

The axolotl genome and the evolution of key tissue formation regulators

Genome Biology

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Introduction

- *Ambystoma mexicanum*
- No metamorphosis
- Extensive regeneration abilities



Figure 1: Axolotl

Genome characteristics

- Large genome: **32 Gb**
- High number of repeats: ~65%
- Mostly long terminal repeats (LTR)

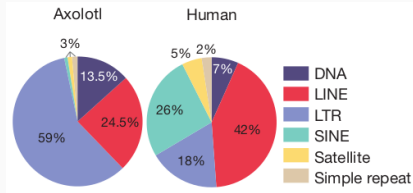


Figure 2: Major repeat classes

- PacBio + Illumina
- Development of a novel genome assembler (MARVEL)
- Thorough assessment of the genome assembly

Genome annotation and analysis

- Protein-coding genes: ~23.000
- Large median intron size: x13 human
- Intron size varies in developmental genes
- Identification of 5 transcripts

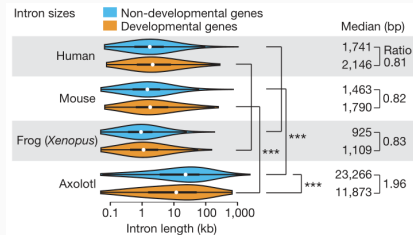


Figure 3: Median intron sizes

Comparative genomics analysis

- Analysis of homologs: **Pax** family
- Deletion of Pax3: functionality present in Pax7
- Mutation experiments: CRISPR and TALEN

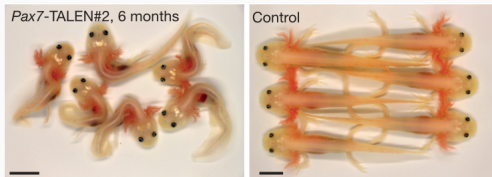


Figure 4: Effect of a Pax7 mutation

- Sequencing and annotation of a challenging organism
- Identification of limb regeneration transcripts
- Foundation to investigate gene regulation in regeneration