MYCOSCIENCE XXX (2016) 1–5

Available online at www.sciencedirect.com

MYCOSCIENCE

ISSN 1340-3540 (print), 1618-2545 (online)

journal homepage: www.elsevier.com/locate/myc

Short communication

Cookeina cremeirosea, a new species of cup fungus from the South Pacific

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ARTICLE INFO

Article history:
Received 22 January 2016
Received in revised form
2 September 2016
Accepted 3 September 2016
Available online xxx

Keywords:
Ascomycota
Pezizales
Phylogenetics
Samoa
Sarcoscyphaceae

ABSTRACT

A new species in the Sarcoscyphaceae from the Samoan Islands, *Cookeina cremeirosea*, is described and illustrated. This species is morphologically and phylogenetically distinct from the other eight species that are currently accepted for the genus. It is closely related to the Asian species *Cookeina indica* from which it can be separated by color and spore morphology.

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Cookeina Kuntze is a small genus of tropical or subtropical cup fungi that typically fruit on woody debris. Members of the genus are often brightly colored and attractive, making them easy to spot in the field and as a consequence they are commonly collected by mycologists. Certain species in the genus such as *C. tricholoma* (Mont.) Kuntze are pantropical in distribution and are rather frequently seen whereas others such as *C. sinensis* Zheng Wang or *C. venezuelae* (Berk. & M.A. Curtis) Le Gal appear to be much more localized in distribution (Iturriaga and Pfister 2006). Twenty four names, including varieties, are listed for *Cookeina* by Index Fungorum (http://www.indexfungorum.org/names/names.asp) although many of these names along with some others were either synonymized or excluded from the genus by Iturriaga and Pfister (2006) leaving 8 taxa that are currently recognized in *Cookeina*.

As the tropical regions of the world are explored by mycologists, new taxa are frequently encountered even in well-studied genera such as *Cookeina*. The objective of this paper is to propose a new Samoan species in the ascomycete genus *Cookeina* and to assess its phylogenetic relationship to other members of the genus.

Fresh specimens of *Cookeina* sp. were photographed against a gray card immediately after returning from the field. Field notes were taken from the material before drying except for the color notations which were done from the digital photographs. Munsell Soil Color Charts (Munsell Color 2000) was used as a color standard. Sections from dried herbarium specimens were mounted in Melzer's reagent or 1% Congo Red to do the microscopic work and to take the photographs used for Fig. 3. Measurements of the ascospores were done using oil immersion and are given as minimum–(average)–maximum (n = 20) whereas measurements for other cells are given as size ranges. The specimens examined for this work were accessioned into the Intermountain Herbarium (UTC) at Utah State University.

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http://dx.doi.org/10.1016/j.myc.2016.09.003

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Please cite this article in press as: Kropp BR, *Cookeina cremeirosea*, a new species of cup fungus from the South Pacific, Mycoscience (2016), http://dx.doi.org/10.1016/j.myc.2016.09.003

Small pieces of tissue from the dried herbarium specimens of *Cookeina* sp. were crushed in liquid nitrogen before DNA was extracted with a modified CTAB mini-prep method that was previously reported by Kropp et al. (1996). Standard PCR protocols were then used with the ITS4 and ITS1 primers of White et al. (1990) to amplify the nuc rDNA ITS1-5.8S-ITS2 region (ITS) from the genomic DNA that had been obtained from the specimens. Sequences of the amplified ITS region were produced using the ITS4 and ITS1 primers and an ABI 3730 DNA Analyzer. The two newly generated sequences were deposited in GenBank (numbers KU306963 and KU306964).

Taxon sampling for the phylogenetic analysis was done using the phylogeny for *Cookeina* done by Weinstein et al. (2002) as a framework for selection. When available, more than one ITS sequence for each of the included species was analyzed although not all of the sequences available for some of the species were included. Sequences of *Microstoma floccosum* (Schwein.) Raitv. were used to root the phylogram.

The ITS sequences that had been selected for the analyses were aligned using Clustal X (Thompson et al. 1997) and adjusted by hand. The alignment used to do the analysis was placed in TreeBASE (18629). Tree searches were done with MrBayes 3.1.2 (Ronquist and Huelsenbeck 2003) using a time reversible model of evolution with a gamma distribution, six base substitution types and some invariant sites (GTR + G + I) (Rodriguez et al. 1990; Maddison 1994). The simulations were run with 8 active MCMC chains heated at 0.2, with each run starting with a randomly chosen neighbor-joining tree. One million generations were run with the trees being sampled every hundred generations. Burnin was set at 2500 and a strict consensus tree was calculated using the last 7500 trees sampled from a 10,000 tree data set. By the end of the analysis, the potential scale reduction factors had converged on 1.000 and the plotted generation versus log likelihood values showed no trend. Thus, stationarity had been achieved in the analyses. TreeView (Page 1996) was used to visualize the consensus tree. Support measures for nodes with less than 70% posterior probability support are not shown in Fig. 1.

The analysis of the ITS sequences of the *Cookeina* sp. specimens yielded a phylogram with well-supported terminal

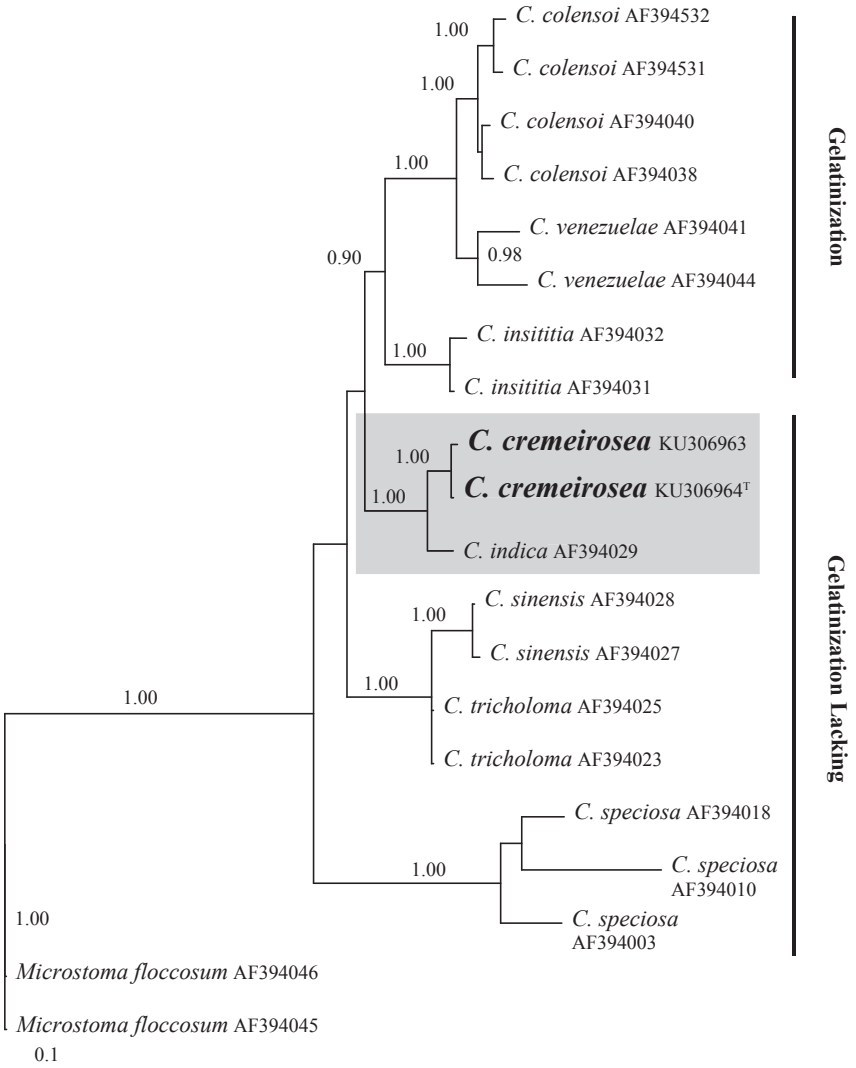

Fig. 1 – Bayesian phylogram based on an ITS data set showing the position of *Cookeina cremeirosea* within its genus. GenBank numbers are shown for the sequences that were used in the analysis. Support measures are not shown for nodes with less than 70% posterior probability support. Vertical lines indicate sections of the genus with and without gelatinized tissue in the excipulum.

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