

Introduction

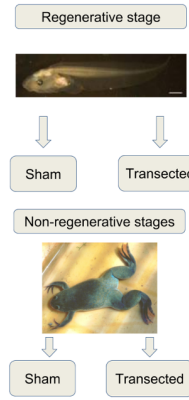
The early development stages of the frog *Xenopus laevis* are known as the regenerative (R) stage, because during that time, it is able to regenerate its spinal cord upon injury. After its metamorphosis into a frog, *X. laevis* goes into its non-regenerative (NR) stage, and it is unable to regenerate its spinal cord. It has been reported that there are differences in the gene repertoire expressed at each stage, and also in its timing. One molecular agent that might influence gene expression and its timing are small non-coding RNAs (snc-RNAs).

Proposal

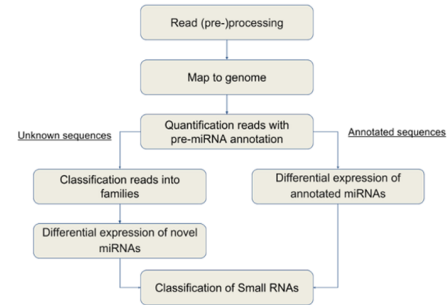
We proposed to study the differential expression of non coding sRNAs in the regenerative stage respect to the non-regenerative stage. And obtain a set of differentially expressed sRNAs divided in two groups, the group of known sRNAs and the group of new sRNAs.

Methods

Experimental Methods



Bioinformatic Pipeline



Results

N° known pre-miRNAs differentially expressed

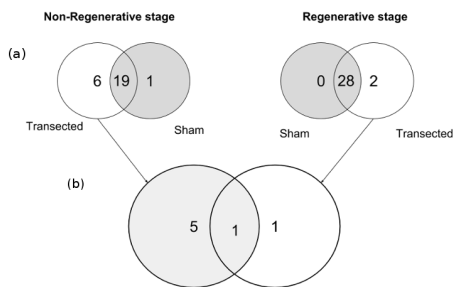


Figure 1. Comparison of the response to spinal cord injury in regenerative and non-regenerative stages. (a) Total pre-miRNAs annotated that responded differently in R and NR-stages, between sham-operated and transected. (b) Venn diagram showing all differentially expressed pre-miRNA detected as differentially expressed.

N° novel sRNA differentially expressed

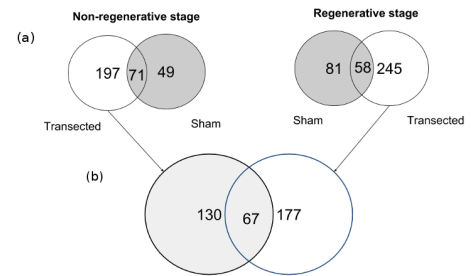


Figure 2. Comparison of the response to spinal cord injury in regenerative and non-regenerative stages. (a) Total novel sRNA that responded differently in R and NR-stages, between sham-operated and transected. (b) Venn diagram showing all differentially expressed novel sRNA detected as differentially expressed.

Genomic location of known pre-miRNAs expressed, between regenerative and non-regenerative stages

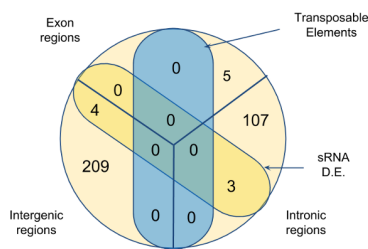


Figure 3. Genomic locations of pre-miRNAs based on the numbers total of pre-miRNAs and differentially-expressed (yellow).

Genomic location of novel sRNA expressed, between regenerative and non-regenerative stages

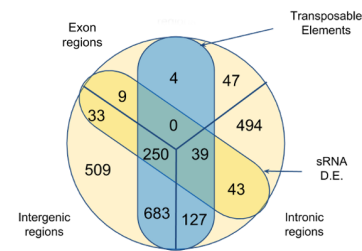


Figure 4. Genomic locations of novel sRNA based on the numbers total of sRNAs and differentially-expressed (yellow).

Conclusions

- 6 known pre-miRNAs are differentially expressed, 1 were regulated in both stages, 1 regulated exclusively in the R-stage and 5 in the NR-stage
- 374 novel sRNAs are differentially expressed, 67 were regulated in both stages, 177 in stage R-stage and 130 in NR-stage.
- 34% of novel sRNA differentially expressed are in intronic regions.
- 374 novel sRNAs are DE. 289 come from TEs, 250 of which are in intergenic regions and 39 are in intronic regions.
- 763 novel sRNA are in gene regions, 700 of which are in intronic regions, but only 39 are differentially expressed.
- In total there are more than 2,000 genomic regions that originate sRNA families in *X. laevis*.

Next step

Predict the target miRNAs of differentially expressed families.

References

- Dasfne Lee-Liu, Mauricio Moreno, Leonardo I Almonacid, Victor S Tapia, Rosana Muñoz, Javier von Marées, Marcia Gaete, Francisco Melo, and Juan Larraín. Genome-wide expression profile of the response to spinal cord injury in *Xenopus laevis* reveals extensive differences between regenerative and non-regenerative stages. *Neuraldevelopment*, 9:12, 2014

Acknowledgements