

Copyright © 2010 · Magnolia Press

Article



Description and molecular phylogeny of *Tethya leysae* sp. nov. (Porifera, Demospongiae, Hadromerida) from the Canadian Northeast Pacific with remarks on the use of microtomography in sponge taxonomy

ISABEL HEIM & MICHAEL NICKEL

Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Friedrich-Schiller-Universität Jena, Erbertstr. 1, 07743 Jena, Germany. E-mail: isabel.heim@uni-jena.de, m.nickel@uni-jena.de. www.porifera.net

Abstract

The sponge Tethya leysae sp. nov. (Porifera, Demospongiae, Hadromerida, Tethyidae) is a new species from the Canadian Northeast Pacific. Its type locality is the infralittoral around Ohiat Islet, Barkely Sound, Vancouver Island in Canada. Tethya leysae sp. nov. is a medium-sized spherical sponge with a vertucose surface, orange-yellow to light red alive and white with a greyish core in ethanol. The highly variable oxyspherasters (25-115 µm in size, R/C 0.34-0.69) are densely scattered almost throughout the entire cortex. The micrasters comprise acanthoxyspherasters, acanthostrongylasters, acanthotylasters and small oxyspherasters, which are present at low densities throughout the sponge and form a dense layer associated with the exopinacoderm. The megascleres and the auxiliary megascleres comprise oxeas and strongyloxeas. The new species is clearly distinguishable from the closely related *T. californiana* by the absence of spherules among the micrasters, the lack of an alveolar cortex and the extremely high density of megasters in the cortex. In addition, the R/C values of the megasters differ between the two species and the oxyspherasters of T. leysae sp. nov. rarely display bent rays. The morphological differences between the species are confirmed by nucleotide and amino acid substitutions within the cytochrome oxidase subunit I (COI) mtDNA gene. Phylogenetic analyses group T. leysae sp. nov. with T. californiana, T. actinia and T. minuta, which together form a sister group to a Mediterranean-North Atlantic species cluster. Morphological analyses of the skeleton included x-ray microtomography (μ CT) and virtual 3D reconstruction, which was used for the first time in conjunction with the description of a new sponge species. Microtomography permitted the visualization and analysis of spicules within the skeletal context or isolated *in silico*. The method represents a valuable extension to the sponge taxonomist's toolbox since it allows morphometric measurements in 3D. µCT will thus supplement classical morphological methods such as light and scanning electron microscopy.

Key words: Sponges, new species, synchrotron radiation based x-ray micro computed tomography, *in silico* morphometry, COI, maximum likelihood, Bayesian analysis

Introduction

The invention of the microscope in the 17th century made it possible to study internal skeletal structures in sponges. Ever since, microscopic mineral spicules and the architecture of the skeleton have been as useful as macroscopic morphological characters such as colour and shape, texture and the like in the determination of sponges. In the 19th century many sponge species, e.g. *Chondrosia reniformis* Nardo, 1847, *Clathrina clathrus* (Schmidt, 1864), *Dysidea fragilis* (Montagu, 1818) and, *Guitarra fimbriata*, Carter, 1874 were described, and often regarded as cosmopolitan due to their wide geographical range (Boury-Esnault *et al.* 1993). However, in recent years many cosmopolitan species have turned out to be 'sponge taxonomist traps', in fact representing complexes of cryptic species that are genetically distinct but which display low variability in most of their morphological characters. In the 1980s molecular techniques were used for the first time to sort among morphotypes thought to pertain to a single species (Solé-Cava & Thorpe 1986). Allozyme electrophoresis which defines products of individual gene loci was used to calculate gene frequencies and estimate exchange