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Deep sequencing of the mantle transcriptome of the great scallop *Pecten maximus*

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Abstract :

RNA-Seq transcriptome data were generated from mantle tissue of the great scallop, Pecten maximus. The consensus data were produced from a time course series of animals subjected to a 56-day thermal challenge at 3 different temperatures. A total of 26,064 contigs were assembled de novo, providing a useful resource for both the aquaculture community and researchers with an interest in mollusc shell production.

Keywords : *Pecten maximus*, RNAseq, Temperature

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1.Introduction

The great scallop *Pecten maximus* is a bivalve mollusc, which occurs over a wide latitudinal gradient, from Spain to Norway, inhabiting depths from 0 m to 500 m (Chauvau*d et a*l., 2005). This is an economically important species, comprising almost 80% of European wild harvested scallops. Furthermore, aquaculture is expanding, especially in France and Ireland where hatchery-produced seed is used to enhance the production in the wild. The transcriptome data were generated as part of a more detailed study, investigating the effect of temperature on growth and development.

One year old scallops (average length : 34.0 +/- 4.1 mm) were obtained from the Tinduff hatchery (Bay of Brest, France). They were cultured at 3 different temperatures: ambient controls at 14.8 ± 0.6°C and also the elevated temperatures of 21.4 ± 0.2°C and 25.2 ± 0.9°C . Individuals in each treatment were sampled over a time course from the beginning of the experiment and then after 3, 7, 14, 21, 27, 42 and 56 days. The scallops were dissected and mantle tissue was flash frozen in liquid nitrogen and stored at -80°C until further analysis. Total RNA was extracted from mantle tissue of 4 individuals per treatment at each time point using TRI Reagent® Solution (Life Technologies) according to manufacturer's instructions. RNA quality and concentration were determined using an Agilent 2100 RNA Nanochip (Agilent, Santa Clara, CA, USA) and a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA), respectively. For each condition, the RNAs from the 4 individuals at each time point were then pooled for RNA-Seq. From these pooled samples, 22 cDNA libraries were produced (cf. Table 1 for details). The production of the Illumina libraries and the transcriptome sequencing using the Illumina HiSeq™2500 (HiSeq 100bp pair-ends) was conducted by the Genome Analysis Centre (Norwich, UK).

Table 1 : Sampling details for the 22 cDNA libraries produced from mantle tissue of *Pecten maximus*

library name	Illumina pair reads	Days of sampling	Water temperature
LIB650	84501929	0	15.21
LIB1034	28360963	3	14.75
LIB530	33666167	3	19.47
LIB651	36249865	3	19.23
LIB531	31338366	7	21.46
LIB532	23236209	7	14.8
LIB533	41914200	7	21.4
LIB1035	29169807	14	24.98
LIB1036	23746508	14	14.94
LIB1037	31458013	14	21.53
LIB654	30034307	21	25.36
LIB655	20315515	21	14.69
LIB660	28367527	21	21.37
LIB656	14723720	27	25.33
LIB657	22531517	27	21.44
LIB661	29224707	27	14.88
LIB658	29214964	42	14.86
LIB662	26693489	42	25.35
LIB663	32078459	42	21.48
LIB1038	15276016	56	25.37
LIB664	28606041	56	14.78
LIB665	26853248	56	21.49

The RNA libraries yielded 667 million paired end reads. Raw reads were filtered and trimmed using the FASTX-toolkit (Version 0.0.13 from Assaf Gordon Hannon lab) and rRNA contamination was removed using riboPicker (Schmieder *et a*l., 2012) and cutadapt (Version 1.1; Martin, 2011), with a final quality check performed using fastQC (Version 0.10.0 ; http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc/).

The contigs were assembled using SOAPdenovo (Luo *et a*l., 2012), and a kmer size of 89 was used to construct the initial *de novo* transcriptome assembly, resulting in 1,311,367 contigs. These contigs were then used in a further assembly with CAP3 (Huang & Madan, 1999). Contigs from both rounds of assemblies that were greater than 500bp, totaling 26 064, were used in a sequence similarity search against an in-house nr database using an e-value cutoff of 1e-10. Putative annotation based on sequence similarity searching could be assigned to approximately 23.5% of the contigs (Table 2).

Table 2 : Statistics for the transcriptome generation from mantle tissue of *Pecten maximus*

Total reads	1335123074
Total Contigs	26064
Average Contig length (bp)	1011
Median length (bp)	815
Max length (bp)	11760
Min length (bp)	490
% Annotated Contigs	23.5%

These data generated from the mantle of *P. maximus* form a valuable addition to those generated from hemocytes of the same species (Pauletto *et a*l., 2014) and, in a more general context, to the transcriptomes generated for other molluscs including the Yesso scallop *Patinopecten yessoensis* (Hou *et a*l., 2011), *Mytilus galloprovincialis* (Craft *et a*l., 2010), *Laternula elliptica* (Clark *et a*l., 2010), *Meretrix meretrix* (Huan *et a*l., 2012), *Ruditapes philippinarum* (Milan *et a*l., 2011), *Haliotis midae* (Franchini *et a*l., 2011), several pearl oysters (Huang *et a*l., 2013) and the oyster genome data (Zhang *et a*l., 2012), thus increasing the sequence resource available for commercially important shellfish species and for researchers investigating shell deposition processes in molluscs.

2. **Nucleotide sequence accession numbers**

The sequence data for this transcriptome has been deposited in the GenBank SRA, accession number: SRP040427. The contigs, and the annotation for those contigs with a match of 1e-10 and lower, are available from http://ramadda.nerc-bas.ac.uk/repository/entry/show/Polar+Data+Centre/NERC-BAS+Datasets/Genomics/

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