Some of the methods used in this paper are slightly modified or identical to those given in Tsutsui & Jordan (2016), and so have been placed in the online supplementary information. In particular, methods related to the photography and semi-automated programme used to take skeletal measurements.

The origin of the sample (E1758) from the island of Mors, Denmark (see Fig. S1), used in this study and currently curated in the Friedrich Hustedt diatom collection (in the Alfred-Wegener-Institut in Bremerhaven, Germany), is unknown but may have been collected by Hustedt himself, or alternatively, it may be a subsample of material collected over 120 years ago and distributed among 19th century diatomists. Indeed, Mors samples were already in circulation by the 1860s and numerous papers were subsequently published, particularly on new taxa (e.g. Heiberg 1863, Grunow 1866, Kitton 1871, Schmidt et al. 1874-1959). Much later, Hustedt published a paper on Eocene marine diatoms, including those from Mors, but did not mention which samples he examined (Hustedt 1950).

The *Corbisema* micrographs in this study were taken using an Olympus BH2 with an ARMS AR-D300C digital camera or BX40 with a CANON EOS Kiss X6i digital camera, and with x10, x20 and x40 objective lenses and KB-3, IF550 and ND25 colour filters. The latter are useful for maintaining photographic conditions. The skeletons featured in the micrographs were then measured using a morphometric programme custom-made for *Corbisema* (Tsutsui & Jordan 2016). In short, the photographic images of the *Corbisema triacantha-apiculata* complex (see examples in Fig. S2a-c) are converted from JPEG to a bitmap, the landmark positions are marked on a wire-frame computerised skeleton (Fig. S2d), measurements are made between two landmark points, and the curve control points are drawn by the quadratic Bézier curve module. The input work of the skeletal parts is done manually, but the identification and arrangement of skeletal points except pikes are fully automated (see Fig. S3 for an example of a screenshot and basic measurements). Although the *Corbisema* skeleton is three-dimensional, the distance from the basal ring to the top of the strut is calculated as if it were two-dimensional (i.e. horizontal distance).

Statistics (kurtosis and skewness) are calculated by Statistical Analysis Software (SAS Institute®) version 9.4, licensed to Yamagata University. If the skewness value is <0, then the normal distribution curve is narrow, while a skewness value >0 has a wide normal distribution curve. In an ideal normal distribution the kurtosis value is 0, if not then the distribution may be bimodal or trimodal.

References

Grunow, A. 1866. Molér aus Jütland, eingesandt von Th. Jensen, analysirt von A. Grunow. *Hedwigia*, **5**(10), 145-146.

Heiberg, P.A.C. 1863. *Conspectus Criticus Diatomacearum Danicarum. Kritisk Oversigt over de Danske Diatomeer*. 78pp., 6 pls. Kopenhagen.

Hustedt, F. 1950. Eozäne Diatomeen. *Mikrokosmos*, **40**(3), 1-5.

Kitton, F. 1871. Diatomaceous deposits from Jutland. *Journal of the Quekett Microscopical Club*, **2**, 99-102, 168-171, 5 pls.

Schmidt, A. *et al*. 1874-1959. *Atlas der Diatomaceen-kunde*. Leipzig and Berlin. [reprinted in 1984 by Koeltz Scientific Books, Koeningstein, W. Germany]

Tsutsui, H. & Jordan, R.W. 2016. A semi-automatic two-dimensional image system for studying the skeletal design of the silicoflagellate genus *Corbisema* (Dictyochales, Dictyochophyceae). *Journal of Nannoplankton Research*, **36** (2), 1-9.

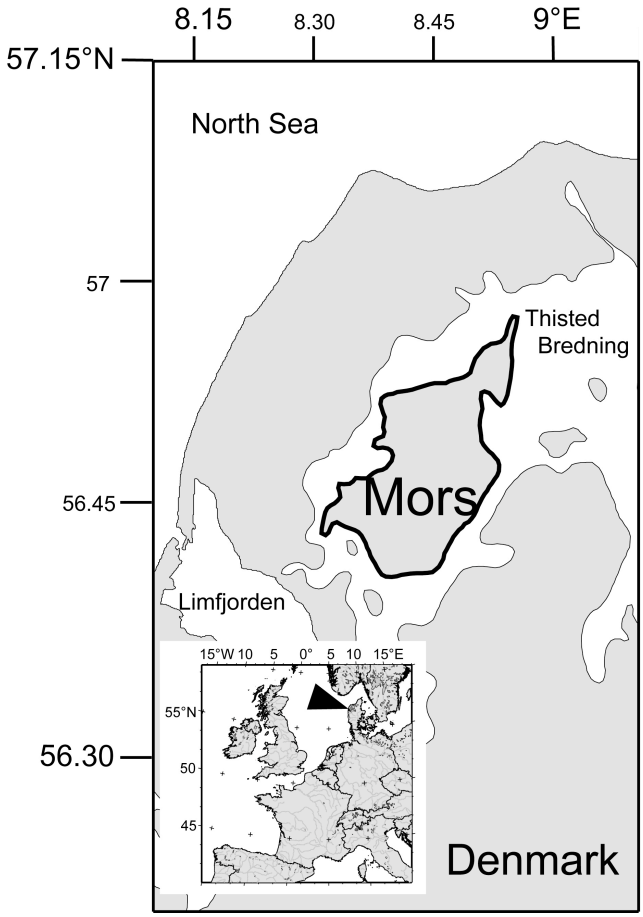

Figure S1. Map, showing the sample location; Mors Island, Jutland, Denmark. Map is based on Collaborative Research Center (SFB) 574, GEOMAR (http://sfb574.geomar.de/gmt-maps.html).

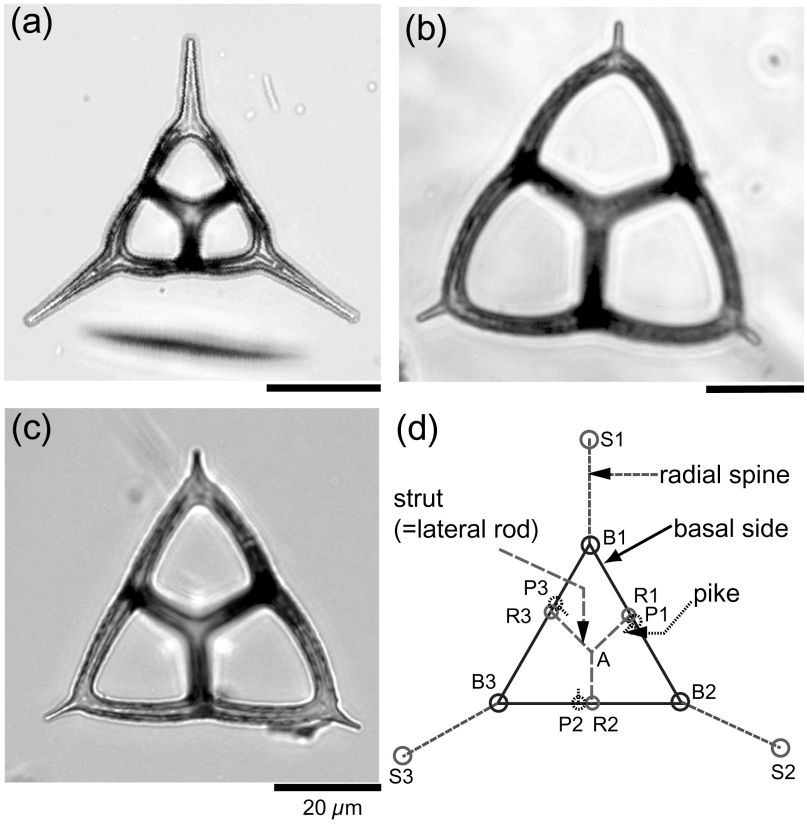

Figure S2. Light micrographs of (a) *Corbisema* group A (*C. triacantha*) and (b-c) *Corbisema* group B (*C. apiculata*), subdivided into B1 (b) and B2 (c), and (d) an annotated computer-generated ideal skeleton. Scale bars = 20 μm.

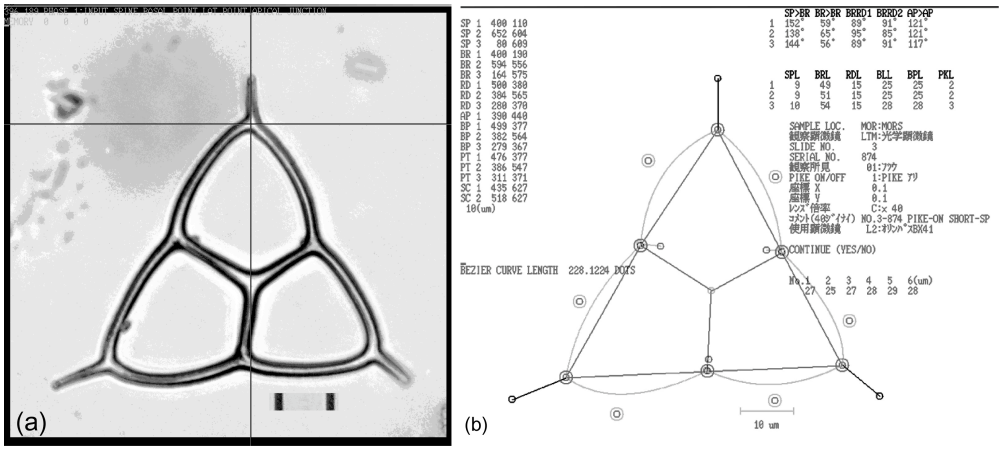

Figure S3. (a) A computer screenshot of a microphotograph loaded into the biometry programme, with the selected coordinates on the computer graphic frame, and (b) a screenshot of the primary measurement result (e.g., length and angles), the coordinate data, and specimen notes. Scale bar = 10 μm.