Assessment of family lineage in *Lobotes surinamensis* aquaculture stocks

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**Introduction:**
- Genomic sequences can be aligned to determine single nucleotide polymorphisms (SNPs), and these variable DNA sites can be used to determine parental lineage.
- We can enhance aquaculture stock of Atlantic tripletail (*Lobotes surinamensis*) offspring at the University of Miami Experimental Hatchery (UMEH) at the Rosenstiel School by defining successful parents.
- My research isolated genomic DNA and created a genotype-by-sequencing (GBS) library to define SNPs and determine parental lineages.

**Results:**
- Library: ~600 bp sequences
- Library concentration: 37.8 ng/μL
- Library volume: 30 μL

**Discussion:**
The gDNA was isolated, digested with restriction enzyme ApeK1, then bar codes used to identify individuals were ligated to the size selected DNA fragments (500-700 bp). Analysis using gel electrophoresis showed that the library had a range from 1000-500 pb before size selection, which was reduced to a range of about 500-700 bp post-size selection. Each individual has a unique DNA barcode, so that SNPs for each individual can be identified using a GBS pipeline. From the SNPs, the full parental lineage of the offspring generation will be determined and used to achieve improved breeding outcomes.

**Conclusion / Future Goals:**
- By identifying the parental lineage of the offspring generation, it may be possible to improve broodstock management regimes.
- Future breeding can be improved by accounting for genotype information.
- One of the key first steps in establishing breeding programs for aquaculture species is genotyping of broodstock and identification of family lineage.
- Presented techniques have potential to reduce the expense and time required to establish an effective breeding program in broodstock fish.

**Methods:**
1. Tag fish and collect fin clips
2. Digest DNA with ApeK1
3. Ligate adapters
4. Pool DNAs & Clean up
5. Perform PCR
6. Clean up PCR
7. Evaluate fragment sizes

**References:**

**Acknowledgements:**
Special Thanks To…
Douglas Crawford
Marjorie Oleksiak
John Stieglitz
Ronald Hoenig
Samantha Sierra-Martinez
Liza Merly

Funding:
SURGE Award Funding
Tripletail Aqua, LLC
All animal handling and sampling procedures conducted in accordance with IACUC Protocol: 23-132.