

1 Microbial Systematics (Short Communication)

2
3 **The Generic Circumscription of *Eremothecium* emend. Kurtzman**

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20 **Keywords:** *Crebrothecium ashbyi*; *Nematospora coryli*; *Eremothecium cymbalariae*;
21 *Ashbya gossypii*; *Holleya sinecauda*.

22
23 **Abstract**

24 In the family Eremotheciaceae, the only genus *Eremothecium* emend. Kurtzman included
25 five species. However, the calculated pair-wise sequence similarities were very low (93.8-
26 96.8%) among the five species, indicating that the emended genus was not taxonomic
27 homogeneous-natured. Therefore, it is adequate to accommodate the five species to their
28 own separate five genera.

29 **Supplementary Abstract**

The subfamily Eremothecioideae

Genus I *Eremothecium* sensu stricto *Eremothecium cymbalariae* Borzi (1888)

Genus II *Nematospora* *Nematospora coryli* Peglion (1897)

Genus III *Ashbya* *Ashbya gossypii* (Ashby et Nowell) Guillielmond (1928)

Genus IV *Crebrothecium* *Crebrothecium ashbyi* Routien (1949)

Genus V *Holleya* *Holleya sinecauda* (Holley) Yamada (1986)

The family Eremotheciaceae

Genus *Eremothecium* emend. *Eremothecium cymbalariae* Borzi (1888)

Eremothecium coryli (Peglion) Kurtzman (1995)

Eremothecium gossypii (Ashby et Nowell) Kurtzman (1995)

Eremothecium ashbyi (Guillielmond) Kurtzman (1995)

Eremothecium sinecaudum (Holley) Kurtzman (1995)

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31 The genus *Holleya* was introduced based on the exceptional distribution of
32 ubiquinone-9 (Q-9) as a respiratory quinone in the species, *Holleya sinecauda* (= *Nematospora sinecauda* Holley) (Yamada 1986).
33
34

35 On the phylogenetic analysis based on the partial base sequencing (Yamada and
36 Nagahama 1991), *Holleya sinecauda* represented considerable base differences (seven
37 bases) from *Nematospora coryli* (Q-5 or Q-6; Yamada et al. 1977, 1981) in positions 1451
38 -1618 (168 bases) of the 18S rRNA, demonstrating that the genus *Holleya* was
39 phylogenetically separable from the genus *Nematospora*. Incidentally, the base differences
40 were only four between *Nematospora coryli* and *Saccharomyces cerevisiae* and eight
41 between *Holleya sinecauda* and *Saccharomyces cerevisiae*.
42

43 On the other hand, Kurtzman (1995) compared the genera *Ashbya*, *Eremothecium*,
44 *Holleya* and *Nematospora* by use of the 580 base-sequences near the 5' end of 26S rDNA.
45 The experimental results showed that the four genera were closely related and the taxa was
46 little divergence. As a conclusion, all the species concerned were placed in the single
47 genus *Eremothecium* emend. Kurtzman.
48

49 This paper deals with the sequence data proposed by Kurtzman (1995) and gives the
50 different conclusion that the four genera (or five genera) are not closely related but
51 phylogenetically independent from one another and constitute their taxonomic
52 homogeneous-natured taxa.
53

54 The first of all, the pair-wise sequence similarities were calculated among the five
55 species. The calculated similarities were 93.8-96.8%, which did not exceed 98% or more
56 (Table 1). For example, the phylogenetic relationship was 98.1% between *Octosporomyces*
57 *octosporus* (= *Schizosaccharomyces octosporus*, Schizosaccharomycetaceae) and
58 *Octosporomyces osmophilus* (= *Schizosaccharomyces osmophilus*) in the 26S rRNA gene
59 D1/D2 domain sequences (Huong et al. 2022a), was 98.0% between *Kockiozyma*
60 *suomiensis* and *Myxozyma geophila* (Lipomycetaceae) (Yamada et al. 2022) in the same
61 sequence region, and were 98.7-99.5% between *Kockiozyma suomiensis* and the related
62 *Myxozyma* species in the 18S rRNA gene sequences (Huong et al. 2022b). The 98% or
63 more is assumed to be one of the most important markers to designate the taxonomic
64 homogeneous-natured genus.
65

66 For example, the calculated sequence similarity between *Holleya sinecauda* and
67 *Eremothecium cymbalariae* was 94.8%, which was much lower than that (95.7%) between
68 *Dipodascopsis uninucleata* and *Lipomyces starkeyi* (Yamada et al. 2022). In addition, the
69 similarity (95.2%) between *Holleya sinecauda* and *Nematospora coryli* was almost the
70 same as that (95.2%) between *Waltomyce lipofer* and *Lipomyces starkeyi*.
71

72 As described above, the five species assigned to the genus *Eremothecium* emend.
73 Kurtzman were adequate to be classified into five genera respectively, as once done by
74 classical yeast taxonomists. The five species were uniquely equipped with chemotaxo-
75 nomically complicated isoprenoid quinone homologues (Q-5, Q-6, Q-7 and Q-9, Yamada
76 et al. 1977, 1981, 1987) and with morphologically very complicated needle-shaped
77 ascospores, in contrast to other members (Q-6) of the family Saccharomycetaceae. To
78 distinguish the taxonomic small and unique group, the subfamily Eremothecioideae rather
79 than the family Eremotheciaceae was appropriately given (Kurtzman 1995, 2011).

80
81 The subfamily Eremothecioideae subfam. nov., the family Saccharomycetaceae

82
83 Genus I *Eremothecium* Borzi MB1883
84 *Eremothecium cymbalariae* Borzi (1888) MB235811
85 Q-7(Q-6)-equipped.

86
87 Genus II *Nematospora* Peglion MB3441
88 *Nematospora coryli* Peglion (1897) MB222583
89 Synonym: *Eremothecium coryli* (Peglion) Kurtzman (1995)
90 Q-6-equipped (Q-5 only in the type strain).

91
92 Genus III *Ashbya* Guillielmond MB389
93 *Ashbya gossypii* (Ashby et Nowell) Guillielmond (1928) MB266255
94 Synonym: *Eremothecium gossypii* (Ashby et Nowell) Kurtzman (1995)
95 Q-6-equipped.

96
97 Genus IV *Crebrothecium* Routien MB1283
98 *Crebrothecium ashbyi* Routien (1949) MB266255
99 Synonym: *Eremothecium ashbyi* (Guillielmond) Kurtzman (1995)
100 Q-6(Q-7)-equipped.

101
102 Genus V *Holleya* Yamada MB25105
103 *Holleya sinecauda* (Holley) Yamada (1986) MB131133
104 Synonym: *Eremothecium sinecaudum* (Holley) Kurtzman (1995)
105 Q-9(Q-8)-equipped.

106
107 As described above, the five species classified in the subfamily Eremothecioideae
108 were unique in the complicated distribution of isoprenoid quinone homologues and the
109 complicated needle-shaped ascospore distribution within the subfamily, in contrast to the
110 family Saccharomycetaceae (Q-6). The complex distribution of isoprenoid quinone
111 homologues in the genus *Eremothecium* emend. was reasonable, since the emended genus
112 was not so taxonomic homogeneous-natured.

113

114 Kurtzman and Robnett (1998) described that the ascus morphology, ascospore
115 ornamentation and composition of coenzyme Q were unreliable predictors of kinship in
116 the paraphyletic genus *Dipodascopsis*. Of the three, the coenzyme Q homologues or the
117 ubiquinone homologues play an important role as taxonomic markers. Of the remaining
118 two, the ascus morphology and the ascospore ornamentation gave valuable taxonomic
119 information in the five species.

120

121 The type strain of *Nematospora coryli* showed Q-5 (Yamada et al. 1981). The other
122 strains examined did Q-6. According to the present author's experiences, such an
123 exceptional distribution of ubiquinone homologues has been restricted to only one species
124 and one strain. Therefore, the isoprenoid quinone homologues have been widely utilized
125 as important microbial taxonomic criteria for Gram-negative and Gram-positive bacteria
126 and also yeasts and fungi.

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Table 1. The pair-wise sequence similarity in *Eremothecium* and related species.

Species	1	2	3	4	5
1. <i>Ashbya gossypii</i>					
2. <i>Crebrothecium ashbyi</i>	94.8				
3. <i>Eremothecium cymbalariae</i>	96.2	96.6			
4. <i>Nematospora coryli</i>	95.7	94.7	96.2		
5. <i>Holleya sinecauda</i>	93.8	94.3	94.8	95.2	
6. <i>Saccharomyces cerevisiae</i>	88.8	88.6	88.4	86.9	86.7

All were the type strains or the authentic strains in the respective species (Kurtzman 1995).
 The calculated sequence similarity (%) was based on the 26S rDNA (positions 63-642, 580
 bases).

177 The original data of base substitution rates were cited from Kurtzman (1995).
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