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# Intra- and interspecific diversity of ultrastructural markers in *Scedosporium*

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ABSTRACT

Ultrastructural features of conidia, lateral walls of aerial and submerged hyphal cells, and of septal pore apparatus of *Scedosporium apiospermum*, *S. boydii*, *Pseudallescheria angusta* and *Scedosporium aurantiacum* were studied. Submerged hyphal cells possessed a thick extracellular matrix. Crystalline satellites accessory to the septal pore apparatus were revealed. Fundamental ultrastructural features appeared to be heterogeneous at low taxonomic levels. The closely interrelated members of the *S. apiospermum* complex showed quantitative ultrastructural variability, but the unambiguously different species *S. aurantiacum* deviated qualitatively by markers of conidial wall structure, Woronin bodies morphology and presence/absence of crystalline satellites of the septal pore apparatus.

## Introduction

Ultrastructure of conidial wall relations and septal pore apparatus hyphal cells differ significantly between major groups of fungi and have extensively been used as primary characters to define higher taxa (Suh & Sugiyama 1993; Ho & Hyde 2004; Healy *et al.* 2013). In recent decades the role of ultrastructural markers has largely been taken over by molecular phylogeny. Quite significantly, however and in contrast to phenotypic characters such as microscopic morphology or physiology, the taxonomic value of Transmission Electron Microscopy (TEM) studies has never been falsified by more recent approaches. Although neglected, they are still useful as markers of diversity, supporting main traits in phylogeny (Moore 1996). On the other hand, molecular methods have led to more precision at all taxonomic levels, and corrected the taxonomy e.g. of groups that appeared to be dramatically polyphyletic, such as *Sporothrix* (de Beer *et al.* 2006). Therefore it may be useful to reconsider the validity and diagnostic power of TEM. In the present study we will focus on lower taxonomic levels, to establish variance and reproducibility of selected TEM markers. This is done with members of *Scedosporium*, a genus of common opportunists causing a wide spectrum of diseases in humans (Cortez *et al.* 2008; de Hoog *et al.* 2014). The name *Pseudallescheria* has been in use for the sexual state of this group of fungi, but this has been replaced by *Scedosporium for the*

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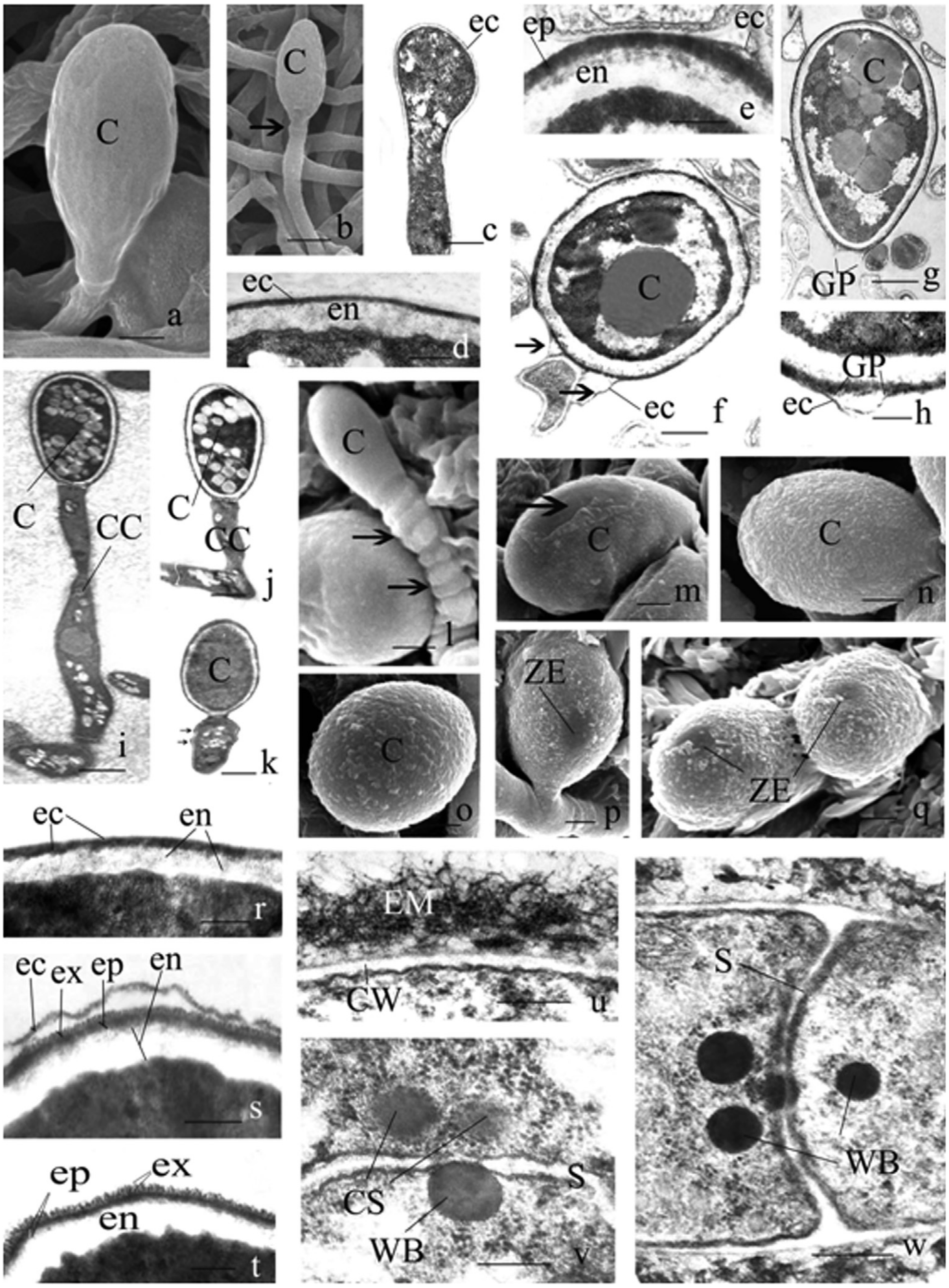

**Fig 1 – Scanning (a, b, l–q) and transmission (c–k, r–w) electron microscopy of *S. apiospermum* (a–k), *S. aurantiacum* (l–q, r–t), *S. boydii* (u, w) and *P. angusta* (v). a–i. RCPFF 1491/1057; j, k. RCPFF 1490/712; m. CBS 116910; l, n, p, q. CBS 136046; r–t. CBS 136047; u. CBS 117432; v – CBS 254.72; w – CBS 301.79. Scale bars: a, b, l–q = 1 μm; c, f, g, i–k = 0.5 μm; d, e, h, r–t, v, w = 0.3 μm; u = 1.5 μm. Abbreviations used: C = conidium, CC = conidiogenous cell, CS = crystalline satellite, CW = cell wall, ec = ectosporium, EM = extracellular matrix, en = endosporium, ep = episporium, ex = exosporium, GP = germ pore, S = septum; WB = Woronin body(ies), ze = zone(s) of exclusion.**

*holomorph* (Lackner et al. 2014) *for most species except for those of doubtful identity, such as Pseudallescheria angusta.*

Limited data on TEM of *Scedosporium* and related fungi in *Microascaceae* are as yet available in the literature. Certain aspects of conidiogenesis have been studied in *Scedosporium apiospermum*, *Scedosporium boydii*, *Lomentospora inflata* and *Scopulariopsis brumptii* (Campbell & Smith 1982; Dykstra *et al.* 1989; Huang *et al.* 1990). The aim of the present work was to compare more fundamental criteria which have been in use at higher taxonomic levels, i.e. mature conidial walls, lateral cell walls, septa and septal pore apparatus. As a model set we used strains of the closely interrelated taxa of the *S.*