



SWEDISH TAXONOMY INITIATIVE RESEARCH REPORT

Project period: 2006–2009

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BRYOZOANS:

Taxonomy and phylogeny of Swedish bryozoans

In addition to my own project, I was acting as supervisor for Judith Fuchs' PhD project with the title "Taxonomy and systematics of Swedish bryozoans". Hence all scientific work regarding the taxonomy and systematics of bryozoans in Sweden reported here was carried out together with Judith Fuchs and her supervisor Per Sundberg (Department of Marine Sciences, University of Gothenburg).

Introduction

Bryozoa (bryozoans or moss animals) is a poorly investigated phylum of aquatic animals with uncertain phylogenetic origins. Between 2006 and 2008 the Swedish Taxonomy Initiative supported my taxonomic and systematic research on these animals.

The project was designed in accordance with the overall research agenda of the Swedish Taxonomy Initiative and pinpointed a number of key questions to be addressed within a 2.5 years of investigation. These were:

- (1) How many bryozoan species live in Swedish waters?
- (2) What are the biogeographic interesting regions and species?
- (3) Are there any new species to science?
- (4) What are the phylogenetic relationships among the major bryozoan groups?
- (5) What are the phylogenetic origins of bryozoans?

After three years of intense focus on these questions we are happy to report a substantial progress in answering most of these questions. We also gained considerable expertise on bryozoans and many other groups of marine invertebrates that live in the same habitats.

Marine inventories

Between 2006 and 2008 I participated in all marine inventories of the Swedish Taxonomy Initiative (e.g. the SAMARIN expedition) and collected moss animals as well as similar benthic invertebrates (hydroids, entoprocts, brachiopods, etc.) during six cruises along the Swedish West coast. I obtained samples from more than 400 locations across Skagerrak and Kattegat.

Our collection currently contains a total of at least 3 000 specimen, including >2 000 bryozoan and >1 000 hydroid specimen. These samples provided the raw material for all taxonomic and phylogenetic work, as well as for ecological and historical comparisons of the marine fauna of Sweden.

Throughout the past three years we have continuously been sorting and identifying the samples in our collection and prepared the specimen for long term storage at the Natural History Museum in Gothenburg.

Taxonomic work

At this point we have built up substantial taxonomic expertise and work routine for processing bryozoans and related taxa. We have sorted and identified about one third of the collected material. Our species record includes more than 120 Swedish bryozoans (including related taxa) with a detailed distribution record for each species, which were analyzed in order to define areas with rare species as well as hotspots.

In comparison with other Scandinavian species lists (e.g. Danmarks Fauna, NEAT), which estimate the number of marine bryozoans to be around 140 in Sweden, our collection recovers approximately 25 % new species for Sweden.

Biogeography

Most of the new records are species known from other European localities, but seem to exist in Swedish water with relatively low abundance. Therefore it is likely that many of the newly recorded species have been present in the past, but remained unrecorded.

At this point we have the impression that there are some bryozoan invaders migrating from the western parts of the European continental shelf. Examples are the cheilostome *Celleporina decipiens*, *Escharina vulgaris*, *Ragionula rosacea*, and the ctenostome *Arachnidium simplex*. However, in these cases we need to investigate the collected material more thoroughly in order to draw firm conclusions.

Alpha-taxonomy

We can report a number of species new to science, which we retrieved from the collection. This concerns a ctenostome, a cyclophoran, and an entoproct. The ctenostome (preliminary name *Nolella franzenii* sp. nov.) develops creeping colonies consisting of semi-solitary zooids, which are possibly connected by slender stolons. The main diagnostic character is the zooid surface, which is densely covered with soft spines that incorporate small silt particles. The type specimen was collected on June 15th 2008 at a depth of 313 m off the coast of Väderöarna, Skagerrak on soft gravel-rich sediment.

The second new species lives on the mouth appendages of the European lobster where it typically grows in dense clusters of up to several thousand individuals. The species is preliminarily named *Symbion gammarus* sp. nov., based on the host's name *Homarus gammarus*. The main diagnostic character is the presence of small posterior lobes in one of the free-living stages, the Prometheus larva.

The third novel species (preliminary name *Loxosoma beaniana* sp. nov.) lives on the coralline bryozoan *Reteporella beaniana* and forms aggregations of up to 100 solitary individuals.

Phylogenetic work

In order to analyze the relationships within Bryozoa we generated a molecular data set from 36 species (32 bryozoans and 4 outgroups), including nuclear (18S, 28S rDNA) and mitochondrial (cox1) gene sequences. Our results show for the first time that bryozoans are monophyletic, with freshwater bryozoans as the most basal clade. Cheilostomes are clearly polyphyletic and seem to have evolved their encrusting and coral-like body forms several times independently from soft-bodied ancestors.

We can also show that marine bryozoans (cyclostomes, ctenostomes, cheilostomes) evolved from a common ancestor, which probably had an anatomy similar to a soft-bodied cyclostome. These results help explaining why bryozoans appear relatively late in the fossil record during Ordovician, while most other animal phyla are already known from the Cambrian. According to our results it seems very likely that bryozoans were actually present in the Cambrium, but did not fossilize.

In order to trace the evolution of the bryozoan body plan along the deeper branches in the animal tree of life we compiled a genomic data set (generating expressed sequence tags from cDNA libraries) from 77 metazoans, including six species of sessile filter feeding protostomes. These are two bryozoans (*B. neritana*, *C. mucedo*), one phoronid (*P. vancouverensis*), one brachiopod (*T. transversa*), one entoproct (*P. cernua*), and one cycliophoran (*S. pandora*).

The alignment of the molecular data yielded more than 1 000 genes applicable to phylogenetic analysis. Our results support clades that split deep in the metazoan tree (i.e. Ecdysozoa, Protostomia, Lophotrochozoa) and suggest a number of new hypotheses for metazoan evolution. One of them clearly refutes the long held Lophophorata concept in which Bryozoa, Phoronida, and Brachiopoda have a common origin.

Our results indicate a group named Polyzoa, uniting bryozoans, entoprocts, and cycliophorans. The results of this work have been a cover story in Nature in 2008 and another publication followed in Proceedings of the Royal Society B.

PUBLICATIONS

All articles can be accessed at <http://marine.gu.se/om-institutionen/personal?userId=xobsma#tabContentAnchor2>

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