Spring 2015 Xenbase Newsletter

The Xenopus ORFeome is here!
The Xenopus ORFeome is a collection of ~9,000 PCR-amplified ORFs from the Xenopus Gene Collection cloned into Gateway entry plasmid vector, pDONR223. The ORFeome collection covers ~7,800 unique genes representing approximately 40% of the non-redundant *X. laevis* genome. Human orthologs were identified for ~7,000 of the validated frog clones, and ~2,200 are associated with human diseases. The ORFeome clones are available as a complete set of 93, 96-well plates from Biodesign Institute, EXRC, GE Healthcare, Harvard Medical School, and Source Bioscience. The Xenopus ORFeome PIs are Todd Stukenberg, David Hill, Michael Gilchrist, and Aaron Zorn. (Supported by NIH/NICHD grant R01HD069352).

A new outbred *Xenopus laevis* Genome- now online
The Michalak Lab at Virginia Tech sequenced an outbred adult *X. laevis* female (ZW) from the Southern Cape Region of South Africa (supplied by Xenopus Express). Illumina Hiseq and 454/Life Sciences sequencing platforms were used to obtain a ~2.67 Gb assembly on 871,573 scaffolds. Almost 30,000 gene models are annotated, with 13,705 mapped to genes. This is a new resource for comparative and population genomics providing insights into genome-scale polymorphisms. The outbred *X. laevis* genome is now available in the Xenbase genome browser and can be queried via BLAST.

New Genome Browser Tracks
- NCBI tracks (*X. tropicalis* v7.1) show alternative splicing, gene variants, pseudo genes and mirs/miRNAs
- new outbred Xenopus laevis genome
- genome details page has been re-vamped, allows downloadable FASTA files
- histone methylation,RNApol2, p300 CHiPseq data mapped to trop 7.1

Data Download/FTP site: now more user-friendly
- Xenbase data exports and stored files are more easily accessible on our FTP/downloads page.
- Each file has a "readme" description associated detailing the contents and format(s) of the file.
- Field names for tab delimited files are contained in the readme information.
- Files organised by data type: gene reports, ChIP-seq, microarrray, movies/videos etc.

Updates to the Xenopus genome editing online resources page
- CCTop now supports Xenla7.1 and XenTro3 genomes.
- GGGenome now supports:
    - X. tropicalis v.7: http://GGGenome.dbcls.jp/Xentr7/
    - X. tropicalis v.8: http://GGGenome.dbcls.jp/Xentr8/

Additional details can be seen at: http://www.xenbase.org/other/static/CRISPr.jsp

New *Xenopus laevis* Chromosome Nomenclature
Xenopus laevis is allotetraploid and has 36 chromosomes consisting of 2 sets of 18 chromosomes. The new chromosome nomenclature for *X. laevis* is based on phylogenetic relationship and chromosome length, i.e. XLA1L, XLA1S, XLA1L, XLA2S, etc. in which the numbering of XLA chromosomes corresponds to the diploid *X. tropicalis*. The postfixes 'L' and 'S' stand for long and short chromosomal homeologous pairs. The last *X. laevis* chromosome set, XLA9L and XLA9S, corresponds to fused XTR9 and XTR10, with XLA9_10L and XLA9_10S as synonyms. See: Matsuda et al., Cytogenet Genome Res. 2015 Apr 8. for more details.

Congratulations to the newly elected members of the National Academy of Sciences:

Marianne Bronner: California Institute of Technology, Pasadena, CA, USA.
Randall Moon: University of Washington, Seattle, WA, USA
Nancy Ip: Hong Kong University of Science and Technology, Kowloon, Hong Kong (China).

Xenbase Forums is the Xenopus community forum - a great place to seek answers to the day-to-day Xenopus life-hacks, dealing with difficult wet lab experiments, frog room drama, pesky reagents, - whatever you need help with - as your community!

Interested in submitting gene expression or other data sets to Xenbase?
Contact the curation team: xenbase@ucalgary.ca