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Biogeographical variability and re-description of an imperfectly known species *Hamatocanthoscypha rotundispora* (Helotiales, Hyaloscyphaceae)

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Abstract

Study on fresh collections and type material of *Hamatocanthoscypha rotundispora* showed that the original description is incomplete and that the variation range in the essential characters is too narrowly defined. In this paper we therefore provide a detailed description, including ascospore morphometry using length, width, length/width ratio and volume. Non-parametric statistics showed significant deviation of normal distribution and high variability of all morphometrical variables, suggesting that use of living material for ascospore morphometrical analysis is more reliable than that of a traditional approach. Geometric criteria for defining the simple spore shape regarding the length/width ratio, polarity and symmetry in straight symmetric spores are proposed. Refractive cytoplasmic globules are described as a new type of inclusions in living cells. Species ecology and biogeography is also discussed.

Key words: Ascomycota, ascospore morphology, biogeography, ecology, methodology, microscopy

Introduction

A *Hamatocanthoscypha* species was collected in the Mediterranean region on fallen *Juniperus phoenicea* twigs beset with leaves in litter. After its study in both living and dead state and comparison to the relevant literature (Huhtinen 1990, Galán & Raitviir 1994, Raitviir 2004) it seemed certain that this collection did not represent any of the known *Hamatocanthoscypha* species. However, after re-examination of the type material our collection appeared to fit quite well *H. rotundispora* Raitv. & R. Galán. The protologue gives erroneously broadly ellipsoid to subglobose spore shapes with a too narrowly defined dimensional range for this species. Because of quite frequently noted inconsistencies in spore shape naming, we here propose clear geometric criteria with a redefined terminology for naming simple shapes of straight symmetric spores by relying mainly on Bas (1969) and Domínguez de Toledo (1994).

In this paper, a detailed modern re-description of *H. rotundispora* is provided. It is based on data obtained from the type material as well as recently collected material in both living and dead states from several European localities.

Materials and methods

H. rotundispora was collected in the maritime areas of Croatia and France during November to December, 2009–2011 which is the expected fructification period. Additionally, type material from AH (Universidad de Alcalá) was loaned and compared in detail with our collections. Macroscopic and microscopic characters based on living cells and tissues were recorded whenever possible using vital taxonomy as described in Baral (1992). Information based on dead cells and tissues were obtained from freshly fixed sections and rehydrated exsiccata. The mounting media were tap water and potassium hydroxide (5% weight aqueous solution). Reagents used were: Lugol's solution (Baral 1987), Brilliant Cresyl Blue solution (Baral 1992) and Melzer's reagent (Huhtinen 1990), the latter was used only in fixed material. Air dried apothecia were rehydrated by spraying with a water mist, and were subsequently examined in tap water and

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When the low global mycobiodiversity exploration level is taken into consideration (Mueller & Schmit 2007, Lumbsch *et al*. 2011), it is clear that there are still a vast number of fungal taxa waiting to be discovered and described. Many of previously described species are inadequately documented and poorly known. Thus, taxonomists should be encouraged to produce high quality re-descriptions for such taxa, especially those described from the sole type collection; to lodge cultures where possible and to produce sequence data. This should include data on living material, on fixed material from the same collections as well as extensive data obtained from re-examined type material whenever possible. Because current mycological practices have shown the existence of many cryptic (sibling) species (Frisvad & Samson 2004, Jaklitsch 2009, 2011, Liu *et al*. 2013, Muggia *et al*. 2014, Perrone *et al*. 2011, etc.) it is advisable to include physiological, chemotaxonomic, ontogenetic and molecular phylogenetic methods because only the polyphasic (holistic) approach could define differences between closely related taxa (Kuhnert *et al.* 2014, Maharachchikumbura *et al*. 2012, Pažoutová *et al*. 2013, Udayanga *et al*. 2011, 2012). This is particular important for plant pathogenic species (Sharma *et al*. 2013, Udayanga *et al*. 2013, Yang *et al*. 2009). Taxon with well-defined variation limits will reduce subsequent misidentification and enable reliable use in applied sciences.

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