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64

Septal micropores in *Zygozyma* and their taxonomic significance

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Abstract

Septal micropores or plasmadesmal canals have been observed in two species of the lipomycetaceous genus *Zygozyma*. The presence of these canals is considered as further evidence for the connexion between the Lipomycetaceae and the Dipodascaceae. The genus *Zygozyma* has been emended.

Introduction

Within the Endomycetales Gäumann, the Lipomycetaceae Novák & Zsolt emend Van der Walt et al. (1987) constitutes a well-defined, but highly diversified family. It is, nevertheless, easily recognized by its conidial states which are characterized by

- an essentially ascomycetous cell-wall, and holoblastic budding by non-hyphal species,
- copious formation of amyloid material which colours blue green with iodine, and
- as a rule, viscous colonies on solid substrates.

While this family has no obvious relations in the Euascomycetes (Von Arx & Van der Walt 1987), it does appear to be connected to the family of the Dipodascaceae Gäumann in terms of its monosaccharide composition of whole cells (Weijman & Van der Walt 1989). In the present communication further evidence for this phylogenetic relationship is presented, based on ultrastructural spetal features in two species of the genus *Zygozyma*, *Z. oligophaga* Van der Walt & Von Arx (Van der Walt et al. 1987) and *Z. smithiae* Van der Walt et al. 1990b).

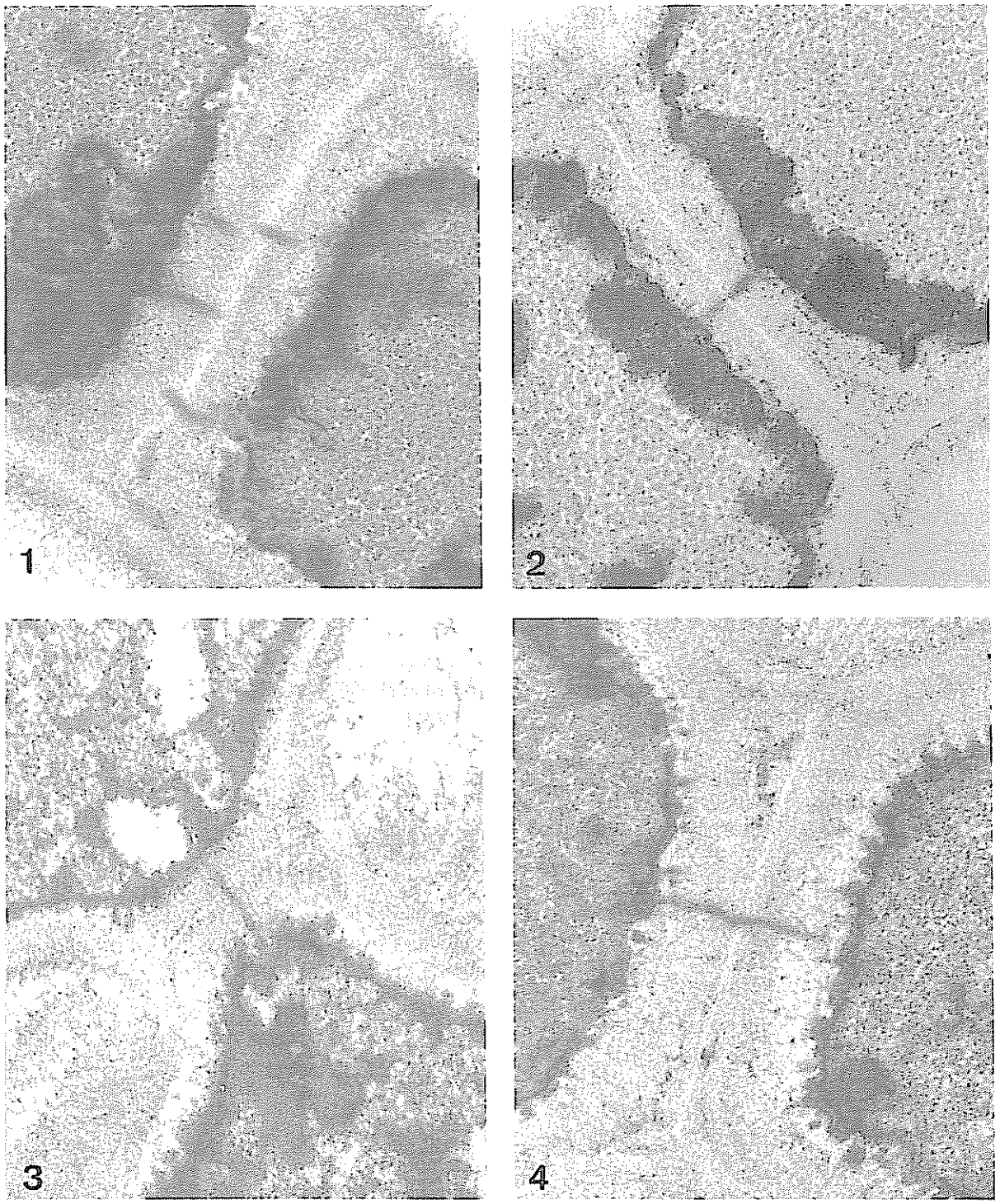
Materials and methods

Strains studied

The strains studied are held by the Yeast Division of the Centraalbureau voor Schimmelcultures in Delft (The Netherlands).

Zygozyma oligophaga	*Zygozyma smithiae*
CBS 7107 T	CBS 7407 T
CBS 7406	CBS 7408

For details of the strains, the publications covering their description may be consulted (Van der Walt et al. 1987, 1990b).



Figs 1–4. Transmission electron micrographs of septa with plasmadesmal canals (50.000X).
(1) *Zygozyma smithiae* CBS 7407 Type strain. (2) *Zygozyma smithiae* CBS 7408. (3) *Zygozyma oligophaga* CBS 7107 Type strain. (4) *Zygozyma oligophaga* CBS 7406.

Transmission electron microscopy

Observations by TEM were based on material from the strains cultured on potato-glucose-agar (*Z. oligophaga*) and 2% malt agar (*Z. smithiae*) at 18–20° C. Material was fixed in 1,5% aqueous potassium permanganate as described by Smith & Batenburg-van der Vegte (1986) and Van der Walt et al. (1983).

Results

Evidence for the formation of septal micropores or plasmadesmal canals (Tsuneda & Murakami 1989) by both *Z. smithiae* and *Z. oligophaga* is shown in Figs 1, 2, 3 and 4. These canals are, nonetheless, not abundant. In the case of *Z. smithiae* up to three canals per septum were found, but as a rule only one, suggestive of a so-called 'closure line'. In *Z. oligophaga* only single canals, some not centrally located, were observed.

Discussion and conclusions

The low numbers of plasmadesmal canals observed per septum in *Z. smithiae* and *Z. oligophaga* might relate to the restricted surface area of the septa which is small. The septa are not obvious by light microscopy. Their sparsity notwithstanding, the presence of these canals in *Z. smithiae* and *Z. oligophaga* establishes that these two species are, in fact, characterized by a rudimentarily hyphal phase. Given the definitive value of plasmadesmal canals in the demarcation of the Dipodascaceae and their anamorphs in *Geotrichum* Link: Fr. (De Hoog et al. 1986; Van der Walt et al. 1983), the presence of such canals in *Z. smithiae* and *Z. oligophaga* consequently provides further ultrastructural evidence for the postulated connexion between the Lipomycetaceae and the Dipodascaceae (Weijman & Van der Walt 1989).

Irrespective of the close agreement in their reproductive structures which serve for multiplication, dispersal and survival, and habitat (Van der Walt et al. 1990b), *Z. oligophaga* and *Z. smithiae*, nevertheless, differ by their respective Coenzyme Q8 and Q9 systems. Since variation in Coenzyme Q systems has already been observed within both yeast and higher fungal species (Yamada et al. 1981; Kuraishi et al. 1985), this biochemical property cannot be considered as generically-definitive in the natural demarcation of *Zygozyma*. The earlier classification of *Z. smithiae* and *Z. arxii* Van der Walt et al. (1990a) consequently requires that the genus be emended as follows:

Zygozyma Van der Walt & Von Arx emend. Van der Walt & M.Th. Smith.

Colonies watery, becoming viscous to glutinous. Cells hyaline, encapsualted, reproducing as a rule by multilateral budding, occasionally by rudimentary septation with the formation of plasmadesmal canals. Asci saccate, one- to multispored, evanescent, arising from enlarging evaginations of single cells, from conjugating cells, or direct transformation of cells. Ascospores allantoid to cymbiform, smooth, amber-coloured, conglutinative when liberated. Amyloid colouring blue-green with iodine, formed.

The genera *Zygozyma* and *Dipodascopsis* Batra & Millner show filiation by their agreement in ascosporal shape and size, dispersal by insects (Van der Walt et al. 1987) and the formation of plasmadesmal canals, which in *Dipodascopsis* have previously been interpreted as 'closure lines' (Kreger-van Rij & Veenhuis 1974). This connexion might not be that close, since mtDNA analyses data presented by Lodolo et al. (1990) unexpectedly suggest the insect-associated, hyphal species, *Dipodascopsis uninucleata* (Biggs) Batra & Millner, to be more nearly related to the soil-borne, budding species, *Lipomyces starkeyi* Lodder & Kreger-van Rij and *Waltomyces lipofer* (Lodder & Kreger-van Rij ex Slooff) Yamada & Nakase, than to *Z. oligophaga* itself. Should such data permit unequivocal inferences to the genealogy of the Lipomycetaceae, the results submitted by Lodolo et al. (1990) suggest rather unusual phylogenetic connexions within this family.

It should, in conclusion, be noted that the genera

Lipomyces Lodder & Kreger-van Rij and *Waltomyces* Yamada & Nakase are currently distinguished by differences in Coenzyme Q composition, and ascosporal topography (Yamada & Nakase 1985; Yamada et al. 1986). In view of the situation which obtains in *Zygozyma*, these two taxa need to be re-evaluated in terms of more fundamental differences in their ascosporal structure.

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