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Transcriptome of the Antarctic amphipod *Gondogeneia antarctica* and its response to pollutant exposure

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ABSTRACT

Gondogeneia antarctica is widely distributed off the western Antarctic Peninsula and is a key species in the Antarctic food web. In this study, we performed Illumina sequencing to produce a total of 4,599,079,601 (4.6 Gb) nucleotides and a comprehensive transcript dataset for *G. antarctica*. Over 46 million total reads were assembled into 20,749 contigs, and 12,461 annotated genes were predicted by Blastx. The RNA-seq results after exposure to three pollutants showed that 658, 169 and 367 genes that were potential biomarkers of responses to pollutants for this species were specifically upregulated after exposure to PCBs (Polychlorinated biphenyls), PFOS (Perfluorooctanesulfonic acid) and PFOA (Perfluorooctanoic acid), respectively. These data represent the first transcriptome resource for the Antarctic amphipod *G. antarctica* and provide a useful resource for studying Antarctic marine species.

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1. Introduction

The Antarctic amphipod *Gondogeneia antarctica* is widely distributed around most of the western Antarctic Peninsula and in some areas represents the dominant faunistic element in the shallow littoral benthic community. This species is also found on the sub-Antarctic islands and in the Magellanic region (Huang et al., 2007; Jazdzewski et al., 2001). Given its abundance, *G. antarctica* plays a key role in the littoral food web of the Southern ocean. *G. antarctica* feeds mainly on benthic microalgae, macroalgae, detritus and small amounts of microcrustaceans, and is preyed on by a large number of different species (Amsler et al., 2005; Barrera-Oro and Piacentino, 2007). Although Antarctica is largely pristine, relatively volatile persistent organic pollutants (POPs) can be carried there by long-range atmospheric transport (Risebrough et al., 1976; Zhao et al., 2012) and pollution from local sources of POPs around research stations (Park et al., 2010). Their highly lipophilic and persistent nature allows ready accumulation in organisms and subsequent biomagnification through the food web (Kim et al., 2010). *G. antarctica* is a potential bioindicator of the metabolic physiology and/or ecotoxicology of global climate alteration and environmental contamination for shallow water Antarctic animals (Gomes et al., 2009; Obermüller et al., 2007). Little is known with regard to its genomic and transcriptomic information (Shin et al., 2012). In this study we present a comprehensive analysis of the *G. antarctica* transcriptome and provide a general view of potential biomarkers involved in response to pollutants for this species.

2. Data description

2.1. Specimens and transcriptome sequencing

G. antarctica was collected from tidal pools in Marian Cove, near King Sejong Station on the northern Antarctic Peninsula (62°14′S, 58°47′W) in January 2011 using a net. Three short-term (3 day) treatments were imposed consisting of three pollutants. 10–12 actively swimming adults of similar size were randomly allocated to the following treatments: PCBs (Polychlorinated biphenyls) 10 ppb, PFOS (Perfluorooctanesulfonic acid) 100 ppb and PFOA (Perfluorooctanoic acid) 100 ppb, plus a control, and pooled for Illumina sequencing. Total RNA was extracted and subjected to poly-A selection and a cDNA library was constructed using the TruSeq RNA sample prep kit (Illumina Inc., SanDiego, CA). RNA-seq was performed in a single lane of an Illumina GAII platform (Illumina Inc., San Diego, CA) at the DNAlink Co. (Seoul, Korea) using a 100-cycle sequencing strategy.

2.2. De novo assembly

The de novo transcriptome assembly was constructed using a CLC Genomics Workbench 7.5 environment (CLC Bio Aarhus, Denmark) and a total of 46,524,315 raw reads (control, 8,911,747; PCBs treated, 12,493,240; PFOS treated, 11,913,909; PFOA treated, 13,205,419), with a minimum allowed contig length of 500 nucleotides and all other

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Table 1
Sequencing, de novo assembly and annotation statistics.

Number of total reads	46,524,315
Total sequencing output	4.6 Gb
Number of assembled contigs	20,749
Maximum contig length	20,822
Mean contig length	880
N50	889
Contigs with BLASTp matches in nr/UniprotKB/Swiss-Prot	12,461
Contigs with Gene Ontology terms (cellular component)	3094
Contigs with Gene Ontology terms (molecular function)	5096
Contigs with Gene Ontology terms (biological process)	4085

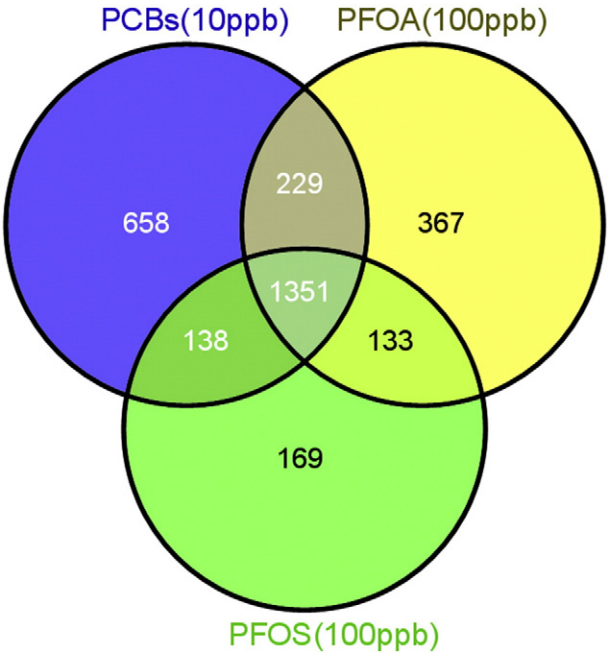

Fig. 1. Comparison between the upregulated (over twofold) genes of *G. antarctica* after exposure to three pollutants. The Venn diagram summarizes the number of genes upregulated in response to each pollutant.

parameters set to the default settings. The assembly process generated 20,749 contigs with a N50 value of 889 (Table 1).

2.3. Transcriptome annotation

Annotation of *G. antarctica* contigs was performed using a BLASTx search against the Uniprot and NCBI nr databases (Altschul et al., 1990). In both cases, the cut-off e-value was $1e^{-6}$. The results comprised 12,461 (61%) contigs with matches. The 12,461 annotated contigs were analyzed by means of GO terms, thus providing a better understanding of the distribution of gene functions. The Blast2GO application was used for the functional annotation of contigs by mapping gene ontology (GO) terms to transcripts with Blast hits (Götz et al., 2008) as obtained from Blast searches against the NR databases. An RNA-seq approach to assess potentially differentially expressed features in response to the pollutants was performed using the CLC Genomics Workbench RNA-seq mapping tool. 1351 genes were commonly upregulated in response to the three pollutants, and 658, 169 and 367 genes were specifically upregulated in response to PCBs, PFOS and PFOA, respectively (Fig. 1 and Supplementary Table S1).

2.4. Data deposition

The raw sequence data from *G. antarctica* were deposited in the NCBI Sequence Read Archive (SRA), with accession numbers SRR2075811, SRR2075812, SRR2075813 and SRR2075814.

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.margen.2015.07.012.

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