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# The Generic Circumscription of *Eremothecium* emend. Kurtzman

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## Abstract

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

## 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) |

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

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

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

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

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

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

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

The subfamily Eremothecioideae subfam. nov., the family Saccharomycetaceae

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

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

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

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

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

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

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

The type strain of *Nematospora coryli* showed Q-5 (Yamada et al. 1981). The other strains examined did Q-6. According to the present author's experiences, such an exceptional distribution of ubiquinone homologues has been restricted to only one species and one strain. Therefore, the isoprenoid quinone homologues have been widely utilized as important microbial taxonomic criteria for Gram-negative and Gram-positive bacteria 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. *Ashbya gossypii* | | | | | |
| 2. *Crebrothecium ashbyi* | 94.8 | | | | |
| *3. Eremothecium cymbalariae* | 96.2 | 96.6 | | | |
| 4. *Nematospora coryli* | 95.7 | 94.7 | 96.2 | | |
| 5. *Holleya sinecauda* | 93.8 | 94.3 | 94.8 | 95.2 | |
| 6. *Saccharomyces cerevisiae* | 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).
The original data of base substitution rates were cited from Kurtzman (1995).