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The coelomic epithelium transcriptome from a clonal sea star, *Coscinasterias muricata*

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ABSTRACT

Coscinasterias is a cosmopolitan genus of large asteroid sea stars with the ability of somatic fission as a clonal reproductive strategy. During fission, the animals tear themselves apart across their central disc, where the lost body parts are regenerated afterwards. Here, we have sequenced and subsequently analysed the transcriptome of the coelomic epithelium of a clonal *Coscinasterias muricata* specimen from New Zealand. Out of the total 389,768 raw reads, 11,344 contigs were assembled and grouped into functions. Raw read and assembled contig sequences are available at NCBI (BioSample: SAMN03371637), while the annotated assembly can be accessed through the project transcriptome browser (compngen.bio.ub.edu/gbrowse/starfish_transcriptome/). Our data is valuable for future detailed exploration of the coelomic epithelium functions as well as for a better understanding of sea star physiology.

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1. Introduction

Coscinasterias is a cosmopolitan genus of large and fissiparous asteroid sea stars that are common in shallow waters at many continents (Waters and Roy, 2003). Sea stars are exclusively marine deuterostomes with features of special interest such as their key stone ecological functions, innate immunity, tissue regeneration and clonal potential. One species in this genus, *Coscinasterias muricata* from New Zealand is particularly interesting because it reproduces only sexually in certain geographical areas and mostly by cloning in others. Upon fission, any of these sea stars tear themselves apart across the central disc to form two or more separate pieces. Thereafter, the wounds heal and missing body parts regenerate. The coelomic epithelium is a tissue layer that covers the dorsal inside of sea stars (see Fig. 1A). It responds to several stimuli by extensive cell proliferation and it is involved in a range of important processes such as wound healing, regeneration and haematopoiesis (Holm et al., 2008; Hernroth et al., 2010). Despite the obvious wide relevance of this tissue, a molecular survey of its transcriptome has not been

conducted, limiting deeper analysis of its functions. In order to provide a larger toolbox for further molecular analysis of sea stars and the coelomic epithelium in particular, we here provide de novo sequencing and subsequent annotation of the transcriptome of the coelomic epithelium from this clonal sea star, *C. muricata*.

2. Data description

2.1. Study object and sample preparation

The analysed sea star of the species *C. muricata* was originally collected from a highly clonal population of the Portobello Aquarium in Otago Harbour, New Zealand (Sköld et al., 2003) and brought to Sven Lovén Centre of Marine Sciences at Kristineberg, University of Gothenburg, Sweden. The animals were kept at 15 °C in running sea water (PSU 33) and fed ad libitum with small blue mussels. Spontaneous fission was observed during their maintenance and followed by regeneration of missing arms. The individual sampled for this study (Fig. 1B) had a diameter of 10 cm and was undergoing regeneration after fission; the presence of eggs indicated that it was a female. Coelomic epithelium was collected using sterile forceps from arms of normal length of the sea star.

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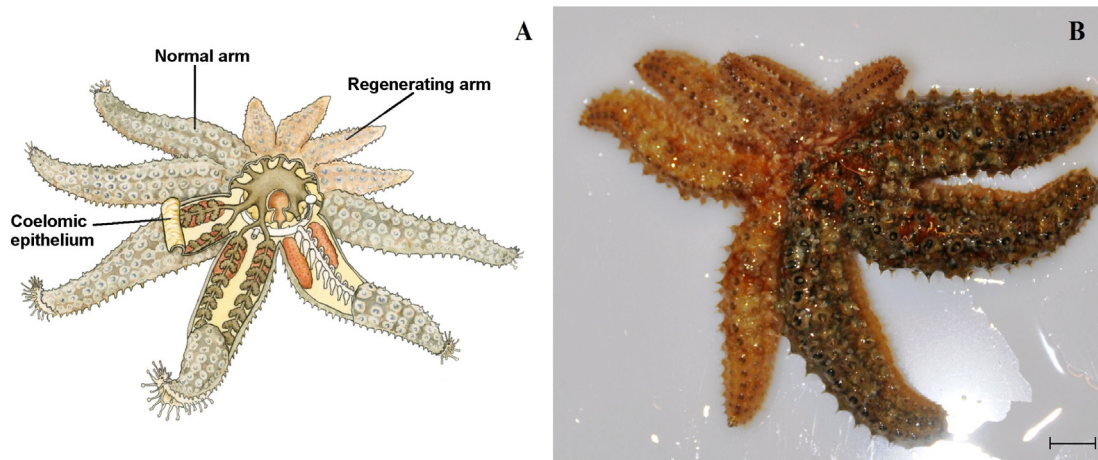


Fig. 1. A) Diagram of relevant anatomical structures of *Coscinasterias muricata*. B) Photograph of an individual sea star collected from the clonal population in Otago Harbour, New Zealand. Coelomic epithelium from normal arms (darker arms to the right) was used to isolate the RNA used in this study. Scale bar: 1 cm.

Tissue was frozen in liquid nitrogen and homogenised with glass pestles. Total RNA extraction was performed with the RiboPure kit (Applied Biosystems, Foster City, CA, USA), following manufacturer's protocol.

Concentration was determined photometrically at 260 nm (NanoDrop ND-1000, Seqlab, Erlangen, Germany) and purity was estimated using the Agilent 2100 Bioanalyzer system (Agilent, Santa Clara, CA, USA).

Sequence Stats	#Seqs	Total.Length	Avg.Length
Raw Reads	389,768	147,624,619bp	378.75bp
Trimmed and Clean Reads	346,201	88,571,400bp	255.84bp
Assembled Transcripts	11,369	5,212,378bp	458.50bp
VBF-Clean Transcripts	11,344	5,204,316bp	458.77bp

Assembly Stats	#Seqs	N50	GC.Pct	Longest Sequence
All Contigs	11,344	529bp	43.61%	
#Contigs >500bp	2,924	948bp	44.68%	9,225bp

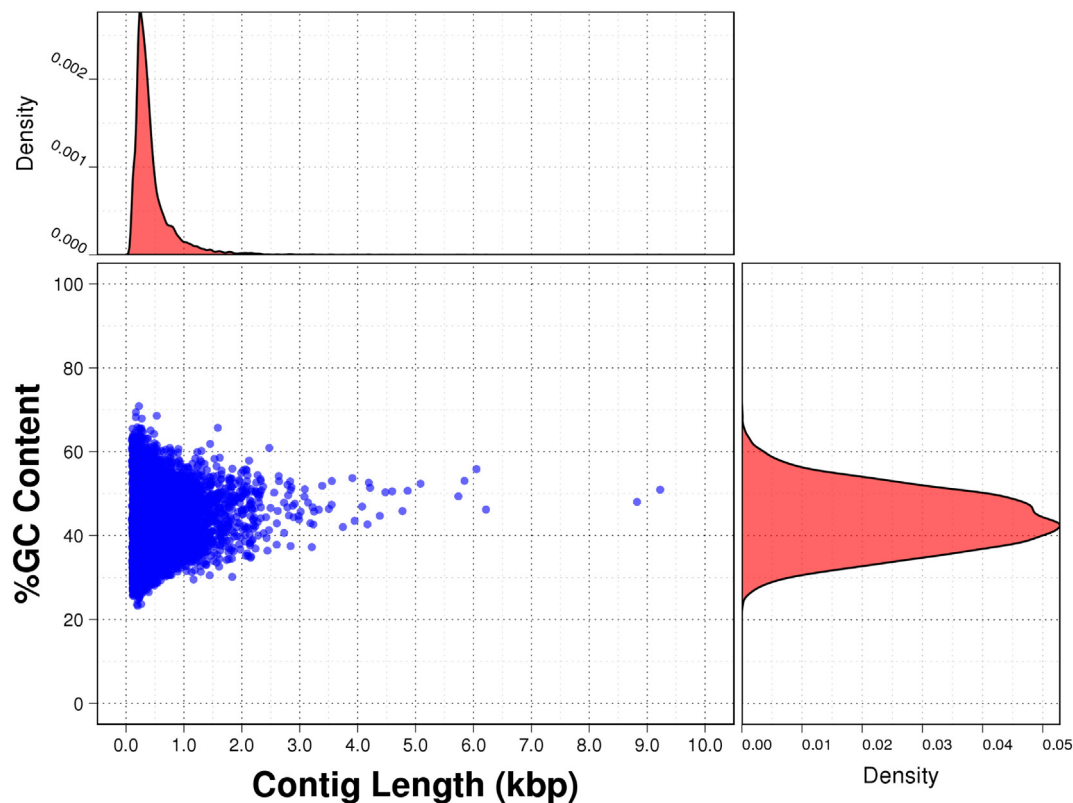


Fig. 2. Assembly statistics: top table summarizes main assembly features, while the bottom figures present a scatterplot with marginal density plots that illustrate the distribution of contig lengths (in base pairs), with values ranging from 100 to 9225 bp, and the average GC content of each contig sequences.

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