Transcriptome of the Antarctic brooding gastropod mollusc *Margarella antarctica*

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Abstract

454 RNA-Seq transcriptome data were generated from foot tissue of the Antarctic brooding gastropod mollusc *Margarella antarctica.* A total of 6,195 contigs were assembled *de novo*, providing a useful resource for researchers with an interest in Antarctic marine species, phylogenetics and mollusc biology, especially shell production.

Keywords

1. Introduction

Margarella antarctica is a small omnivorous topshell (up to 10mm) that is abundant and widely distributed throughout the Antarctic. Poor genetic connectivity between populations is expected in this species because it is a direct developer and the adults have low motility with a limited ability to disperse over soft sediments compared with hard rock substrata such as bed rock and loose rubble (Picken, 1979). It has already been subject to some preliminary population analyses, using AFLPs, as part of a comparative study to investigate the link between life history and genetic structure in the Antarctic ecosystem (Hoffman *et al.* 2011; 2012; 2014). The data revealed strong population structure in *M. antarctica* sampled from sites along the Antarctic Peninsula separated by distances of at least 6km. At smaller spatial scales *M. antarctica* populations are still significantly structured, although weakly so on AFLP criteria and the isolation-by-distance pattern is non-linear (Hoffman *et al.* 2014) and cannot be explained by simple dispersal limitation. Thus this species is now the subject of further population analyses to determine the factors affecting micro-population structuring and the data described here will provide a resource for those studies.

M. antarctica were collected by SCUBA divers from depths of 10-15 m from South Cove, near Rothera research station, Adelaide Island, Antarctic Peninsula (67^{o} 34 ′07″ S, 68^{o} 07 ′30″ W) in the austral summer of 2012. 20 animals were dissected and the foot tissue flash frozen in liquid nitrogen and stored at -80°C until further analysis. Total RNA was extracted from all 20 individuals TRIsure Reagent (Bioline) according to manufacturer's instructions. RNA quality and concentration were determined using a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA), respectively. The RNAs from all the individuals were pooled for RNA-Seq. The production of the 454 library and the transcriptome sequencing was performed at the University of Cambridge Sequencing Service in the Biochemistry Department (Cambridge, UK). The RNA library yielded 487326 million reads. The contigs were trimmed and assembled using Newbler (www.454.com). *De novo* assembly led to a total number of 6,195 contigs, of which 3,313 contained at least 10 reads each. These were annotated using an in-house GenBank nr database (Benson *et al.,* 2007) using a threshold value for annotation of below 1e^{-10}. Putative annotation based on sequence similarity searching could be assigned to 1,830 contigs (30%) of the contigs (Table

1). With regard to population work, 10,054 high confidence SNPs were identified in 1,974 contigs.

Table 1 : Statistics for the transcriptome generation from foot tissue of *Margarella antarctica*

Total reads	487,326
Total Contigs	6,195
Average Contig length (bp)	597
Median length (bp)	509
Max length (bp)	4597
Min length (bp)	100
% Annotated Contigs	30

RNA-Seq transcriptome data for Antarctic marine invertebrates is still limited, but encompasses a wide range of phyla including the Antarctic clam *Laternula elliptica* (Clark *et al*., 2010; Husmann et al., 2013; Sleight et al., 2015); the krill *Euphasia superba* (Clark *et al.,* 2011; Toullec *et al.,* 2013; Meyer *et al.,* 2015), the brittlestar *Ophionotus victoriae* (Burns *et al.*, 2013) and the limpet *Nacella concinna* (Fuenzalida *et al.,* 2014). Thus the data from *M. antarctica* will form a valuable resource to understanding how life evolved and is maintained in the freezing waters of the Southern Ocean. These data will also provide a useful resource for researchers with an interest in mollusc biology, phylogeny, population genetics and mollusk shell production.

2. **Nucleotide sequence accession numbers**

The sequence data for this transcriptome has been deposited in the GenBank SRA, accession number: SRP058232. The contigs are available from http://tinyurl.com/p9nlwww

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