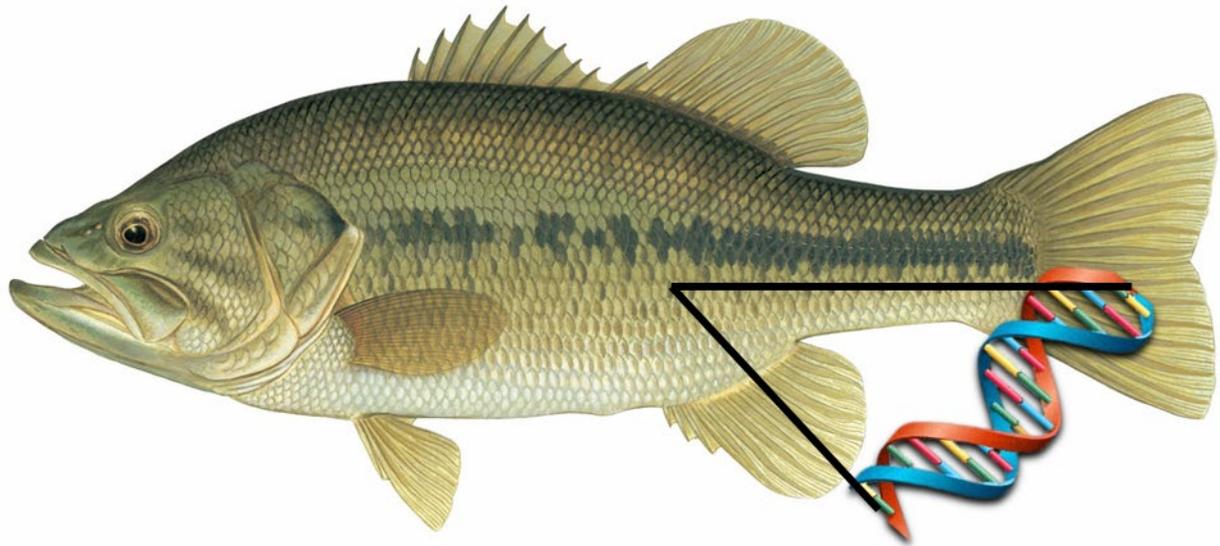


Thoroughbred Bass Program

Interim Progress Report
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by

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The Thoroughbred Bass Program

The new KDFWR Thoroughbred Bass Program uses cutting-edge genetic sequencing to identify genetic markers—known as single nucleotide polymorphisms (SNPs)—associated with trophy-sized Largemouth Bass. By selectively breeding native Largemouth Bass with these markers in our hatcheries, we aim to stock public waters with fish that have a higher potential for large size.

This approach offers key advantages:

1. **Native Adaptation:** Thoroughbred Bass will be locally adapted Largemouth Bass, bass from Kentucky waters, ensuring the best survival and performance in Kentucky’s climate. Since they are simply a “better version” of what has always been here, Thoroughbred Bass are adapted to thrive in our state’s unique environmental conditions and are best suited to handle the seasonal temperature fluctuations and day length periods of our latitude.
2. **Selective Breeding:** Every Thoroughbred Bass will be bred with genetic markers linked to trophy size potential. In comparison, when stocking Florida Bass or first generation (F1) hybrids, only some of the individual fish possess the genetic potential for trophy size. This is akin to planting a field with premium, carefully selected seeds versus a random assortment. This approach should achieve more consistent and superior outcomes in growth potential.
3. **Sustainable Improvements:** Maximum size potential in bass is influenced by multiple genes. Over time, the Thoroughbred Bass Program aims to identify and propagate bass with increasingly complete sets of genetic markers for large size potential. This means that each generation of stocked Thoroughbred Bass should be better than the last. Stocked Thoroughbred Bass will not only contribute directly to fisheries but also pass on these desirable genetics to future generations through natural reproduction. As a result, the program has the potential to gradually transform the genetic makeup of bass populations in stocked waterbodies, increasing the percentage of trophy-potential fish over time. Even if Kentucky had a suitable climate for Florida Bass genetics, the Thoroughbred Bass approach offers a more sustainable, science-driven alternative. F1 hybrids, for example, only exhibit increased size potential in the first generation. Thoroughbred Bass, by contrast, could pass on and integrate their genetic improvements into the broader bass population through natural reproduction.
4. **Reversal of Angling Effects:** Research shows that angling can negatively impact the genetics of a fish population by selectively removing bass that are larger or more aggressive. These effects are particularly intense when harvest rates are high, but even in low-harvest situations, angling still disproportionately affects certain fish.

For example:

1. **Aggressive Bass Vulnerability:** Aggressive bass are more likely to strike at a lure and therefore more likely to experience angling mortality.
2. **Tournament Stress:** Larger bass are often removed during fishing tournaments, when handling stress can lead to higher mortality rates.

3. **Spawning Disruption:** The largest and most aggressive bass, which are critical for reproduction, are more likely to be removed from their nests by fishing during spawning. This limits their ability to pass on their genetics, because even in catch-and-release fishing, nest abandonment or failure can occur, reducing the recruitment of trophy-potential offspring.

This initial research project is only focused on maximizing potential size, but by identifying genetic markers associated with these desirable traits and reintroducing these genetics into the population through selective breeding, we may be able to reverse these angling-induced effects. Over time, this approach could help restore the natural balance and ensure that Kentucky's bass populations remain robust and sustainable.

How it Works

The Thoroughbred Bass Program employs a Genome-Wide Association Study (GWAS), a technique widely used in medical and agricultural research, to identify genes linked to specific traits. In our study, we collected fin clip samples from Largemouth Bass across Kentucky:

- **Trophy Group:** Samples from bass over 5 pounds.
- **Non-Trophy Group:** Samples from bass under 3.5 pounds.

We collected 150 samples for each group from 30 different lakes statewide. These samples were tested by the Center for Aquaculture Technologies (CAT) to confirm they were pure Largemouth Bass. Then, researchers at CAT sequenced each fish's entire genome, and looked for genetic markers which were common in the trophy group but were not commonly found in the non-trophy group. That analysis revealed a number of genetic markers associated with the trophy fish group. Further statistical testing will refine that initial list of markers down to the best or most useful markers. We anticipate identifying approximately 20–50 of the most promising markers for incorporation into the actual trophy marker testing panel, although the exact number is still to be determined. Once the testing panel is developed it will be used to select individual broodfish with the highest trophy potential at our hatcheries.

Establishing a Reference Genome for Future Research

One major outcome of this research is the creation of a reference genome for Largemouth Bass in Kentucky. A reference genome serves as a detailed map of a species' genetic makeup, allowing future studies to focus on specific traits with much lower costs. For example, once the reference genome is complete, researchers can use it to more quickly and cheaply identify genetic markers for other desirable traits, such as aggression or catchability, without having to conduct the costliest form of genome sequencing again. This is similar to having a master key that makes unlocking future discoveries faster and more affordable. The reference genome will not only benefit Kentucky but could also be a valuable resource for other states looking to enhance their Largemouth Bass populations.

Frequently Asked Questions

1. How big will the Thoroughbred Bass grow?

Genetics determine potential, but environmental conditions—such as forage availability and habitat quality—are crucial for growth. If the environment is poor the genetics won't make a difference. By combining optimal environments with trophy genetic markers, Thoroughbred Bass are expected to surpass the size potential of our naturally occurring bass. For example, if we identify 30 genetic markers for trophy size and are able to selectively breed fish with all 30 of them, those fish should grow larger

than any naturally occurring bass, which might only have a few of these markers. Selective breeding in aquaculture has frequently produced gains of 10–15% per generation when larger size is the primary objective.

2. *Are Thoroughbred Bass genetically modified?*

No, the breeding process uses traditional techniques. The naturally existing genetic markers are identified through advanced technology, but the breeding itself relies on time-tested methods used in agriculture for thousands of years.

3. *When will Thoroughbred Bass be available?*

We had originally hoped to produce the first batch in 2026, but at this point it's unfortunately likely that we will miss that goal. The low-density testing panel is still in development, and we don't anticipate getting our broodfish test results back until the hatchery is preparing to spawn the fish. Because bass spawn only once per year, even a one-week delay in receiving results after spawning begins would cause us to miss that window. Regardless, our biologists will spend significant time this spring and summer collecting and testing wild fish to ensure we have the best possible broodfish available for 2027 production. Each production year will build on the previous one, with continual improvements to the broodstock.

4. *How much does the research project cost?*

The research phase to identify genetic markers was budgeted for \$100,000 and the project is under budget. This is a significant investment, but far more feasible than it was just a decade ago. Advances in genome sequencing have drastically reduced costs. For example, the Human Genome Project which only sequenced the genome of a single human cost \$2.7 billion in 2003, while this project will sequence 300 individual bass genomes for a fraction of that cost.

5. *Can other genetic traits, like aggression, be studied?*

Yes. Traits like aggression and catchability, which are known to have genetic components, could be studied using this technique. The current focus is on trophy size, but future research could expand to other traits. For instance, studying catchability could help identify fish more likely to strike at a lure, making fishing easier.

6. *Why was 5 pounds the cutoff for the analysis? Why not higher?*

Five pounds was chosen as the cutoff for data collection because a fish above 5 pounds is certainly in the top 1% of the population in any body of water in Kentucky. The 150 chosen for the trophy group ranged from 5.02 – 8.46 pounds and came from 30 different waterbodies.

7. *Can this approach be used for other species?*

Yes, this technique can theoretically be applied to any fish species, including Smallmouth Bass. While Largemouth Bass are the initial focus due to their popularity and widespread distribution in our state, a Thoroughbred Smallmouth program could be developed in the future.

8. *Has this strategy previously been used for bass management, or will Kentucky be the first?*

Yes, this strategy has been used for genetic improvements in Florida Bass by at least one hatchery in the private industry (Red Hills Fishery) and is on the verge of deployment by state agencies in Texas and Arkansas. However, to our knowledge, Kentucky will be the first state to use this approach for Largemouth Bass.

9. Is this project similar to a Sharelunker style program?

Yes, it is similar in that both approaches rely on the theory that greater potential for trophy size is partially an inherited trait which can be passed on to offspring. One key difference is that using trophy markers allows us to identify high-potential fish long before they reach trophy size. This is critical because fish that have already reached trophy size are rare and are often beyond their most productive breeding years despite having a high number of eggs. This greatly limits how many offspring can be produced. For example, until very recently only about 200,000-300,000 ShareLunker offspring were typically produced annually in Texas, despite their hatcheries producing roughly 5,000,000 total Florida Bass each year. The genetic marker approach allows potential trophy fish to be identified much earlier, when they are still productive breeders with many spawning seasons ahead. The trophy marker approach is also more advantageous than Sharelunker style programs for more technical reasons. For example, say we find 20 genetic markers highly associated with trophy size. Because bass have one copy of chromosomes from each parent, each potential broodstock has a chance of having zero copies of that good trophy marker, 1 copy (heterozygous), or 2 copies (homozygous). By knowing which markers and how many copies each broodfish has, we can make smarter decisions about which fish to breed together. This type of complementary advanced matchmaking is not possible if the only thing you know about the broodfish is that it reached trophy size.

10. What will be the ongoing costs of this project?

As this project is cutting edge, we can't predict every cost, but it should be relatively low once the initial research is conducted. The fish themselves will be produced at our own hatcheries so rearing costs should not exceed what we already spend to produce bass. Any new broodfish will need to be tested to ensure they are genetically pure Largemouth Bass but since that testing will occur simultaneously with the screening for trophy markers there is really no additional cost. Results for each broodfish are expected to provide the following information: (1) the percentage of Largemouth Bass ancestry; (2) the probability of reaching trophy size based on the presence of trophy markers; and (3) the degree of relatedness to other broodfish. Using these data, geneticists at CAT will develop a breeding matrix identifying the most suitable candidates for each cohort of Thoroughbred Bass broodstock. Additionally, fish larger than 5 pounds from across the state will be tested to confirm the validity of the genetic markers. It's possible that through those validity tests we will discover that some of the trophy markers are more important than others or that some are not good markers for determining trophy status. The cost for this low-density testing is much cheaper than whole genome sequencing and should be well under \$5,000 per year. If the project continues to show promise, upgrades to the hatcheries may be necessary in the future to increase capacity.