

Nomenclatural Validation of *Desmodesmus dohacommunis* (Chlorophyta)

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Abstract Although *Desmodesmus dohacommunis* Demura was described in Demura *et al.* (2021), it was invalid because the protologue did not designate the valid holotype. Nomenclatural validation of this species is made with the dried herbarium specimen according to Art. 40.7 and 40.8 (Shenzhen Code) in this study.

Keywords: *Desmodesmus dohacommunis* Demura, Holotype, ICN, nomenclature.

Introduction

Desmodesmus dohacommunis Demura was described in Demura *et al.* (2021) based on its unique outer cell wall structure and distinctive sequence of the internal transcribed spacer 2 (ITS2) region of nuclear ribosomal DNA. However, it was invalid because of lacking the valid holotype designation in the protologue according to the International Code of Nomenclature for algae, fungi, and plants (ICN, Shenzhen Code: Turland *et al.*, 2018), Art. 40.7 and 40.8. The designation of the holotype was validly made in this paper.

Taxon

Desmodesmus dohacommunis Demura, sp. nov.
≡ *Desmodesmus dohacommunis* Demura, nom. inval. in Demura *et al.*, biomass **2021(1)**: 116. f. 2, 4c. 2021.

Holotype (designated here): TNS-AL-58987 in TNS (Department of Botany, National Museum of Nature and Science), Japan. This is the dried algal material for Scanning Electric Microscope (SEM) observation prepared from a strain

dSgDes-b.

Ex-holotype strain: a strain dSgDes-b. Isolated from Oyako-tsutsumi, Saga City, Saga Prefecture, Japan (N33.326, E130.312).

Description: Cell size was 9.4–15.8 × 3.2–4.7 μm. Coenobia of four cells were observed, outer cells of which had spines. This strain could not be distinguished from *D. communis* and its related species using optical microscopy. Rosettes of this strain were complex and had a large number of outer tubes (eight–nine), similar to those of *D. pseudocommunis*; however, rarely, rosettes of four–five tubes were observed. The net-like structure of the outer cell wall layer had regular and smaller meshes than those of *D. communis*. The sequences and the secondary structure of the ITS2 region distinguish the new species from *D. communis* and *D. pseudocommunis* (see Demura *et al.*, 2021).

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