Data in Brief 9 (2016) 699–703

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data on microRNAs and microRNA-targeted mRNAs in *Xenopus* ectoderm

Vrutant V. Shah [a], Benjamin Soibam [b,d], Ruth A. Ritter [a], Ashley Benham [b], Jamina Oomen [c], Amy K. Sater [a,*]

[a] *University of Houston, Houston, TX, USA*
[b] *Texas Heart Institute, Houston, TX, USA*
[c] *Stonybrook Univ., Stonybrook, NY, USA*
[d] *Department of Computer Science and Engineering technology, University of Houston-Downtown, Houston, TX, USA*

ARTICLE INFO

Article history:
Received 19 August 2016
Received in revised form
27 September 2016
Accepted 30 September 2016
Available online 14 October 2016

Keywords:
microRNA
Neural
Ectoderm
Xenopus

ABSTRACT

Small RNAs from early neural (i.e., Noggin-expressing, or NOG) and epidermal (expressing a constitutively active BMP4 receptor, CABR) ectoderm in *Xenopus laevis* were sequenced to identify microRNAs (miRs) expressed in each tissue. Argonaute-associated mRNAs were isolated and sequenced to identify genes that are regulated by microRNAs in these tissues. Interactions between these ectodermal miRs and selected miR-regulated mRNAs were predicted using the PITA algorithm; PITA predictions for over 600 mRNAs are presented. All sequencing data are available at NCBI (NCBI Bioproject Accession number: PRJNA325834). This article accompanies the manuscript "MicroRNAs and ectodermal specification I. Identification of miRs and miR-targeted mRNAs in early anterior neural and epidermal ectoderm" (V.V. Shah, B. Soibam, R. A. Ritter, A. Benham, J. Oomen, A.K. Sater, 2016) [1].

DOI of original article: http://dx.doi.org/10.1016/j.ydbio.2016.08.017
* Corresponding author.
E-mail address: asater@uh.edu (A.K. Sater).

http://dx.doi.org/10.1016/j.dib.2016.09.054

Specifications Table

Subject area	Developmental Biology and Genomics
More specific subject area	microRNAs and early ectodermal development
Type of data	Supplementary tables
How data was acquired	Next-Generation Sequencing; multiple instruments
Data format	Analyzed
Experimental Factors	Xenopus ectoderm in which BMP signals are either inhibited (NOG) or activated (CABR) to give rise to either neural or epidermal tissue, respectively.
Experimental features	We generated ectoderm overexpressing either noggin (NOG) to elicit an anterior neural state, or a constitutively active BMP4 receptor (CABR) to elicit an epidermal state of specification. These tissues were used to prepare microRNAs and argonaute-associated mRNAs (thus regulated by microRNAs) for sequencing and analysis.
Data source location	Houston, TX, USA
Data accessibility	Data are submitted with this publication; sequencing reads are also available through NCBI Bioproject Accession number: PRJNA325834 at http://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA325834

Value of the data

- Sequence data and target predictions provide a foundation for subsequent functional analyses of miR-mRNA interactions. Large-scale microRNA target predictions have not previously been generated for *Xenopus laevis*.
- These datasets can support future studies on microRNA-dependent translational control in embryonic systems, and they can be used to establish the extent of conservation of microRNA-targeted mRNA interactions.
- These datasets can be used to investigate the roles of microRNAs in the establishment of neural vs epidermal ectoderm, the transition from the early neural gene regulatory network to the neural proliferative and neurogenic networks, and the restriction of pluripotency in embryonic ectoderm.

1. Data

These data include:

1) The identification and genomic locations of microRNAs expressed in early neural and epidermal ectoderm from *Xenopus laevis* embryos. Sequence reads for 3 biological replicates, as well as the accompanying DESeq analysis, are provided. (Supplementary Table 1 in Ref. [1] and Supplementary Table 2).
2) The identification of RNAs in the Argonaute Ribonucleoprotein complex (Ago–RNP) from in early neural and epidermal ectoderm from *Xenopus laevis* embryos (Supplementary Table 3). Total RNAs present in both samples are also identified (Supplementary Table 4).
3) Predicted miR-mRNA interactions for “High Confidence” miR-targeted ectodermal mRNAs from the Ago–RNP pools for early neural and epidermal ectoderm (Supplementary Table 5).
4) Gene Ontology (GO) categories and associated genes among the “High Confidence” miR-targeted ectodermal mRNAs (Supplementary Table 6).
5) Conserved targets of pou5f3 among the miR-targeted mRNAs for NOG and CABR Ago-associated mRNAs and predictions of miR –mRNA interactions for the genes (Supplementary Table 7).