Three new combinations from the *Cryptococcus laurentii* complex: *Cryptococcus aureus*, *Cryptococcus carnescentis* and *Cryptococcus peneaus*

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Fifteen strains of the *Cryptococcus laurentii* complex were reclassified based on sequence analyses of 18S rDNA, the D1/D2 region of the 26S rDNA and the internal transcribed spacer regions, as well as physiological and biochemical properties. The strains were divided into phylogenetic groups I and II. The type strain of *C. laurentii* (CBS 139^T=ATCC 18803^T=JCM 9066^T=MUCL 30398^T=NRRL Y-2536^T) was in phylogenetic group I. Phylogenetic group II, which was phylogenetically distant from phylogenetic group I, clustered with *Cryptococcus dimennae* and *Bullera globispora*. In phylogenetic group I, the type strain of *Torula aurea* (CBS 318^T=ATCC 32063^T=IFO 0372^T=NRRL Y-1582^T) appeared to be a separate species from *C. laurentii*, and the designation *Cryptococcus aureus* comb. nov. is proposed for *Torula aurea*. *Cryptococcus flavescens* (formerly *Torula flavescens*, type strain CBS 942^T=ATCC 10668^T=DBVPG 6007^T=MUCL 30414^T) was treated as a synonym of *C. laurentii*; however, this is a distinct species. The type strains of *Torulopsis carnescentis* (CBS 973^T=ATCC 32064^T=MUCL 30641^T=NRRL Y-1503^T), *Rhodotorula peneaus* (CBS 2409^T=ATCC 13546^T=MUCL 30643^T=NRRL Y-2005^T) and *Cryptococcus victoriae* belonged to phylogenetic group II. Two new combinations, *Cryptococcus carnescentis* comb. nov. (type strain CBS 973^T=ATCC 32064^T=MUCL 30641^T=NRRL Y-1503^T) and *Cryptococcus peneaus* comb. nov. (type strain CBS 2409^T=ATCC 13546^T=MUCL 30643^T=NRRL Y-2005^T), are proposed from this group.

INTRODUCTION

Cryptococcus laurentii (Kufferath) C. E. Skinner has been isolated from plants, soil and clinical specimens (Fell & Statzell-Tallman, 1998). This species is reported to be heterogeneous based on the wide range of nuclear DNA G+C contents and whole-cell protein electrophoretic patterns (Nakase & Komagata, 1971; Vancanneyt *et al.*, 1994). Recently, a high degree of intraspecific heterogeneity has been reported in *C. laurentii* based on sequences of the

D1/D2 region of 26S rDNA and internal transcribed spacer (ITS) regions (Sugita *et al.*, 2000). Ten strains, including the type strain, were divided into phylogenetic groups I and II. The type strain of the species (CBS 139^T=ATCC 18803^T=JCM 9066^T=MUCL 30398^T=NRRL Y-2536^T) was in phylogenetic group I. Phylogenetic group II was phylogenetically distinct from group I and clustered with *Cryptococcus dimennae* Fell & Phaff and *Bullera globispora* Johri & Bandoni. Four species that have been treated as synonyms of *C. laurentii*, *Torula aurea* Saito (type strain CBS 318^T=ATCC 32063^T=IFO 0372^T=NRRL Y-1582^T), *Torula flavescens* Saito (type strain CBS 942^T=ATCC 10668^T=DBVPG 6007^T=MUCL 30414^T), *Torulopsis carnescentis* Verona & Luchetti (type strain CBS 973^T=ATCC 32064^T=MUCL 30641^T=NRRL Y-1503^T) and *Rhodotorula peneaus* Phaff, Mrak & Williams (type strain CBS 2409^T=ATCC 13546^T=MUCL 30643^T=NRRL Y-2005^T), seemed to be distinct species.

Abbreviation: ITS, internal transcribed spacer.

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The GenBank/EMBL/DDBJ accession numbers for the sequences determined in this study are AB085795–AB085812.

In addition to these strains, five other strains in the *C. laurentii* complex were included in this study. Four were strains of opposite mating types from wheat and corn (JCM 9909, JCM 9910, JCM 9911, JCM 9912) isolated by Kurtzman (1973). These strains were identified as *C. laurentii*, but did not mate with the type strains of *C. laurentii*, *C. laurentii* var. *flavescens* or *C. laurentii* var. *magnus* (Kurtzman, 1973). Guého *et al.* (1993) confirmed this heterogeneity by sequence analysis of the D1/D2 region of the 26S rDNA. A final strain, JCM 5945, isolated by Tokuoka *et al.* (1985) from a flower, was also included. This paper clarifies the taxonomic assignment of these strains.

METHODS

Yeast strains. The strains used in this study are listed in Table 1. They were stock cultures identified as *C. laurentii* in the Centraalbureau voor Schimmelcultures (CBS) and the Japan Collection of Microorganisms (JCM).

Morphological, physiological and biochemical characteristics.

Most of the morphological, physiological and biochemical characteristics were examined according to the methods of Yarrow (1998). The assimilation of nitrogen compounds was investigated on solid media using starved inoculum. Vitamin requirements were determined by the method of Komagata & Nakase (1967). The maximum growth temperature was determined in YM broth (Difco) using thermoregulated metal block heaters.

Major ubiquinones. Cells were grown in 500 ml Erlenmeyer flasks containing 250 ml YM broth on a rotary shaker at 150 r.p.m. at 25 °C and were harvested in the early stationary growth phase and then washed with distilled water. Extraction, purification and identification of ubiquinones were carried out according to the method of Nakase & Suzuki (1986).

DNA base composition. Cells were grown as described above and were harvested in the exponential growth phase and then washed with distilled water and freeze-dried. Isolation and purification of nuclear DNA were done according to Takashima & Nakase (2000). The DNA base composition was determined by HPLC after enzymic digestion of DNA to deoxyribonucleosides as described by Tamaoka & Komagata (1984). The DNA-GC kit (Yamasa Shoyu) was used as the quantitative standard.

Sequencing and phylogenetic analysis. Nuclear DNA was extracted by the method of Makimura *et al.* (1994). The 18S rDNA and ITS regions, including 5.8S rDNA, were amplified by PCR according to Sugita & Nakase (1999). The D1/D2 region of the 26S rDNA was amplified according to Kurtzman & Robnett (1997). PCR products were sequenced directly using an ABI Prism BigDye Terminator cycle sequencing ready reaction kit (Applied Biosystems) and analysed with an Applied Biosystems sequencer model 310 according to the manufacturer's instructions. Reference sequences used for the phylogenetic study were obtained from the DDBJ/GenBank/EMBL database. Sequences were aligned with those of related species using CLUSTAL W version 1.8 (Thompson *et al.*, 1994) and checked visually. Phylogenetic trees were constructed using the neighbour-joining method (Saitou & Nei, 1987). Evolutionary distances were calculated according to Kimura (1980). Sites where gaps existed in any sequences were excluded. Bootstrap analyses (Felsenstein, 1985) for the neighbour-joining method were performed from 100 random resamplings.

RESULTS AND DISCUSSION

Phylogenetic group I

The phylogenetic relationships among *C. laurentii* strains used in this study are shown in Fig. 1. Strains JCM 9066^T, CBS 318^T, CBS 942^T and JCM 9909 belong to phylogenetic group I. *Bulleromyces albus* Boekhout & A. Fonseca, *Bullera hanna* Hamamoto & Nakase, *Bullera pseudoalba* Nakase & Suzuki, *Bullera penniseticola* Takashima & Nakase and *Bullera unica* Hamamoto & Nakase were included in this cluster. The type strain of *C. laurentii*, JCM 9066^T, clustered with CBS 2174 and CBS 8648, as shown previously (Sugita *et al.*, 2000). Sequences of the ITS region and D1/D2 region of the 26S rDNA in CBS 2174 and CBS 8648 were identical, although three and one base differences, respectively, were detected between each of these two strains and JCM 9066^T. Physiological and biochemical characteristics were almost the same among them. Based on these results, CBS 2174 and CBS 8648 were classified as *C. laurentii*.

The type strain of *Torula flavescens*, CBS 942^T, belongs to phylogenetic group I and is thought to be distinct from *C. laurentii*. *Torula flavescens* was described by Saito in 1922 and was transferred to the genus *Torulopsis* as *Torulopsis flavescens* (Saito) Lodder in 1934, to *Cryptococcus flavescens* (Saito) Skinner in 1950 and then to *C. laurentii* var. *flavescens* (Saito) Lodder & Kreger-van Rij in 1952. Since the treatment by Rodrigues de Miranda (1984), this species has been viewed as a synonym of *C. laurentii*. As described previously, CBS 942^T is distinct from *C. laurentii* based on sequence analyses. Strain CBS 8645, a clinical isolate, and '*Cryptococcus nodaensis*' G60 showed high sequence similarity to CBS 942^T (99.1% for the D1/D2 region of 26S rDNA and 100% for overall ITS region) (Sugita *et al.*, 2000). It has been stated previously that CBS 942 and CBS 8645 are the same species as '*C. nodaensis*'; however, '*C. nodaensis*' is a *nomen invalidum* because no Latin description has been given (Sato *et al.*, 1999). CBS 8645 was identified as *C. flavescens*.

The ITS sequences of JCM 9909, 9910, 9911 and 9912, and the D1/D2 region of JCM 9909 were identical to those of *C. flavescens* CBS 942^T. The four former strains were isolated from wheat or corn and their mating was observed by Kurtzman (1973). Although these strains were reported to represent an anamorphic species because the complete life cycle was not determined, it is assumed that some morphological characteristics are similar to those of *Bulleromyces albus*. When the complete life cycle of these strains is observed, it will be described as a teleomorph of *C. flavescens*. In this paper, these strains have been identified as *C. flavescens* based on the results of sequencing analyses and physiological and biochemical properties.

The type strain of *Torula aurea*, CBS 318^T, belongs to phylogenetic group I and is thought to be distinct from *C. laurentii* and *C. flavescens*. *Torula aurea* was described by Saito in 1922, was transferred to *Chromotorula aurea* by F. C.

Table 1. Strains used in this study

Strain	Source	Co-Q*	G + C content (mol%)*
<i>Cryptococcus laurentii</i>			
JCM 9066 ^T (=ATCC 18803 ^T =CBS 139 ^T =MUCL 30398 ^T =NRRL Y-2536 ^T)	Palm wine; type strain of <i>Torula laurentii</i> Kufferath	Q-10 ^a	56.4 ^b , 59.0 ^c
CBS 2174	Tumour		54.7 ^b
CBS 8648	Lung		
<i>Cryptococcus aureus</i>			
CBS 318 ^T (=ATCC 32063 ^T =IFO 0372 ^T =NRRL Y-1582 ^T)	Atmosphere; type strain of <i>Torula aurea</i> Saito	Q-10 ^a	55.0 ^b
JCM 5945	Flower		
<i>Cryptococcus flaveszens</i>			
CBS 942 ^T (=ATCC 10668 ^T =DBVPG 6007 ^T =MUCL 30414 ^T)	Atmosphere; type strain of <i>Torula flaveszens</i> Saito	Q-10 ^d	57.2 ^b
JCM 9909 (=ATCC 26021=CBS 6473=IFO 1898=NRRL Y-7139)	Wheat	Q-10 ^d	58.9 ^d
JCM 9910 (=ATCC 26022=CBS 6475=NRRL Y-7371)	Wheat		
JCM 9911 (=ATCC 26023=CBS 6476=NRRL Y-7373)	Wheat		
JCM 9912 (=NRRL Y-7376)	Wheat		
CBS 8645 (=DBVPG 7166)	Cerebrospinal fluid of male AIDS patient with meningitis	Q-10 ^d	58.4 ^d
<i>Cryptococcus carnescens</i> CBS 973 ^T (=ATCC 32064 ^T =MUCL 30641 ^T =NRRL Y-1503 ^T)	Muscatel grape; type strain of <i>Torulopsis carnescens</i> Verona & Luchetti	Q-10 ^d	
<i>Cryptococcus peneaus</i> CBS 2409 ^T (=ATCC 13546 ^T =MUCL 30643 ^T =NRRL Y-2005 ^T)	Surface of shrimp; type strain of <i>Rhodotorula peneaus</i> Phaff <i>et al.</i>	Q-10 ^d	52.3 ^b , 51.2 ^c
<i>Cryptococcus</i> sp. CBS 2993 (=DBVPG 7158=MUCL 30644)	Bronchus of lung patient	Q-10 ^d	50.8 ^b
<i>Cryptococcus</i> sp. CBS 6578 (=MUCL 30680)	Sea water	Q-10 ^d	51.8 ^b
<i>Trimorphomyces papilionaceus</i>			
JCM 9899 (=MAFF 235184)	Associated with <i>Arthrinium</i> sp. on dead culm of <i>Sasa</i>		
JCM 11071	Dead culm of bamboo with <i>Arthrinium</i> sp.		
JCM 11072	Dead culm of bamboo with <i>Arthrinium</i> sp.		
CBS 200.94	Bamboo with <i>Arthrinium</i> sp.		

*Data from: *a*, Yamada & Kondo (1973); *b*, Vancanneyt *et al.* (1994); *c*, Nakase & Komagata (1971); *d*, this study.

Fig. 1. Neighbour-joining tree of *Cryptococcus laurentii* and related species based on sequences of 18S rDNA (a) and the D1/D2 region of the 26S rDNA (b). Evolutionary distances were calculated according to Kimura (1980). Numbers at nodes represent percentages from 100 replicate bootstrap samplings (frequencies less than 50% not shown). Sequences were retrieved from the DDBJ/GenBank/EMBL databases under the accession numbers indicated. *Trichosporon ovoides* was used as an outgroup.

Harrison in 1928 and then to *Rhodotorula aurea* by Lodder in 1934. Lodder & Kreger-van Rij (1952) considered this species to be a member of the *C. laurentii* complex. Phaff & Fell (1970) treated this species as a member of *C. laurentii* var. *flavescent*. Since no strains have been reported to be phylogenetically close to this one, it has been described as *Cryptococcus aureus* comb. nov. in this paper. JCM 5945, which was isolated from a flower and identified as *C. laurentii* (Tokuoka *et al.*, 1985), was reclassified as *C. aureus* based on identical ITS1 and ITS2 sequences and on physiological and biochemical properties.

Phylogenetic group II

Phylogenetic group II consisted of CBS 973^T, CBS 2409^T, CBS 2993 and CBS 6578. *Cryptococcus victoriae* (Montes *et al.*, 1999) also belongs to phylogenetic group II. This group constituted a cluster with *Bullera globispora* and *C. dimennae* in phylogenetic trees based on sequences of 18S rDNA and the D1/D2 region of the 26S rDNA. The type strain of *Rhodotorula peneaus*, CBS 2409^T, which was described by Phaff *et al.* (1952) and placed in *C. laurentii* var.

flavescent by Phaff & Fell (1970), was shown to be a distinct species. The name *Cryptococcus peneaus* comb. nov. is proposed for this strain.

Torulopsis carnescent was described by Verona & Luchetti (1936) and treated as a synonym of *C. laurentii* by Lodder & Kreger-van Rij (1952). Our previous paper (Sugita *et al.*, 2000) stated that the ITS region and D1/D2 region of the 26S rDNA of the type strain of this species, CBS 973^T, had sequences identical to those of *Trimorphomyces papilionaceus* Bandoni & Oberwinkler (AF075491, source strain CBS 445.92). When the 18S rDNA sequence of CBS 973^T was determined and analysed using a phylogenetic tree, the position of this strain was far from *Trimorphomyces papilionaceus* (AF053716, source strain RJB 75-9458-B). To resolve this conflict, attempts to determine the sequence and to confirm the morphology of CBS 445.92 were made but, unfortunately, a living culture could not be obtained. Strain CBS 200.94, labelled *Trimorphomyces papilionaceus*, had a D1/D2 region that was identical to sequence AF075491 (source strain CBS 445.92), but the distinct morphological characteristic 'papilionaceus' was not observed in this strain (G. Okada, personal communication). Recently, the

sequence data of AF075491 have been corrected using another strain (CBS 443.92). Whereas *Trimorphomyces papilionaceus* JCM 9899, JCM 11071 and JCM 11072 were

almost identical and differed by 12–13 bp from CBS 443.92 in the D1/D2 region of their 26S rDNA, these strains had more than 67 base differences when compared with

Table 2. Physiological and chemotaxonomic characteristics among the *C. laurentii* complex

Strains/species: 1, *C. laurentii* JCM 9066^T, CBS 2174 and CBS 8648; 2, *C. aureus* CBS 318^T and JCM 5945; 3, *C. flavescens* CBS 942^T, CBS 8645, JCM 9909, JCM 9910, JCM 9911 and JCM 9912; 4, *C. carnescens* CBS 973^T; 5, *C. peneaus* CBS 2409^T; 6, *C. victoriae* (data from Montes *et al.*, 1999); 7, *Cryptococcus* sp. CBS 2993; 8, *Cryptococcus* sp. CBS 6578. +, Positive; –, negative; L, latent; W, weak; LW, latent and weak; ND, no data; st, stimulative. All strains examined in this study can assimilate ammonium sulfate as a sole nitrogen source and are positive for production of starch-like substances, urease, Diazonium blue B complex and assimilation of glucose, galactose, sucrose, maltose, cellobiose, melibiose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, 2- and 5-ketogluconic acids and saccharate. All strains are negative for fermentation of glucose, acid production from glucose, liquefaction of gelatin and assimilation of methanol, hexadecane and 2,3-butanediol.

Characteristic	Phylogenetic group I			Phylogenetic group II				
	1	2	3	4	5	6	7	8
Assimilation of carbon compounds:								
L-Sorbose	–, LW	–	–, LW	–	L	–	–	–
Trehalose	+	+	+	+	+	+	L	+
Lactose	+	+	+	+	+	+	L	+
Inulin	–	LW	–	–	–	+	–	–
D-Arabinose	+	+	+	L	L	+	LW	+
D-Ribose	+	+	+	L	+	L	L	L
L-Rhamnose	+	–, +	+	L	+	+	L	L
D-Glucosamine	+	L, LW	–	L	+	–	L	–
N-Acetyl-D-glucosamine	+	L, +	–	W	+	–	+	–
Ethanol	+, L	–, L	+	–	–	–	–	–
Glycerol	+, L	LW, +	+, –	L	L	L	LW	L
Erythritol	+	–, L	+, L	L	+	+	L	L
Ribitol	+	+	+	+	+	+	LW	L
Galactitol	+	L, +	+	+	+	+	L	+
D-Mannitol	+	+	+	+	+	+	L	L
D-Glucitol	+	+	+	+	+	+	L	L
Methyl α -D-glucoside	+	L, +	+, L	+	+	+	+	+
Salicin	+, W	L, +	+	+	+	+	+	+
Glucono- δ -lactone	+	–, +	+	–	L	–	–	–
D-Gluconate	+	L, +	+	+	+	+	L	+
DL-Lactic acid	+, W	–	W	LW	–	–	–	–
Succinic acid	+	L, +	+	+	+	+	+	L
Citric acid	+	L, +	+, W	L	L	+	+	–
Inositol	+	+	+	L	+	+	+	L
Xylitol	+	+	+	+	+	+	+	L
L-Arabinitol	+	+	+	+	+	L	LW	L
1,2-Propanediol	–	–	LW, +	–	–	–	–	–
D-Glucuronic acid	+	+	+	+	+	+	L	+
D-Galacturonic acid	+	LW, +	+	+	+	+	L	+
Assimilation of nitrogen compounds:								
Potassium nitrate	–	–	–	–	–	+	–	–
Sodium nitrite	–	–	+	+	+	–	+	L
Ethylamine hydrochloride	+	+	+	+	+	–	+	–
L-Lysine hydrochloride	+	+	+	+	+	L	+	L
Cadaverine dihydrochloride	+	+	+	+	+	–	+	–
Vitamins required	Thiamin	Thiamin	None	Thiamin	Thiamin	None	Thiamin (st)	Thiamin
Maximum growth temperature (°C)	34–35	30–33	30–35	28–29	30–31	ND	29–30	29–30
Growth on 50 % (w/w) glucose/yeast extract agar	–	–	W, –	–	–	–	–	–
Hydrolysis of fat	–	–	–	–	–	ND	+	–

CBS 973^T. CBS 973^T apparently does not belong to *Trimorphomyces papilionaceus*.

It is very interesting that the 18S rDNA of CBS 973^T was identical to that of '*Taphrina*' *maculans* in the database (AB000953, source strain CBS 427.69). Sjamsuridzal *et al.* (1997) assumed that this strain might have been misidentified as *Taphrina* based on morphological, chemotaxonomic or physiological and biochemical characteristics, in addition to the sequence analysis. Since '*Taphrina*' *maculans* CBS 427.69 is not available for distribution from the CBS, this strain has not been compared with CBS 973^T in our laboratory, but it is assumed that CBS 973^T, '*Taphrina*' *maculans* CBS 427.69 and '*Taphrina*' *californica* CBS 374.39 (Sjamsuridzal *et al.*, 1997) are closely related strains.

The morphological, physiological and biochemical characteristics of CBS 973^T closely matched those of *Torulopsis carnescentis* described by Verona & Luchetti (1936), although lactose was not assimilated according to their description. In this paper, CBS 973^T is described as *C. carnescentis* as enough data were obtained to confirm the identity of this strain. The taxonomic position of '*Taphrina*' *maculans* CBS 427.69 and '*Taphrina*' *californica* CBS 374.39 should be studied further.

Recently, Vishniac (2002) proposed two species, *Cryptococcus heimaeyensis* and *Cryptococcus tephrensensis*, for isolates from Iceland. *C. heimaeyensis* was phylogenetically closely related to CBS 2993 and *C. tephrensensis* was closely related to CBS 6578. CBS 2993 was isolated from bronchus of a lung patient in France by G. Cochet (strain no. 237) and CBS 6578 was isolated from sea water by J. W. Fell (ML 24-237); these two strains were respectively deposited in the CBS in November 1957 and March 1972. Both strains were tentatively identified as *C. laurentii* and kept in the CBS. Since only two and three base differences, respectively, were detected in the D2 regions of 26S rDNA in the former and latter pair, DNA–DNA reassociation experiments will be necessary to confirm the taxonomic positions of CBS 2993 and CBS 6578.

As shown in Table 2, the physiological and biochemical characteristics of the various species in the *C. laurentii* complex are very similar, but members of phylogenetic group I are distinguishable by the combination of assimilation patterns of D-glucosamine, N-acetyl-D-glucosamine, DL-lactic acid, 1,2-propanediol and sodium nitrite and vitamin requirements. *C. carnescentis*, *C. peneaus* and *C. victoriae* could be differentiated by assimilation patterns of L-sorbose, inulin, D-glucosamine, N-acetyl-D-glucosamine, glucono-δ-lactone, DL-lactic acid, potassium nitrate, sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride. *Cryptococcus* sp. CBS 2993 could hydrolyse fat, indicating that this is a unique strain within the *C. laurentii* complex.

In this study, several species were identified as members of

the genus *Cryptococcus*, although they should be reclassified into other appropriate genera in the future because they are considerably phylogenetically distant from *Cryptococcus neoformans* (type species of the genus) (Fell *et al.*, 2000; Takashima & Nakase, 1999).

Taxonomic treatment

Cryptococcus laurentii (Kufferath) C. E. Skinner, in *Am Midl Nat* 43, 249 (1950).

≡ *Torula laurentii* Kufferath, in *Ann Soc R Sci Méd Nat Brux* 74, 45 (1920).

≡ *Torulopsis laurentii* (Kufferath) Lodder, in *Verh K Ned Akad Wet Afd Natuurkd Sect II* 32, 160 (1934).

≡ *Rhodotorula laurentii* (Kufferath) Hasegawa, Banno & Yamauchi, in *J Gen Appl Microbiol* 6, 212 (1960).

Cryptococcus aureus (Saito) Takashima, Sugita, Shinoda & Nakase comb. nov.

≡ *Torula aurea* Saito, in *Mitt Jpn J Bot* 1, 44 (1922).

≡ *Chromotorula aurea* (Saito) F. C. Harrison, in *Trans R Soc Can Sect V* 22, 202 (1928).

≡ *Rhodotorula aurea* (Saito) Lodder, in *Verh K Ned Akad Wet Afd Natuurkd Sect II* 32, 125 (1934).

Type strain: CBS 318^T (=ATCC 32063^T=IFO 0372^T=NRRL Y-1582^T).

Cryptococcus flavescens (Saito) C. E. Skinner (1950).

≡ *Torula flavescens* Saito, in *Mitt Jpn J Bot* 1, 43 (1922).

≡ *Torulopsis flavescens* (Saito) Lodder, in *Verh K Ned Akad Wet Afd Natuurkd Sect II* 32, 166 (1934).

≡ *Cryptococcus laurentii* (Kufferath) C. E. Skinner var. *flavescens* (Saito) Lodder & Kreger-van Rij in '*The Yeasts, a Taxonomic Study*', p. 381 (1952).

Cryptococcus carnescentis (Verona & Luchetti) Takashima, Sugita, Shinoda & Nakase comb. nov.

≡ *Torulopsis carnescentis* Verona & Luchetti, in *Boll Reg Inst Super Agrar Pisa* 280 (1936).

Type strain: CBS 973^T (=ATCC 32064^T=MUCL 30641^T=NRRL Y-1503^T).

Cryptococcus peneaus (Phaff, Mrak & Williams) Takashima, Sugita, Shinoda & Nakase comb. nov.

≡ *Rhodotorula peneaus* Phaff, Mrak & Williams, in *Mycologia* 44, 438 (1952).

Type strain: CBS 2409^T (=ATCC 13546^T=MUCL 30643^T=NRRL Y-2005^T).

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