



**HAL**  
open science

## RNA-Seq transcriptome data of undifferentiated and differentiated gonads of Siberian sturgeon

Christophe C. Klopp, André Lasalle, Santiago Di Landro, Denise Vizziano-Cantonnet

► **To cite this version:**

Christophe C. Klopp, André Lasalle, Santiago Di Landro, Denise Vizziano-Cantonnet. RNA-Seq transcriptome data of undifferentiated and differentiated gonads of Siberian sturgeon. *Data in Brief*, 2020, 31, 10.1016/j.dib.2020.105741 . hal-03182864

**HAL Id: hal-03182864**

**<https://hal.inrae.fr/hal-03182864>**

Submitted on 26 Mar 2021

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



## Data Article

# RNA-Seq transcriptome data of undifferentiated and differentiated gonads of Siberian sturgeon



Christophe Klopp<sup>a</sup>, André Lasalle<sup>b</sup>, Santiago Di Landro<sup>b</sup>,  
Denise Vizziano-Cantonnet<sup>b,\*</sup>

<sup>a</sup> INRA, SIGENAE, Genotoul Bioinfo, MIAT UR875, Chemin de Borde-Rouge - Auzeville BP 52627, 31326 CASTANET-TOLOSAN CEDEX, France

<sup>b</sup> Laboratorio de Fisiología de la Reproducción y Ecología de Peces, Instituto de Biología, Facultad de Ciencias, Universidad de la República Oriental del Uruguay, Iguá 4225, Montevideo 11400, Uruguay

## ARTICLE INFO

## Article history:

Received 18 February 2020

Revised 7 May 2020

Accepted 15 May 2020

Available online 22 May 2020

## Keywords:

RNA sequencing

gonads

*Acipenser baerii*

sex differentiation

gametogenesis

## ABSTRACT

RNA-Seq transcriptome data from twenty Siberian sturgeon gonads at different developmental stages is described: ten undifferentiated gonads, six gonads of immature males and four gonads from immature females. Siberian sturgeon, *Acipenser baerii*, is long-lived, late-maturing fish farmed in 50 countries but its production remains on a craftsman scale when compared to industrial species. Sturgeon genetic and physiological studies are less developed than for industrial fish. The data presented hereafter enables fundamental studies on the regulatory mechanisms of sturgeon gonad development, which can further be applied both in aquaculture and in fundamental research.

© 2020 The Author(s). Published by Elsevier Inc.

This is an open access article under the CC BY license.

(<http://creativecommons.org/licenses/by/4.0/>)

\* Corresponding author: Denise Vizziano Cantonnet. Laboratorio de Fisiología de la Reproducción y Ecología de Peces, Instituto de Biología, Facultad de Ciencias, Universidad de la República Oriental del Uruguay, Iguá 4225, Montevideo 11400, Uruguay. Phone: +598 2 525 86 18x7150.

E-mail address: [vizziano@gmail.com](mailto:vizziano@gmail.com) (D. Vizziano-Cantonnet).

<https://doi.org/10.1016/j.dib.2020.105741>

2352-3409/© 2020 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY license. (<http://creativecommons.org/licenses/by/4.0/>)

## Specifications Table

|                                |  |
|--------------------------------|--|
| Subject                        | Biology  |
| Specific subject area          | Transcriptomics, sex determination and differentiation   |
| Type of data                   | Raw RNA-Seq data and assembled reference transcriptome assembly  |
| How data were acquired         | Illumina HiSeq 2500  |
| Data format                    | Raw data and assembly information  |
| Parameters for data collection | Gonads from 10 sex undifferentiated fish of 3 to 6 months of age   |
| Description of data collection | Gonads from 4 immatures males (only spermatogonias) before first maturity and from 6 immatures females (with oogonias and pre-vitellogenic oocytes) Gonads were collected from Siberian sturgeons farmed at Estuario del Plata (San Gregorio de Polanco, Uruguay) under natural conditions. The gonad stage was identified by histology for fish $\geq 6$ months of age.   |
| Data source location           | Laboratorio de Fisiología de la Reproducción y Ecología de Peces, Facultad de Ciencias, Universidad de la República Oriental del Uruguay.<br>Country: Uruguay<br>Site of collection: Estuario del Plata sturgeon farm, San Gregorio de Polanco, Tacuarembó, Uruguay  |
| Data accessibility             | Raw data of RNA Seq analysis are available on Sequence Read Archive (SRA) database and connected with BioProject PRJNA589957<br><a href="https://www.ncbi.nlm.nih.gov/bioproject/PRJNA589957">https://www.ncbi.nlm.nih.gov/bioproject/PRJNA589957</a><br>Reference transcriptome assembly is available at the NCBI in TSA<br><a href="https://www.ncbi.nlm.nih.gov/nucore/GICD00000000">https://www.ncbi.nlm.nih.gov/nucore/GICD00000000</a> |

## Value of Data

- This data set will benefit the community of scientists working on sex determination/sex differentiation mechanisms and gametogenesis as well as fish evolution.
- This data set includes RNA-Seq of gonads at several stages before and after sex differentiation enabling to better understand the control of sex differentiation.
- This data will facilitate the development of sex control strategies to increase aquaculture production of Siberian sturgeon.

## 1. Data Description

Gonadal development, from sex differentiation to the end of gametogenesis and gamete production is a key process for species perpetuation. Understanding the different regulation steps of gonad development is a key point in reproduction studies. These studies may have an impact at the applied level in the control of sex and production of gametes in aquaculture; and they also can be useful for the understanding of the general mechanisms of sex differentiation and its evolution. The Siberian sturgeon is a long lived and late maturing fish for which mechanisms of sex differentiation and gametogenesis are not well understood [1]. The unraveling of the molecular control of sex differentiation and early gametogenesis can profit from gonad RNA-seq data sets at different maturation stages. We provide here a high-quality data set including 10 gonads from sex undifferentiated animals and 10 immature gonads at early stages of gametogenesis.

Gonad samples were taken from fish at several stages of sex undifferentiated period (2.5, 3, 5, and 6 months of age), males at immature stage containing only spermatogonia (8, 9, 14 and 17 months of age), and females with oogonias and different stages of oocyte development previous to vitellogenesis (9 and 17 months of age) [1]. The gonads were sequenced individually using Illumina HiSeq 2500, except at 2.5 months for which gonads of 13 fish were collected individually under binocular loupe and pooled before RNA extraction. Raw data correspond to Fastq for RNA-Seq reads and fasta for assembled contigs. The library identification and the corresponding SRA files are given in the Table 1.

**Table 1**  
Fish identification (Id), library name, SRA files, SAMN files, sequencer and quality of sequences produced

| Fish Id | Tissue samples         | Library name | SRA files   | SAMN files   | Sequencer           | Nb of bases <sup>(1)</sup> | Alignment rate <sup>(2)</sup> | Q20 ratio <sup>(3)</sup> |
|---------|------------------------|--------------|-------------|--------------|---------------------|----------------------------|-------------------------------|--------------------------|
| I1      | Undifferentiated gonad | 186          | SRR10466921 | SAMN13294989 | Illumina HiSeq 2500 | 2590499400                 | 93,25                         | 96,19                    |
| I2      | Undifferentiated gonad | 414          | SRR10466920 | SAMN13294990 | Illumina HiSeq 2500 | 3599333200                 | 95,09                         | 90,54                    |
| I3      | Undifferentiated gonad | 417          | SRR10466909 | SAMN13294991 | Illumina HiSeq 2500 | 2951092800                 | 94,45                         | 90,50                    |
| I4      | Undifferentiated gonad | 640          | SRR10466908 | SAMN13294992 | Illumina HiSeq 2500 | 3356820000                 | 95,26                         | 90,16                    |
| I5      | Undifferentiated gonad | 649          | SRR10466907 | SAMN13294993 | Illumina HiSeq 2500 | 3016267800                 | 94,51                         | 89,90                    |
| I6      | Undifferentiated gonad | 961          | SRR10466906 | SAMN13294994 | Illumina HiSeq 2500 | 8362045600                 | 94,38                         | 90,12                    |
| I7      | Undifferentiated gonad | 302          | SRR10466905 | SAMN13294995 | Illumina HiSeq 2500 | 1,2866E+10                 | 96,53                         | 96,92                    |
| I8      | Undifferentiated gonad | 306          | SRR10466904 | SAMN13294996 | Illumina HiSeq 2500 | 2,4061E+10                 | 95,53                         | 96,86                    |
| I9      | Undifferentiated gonad | 313          | SRR10466903 | SAMN13294997 | Illumina HiSeq 2500 | 1,2309E+10                 | 97,02                         | 96,20                    |
| I10     | Undifferentiated gonad | 214          | SRR10466902 | SAMN13294998 | Illumina HiSeq 2500 | 1,245E+10                  | 96,73                         | 97,09                    |
| M1      | Immature testis        | 152          | SRR10466919 | SAMN13294999 | Illumina HiSeq 2500 | 1,5511E+10                 | 95,72                         | 96,40                    |
| M2      | Immature testis        | 165          | SRR10466918 | SAMN13295000 | Illumina HiSeq 2500 | 5879588200                 | 94,92                         | 96,54                    |
| M3      | Immature testis        | 172          | SRR10466917 | SAMN13295001 | Illumina HiSeq 2500 | 5963519600                 | 96,24                         | 96,72                    |
| M4      | Immature testis        | 175          | SRR10466916 | SAMN13295002 | Illumina HiSeq 2500 | 1,0986E+10                 | 94,63                         | 96,65                    |
| M5      | Immature testis        | 259          | SRR10466915 | SAMN13295003 | Illumina HiSeq 2500 | 2511126800                 | 95,24                         | 96,85                    |
| M6      | Immature testis        | 260          | SRR10466914 | SAMN13295004 | Illumina HiSeq 2500 | 3239050400                 | 95,37                         | 96,59                    |
| F1      | Immature ovary         | 171          | SRR10466913 | SAMN13295005 | Illumina HiSeq 2500 | 3099329000                 | 94,01                         | 96,31                    |
| F2      | Immature ovary         | 173          | SRR10466912 | SAMN13295006 | Illumina HiSeq 2500 | 3117568600                 | 94,18                         | 96,54                    |
| F3      | Immature ovary         | 261          | SRR10466911 | SAMN13295007 | Illumina HiSeq 2500 | 2092346200                 | 97,92                         | 96,51                    |
| F4      | Immature ovary         | 262          | SRR10466910 | SAMN13295008 | Illumina HiSeq 2500 | 2587806600                 | 97,91                         | 96,64                    |

<sup>(1)</sup> Number of bases

<sup>(2)</sup> Alignment rate: is the number of sequences aligned on the de novo transcriptome reference divided by the total number of sequences of the sample expressed in percent

<sup>(3)</sup> Q20 ratio is the number of raw read base pairs having a quality score equal or over 20 divided by the total number of read base pairs of the sample expressed in percent.

## 2. Experimental Design, Materials, and Methods

### 2.1. Ethics statement

Research procedures involving animal experimentation complied with international principles on the use and care of laboratory animals and Uruguayan regulations on animal welfare (Comisión Honoraria de Experimentación Animal: CHEA). The protocol was approved by the “Comisión de Etica en el Uso de Animales” from the Comisión Honoraria de Experimentación Animal CHEA of Uruguay (Authorization Number 006-11).

### 2.2. Experimental animals and rearing procedures

Siberian sturgeon (*Acipenser baerii*) individuals were obtained from a fish farm (Estuario del Plata, Uruguay). The embryos come from Poland, and were hatched and reared at natural temperature at the sturgeon farm [2]. The fish were sacrificed by spinal transection. Gonad samples for transcriptome studies were used individually for RNA extraction, except for the 2.5-month-old individuals, for which gonads of 13 fish were pooled for RNA extraction due to their minute size. The external gonad characteristics were observed for fish aged 2.5–5 months that were considered as sex undifferentiated following previous studies made in our Laboratory [1, 3]. For 6-month-old fish, gonad staging was performed in fish from the same cohort as the fish used for RNA extraction, as the gonads are too small to at this age to allow for RNA extraction and histological gonad staging in the same fish. In fish >6 months of age, one gonad was frozen in liquid nitrogen and stored at -80°C until RNA extraction, and the contralateral gonad was stored in 10% formaldehyde for histological analysis). Histological data were reported previously [3].

### 2.3. RNA extraction, cDNA library construction, and Illumina sequencing

RNA was extracted using the Illustra RNeasy Mini RNA Isolation Kit (GE Healthcare, Little Chalfont, UK) according to manufacturer instructions, and quality was assessed using an Agilent 2100 Bioanalyzer. The cDNA libraries were developed from the total RNA of the individual samples. The RNA samples conformed to the required purity criteria (A260/A230 and A260/A280 >1.8) and quality levels (RIN >8) (Agilent 2100 Bioanalyzer) for library preparations for sequencing. The cDNA libraries were constructed on a Tecan EVO200 liquid handler using the Illumina TruSeq Stranded mRNA sample prep kit for RNA analysis. Briefly, the mRNA molecules containing poly (A) were purified using magnetic poly (T) beads from each total RNA sample. A fragmentation buffer was added to break the mRNA into short fragments with an average length of 155 base pairs (bp) (120–210 bp). From these fragments, the first strand cDNA was synthesized using random hexamer primer. The second cDNA strand was synthesized. After purification and end repair, these short cDNA were ligated to the sequencing adapters (60 bp on each side) and enriched by polymerase chain reaction (PCR, 12 cycles). Libraries were checked using an Agilent High Sensitivity DNA Kit and quantified with a KAPA Library Quantification Kit to ensure accuracy. RNA-seq experiments were performed on the Illumina HiSeq 2500 platform (high-throughput mode) with a paired-end read length of 2 × 100 bp and an Illumina TruSeq SBS kit, v3.

### 2.4. Transcriptome assembly

The reads were assembled using the methods presented in [1] and released at in NCBI in TSA (Transcriptome Shotgun Assembly): <https://www.ncbi.nlm.nih.gov/nucore/GICD00000000>. The

quality assessment results of the assembled transcriptome were presented in [3] and resumed in Table 1.

## Author Contributions

C.K. and D.V.C. conceived and designed the experiments; D.V.C. directed the research project, acquired the funding and administrate the projects; A.L. and SDL performed the experiments; C.K. and D.V.C. analyzed the data and organized the datasets; the manuscript was written by C.K. and D.V.C.

## Funding

This work was supported by the Comisión Sectorial de Investigación Científica (CSIC), Universidad de la República Oriental del Uruguay, Grant C225-348-Uruguay; the Agencia Nacional de Investigación e Innovación-Dirección Nacional de Recursos Acuáticos ANII-DINARA – FPA 9975-Uruguay; and Agencia Nacional de Investigación e Innovación – FMV\_1\_2017\_1\_135908.

## Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper

## Acknowledgements

The authors acknowledge the chief executive officer of Estuario del Plata Facundo Márquez, to Dr. Vet. Andres Ryncowski, Mr. Eduardo Oliver, and all of the Estuario del Plata (Uruguay) staff for their ample support and kindness during the development of this work.

## Supplementary Materials

Supplementary material associated with this article can be found, in the online version, at doi:[10.1016/j.dib.2020.105741](https://doi.org/10.1016/j.dib.2020.105741).

## References

- [1] D. Vizziano-Cantonnet, A. Lasalle, S. Di Landro, C. Klopp, C. Genthon, *De novo* transcriptome analysis to search for sex-differentiation genes in the Siberian sturgeon, *Gen. Comp. Endocrinol.* 268 (2018) 96–109 <https://doi.org/10.1016/j.ygcen.2018.08.007>.
- [2] D. Vizziano-Cantonnet, S. Di Landro, A. Lasalle, Sex determination and differentiation of the Siberian sturgeon: morphological and molecular approaches, in: P. Williot, G. Nonnote, D. Vizziano (Eds.), *The Siberian Sturgeon (Acipenser Baerii, Brand. 1869)*, Springer, 2018 [https://doi.org/10.1007/978-3-319-61664-3\\_6](https://doi.org/10.1007/978-3-319-61664-3_6).
- [3] D. Vizziano-Cantonnet, S. Di Landro, A. Lasalle, A. Martínez, T.S. Mazzoni, I. Quagio-Grassiotto, Identification of the molecular sex-differentiation period in the siberian sturgeon, *Mol. Reprod. Dev* (2016) 83 <https://doi.org/10.1002/mrd.22589>.