

1 Microbial Systematics

2

3 **The Subdivision of the Genus *Kazachstania* Zubkova (1971) (Saccharomycetaceae)**

4

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

33

34

35 **Abstract**

36 The genus *Kazachstania* Zubkova was introduced as a monotypic genus including
37 *Kazachstania viticola* Zubkova (1971). Later, a large number of species were accom-
38 modated to the genus. However, the phylogenetic analyses indicated that the genus was
39 extremely diverse, since the species concerned, including the type species, *Kazachstania*
40 *viticola*, showed extremely long branches in the phylogenetic trees. The calculated pair-
41 wise sequence similarities of *K. viticola* were quite low (89.4 - 94.6%) to the remaining 17

42 representative species. The phylogenetic data obtained indicated that the genus formed the
43 so-called *Kazachstania* complex, which was subdivided into 10 taxa at the generic level.

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45
46 The genus *Kazachstania* Zubkova was introduced as a monotypic genus with
47 *Kazachstania viticola* Zubkova (1971). Later, a large number of species were
48 accommodated to the genus (Kurtzman 2003). However, many species of the genus had
49 quite long phylogenetic branches, as well as the type species, *K. viticola*, in the resulting
50 phylogenetic trees (Kurtzman 2003; Vaughan-Martini et al. 2011; Goulianova and
51 Dimitrov 2020). Such a phenomenon suggests that the genus is quite diverse phylogenetic-
52 cally and taxonomic heterogeneous-natured.

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

58
59 This paper deals with the presently available sequence data and gives the different
60 conclusion that the genus *Kazachstania* was subdivided into 10 groups at the generic
61 level.

62
63 The phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences was
64 constructed by the neighbour-joining method for 32 species of the genus *Kazachstania*
65 (Fig. 1). The type species, *K. viticola* produced a long branch with *K. kunashirensis*. The
66 calculated pair-wise sequence similarity was 95.2% between the two species (Table 1), the
67 value of which was almost similar to that (94.1%) between *Vanderwaltozyma polyspora*
68 and *Saccharomyces cerevisiae* used as reference standards (Malimas et al. 2023c). In the
69 additional phylogenetic tree derived from the maximum parsimony method (Fig. 2), *K.*
70 *kunashirensis* was located at a different position independently apart from the type
71 species, *K. viticola*, as found previously in the relationship between *Dipodascopsis*
72 *uninucleata* and *Neoaidaea tothii* (= *Dipodascopsis tothii*) (Lipomycetaceae) (Yamada et
73 al. 2022). Namely, the two species were not tightly coupled but loosely phylogenetically.
74 As a result, *K. viticola* constituted the monotypic genus *Kazachstania*. Incidentally, the
75 calculated pair-wise sequence similarities of *K. viticola* were very low (89.4 - 94.6%) to
76 the remaining 17 representative species of the 31 in the genus (Malimas et al. 2023c).

77 78 Genus I *Kazachstania* Zubkova

79 The type species is *Kazachstania viticola*.

80 1. *Kazachstania viticola* Zubkova (1971)

81 The type strain is NRRL Y-27206.

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

83 The type strain is NRRL Y-27209.

84

85 As mentioned above, *K. kunashirensis* was not able to be classified phylogenetically in
86 the genus *Kazachstania*. However, the species was temporarily accommodated to the
87 genus (Malimaset al. 2023b, c).

88

89 Genus II *Vanderwaltomyces* Malimas, Vu, Yukphan, Tanasupawat et Yamada

90 The type species is *Vanderwaltomyces africanus*.

91 1. *Vanderwaltomyces africanus* (van der Walt) Malimas, Vu, Yukphan, Tanasupawat et
92 Yamada (2023)

93 The type strain is NRRL Y-8276.

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

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

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

99 The type strain is NRRL Y-409.

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

101

102 The calculated pair-wise sequence similarity was 94.1% between *Vanderwaltomyces*
103 *africanus* and *K. viticola* (Table 1). In the phylogenetic tree derived from the neighbour-
104 joining method, *Vandervaltomyces africanus* and *K. martiniae* constituted a common
105 cluster. However, the calculated sequence similarity was 97.0% between the two species,
106 i.e., not “98% or more” nor “beyond the 98% wall” (Yamada et al. 2022; Vu et al. 2022a,
107 b; Malimas et al. 2023a, b). Therefore, the relationship between the two species was
108 similar to that (94.0%) between *Kloeckeraspora osmophilus* (subgroup *a-1*) and
109 *Kloeckeraspora occidentalis* (subgroup *a-2*) (Malimas et al. 2023b).

110

111 Genus III *Arxiozyma* van der Walt et Yarrow

112 The type species is *Arxiozyma telluris*.

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

114 The type strain is YB-4302.

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

116 2. *Arxiozyma bovina* (Kurtzman et Robnett) Malimas, Vu, Yukphan, Tanasupawat et
117 Yamada (2023) comb. nov.

118 Basionym: *Kazachstania bovina* Kurtzman et Robnett, J. Clin. Microbiol. 43:105.
119 2005.

120 The type strain is NRRL Y-7283.

121 3. *Arxiozyma heterogenica* (Kurtzman et Robnett) Malimas, Vu, Yukphan,
122 Tanasupawat et Yamada (2023) comb. nov.

123 Basionym: *Kazachstania heterogenica* Kurtzman et Robnett, J. Clin. Microbiol.
124 43:107. 2005.
125 The type strain is NRRL Y-27499.
126 4. *Arxiozyma pintolopesii* (Kurtzman, Robnett, Ward et Walsh) Malimas, Vu, Yukphan,
127 Tanasupawat et Yamada (2023) comb. nov.
128 Basionym: *Kazachstania pintolopesii* Kurtzman, Robnett, Ward et Walsh, J. Clin.
129 Microbiol. 43:108. 2005.
130 The type strain is NRRL Y-27500.
131 5. *Arxiozyma slooffiae* (Kurtzman et Robnett) Malimas, Vu, Yukphan, Tanasupawat et
132 Yamada (2023) comb. nov.
133 Basionym: *Kazachstania slooffiae* Kurtzman et Robnett, J. Clin. Microbiol. 43:109.
134 2005.
135 The type strain is NRRL YB-4349.
136
137 The calculated pair-wise sequence similarity was 88.8% between *Arxiozyma telluris*
138 and *K. viticola* (Table 1). The sequence similarities were 96.8 - 98.1% among the four
139 except for *Arxiozyma slooffiae*. Between *Arxiozyma slooffiae* and *Arxiozyma telluris*, the
140 calculated similarity was 95.0%.
141
142 Genus IV *Pachytichospora* van der Walt.
143 The type species is *Pachytichospora transvaarensis*.
144 1. *Pachytichospora transvaarensis* van der Walt (1978)
145 The type strain is NRRL Y-17245.
146 Synonym: *Kazachstania transvaarensis* (van der Walt) Kurtzman (2003).
147 2. *Pachytichospora humatica* (Mikata et Ueda-Nishimura) Malimas, Vu, Yukphan,
148 Tanasupawat et Yamada (2023)
149 Basionym: *Saccharomyces humatica* Mikata et Ueda-Nishimura, Int. J. Syst. Evol
150 Microbiol., 51: 2193. 2001.
151 The type strain is NBRC 10673.
152 Synonym: *Kazachstania humatica* (Mikata et Ueda-Nishimura) Kurtzman (2003).
153 3. *Pachytichospora yakushimaensis* (Mikata et Ueda-Nishimura) Malimas, Vu,
154 Yukphan, Tanasupawat et Yamada (2023)
155 Basionym: *Saccharomyces yakushimaensis* Mikata et Ueda-Nishimura, Int. J. Syst.
156 Evol Microbiol. 51: 2194. 2001.
157 The type strain is IFO 1889.
158 Synonym: *Kazachstania yakushimaensis* (Mikata et Ueda-Nishimura) Kurtzman
159 (2003).
160 4. *Pachytichospora jainica* (Lee, Liu, Young et Chang) Malimas, Vu, Yukphan,
161 Tanasupawat et Yamada (2023)
162 Basionym: *Kazachstania jainica* Lee, Liu, Young et Chang, FEMS Yeast Res. 8: 116
163 (2008).

164 The type strain is SF1S05.

165

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

170 According to MycoBank Database, the genus *Grigorovia* Gouliamova et Dimitrov
171 (2020) appears to be a synonym of the genus *Pachytichospora* van der Walt (1978) (van
172 der Walt 1978; Goulianova and Dimitrov 2020).

173

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

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

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

183 The type species is *Mikataea zonata*.

184 1. *Mikataea zonata* (Imanishi, Ueda-Nishimura et Mikata) Malimas. Vu, Yukphan,
185 Tanasupawat et Yamada (2023) comb. nov.

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

188 The type strain is NBRC 100504.

189 2. *Mikataea gamospora* (Imanishi, Ueda-Nishimura et Mikata) Malimas. Vu, Yukphan,
190 Tanasupawat et Yamada (2023) comb. nov.

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

193 The type strain is NBRC 11056.

194

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

197

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

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

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

205 The type species is *Sinensiomyces sinensis*.
206 1. *Sinensiomyces sinensis* (Li, Fu et Tang) Malimas, Vu, Yukphan, Tanasupawat et
207 Yamada comb. nov.
208 Basionym: *Kluyveromyces sinensis* Li, Fu et Tang, Acta Microbiol. Sin. 30: 96. 1990.
209 The type strain is. NRRL Y-27222.
210 2. *Sinensiomyces naganishii* (Mikata, Ueda-Nishimura et Hisatomi) Malimas, Vu,
211 Yukphan, Tanasupawat et Yamada comb. nov.
212 Basionym: *Saccharomyces naganishii* Mikata, Ueda-Nishimura et Hisatomi, Int. J.
213 Syst. Evol. Microbiol. 51: 2191, 2001.
214 The type strain is NBRC 10181.
215 Synonym: *Kazachstania naganishii* (Mikata, Ueda-Nishimura et Hisatomi) Kurtzman
216 (2003).
217
218 The calculated pair-wise sequence similarity was 91.6% between *Sinensiomyces*
219 *sinensis* and *K. viticola* (Table2). The sequence similarity was 99.2% between the two
220 species.
221
222 Genus VII *Baiomyces* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov
223 *Baiomyces* (Ba.i.o.my'ces. N. L. masc. n. *Baiomyces*, Bai fungus, in honour of Dr. F.-
224 Y. Bai, the yeast taxonomist in China, who contributed greatly in the yeast systematics)
225 Cells are globose to subglobose and occur singly, in pairs or in groups (Vaughan-
226 Martini et al. 2011). Budding is multilateral on a narrow base. Pseudohyphae are not
227 formed. Budding cells are transformed into persistent asci, each of which contains one
228 ascospore. Glucose and galactose were fermented. Growth occurs on glucose and
229 galactose (Vaughan-Martini et al. 2011).
230 The type species is *Baiomyces aquatica*.
231 1. *Baiomyces aquatica* (Bai et Wu) Malimas, Vu, Yukphan, Tanasupawat et Yamada
232 (2023) comb. nov.
233 Basionym: *Kazachstania aquatica* Bai et Wu, Int. J. Syst. Evol. Microbiol. 55: 2221,
234 2005.
235 The type strain is AS 2.0706.
236 2. *Baiomyces siamensis* (Limtong, Yongmanitchai, Tun, Kawasaki et Seki) Malimas,
237 Vu, Yukphan, Tanasupawat et Yamada (2023) comb. nov.
238 Basionym: *Kazachstania siamensis* Limtong, Yongmanitchai, Tun, Kawasaki et Seki,
239 Int. J. Syst. Evol. Microbiol. 57: 421, 2007.
240 The type strain is NBRC 101968.
241
242 The calculated pair-wise sequence similarity was 94.6% between *Baiomyces aquatica*
243 and *K. viticola* (Table 1). The sequence similarity was 97.0% between the two species.
244
245 Genus VIII *Neoyamazakia* Malimas, Vu, Yukphan, Tanasupawat et Yamada gen. nov.

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

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

254 The type species is *Neoyamazakia rosinii*.

255 1. *Neoyamazakia rosinii* (Vaughan-Martini, Barcaccia et Pollacci) Malimas, Vu,
256 Yukphan, Tanasupawat et Yamada (2023) comb. nov.

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

259 The type strain is NRRL Y-17919.

260 Synonym: *Kazachstania rosinii* (Vaughan-Martini, Barcaccia et Pollacci) Kurtzman
261 (2003).

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

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

266 The type strain is NRRL Y-17977.

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

268 3. *Neoyamazakia lodderae* (van der Walt et Tscheuschner) Malimas, Vu, Yukphan,
269 Tanasupawat et Yamada (2023) comb. nov.

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

272 The type strain is NRRL Y-8280.

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

274 4. *Neoyamazakia spencerorum* (van der Walt et Tscheuschner) Malimas, Vu, Yukphan,
275 Tanasupawat et Yamada (2023) comb. nov.

276 Basionym: *Saccharomyces spencerorum* Vaughan-Martini, Antonie van Leeuwenhoek
277 68: 116. 1995.

278 The type strain is NRRL Y-17920.

279 Synonym: *Kazachstania spencerorum* (van der Walt et Tscheuschner) Kurtzman
280 (2003).

281

282 The calculated pair-wise sequence similarity was 92.8% between *Neoyamazakia*
283 *rosinii* and *K. viticola* (Table 1). The sequence similarities were 95.2 - 97.7% among the
284 four species within the genus, as already shown in the genus *Kloeckeraspora* (subgroups
285 *a-1* and *a-2*) and the genus *Hanseniaspora* (subgroups *b-1* and *b-2*) (Malimas et al.
286 2023b).

287

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

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

291 Cells are subglobose to ellipsoidal and occur singly or in pairs (Vaughan-Martini et
292 al. 2011). Budding cells are transformed directly into asci usually containing one, but
293 occasionally up to four, globose to short ellipsoidal ascospores. Glucose and galactose are
294 fermented. Growth occurs on glucose, galactose and trehalose (Vaughan-Martini et al.
295 2011).

296 The type species is *Capriottia servazzii*.

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

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

300 The type strain is NRRL Y-12661.

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

302 2. *Capriottia unispora* (Jörgensen) Malimas, Vu, Yukphan, Tanasupawat et Yamada
303 (2023) comb. nov.

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

306 The type strain is NRRL Y-1556.

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

308 3. *Capriottia solicola* (Bai et Wu) Malimas, Vu, Yukphan, Tanasupawat et Yamada
309 (2023) comb. nov.

310 Basionym: *Kazachstania solicola* Bai et Wu, Int. J. Syst. Evol. Microbiol. 55: 2222.
311 2005.

312 The type strain is CBS 6904.

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

315 Basionym: *Kazachstania aerobia* Lu, Cai, Wu et Bai, Int. J. Syst. Evol. Microbiol. 54:
316 2434. 2004.

317 The type strain is AS 2.2384.

318

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

322

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

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

327 Cells are globose or slightly ovoid and occur singly or in pairs (Vaughan-Martini et al.
328 2011). Pseudohyphae are absent. Asci formed one or two globose ascospores. Glucose,
329 galactose and sucrose are fermented. Growth occurs on glucose, sucrose, raffinose,
330 galactose and trehalose (Vaughan-Martini et al. 2011).

331 The type species is *Neovaughania barnettii*.

332 1. *Neovaughania barnettii* (Vaughan-Martini) Malimas, Vu, Yukphan, Tanasupawat et
333 Yamada (2023) comb. nov.

334 Basionym: *Saccharomyces barnettii* Vaughan-Martini, Antonie van Leeuwenhoek 68:
335 116. 1995.

336 The type strain is NRRL Y-27223.

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

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

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

342 The type strain is NRRL Y-27203.

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

345 3. *Neovaughania exigua* (Reess ex Hansen) Malimas, Vu, Yukphan, Tanasupawat et
346 Yamada (2023) comb. nov.

347 Basionym: *Saccharomyces exiguus* Reess ex Hansen, Trav. Lab. Carlsberg 2: 146.
348 1888.

349 The type strain is NRRL Y-12640.

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

351 4. *Neovaughania turicensis* (Wyder, Meile et Teuber) Malimas, Vu, Yukphan,
352 Tanasupawat et Yamada (2023) comb. nov.

353 Basionym: *Saccharomyces turicensis* Wyder, Meile et Teuber, Syst. Appl. Microbiol.
354 22: 423. 1999.

355 The type strain is NRRL Y-27345.

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

357

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

363

364 As described above, the genus *Kazachstania* was extremely diverse phylogenetically
365 and produced the so-called *Kazachstania* complex. In future, a large number of species
366 will be described within the so-called *Kazachstania* complex.

367

368

369 Acknowledgements

370 The present authors express their sincere thanks for citing the experimental data of the
371 authors.

372

373 Funding information

374 The present authors received no grant from any funding agency.

375

376 Conflict of interest

377 The authors declare that there are no conflicts of interest.

378

379 Author contributions

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

383

384

385 **References**

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387 and other members of the Saccharomycetaceae and the proposal of the new genera
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390 Goulianova, D. and Dimitrov, R. (2020) *Kazachstania chrysolinae* and *Kazachstania*
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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	92.1	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	92.8	92.8	92.8	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.

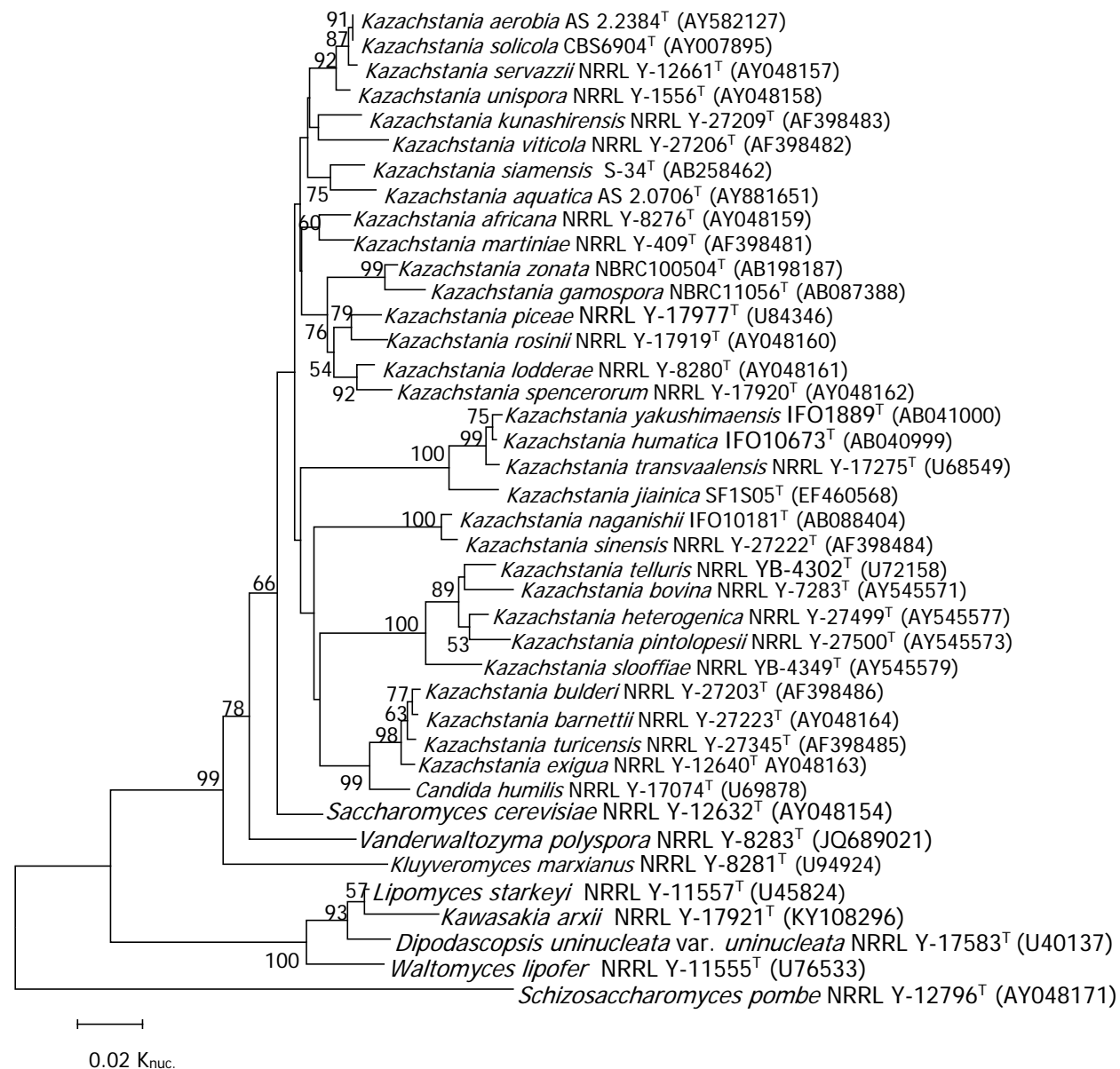


Fig. 1. The phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences with 502 bases derived from the neighbour-joining method. The numerals at the nodes of respective branches indicate bootstrap values (%) deduced from 1000 replications

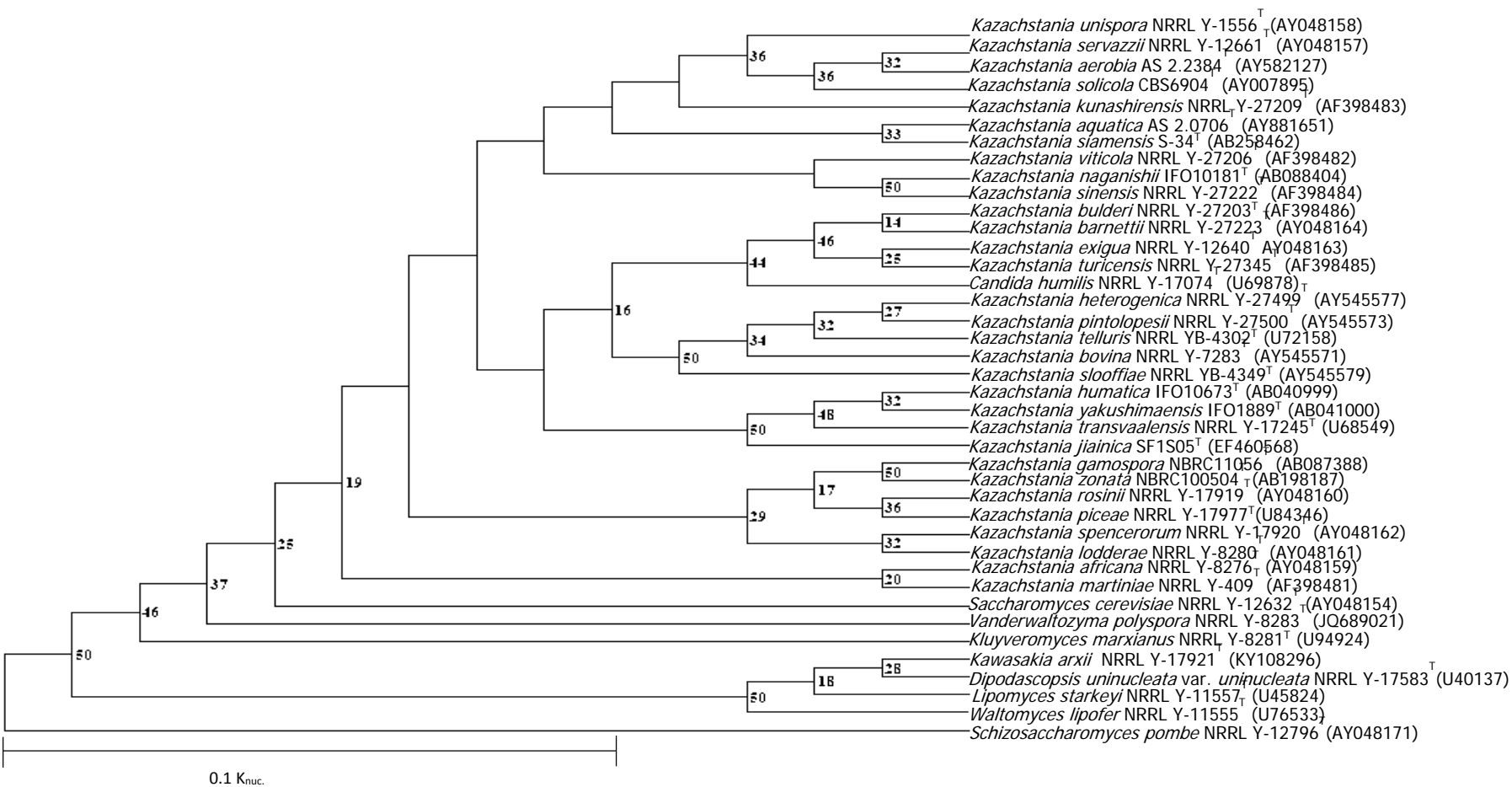


Fig. 2. The phylogenetic tree based on the 26S rRNA gene D1/D2 domain sequences with 502 bases derived from the Maximum Parsimony method. The numerals at the nodes of respective branches indicate bootstrap values (%) deduced from 1000 replications