# Biological Science

Robust estimations of the phylogentic relationship and divergence time among five major orders in Foraminifera

Prior to this study, the major branching order in Foraminifera has hot been resolved with confidence. We obtained the RNA-seq data (~0.7-1.2 Gb) from the species representing orders Textulariida, Spirillinida, Milliolida and Rotallida, and assembled a 157-protein alignments (41,365 positions). Our phylogenomic analyses recovered the robust relationship among the five orders, and estimated ~588 Mya in the Ediacaran for the first divergence of Foraminifera (highlighted by a blue arrowhead) with a 95% confidence of ~544-632 Mya.
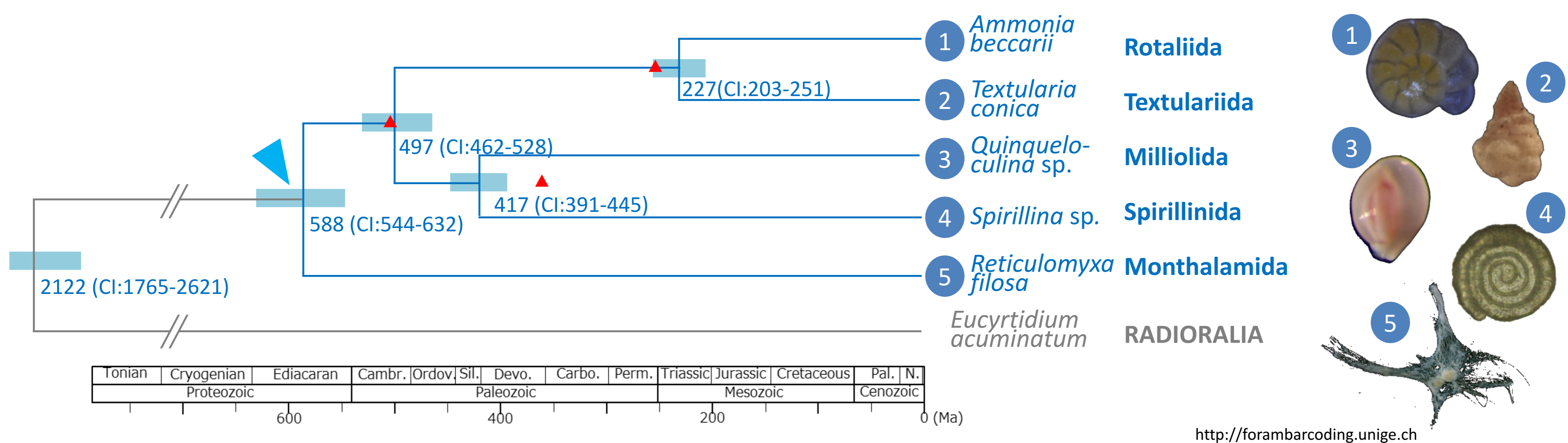
Fig. 1: Chronogram of five foram species representing the five major orders. The foram clade was shown in blue. We generated the sequence data from the species labelled as ①-④. Node ages were inferred using Bayesian inference with an uncorrelated relaxed clock model. Values at nodes indicate ages estimated by median heights of clade, blue bars at nodes represent 95% confidence intervals and red triangles correspond to the lower constraints based on fossil records.

Phylogenomics analyses revealed a novel microeukaryote strain SRT308 is a basal-branching eugolenozoan.

We isolated a novel microeukryote strain SRT308 (Fig. 2a) from marine sediment sample collected in Republic of Palau. In a phylogenetic analysis of small subunit ribosomal DNA sequences, SRT308 shows no strong affinity with major eukaryotic lineages (data not shown). However, our phylogenomic analysis using 153 protein-coding genes placed SRT308 at the base of Euglenozoa with strong statistical support, suggesting this organism is the most basal-branching member of Eugolenozoa known to date (Fig. 2b).
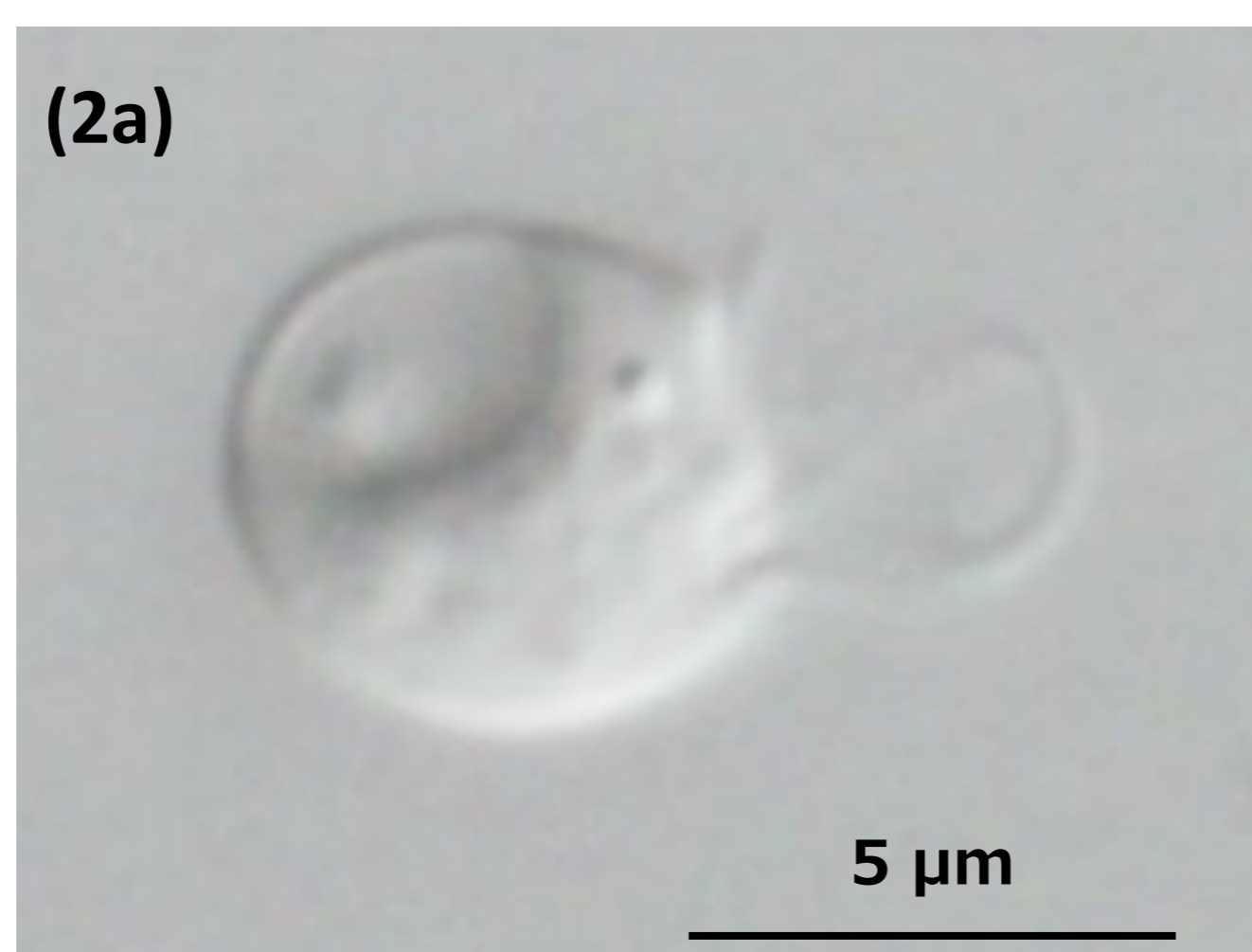
Fig. 2a: Microeukaryote strain SRT308.

Photo by Dr. T. Shiratori (Univ. Tsukuba)

Fig. 2b: ML phylogeny based on a 153-protein alignment (38,592 amino acid positions). MLBP (above) and BPPs (below) are shown at nodes. The nods with full MLBP and are highlighted by dots.