

***Babjevia* gen. nov. – a new genus of the Lipomycetaceae**

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Abstract

The species described as *Lipomyces anomalus* Babjeva & Gorin shows significant genetic and phenotypic divergence from the type species *Lipomyces starkeyi* Lodder & Kreger-van Rij in terms of rRNA base sequence substitution and ascosporal and septal ultrastructure. The species is consequently reclassified in the new, unispecific genus *Babjevia*, as *Babjevia anomala*.

Introduction

Babjeva & Gorin (1975), during a study of yeasts associated with podzolic soils of the northern taiga subzone in Russia, recovered strains of an undescribed species, which, because of its formation of attached, multispored, saccate asci, they regarded as representative of the genus *Lipomyces* Lodder & Kreger-van Rij (1952). Nevertheless, they stressed the fact that the new species differed from the type species, *L. starkeyi* Lodder & Kreger-van Rij (1952), by the formation of non-encapsulated cells, pseudophyphal cell-aggregates and pulvinate colonies on solid substrates. The new species also had a lower optimal growth temperature and utilized relatively few carbon sources. In view of these deviating characters, the species was described as *L. anomalus* Babjeva & Gorin (1975).

Comparative rRNA base sequence analysis by Yamada & Nogawa (1990) and Kurtzman & Liu (1990) of the type strains of *L. anomalus*, *L. kononenkoae*, *L. lipofer*, *L. starkeyi* and *L. tetrasporus*, have, however, established that *L. anomalus* diverges from the other four species by disproportionate differences in the nucleotide substitutions in its 18S, 25S and 26S subunits. Yamada & Nogawa (1990) also reported that in the respective 18S rRNA regions (positions 1451–1618), *L. kononenkoae*, *L. lipofer*, *L. tetrasporus*, and

L. starkeyi were consistently characterized by the fingerprint sequence UUA, and *L. anomalus* by the deviating sequence, UAAUCUA. Given this genetic divergence, Yamada & Nogawa (1990) concluded that *L. anomalus* could be assigned to a separate genus.

Re-examination of the three available strains of *L. anomalus* confirmed that it not only differs significantly from the type species, *L. starkeyi*, in its cultural, morphological, reproductive and generative characters but has many properties in common with species of the genus *Dipodascopsis* Batra & Millner (Batra 1978). On solid substrates, *L. anomalus*, like *D. uninucleata* (Biggs) Batra & Millner and *D. tothii* (Zsolt) Batra & Millner, forms butyrous, raised, restricted and more or less pulvinate colonies, unlike the viscous, confluent growth of *L. starkeyi* and other members of the genus. The relationship with *Dipodascopsis* is also supported by its formation of short hyphal units with open, centrally located septal pores (Figs 1a, b, c), different from the micropores observed in *L. starkeyi* (Fig. 1d) and further by the aspirin-sensitive production of arachidonic acid metabolites (Kock et al. 1992) – two characters not observed in *Lipomyces*. Like the allantoid ascospores of *Dipodascopsis*, the globose to ellipsoid ascospores of *L. anomalus* are hyaline, lacking the amber colour characteristic of *Lipomyces* species.

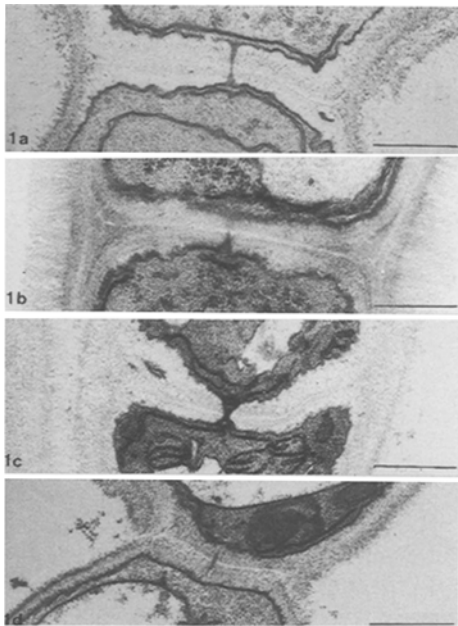


Fig. 1. Transmission electron micrographs of septa with open pores in a. CBS 6740 *L. anomalus*; b. CBS 190.37 *D. uninucleata*; CBS 759.85 *D. tothii*; and with microspore in d. CBS 1807 *L. starkeyi*. Bars represent 0,5 μm (Fixation: 2% KMnO_4).

Ultrastructurally, as revealed by transmission electron microscopy, the ascospores of *L. anomalus* differ fundamentally from those of *Lipomyces* and *Dipodascopsis*. The spores of *L. anomalus* appear glabrous, but the ascospore wall is atypical in consisting of a single, dark, electron-opaque layer (Fig. 2a), lacking the lighter, electron-translucent inner layer which, as a rule, characterizes the ascospore wall of ascomycetous yeasts (Fig. 2d). These unusual ascospores may sometimes be surrounded by a membrane, possibly of endoplasmic origin (Figs 2b, c). This phenomenon could account for the report by Babjeva & Gorin (1975) that the spores of this species are associated with an 'exosporium'.

Given the genetic divergence and phenotypic differences that distinguish *L. anomalus* from the type species of *Lipomyces* and *Dipodascopsis*, the proposal of Yamada & Nogawa (1990) is followed by classifying *L. anomalus* in a new genus:

Babjevia Van der Walt & M.Th. Smith, gen. nov. (Lipomycetaceae)

Coloniae butyrosae pulvinatae restrictae. Status vegetativus dimorphus, ex hyphis brevibus septatis poris septalibus singulis apertis centralibus praeditis, et

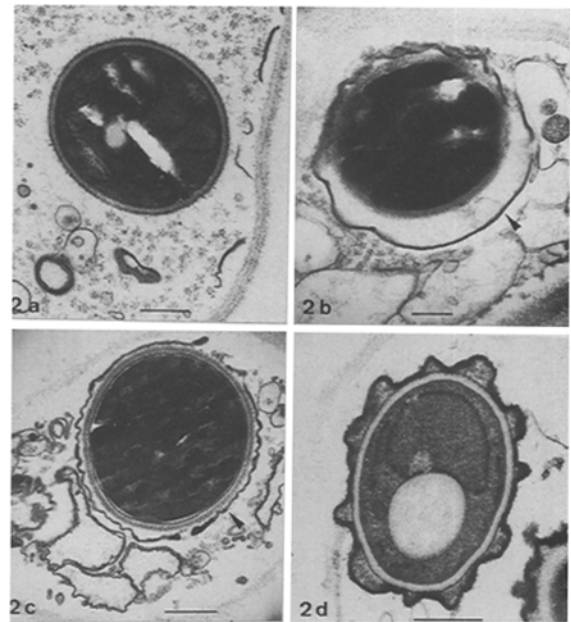


Fig. 2. Transmission electron micrographs of a. CBS 6740 *L. anomalus*. Ascospore with single layered wall; b. CBS 6740 and c. CBS 7606 *L. anomalus*. Ascospores surrounded by endoplasmic membranes (arrows); d. CBS 1807 *L. starkeyi*. Ascospore wall consisting of light inner layer and dark outer layer. Bars represent 0,5 μm (Fixation 2% KMnO_4).

cellulis zymoticis multilateraliter gemmantibus, constans. Asci affixi, saccati, uni- vel multispori. Ascosporae hyalinae, globosae velle ellipsoideae, glabrae, pariete unistrato. Imidazole pro fonte nitrogeni utens.

Colonies butyrous, pulvinate, restricted. Vegetative state dimorphic, composed of short, septate hyphae with single, open, central pores, and multilaterally budding yeast cells. Asci saccate, attached, one- to multisporous. Ascospores hyaline, globose to ellipsoid, smooth with a single-layered wall. Imidazole is utilized as source of nitrogen.

Typus: *Babjevia anomala* (Babjeva & Gorin) Van der Walt & M.Th. Smith comb. nov. (Basionym: *Lipomyces anomalus* Babjeva & Gorin in Antonie van Leeuwenhoek 41: 186: 1975).

The genus is named for Prof. Dr. Inna P. Babjeva, in recognition of her services to yeast systematics.

Although Yamada & Nogawa (1990) and Kurtzman & Liu (1990) did not include *Dipodascopsis* species in their studies, it can be anticipated that rRNA base sequence analyses will confirm the postulated connexion between *Babjevia* and *Dipodascopsis*. While the segregation *Babjevia* imparts greater homogeneity

to *Lipomyces*, it also calls for a re-evaluation of the genus *Waltomyces* Yamada & Nakase (1985) based on *L. lipofer*. Since, (a) the comparative data of Yamada & Nogawa (1990) and Kurtzman & Liu (1990) established that the type strain of *L. lipofer* shows no disproportionate differences in its rRNA base substitutions, and (b) the criteria originally adopted for the demarcation of the genus (differences in ascospore topography and ubiquinone isoprenologue composition) no longer serve for generic differentiation in the Lipomycetaceae (Van der Walt 1992), the segregation of *Waltomyces* from *Lipomyces* does not seem justified.

The more recently described species, *L. japonicus* Van der Walt et al. (1989), not dealt with by either Yamada & Nogawa (1990) or Kurtzman & Liu (1990), is excluded from *Babjevia* in terms of its (a) typically double-layered, ascomycetous ascospore wall (Van der Walt et al. 1989), and (b) characteristic 18S rRNA UUA fingerprint sequence in the 1488–1491 position (Y. Yamada, 1994; personal communication).

Lipomyces consequently comprises the currently known species, *L. japonicus*, *L. kononenkoae*, *L. lipofer*, *L. starkeyi* and *L. tetrasporus*.

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