Short Communication

The Subdivison of the Genus *Kazachstania* Zubkova 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.

Keywords: *Kazachstania viticola*; *Vanderwaltomyces africanus*; *Arxiozyma telluris*; *Neovaughania barnettii*; *Pachytichospora transvaarensis*.

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 & Dimitrov, 2020). Such a phenomenon suggested that the genus was quite diverse phylogenetically and taxonomic heterogeneous-natured (Yamada, 2023; Yamada et al, 2022; Vu et al., 2022a, b; Malimas et al., 2023a).

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 *Vanzderwaltomyces 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.

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 calculated 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*) (Lipomycetaceae) (Yamada et al. 2022; Jindamorakot et al., 2012). Namely, the two *Kazachstania* species were not tightly coupled phylogenetically. As a result, *K. viticola* constituted the monotypic genus. 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 strico (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 ware recognized as follows.

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

MycoBank848374

Vanderwaltomyces (Van.der.wal'to.my.ces. N. L. masc. n. *Vaanderwaltomyces*, 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 were formed. The spores are liberated from the ascus soon after formation. Glucose and galactose are feremnted. Growh 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. MycoBank848376

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

The type strain is CBS 2517.

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

2. *Vanderwaltoyces martiniae* (James, Cai, Roberts et Collins) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank848375

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, *Vandervaltomyces 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. 2022a, b; Malimas et al. 2023a, b). 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 (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. MycoBank848372

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. MycoBank848373

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

The type atrain is NRRL Y-27499.

4. *Arxiozyma pintolopesii* (Kurtzman, Robnett, Ward et Walsh) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank848378

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. MycoBank848379

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 tellulis*, the similarity was 95.0%.

Genus IV *Pachytichospora* van der Walt (MycoBank3680)

The type species is *Pachytichospora transvaarensis*.

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

The type strain is NRRL Y-17245.

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

2. *Pachytichospora humatica* (Mikata et Ueda-Nishimura) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) MycoBank848408

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) MycoBank848381

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) MycoBank848380

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

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

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

MycoBank848382

Mikataea (Mi.ka'ta.e.a. N. L. fem. n. *Mikataea*. Mikata, in honour of Kozaburo Mikata, the research scientist, Institute of 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. MycoBank848383

Bsionym: *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. MycoBank848384

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.

MycoBank848385

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

Cells are subglobose to elliposoidal 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 sinensi*s.

1. *Sinensiomyces sinensi*s (Li. Fu et Tang) Malimas, Vu, Yukphan, Tanasupawat et Yamada comb. nov. MycoBank848386

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 comb. nov. MycoBank848387

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 *Synensiomyces* species.

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

MycoBank848388

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 were 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. MycoBank848389

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. MycoBank848390

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.

MycoBan848391

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* (Vaoghan-Martini, Barcaccia et Pollacci) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank848392

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

The type strain is NRRL Y-17919.

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

2. *Neoyamazakia piceae* (Weber, Sapaaij et van der Walt) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank848393

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. MycoBank848394

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. MycoBank848395

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). The sequence similarities were 95.2 - 97.7% among the four species within the genus, 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* (subgrouo *b-1*) and *Hanseniaspora valbyensis* (subgroup *b-2*)] (Malimas et al. 2023b).

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

MycoBank848396

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 elliposoidal 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 comb. nov. MycoBank848397

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

The type strain is NRRL Y-12661.

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

2. *Capriottia unispora* (Jörgensen) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank848398

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

The type strain is NRRL Y-1556.

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

3. *Capriottia solicola* (Bai et Wu) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank848399

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. MycoBank848400

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 C*apriottia servazzii* and *K. viticola* (Table 1). The sequence similarities were 98.8 - 100% among the four *Capriottia* species.

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

MycoBank848401

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. MycoBank848402

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

The type strain is NRRL Y-27223.

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

2. *Neovaughania bulderi* (Middelhoven, Kurtzman et Vaughan-Martini) Malimas, Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov. MycoBank848404

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. MycoBank848403

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. MycoBank848406

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. 2022a, b; Malimas et al. 2023a, b).

As described above, the genus *Kazachstania* Zubkova sensu Kurtzman (2003) was extremely diverse and produced the so-called *Kazachstania* complex. In future, a large number of species will be described within the so-called *Kazachstania* complex.

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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.

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The Genus *Kazachstania* Zubkova sensu Kurtzman (2003) の分割: (Sacchromycetaceae)

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The genus *Kazachstania* sensu Kurtzman (2003)は，当初，monotypic genus として，*Kazachstania viticola* Zubkova (1971) をもって提案された．後に，多くの種がこの属に移された．しかし，本属の系統解析によると，基準種を含む大多数の種は系統樹の中で極端に長い系統枝をもつことが判明した．基準種の他の30種に対する 26S rRNA遺伝子部分塩基配列での類似度は極めて低く，88.8 - 95.2% であった．この結果，本属は いわゆる*Kazachstania* complex なるグループを形成，10個の属に分割された．

Table 1. The pair-wise sequence similarity in the 26S rRNA gene D1/D2 domain sequences in *Kazchstania* 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	89.2	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	89.8	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	98.8	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	100				
28	91.3	93.5	91.7	92.4	91.9	91.1	92.2	92.1	91.1	89.1	88.8	88.8	90.4	91.3	91.0	91.6	91.2	93.2	92.	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	89.1	88.8	88.8	90.4	91.3	91.0	91.6	91.2	92.8	92.7	92.1	91.9	92.6	92.3	93.0	92.8	93.2	93.2	99.6	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	928	98.7	98.7	100	
31	91.5	93.7	91.9	92.3	91.3	91.0	91.7	91.5	91.0	89.3	89.0	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	99.4	99.4	98.8	100

1, *Kazachstania viticola*; 2, *Kazachstania kunashirensis*; 3, *Vanderwaltomyces africanus*; 4*, Vanderwaltoyces 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 jiainica*; 14*, Mikataea zonata*; 15, *Mikataea gamospora*, 16, *Sinensiomyces sinensis*; 17, *Sinensiomyces naganishii*; 18, *Baiomyces aquatica*; 19, *Baiomyces siamensis*; 20, *Neoyamazakia rosinii*; 21, *Neoyamazakia piceae*; 22, *Neoyamazakia lodderae*; 23, *Neoyamazakia spencerorum*; 24, *Capriottia servazzii*;25, *Capriottia unispora*; 26, *Capriottia solicola*; 27, *Capriottia aerobia*; 28, *Neovaughania barnettii*, 29, *Neovaughania bulderi*; 30, *Neovaughania exigua*; 31, *Neovaughania turicensis*. For calculating the sequence similarity, 542-548 bases were used.

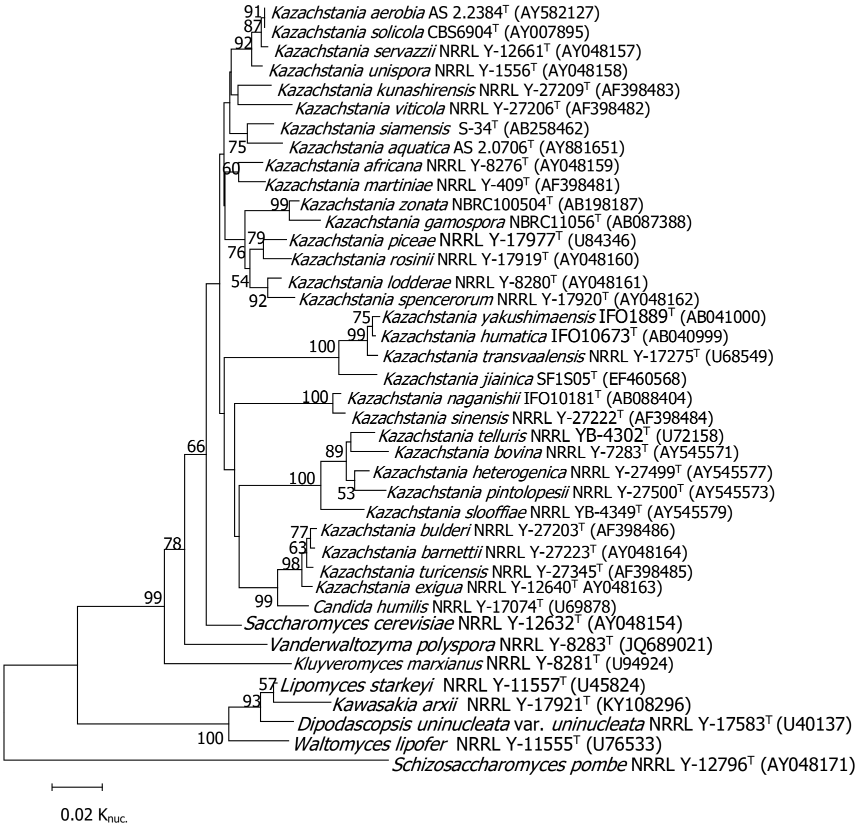

Fig. 1. The phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences with 502 bases in *Kazachstania* species derived from the neighbour-joining method. The numerals at the nodes of respective branches indicate bootstrap values (%) deduced from 1000 replications

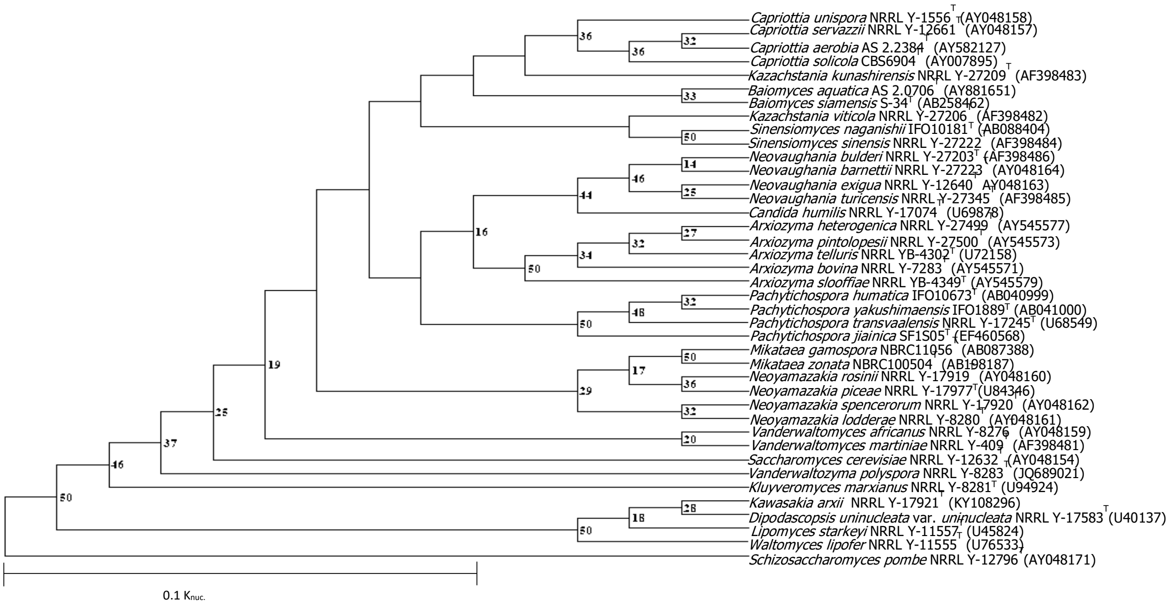

Fig. 2. The phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences with 502 bases in *Kazachstania* and related species derived from the maximum parsimony method. The numerals at the nodes of respective branches indicate bootstrap values (%) deduced from 1000 replications