Exploring the genetic architecture of vocal communication in *Xenopus*

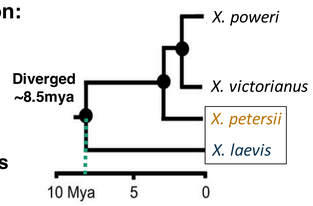
Young Mi Kwon[1], Ursula Kwong-Brown[1], Christa Baker[2], Therese Mitros[3], Avelyne Villain[1], Andres Bendesky[1,4,5], Darcy Kelley[1,5]

[1]Department of Biological Sciences, Columbia University, [2]Princeton University, [3]University of California Berkeley, [4]Department of Ecology, Evolution and Environmental Biology, [5]Zuckerman Mind Brain Behavior Institute

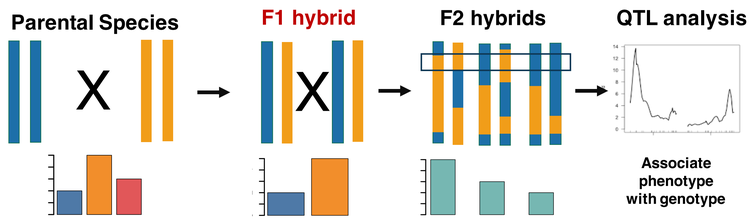
1 Overview of Xenopus

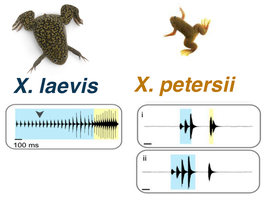
Xenopus **is a model for vocal communication:**

- Unique, innate vocal system
- Characterized vocal patterns and hindbrain neural circuitry
- Defined phylogeny with inter-breeding species



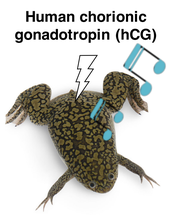
F2 Intercross:

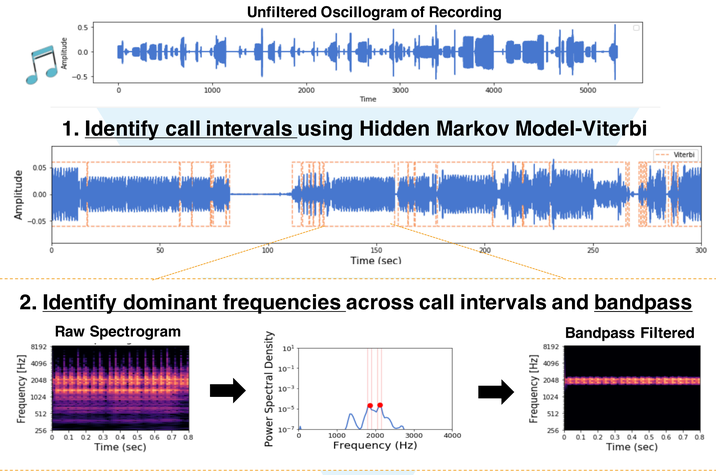


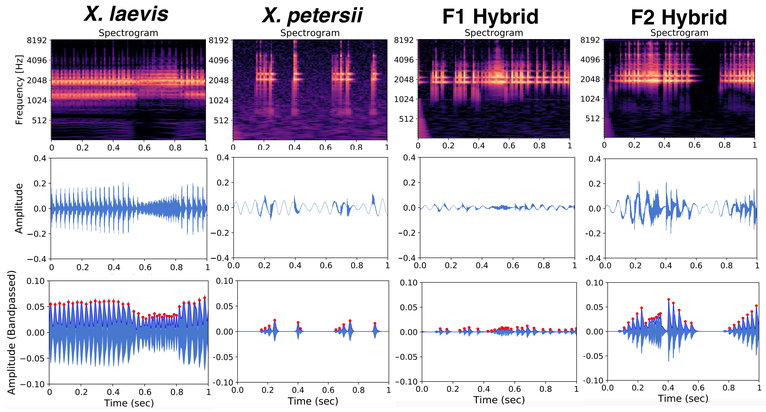


We will investigate the genetics of vocal communication in *Xenopus* using an F2 intercross

2 A pipeline for extracting temporal and spectral features of a recording for vocal analysis

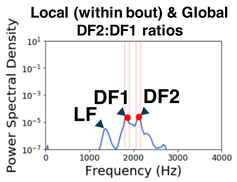




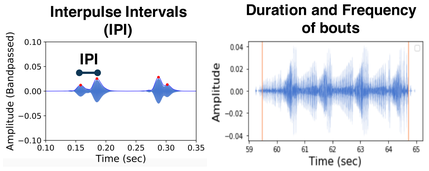


After call and pulse extraction, we assess for each individual:

Spectral Features

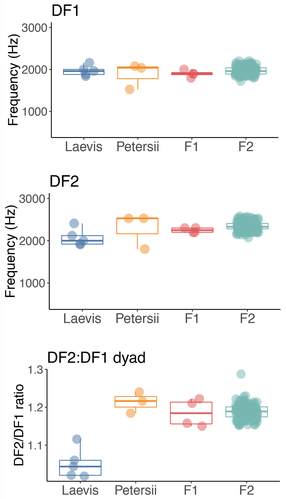


Temporal Features

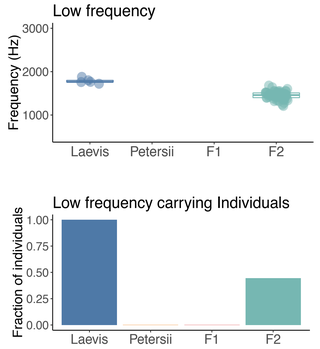


3 Analysis of male vocalization across the F2 intercross

Spectral Features: Dominant Frequency dyads



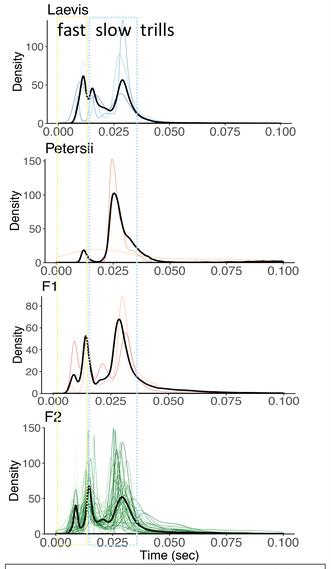
X. laevis **produce a lower frequency (LF) below the dominant frequencies (DF)**



F2 hybrids' dyads are more similar to *X. petersii*

F2 hybrids produce a lower frequency that is not observed in either *X. petersii* or F1 hybrids

Temporal Features: IPIs

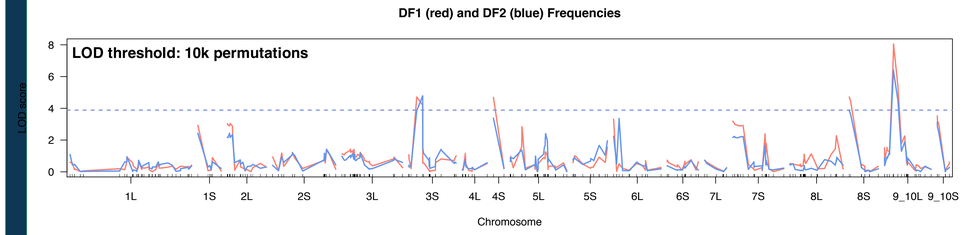


F1 hybrids show IPIs that differ from both parental species

4 Preliminary quantitative trait loci (QTL) analysis

1. Identified ~3.8 million candidate SNPs after analyzing whole genome sequences (WGS) of *X. laevis* ,*X. petersii* (including the founders of the F2 intercross), and the F1 hybrids
2. Whole genome sequenced 129 F2 hybrids at ~0.01-0.03x coverage
3. Called, imputed, and pruned SNPs in the F2s to obtain 533 informative genome-wide markers
4. QTL analysis of the vocal characteristics

Species	# of individuals	Coverage
X. laevis	4	16-28x
X. petersii	2	10-12x
F1 hybrids	4	0.5x



A pilot QTL suggests that a potential loci in Chr 9_10L may contribute to the variation observed in the dominant frequency dyads (DF1, DF2) in the F2s

5 Conclusions

1. We developed a pipeline that recapitulates previous findings on the spectral and temporal patterns across the *Xenopus* phylogeny.
2. We newly characterized a lower frequency (LF) that is specific to *X. laevis.*
3. We identified putative loci that may regulate the dominant frequencies using QTL.

6 Current Directions

1. Increase sample size of F2 hybrids for vocal characterization and genotyping for QTL
2. Investigate the specificity of the F2 female response to male advertisement calling
3. Examine the genes that may be involved in the regulation of male vocalization through the brain and larynx in *X. laevis* and *X. petersii.*

7 Acknowledgments

We would like to give thanks to Charlotte Barkan and Erik Zornick for their input and funding from the Columbia RISE and NIH (NS234684) grants.