. 2012). Namely, the two *Kazachstania* species were not tightly coupled phylogenetically to one another. As a result, *K. viticola* constituted the monotypic genus *Kazachstania*. Incidentally, the calculated pair-wise sequence similarities of *K. viticola* were very low (88.8 - 95.2%) to the remaining 30 species.

Genus I *Kazachstania* Zubkova sensu stricto MycoBank2550

The type species is *Kazachstania viticola*.

1. *Kazachstania viticola* Zubkova (1971) MycoBank316014

The type strain is NRRL Y-27206.

2. *Kazachstania kunashirensis* (James, Cai, Roberts et Collins) Kurtzman (2003)

MycoBank487712

Basionym: *Saccharomyces kunashirensis* James, Cai, Roberts et Collins, Int. J. Syst. Bacteriol. 47: 458, 1997.

The type strain is NRRL Y-27209.

As mentioned above, *K. kunashirensis* was not able to be classified phylogenetically in the genus *Kazachstania*. The pair-wise sequence similarity between the two species was 95.2%, however, the species was temporarily accommodated to the genus (Malimas et al. 2023b, c). Additional nine genera were recognized as follows.

Genus II *Vanderwaltomyces* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov.

MycoBank number is 848374.

*Vanderwaltomyces* (Van.der.wal'to.my.ces. N. L. masc. n. *Vanderwaltomyces*, van der Walt fungus, in honour of Professor Dr. Johannes P. van der Walt, South African yeast taxonomist, who contributed greatly to the yeast systematics)

Cells occur singly, in pairs or short chain (Vaughan-Martini et al. 2011). Conjugating cells may be present. Growth is butyrous. Asci arise directly from diploid cells. One to 16 or more oblong or reniform ascospores are formed. The spores are liberated from the ascus soon after formation. Glucose and galactose are fermented. Growth occurs on glucose, galactose, DL-lactate and D-gluconate (Vaughan-Martini et al. 2011).

The type species is *Vanderwaltomyces africanus*.

1. *Vanderwaltomyces africanus* (van der Walt) Malimas, Vu, Yukphan, Tanasupawat et Yamada comb. nov.

MycoBank number is 848376.

Basionym: *Kluyveromyces africanus* van der Walt, Antonie van Leeuwenhoek 22: 325, 1956.

The type strain is CBS 2517.

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Synonym: *Kazachstania africana* (van der Walt) Kurtzman (2003).

2. *Vanderwaltomyces martiniae* (James, Cai, Roberts et Collins) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848375.

Basionym: *Sacchromyces martiniae* James, Cai, Roberts et Collins. Int. J. Syst. Bacteriol. 47: 458, 1997.

The type strain is NRRL Y-409.

Synonym: *Kazachstania martiniae* (James, Cai, Roberts et Collins) Kurtzman (2003).

The calculated pair-wise sequence similarity was 94.1% between *Vanderwaltomyces africanus* and *K. viticola* (Table 1). In the phylogenetic tree derived from the neighbour-joining method, *Vanderwaltomyces africanus* and *K. martiniae* constituted a common cluster. However, the calculated sequence similarity was 97.0% between the two species, i.e., neither “98% or more” nor “beyond the so-called 98% wall” the similarity was (Yamada et al. 2022; Vu et al. 2022; Malimas et al. 2023f). Therefore, the relationship between the two species was similar to that (94.0%) between *Kloeckeraspora osmophilus* (subgroup *a-1*) and *Kloeckeraspora occidentalis* (subgroup *a-2*) (Malimas et al. 2023b).

Genus III *Arxiozyma* van der Walt et Yarrow nom. rev. MycoBank25498

The type species is *Arxiozyma telluris*.

1. *Arxiozyma telluris* (van der Walt) van der walt et Yarrow (1984)

The type strain is YB-4302. MycoBank105932

Synonym: *Kazachstania telluris* (van der Walt) Kurtzman (2003).

2. *Arxiozyma bovina* (Kurtzman et Robnett) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848372.

Basionym: *Kazachstania bovina* Kurtzman et Robnett, J. Clin. Microbiol. 43:105. 2005.

The type strain is NRRL Y-7283.

3. *Arxiozyma heterogenica* (Kurtzman et Robnett) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848373.

Basionym: *Kazachstania heterogenica* Kurtzman et Robnett, J. Clin. Microbiol. 43:107. 2005.

The type strain is NRRL Y-27499.

4. *Arxiozyma pintolopesii* (Kurtzman, Robnett, Ward et Walsh) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848378.

Basionym: *Kazachstania pintolopesii* Kurtzman, Robnett, Ward et Walsh, J. Clin. Microbiol. 43:108. 2005.

The type strain is NRRL Y-27500.

5. *Arxiozyma slooffiae* (Kurtzman et Robnett) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848379.

Basionym: *Kazachstania slooffiae* Kurtzman et Robnett, J. Clin. Microbiol. 43:109. 2005.

The type strain is NRRL YB-4349.

The calculated pair-wise sequence similarity was 88.8% between *Arxiozyma telluris* and *K. viticola* (Table 1). The sequence similarities were 96.8 - 98.1% among the four species except for *Arxiozyma slooffiae*. Between *Arxiozyma slooffiae* and *Arxiozyma telluris*, the similarity was 95.0%.

Genus IV *Pachytichospora* van der Walt nom. rev. MycoBank3680

The type species is *Pachytichospora transvaalensis*.

1. *Pachytichospora transvaalensis* van der Walt (1978) MycoBank319094

The type strain is NRRL Y-17245.

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Synonym: *Kazachstania transvaalensis* (van der Walt) Kurtzman (2003).

2. *Pachytichospora humatica* (Mikata et Ueda-Nishimura) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848408.

Basionym: *Saccharomyces humaticus* Mikata et Ueda-Nishimura, Int. J. Syst. Evol Microbiol. 51: 2193. 2001.

The type strain is NBRC 10673.

Synonym: *Kazachstania humatica* (Mikata et Ueda-Nishimura) Kurtzman (2003).

3. *Pachytichospora yakushimaensis* (Mikata et Ueda-Nishimura) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848381.

Basionym: *Saccharomyces yakushimaensis* Mikata et Ueda-Nishimura, Int. J. Syst. Evol Microbiol. 51: 2194. 2001.

The type strain is IFO 1889.

Synonym: *Kazachstania yakushimaensis* (Mikata et Ueda-Nishimura) Kurtzman (2003).

4. *Pachytichospora jiainica* (Lee, Liu, Young et Chang) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848380.

Basionym: *Kazachstania jiainica* Lee, Liu, Young et Chang, FEMS Yeast Res. 8: 116 (2008).

The type strain is SF1S05.

The calculated pair-wise sequence similarity was 89.5% between *Pachytichospora transvaalensis* and *K. viticola* (Table 1). The sequence similarities were 98.7 - 99.4% among the three species except for *Pachytichospora jiainica*. Between *Pachytichospora jiainica* and *Pachytichospora transvaalensis*, the calculated similarity was 96.1%.

According to MycoBank Database, the generic name of *Pachytichospora* van der Walt has precedence over that of *Grigorigia* Gouliamova et Dimitrov (van der Walt 1978; Goulianova and Dimitrov 2020).

Genus V *Mikataea* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov.

MycoBank number is 848382.

*Mikataea* (Mi.ka'ta.e.a. N. L. fem. n. *Mikataea*. Mikata, in honour of Kozaburo Mikata, the research scientist, Institute for Fermentation Osaka, Japan, who contributed greatly to the yeast systematics)

Cells are globose and occur singly or in pairs (Vaughan-Martini et al. 2011). Budding cells are transformed to persistent asci containing two ascospores with a belt-intersporal body and warty wall. Glucose, sucrose and raffinose were fermented. Growth occurs on glucose, sucrose, raffinose, trehalose, inulin, glycerol, ethanol and DL-lactate (Vaughan-Martini et al. 2011). Q-6 is present.

The type species is *Mikataea zonata*.

1. *Mikataea zonata* (Imanishi, Ueda-Nishimura et Mikata) Malimas. Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848383.

Basionym: *Kazachstania zonata* Imanishi, Ueda-Nishimura et Mikata, FEMS Yeast Res. 7: 335, 2007.

The type strain is NBRC 100504.

2. *Mikataea gamospora* (Imanishi, Ueda-Nishimura et Mikata) Malimas. Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848384.

Basionym: *Kazachstania gamospora* Imanishi, Ueda-Nishimura et Mikata, FEMS Yeast Res. 7: 336, 2007.

The type strain is NBRC 11056.

The calculated pair-wise sequence similarity was 93.7% between *Mikataea zonata* and *K. viticola* (Table 1). The sequence similarity was 97.6% between the two *Mikataea* species.

Genus VI *Sinensiomyces* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov.

MycoBank number is 848385.

*Sinensiomyces* (Si.nen'si.o.my.ces. N. L. masc. n. *Sinensiomyces*, China fungus)

Cells are subglobose to ellipsoidal and occur singly or in pairs (Vaughan-Martini et al. 2011). Budding cells are transformed directly into asci containing two to four cylindrical ascospores, which are able to be liberated from the ascus and agglutinated. Glucose, galactose (+ or s), sucrose (+ or v) and raffinose were fermented. Growth occurs on glucose, sucrose (+ or -), raffinose and trehalose (Vaughan-Martini et al. 2011).

The type species is *Sinensiomyces sinensis*.

1. *Sinensiomyces sinensis* (Li. Fu et Tang) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov.

MycoBank number is 848386.

Basionym: *Kluyveromyces sinensis* Li, Fu et Tang, Acta Microbiol. Sin. 30: 96. 1990.

The type strain is NRRL Y-27222.

Synonym: *Kazachstania sinensis* (Li, Fu et Tang) Kurtzman (2003).

2. *Sinensiomyces naganishii* (Mikata, Ueda-Nishimura et Hisatomi) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848387.

Basionym: *Saccharomyces naganishii* Mikata, Ueda-Nishimura et Hisatomi, Int. J. Syst. Evol. Microbiol. 51: 2191, 2001.

The type strain is NBRC 10181.

Synonym: *Kazachstania naganishii* (Mikata, Ueda-Nishimura et Hisatomi) Kurtzman (2003).

The calculated pair-wise sequence similarity was 91.6% between *Sinensiomyces sinensis* and *K. viticola* (Table2). The sequence similarity was 99.2% between the two *Sinensiomyces* species.

Genus VII *Baiomyces* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov.

MycoBank number is 848388.

*Baiomyces* (Ba.i.o.my'ces. N. L. masc. n. *Baiomyces*, Bai fungus, in honour of Dr. F.-Y. Bai, the yeast taxonomist in China, who contributed greatly in the yeast systematics)

Cells are globose to subglobose and occur singly, in pairs or in groups (Vaughan-Martini et al. 2011). Budding is multilateral on a narrow base. Pseudohyphae are not formed. Budding cells are transformed into persistent asci, each of which contains one ascospore. Glucose and galactose are fermented. Growth occurs on glucose and galactose (Vaughan-Martini et al. 2011).

The type species is *Baiomyces aquaticus*.

1. *Baiomyces aquaticus* (Bai et Wu) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848389.

Basionym: *Kazachstania aquatica* Bai et Wu, Int. J. Syst. Evol. Microbiol. 55: 2221, 2005.

The type strain is AS 2.0706.

2. *Baiomyces siamensis* (Limtong, Yongmanitchai, Tun, Kawasaki et Seki) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848390.

Basionym: *Kazachstania siamensis* Limtong, Yongmanitchai, Tun, Kawasaki et Seki, Int. J. Syst. Evol. Microbiol. 57: 421, 2007.

The type strain is NBRC 101968.

The calculated pair-wise sequence similarity was 94.6% between *Baiomyces aquatica* and *K. viticola* (Table 1). The sequence similarity was 97.0% between the two *Baiomyces* species.

Genus VIII *Neoyamazakia* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov.

MycoBank number is 848391.



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*Neoyamazakia* (Ne.o.ya.ma.za'ki.a. N. L. fem. n. *Neoyamazakia*, New Yamazaki, in honour of Dr. Atsushi Yamazaki, NITE Biotechnology Center (NBRC), who contributed greatly to the yeast systematics)

Cells are ovoid or elongate and occur singly or in pairs (Vaughan-Martini et al. 2011). Budding is at various positions near the pole of the cells. Pseudohyphae are not produced. Asci are elongated, persistent and contain one occasionally two or four spherical ascospores. Glucose and galactose are fermented. Growth occurs on glucose and galactose (Vaughan-Martini et al. 2011).

The type species is *Neoyamazakia rosinii*.

1. *Neoyamazakia rosinii* (Vaughan-Martini, Barcaccia et Pollacci) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848392.

Basionym: *Saccharomyces rosinii* Vaughan-Martini, Barcaccia et Pollacci, Int. J. Syst. Bacteriol. 46: 616. 1996.

The type strain is NRRL Y-17919.

Synonym: *Kazachstania rosinii* (Vaughan-Martini, Barcaccia et Pollacci) Kurtzman (2003).

2. *Neoyamazakia piceae* (Weber, Sapaaij et van der Walt) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848393.

Basionym: *Kluyveromyces piceae* Weber, Sapaaij et van der Walt, Antonie van Leeuwenhoek 62: 240. 1992.

The type strain is NRRL Y-17977.

Synonym: *Kazachstania piceae* (Weber, Sapaaij et van der Walt) Kurtzman (2003).

3. *Neoyamazakia lodderae* (van der Walt et Tscheuschner) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848394.

Basionym: *Saccharomyces lodderae* van der Walt et Tscheuschner, Antonie van Leeuwenhoek 23: 188. 1957.

The type strain is NRRL Y-8280.

Synonym: *Kazachstania lodderae* (van der Walt et Tscheuschner) Kurtzman (2003).

4. *Neoyamazakia spencerorum* (van der Walt et Tscheuschner) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848395.

Basionym: *Saccharomyces spencerorum* Vaughan-Martini, Antonie van Leeuwenhoek 68: 116. 1995.

The type strain is NRRL Y-17920.

Synonym: *Kazachstania spencerorum* (van der Walt et Tscheuschner) Kurtzman (2003).

The calculated pair-wise sequence similarity was 92.8% between *Neoyamazakia rosinii* and *K. viticola* (Table 1). Among the four species of the genus, the sequence similarities were 95.2 - 97.7% as shown in the genus *Kloeckeraspora* (94.0%) [*Kloeckeraspora osmophila* (subgroup *a-1*) and *Kloeckeraspora occidentalis* (subgroup *a-2*)] and the genus *Hanseniaspora* (96.5%) [*Hanseniaspora uvarum* (subgroup *b-1*) and *Hanseniaspora valbyensis* (subgroup *b-2*)] (Malimas et al. 2023b).

Genus IX *Capriottia* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov.

MycoBank number is 848396.

*Capriottia* (Cap.ri.ot'ti.a N. L. fem. n. *Capriottia*, in honour of Dr. A. Capriotti, Italian yeast taxonomist, who contributed to the yeast systematics)

Cells are subglobose to ellipsoidal and occur singly or in pairs (Vaughan-Martini et al. 2011). Budding cells are transformed directly into asci usually containing one, but occasionally up to four, globose to short ellipsoidal ascospores. Glucose and galactose are fermented. Growth occurs on glucose, galactose and trehalose (Vaughan-Martini et al. 2011).

The type species is *Capriottia servazzii*.

1. *Capriottia servazzii* (Capriotti) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov.

MycoBank number is 848397.

Basionym: *Saccharomyces servazzii* Capriotti, Ann. Microbiol. Enzymol. 17: 83. 1967.

The type strain is NRRL Y-12661.

Synonym: *Kazachstania servazzii* (Capriotti) Kurtzman (2003).

2. *Capriottia unispora* (Jørgensen) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov.

MycoBank number is 848398.

Basionym: *Saccharomyces unisporus* Jørgensen, Die Mikroorganismen der Gärungs-industrie, 5te Aufl., p. 371, 1909. P. Parey, Berlin.

The type strain is NRRL Y-1556.

Synonym: *Kazachstania unispora* (Jørgensen) Kurtzman (2003).

3. *Capriottia solicola* (Bai et Wu) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov.

MycoBank number is 848399.

Basionym: *Kazachstania solicola* Bai et Wu, Int. J. Syst. Evol. Microbiol. 55: 2222. 2005.

The type strain is CBS 6904.

4. *Capriottia aerobia* (Lu, Cai, Wu et Bai) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov.

MycoBank number is 848400.

Basionym: *Kazachstania aerobia* Lu, Cai, Wu et Bai, Int. J. Syst. Evol. Microbiol. 54: 2434. 2004.

The type strain is AS 2.2384.

The calculated pair-wise sequence similarity was 94.1% between *Capriottia servazzii* and *K. viticola* (Table 1). Among the four *Capriottia* species, the sequence similarities were 98.8 - 100%.

Genus X *Neovaughania* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov.

MycoBank number is 848401.

*Neovaughania* (Ne.o.va.ug'ha.ni.a. N. L. fem. n. *Neovaughania*, New Vaughan, in honour of Dr. Vaughan-Martini, the yeast taxonomist in Italy, who contributed greatly to the yeast systematics)

Cells are globose or slightly ovoid and occur singly or in pairs (Vaughan-Martini et al. 2011). Pseudohyphae are absent. Asci formed one or two globose ascospores. Glucose, galactose and sucrose are fermented. Growth occurs on glucose, sucrose, raffinose, galactose and trehalose (Vaughan-Martini et al. 2011).

The type species is *Neovaughania barnettii*.

1. *Neovaughania barnettii* (Vaughan-Martini) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848402.

Basionym: *Saccharomyces barnettii* Vaughan-Martini, Antonie van Leeuwenhoek 68: 116. 1995.

The type strain is NRRL Y-27223.

Synonym: *Kazachstania barnettii* (Vaughan-Martini) Kurtzman (2003).

2. *Neovaughania bulderi* (Middelhoven, Kurtzman et Vaughan-Martini) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848404.

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Basionym: *Sacchromyces bulderi* Middelhoven, Kurtzman et Vaughan-Martini, Antonie van Leeuwenhoek 77: 224. 2000.

The type strain is NRRL Y-27203.

Synonym: *Kazachstania bulderi* (Middelhoven, Kurtzman et Vaughan-Martini) Kurtzman (2003).

3. *Neovaughania exigua* (Reess ex Hansen) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848403.

Basionym: *Saccharomyces exiguus* Reess ex Hansen, Trav. Lab. Carlsberg 2: 146. 1888.

The type strain is NRRL Y-12640.

Synonym: *Kazachstania exigua* (Reess ex Hansen) Kurtzman (2003).

4. *Neovaughania turicensis* (Wyder, Meile et Teuber) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank number is 848406.

Basionym: *Saccharomyces turicensis* Wyder, Meile et Teuber, Syst. Appl. Microbiol. 22: 423. 1999.

The type strain is NRRL Y-27345.

Synonym: *Kazachstania turicensis* (Wyder, Meile et Teuber) Kurtzman (2003).

The calculated pair-wise sequence similarity was 91.3% between *Neovaughania barnettii* and *K. viticola* (Table 1). The sequence similarities were 98.7 - 99.6% among the four *Neovaughania* species. Accordingly, the four species constituted a taxonomic homogeneous-natured genus, since the calculated similarities were “98% or more” or “beyond the so-called 98% wall” (Yamada et al. 2022; Vu et al. 2022; Malimas et al. 2023f).

### 3. CONCLUSION

As described above, the genus *Kazachstania* Zubkova (1971) sensu Kurtzman (2003) was extremely diverse and produced the so-called *Kazachstania* complex, as found in the genus *Wickerhamomyces* Kurtzman et al. (2008) (Malimas et al. 2023e) as well as the genus *Schizosaccharomyces* Lindner (1893) sensu Kurtzman et Robnett (1991) (Malimas et al. 2023f).

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#### Conflict of interest

The authors declare that there are no conflicts of interest.

#### Author contributions

T. M., H.T.L. V., P. Y., S. T. and Y. Y. designed the study. T. M. performed the main experiments. H.T.L. V. and P. Y. instructed the experiments. Y. Y. prepared the manuscript. The detailed discussions were made among the five.

### REFERENCES

- [1] Kurtzman, C.P., 2003. Phylogenetic circumscription of *Saccharomyces*, *Kluyveromyces* and other members of the Saccharomycetaceae and the proposal of the new genera *Lachancea*, *Nakaseomyces*, *Naumovia*, *Vanderwaltozyma* and *Zygorulasporea*. *FFEMS Yeast Res* 4: 233-245.
- [2] Goulianova, D. and Dimitrov, R., 2020. *Kazachstania chrysolinae* and *Kazachstania bozae*, two new species of the genus *Kazachstania*: Transfer of four *Kazachstania* species to *Grigorovia* gen. nov. as new combinations. *C. R. Acad. Bulg. Sci.* 73: 48-57.
- [3] Jindamorakot, S., Yukphan, P. and Yamada, Y., 2012. *Kockiozyma* gen. nov., for *Zygozyma suomiensis*: the phylogeny of the Lipomycetaceous yeasts. *Ann. Microbiol.* 62: 1831-1840.
- [4] Malimas, T., Vu, H.T.L., Yukphan, P., Tanasupwat, S. and Yamada, Y., 2023a. The subdivision of the genus *Eremolthecium* Borzi emend. Kurtzman. *Jxiv* (DOI: <https://doi.org/10.51094/jxiv.285>).



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- [5] Malimas, T., Vu, H.T.L., Yukphan, P., Tanasupwat, S. and Yamada, Y., 2023b. The reinstatement of the genus *Kleckeraspora* Niehaus (1932) (apiculate yeasts). Jxiv (DOI: <https://doi.org/10.51094/jxiv.317>).
- [6] Malimas, T., Vu, H.T.L., Yukphan, P., Tanasupwat, S. and Yamada, Y., 2023c. The generic circumscription of *Kazachstania* Zubkova (1971) (Saccharomycetaceae): The proposal of the new genus *Vanderwaltomyces*. Jxiv (DOI: <https://doi.org/10.51094/jxiv.328>).
- [7] Malimas, T., Vu, H.T.L., Yukphan, P., Tanasupwat, S. and Yamada, Y., 2023d. The subdivision of the genus *Kazachstania* Zubkova sensu Kurtzman (2003) (Saccharomycetaceae) Jxiv (DOI: <https://doi.org/10.51094/jxiv334>).
- [8] Malimas, T., Vu, H.T.L., Yukphan, P., Tanasupwat, S. and Yamada, Y., 2023e. The genus *Hansenula* Sydow et Sydow (1919) nom. rev. and the genus *Wickerhamomyces* Kurtzman et al. (2008). Int J Nov Res Life Sci **10**: 42-47.
- [9] Malimas, T., Vu, H.T.L., Yukphan, P., Tanasupwat, S. and Yamada, Y., 2023f. The revision of Schizosacchromycetaceae. Int J Nov Res Phys Chem Math **10**: 100-106.
- [10] van der Walt, J.P. (1978) The genus *Pachytichospora* gen. nov. (Saccharomycetaceae). Bothalia **12**: 563-564.
- [11] Vaughan-Martini, A., Lachance, M.-A. and Kurtzman, C.P., 2011. *Kazachstania* Zubkova (1971) In: Kurtzman, C.P., Fell, J.W. and Boekhout, T. (ed). The Yeasts: A Taxonomic Study, 5th edition, vol. 2. London: Elsevier, p. 439-470.
- [12] Vu, H.T.L., Yukphan, P., Tanasupawat, S. and Yamada, Y., 2022. The generic circumscription of *Kockiozyma* (Lipomycetaceae). Jxiv (DOI: <https://doi.org/10.51094/jxiv.221>).
- [13] Yamada, Y., 2023. The generic circumscription of *Eremothecium* emend. Kurtzman, Jxiv (DOI: <https://doi.org/1051094/jxiv.270>).
- [14] Yamada, Y., Vu, H.T.L., Yukphan, P. and Tanasupawat, S., 2022. The revision of Lipomycetaceae. Jxiv (DOI: <https://doi.org/10.51094/jxiv.189>).

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Table 1. The pair-wise sequence similarity in 26S rRNA gene D1/D2 domain sequences of 31 *Kazachstania* and related species.

Sp.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31						
1	100																																				
2	95.2	100																																			
3	94.1	94.1	100																																		
4	94.8	95.0	97.0	100																																	
5	88.8	90.6	89.3	90.4	100																																
6	89.0	90.3	89.0	90.1	97.4	100																															
7	89.7	90.4	90.3	91.0	97.6	96.8	100																														
8	88.8	89.9	88.2	90.1	97.7	97.0	98.1	100																													
9	90.3	91.4	90.4	91.5	95.0	95.7	95.5	94.6	100																												
10	89.5	90.6	91.7	91.3	88.4	88.4	88.2	88.1	87.9	100																											
11	89.7	90.8	92.4	91.7	88.7	87.7	88.2	87.5	87.9	99.2	100																										
12	89.3	90.4	92.4	92.0	87.9	87.5	88.4	87.7	87.9	98.7	99.4	100																									
13	89.7	90.8	91.5	91.1	87.7	87.7	88.6	87.2	88.4	96.1	96.1	95.9	100																								
14	93.7	94.6	94.3	95.4	89.9	89.9	90.1	89.2	90.8	91.1	91.0	90.6	90.0	100																							
15	92.6	93.0	93.0	93.3	88.8	88.4	89.2	88.2	89.3	90.9	90.8	90.8	89.6	97.6	100																						
16	91.6	92.3	91.2	91.6	89.5	89.4	89.9	90.3	90.3	87.9	87.9	87.9	88.1	91.0	90.1	100																					
17	91.9	92.7	91.6	91.9	89.9	89.9	90.3	90.6	90.6	88.3	88.3	88.3	87.7	91.0	90.5	99.2	100																				
18	94.6	95.7	95.0	96.8	91.2	90.6	92.1	90.8	91.7	90.6	90.8	90.8	90.4	95.0	93.4	92.7	93.0	100																			
19	94.1	94.5	93.9	94.8	91.4	91.6	92.3	91.0	92.1	90.6	90.6	90.3	89.7	93.9	92.8	92.3	92.7	97.0	100																		
20	92.8	93.4	94.6	95.4	89.7	89.3	90.6	89.5	90.3	90.8	91.1	91.1	90.6	95.0	94.3	91.6	91.9	94.5	93.9	100																	
21	94.1	94.3	95.7	96.3	89.5	89.2	90.8	89.7	90.4	90.6	91.3	91.3	90.6	95.7	95.0	91.2	91.6	95.0	94.3	97.7	100																
22	93.9	94.8	95.5	96.5	90.8	90.4	91.7	90.6	91.5	90.1	90.4	90.4	90.1	95.9	94.3	92.5	92.8	95.4	94.3	96.5	97.4	100															
23	94.5	93.9	94.8	95.0	89.5	89.5	90.8	89.7	90.3	89.9	90.1	89.7	89.1	95.4	93.9	91.9	92.3	94.6	93.2	95.2	96.5	97.6	100														
24	94.1	95.9	95.7	97.2	91.9	91.0	92.1	91.5	91.9	91.5	91.5	91.9	90.6	95.6	93.5	92.8	93.2	97.0	95.4	95.2	95.7	96.1	94.8	100													
25	94.6	96.1	96.5	96.8	91.5	91.0	92.1	91.4	92.3	91.2	91.9	91.9	91.0	95.2	93.5	92.8	93.2	96.7	95.8	95.7	96.6	96.3	95.0	96.8	100												
26	94.3	96.1	96.1	96.8	91.9	91.0	92.1	91.5	91.9	91.5	91.5	91.5	91.0	95.6	93.5	93.0	93.4	97.0	95.4	95.4	95.9	96.3	95.0	99.6	99.2	100											
27	94.3	96.1	96.1	96.8	91.9	91.0	92.1	91.5	91.9	91.5	91.5	91.5	91.0	95.6	93.5	93.0	93.4	97.0	95.4	95.4	95.9	96.3	95.0	99.6	99.2	100											
28	91.3	93.5	91.7	92.4	91.9	91.1	92.2	92.1	91.1	88.1	88.8	88.8	90.4	91.3	91.0	91.8	91.2	92.8	92.7	92.1	91.9	92.6	92.3	93.4	92.8	93.5	93.5	100									
29	91.3	93.5	91.7	92.4	91.5	91.5	91.9	91.7	91.1	88.1	88.8	88.8	90.4	91.3	91.0	91.8	91.2	92.8	92.7	92.1	91.9	92.6	92.3	93.0	92.8	93.2	93.2	93.2	100								
30	91.5	93.5	92.3	92.8	91.1	90.8	91.5	91.3	91.1	88.8	88.8	88.8	90.1	91.0	90.4	91.0	90.6	93.2	93.0	91.7	91.9	92.3	91.7	92.6	92.8	92.8	92.8	92.8	92.8	96.7	96.7	100					
31	91.5	93.7	91.9	92.3	91.3	91.0	91.7	91.5	91.0	88.3	88.0	89.0	90.6	91.5	91.2	91.7	91.4	93.0	92.8	92.3	92.1	92.4	92.1	93.2	93.0	93.4	93.4	93.4	99.4	99.4	98.8	100					

1, *Kazachstania viticola*; 2, *Kazachstania kunashirensis*; 3, *Vandervaltomyces africanus*; 4, *Vandervaltomyces martiniae*; 5, *Arxiozyma telluris*; 6, *Arxiozyma bovina*; 7, *Arxiozyma heterogenica*; 8, *Arxiozyma pintolopesii*; 9, *Arxiozyma slooffiae*; 10, *Pachytichospora transvaarensis*; 11, *Pachytichospora humatica*; 12, *Pachytichospora yakushimaensis*; 13, *Pachytichospora jiaunica*; 14, *Pachytichospora jiaunica*; 15, *Mikataea gamospora*; 16, *Sinensiomyces sinensis*; 17, *Sinensiomyces naganishii*; 18, *Baiomyces aquatica*; 19, *Baiomyces siamensis*; 20, *Neoyamazakia rosini*; 21, *Neoyamazakia piceae*; 22, *Neoyamazakia lodderae*; 23, *Neoyamazakia spencerorum*; 24, *Capriottia servazzii*; 25, *Capriottia unisporea*; 26, *Capriottia solicola*; 27, *Capriottia aerobia*; 28, *Neovaughania barnettii*; 29, *Neovaughania bulderi*; 30, *Neovaughania exigua*; 31, *Neovaughania turicensis*. To calculate % similarity, 542-548 bases were used. For construction of phylogenetic trees and calculation of sequence similarities, refer to Yamada et al. (2022).

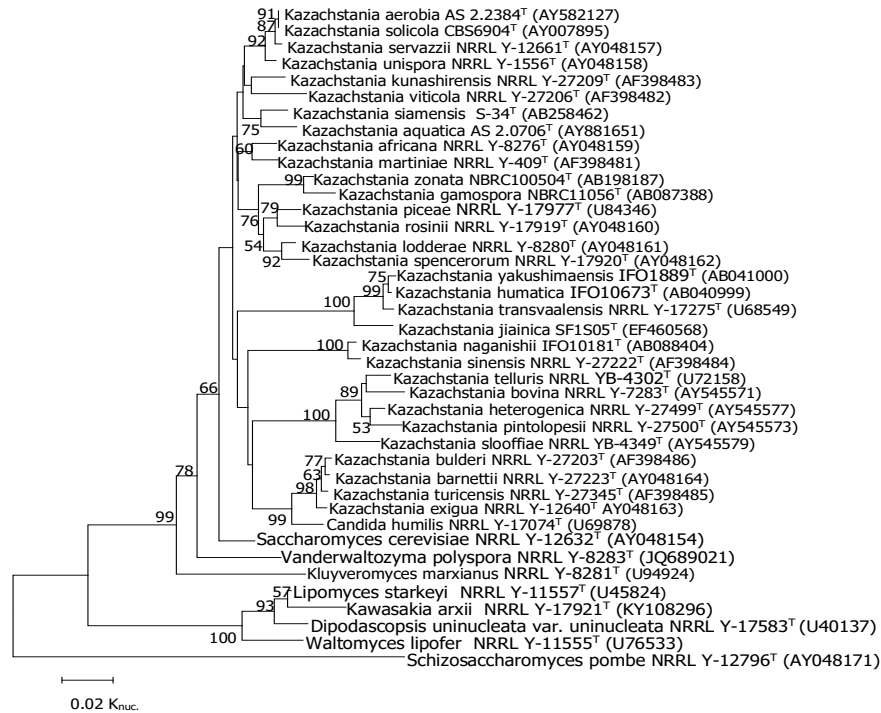


Fig. 1. The phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences with 502 bases derived from the neighbour-joining method. The numerals at the nodes of respective branches indicate bootstrap values (%) deduced from 1000 replications.

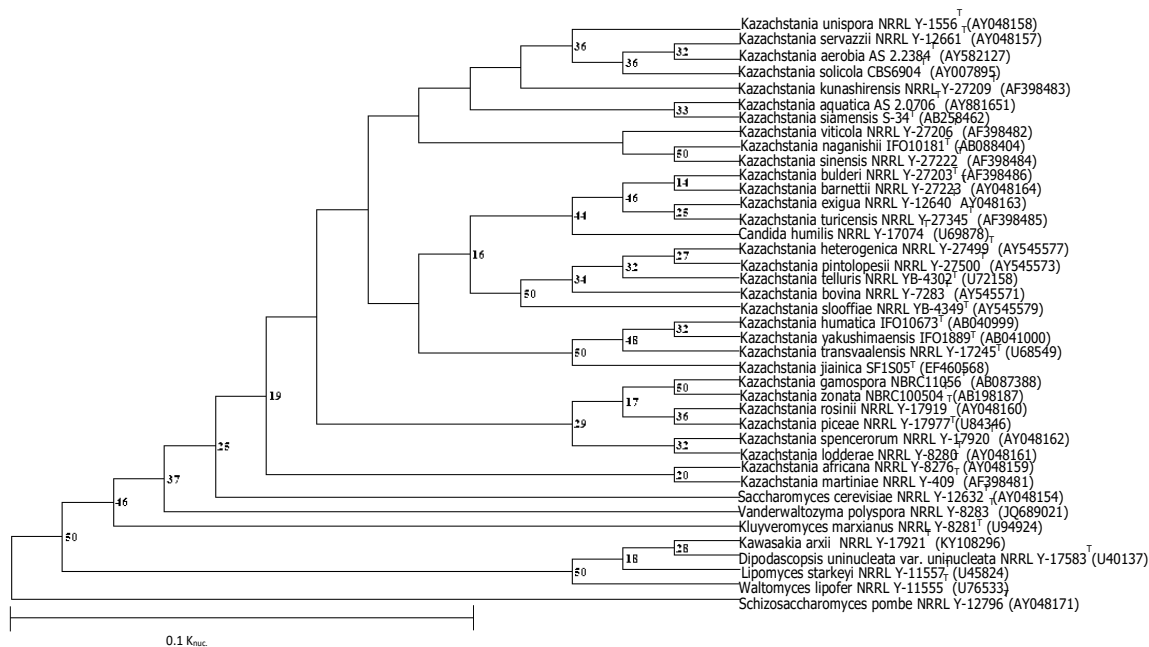


Fig. 2. The phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences with 502 bases derived from the Maximum Parsimony method. The numerals at the nodes of respective branches indicate bootstrap values (%) deduced from 1000 replications.