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

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Received 9 December 1993; accepted in revised form 29 March 1994

**Key words: Babjevia anomala, Lipomycetaceae, yeast taxonomy**

**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 ascosporous 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 sub-zone in Russia, recovered strains of an undescribed species, which, because of its formation of attached, multisporous, 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.
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 ascosporal 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 ascosporal 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:

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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 multispor. Ascopores hyaline, globose to ellipsoid, smooth with a single-layered wall. Imidazole is utilized as source of nitrogen.


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