

Workshop Title: Understanding Genetics for Successful Conservation and Restoration of Resilient Chesapeake Bay Brook Trout Populations (Responsive)

Submitted by: Habitat Goal Implementation Team (HGIT) Brook Trout Work Group

Workshop Steering Committee:

Dr. David Kazyak, Chair (USGS Leetown Science Center /HGIT Brook Trout Work Group)

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Workshop Description:

Traditionally, fisheries management has focused on the abundance, distribution, and size structure of populations. Although these factors remain key aspects of management, a large and growing body of evidence highlights the importance of genetics in conserving wild populations, especially when populations are small and isolated (Frankham et al. 2017). Local adaptations are very common among fishes and help populations cope with specific conditions in their local environment (Fraser et al. 2011). The field of conservation genetics and genomics is highly technical and has advanced rapidly in recent years, offering a wealth of information to support brook trout conservation and restoration. A major impediment to successfully incorporating these advances into conservation outcomes is that most fisheries managers have only a basic understanding of fish genetics and its relevance to their management decisions.

The proposed two-day workshop will bring experts in the field of fish and brook trout genetics together with fishery managers and practitioners to provide the latter with the both the general knowledge of fish genetics and recent scientific advances. The main objectives are to: (1) communicate the importance of genetic information for Brook Trout management and review key conservation genetics concepts and (2) explore available genetics datasets and explain how they can be used to support management.

In order to achieve the Brook Trout Outcome of increasing occupied habitat by eight percent by 2025, it is essential that Brook Trout genetics be incorporated into conservation and restoration decisions to ensure we are restoring resilient populations with the genetic diversity and adaptations to survive in a future landscape that will likely be more disturbed with increased habitat stressors, including increasing stream temperatures. Programmatic priorities and restoration decisions are being made every day right now, so it is urgent that this information is communicated to managers as soon as possible.

Background: We now understand that substantial variation exists within many species, and these differences can have major impacts on the productivity, resilience, and long-term persistence of populations. Intraspecific variation of many key traits is underpinned by heritable genetic variation. Introgression of poorly adapted, stocked lineages into wild populations is a major conservation concern, but is difficult to evaluate without molecular data. Coldwater habitats occupied by Brook Trout are expected to change in the future, and in sometimes unprecedented ways. Since many wild Brook Trout populations are restricted to isolated headwater reaches, their persistence is contingent on the ability of populations to adapt in place. Consequently, it is important to conserve existing genetic diversity to

ensure wild populations have the greatest opportunity to survive in a changing environment, as they will need to rely on local genetic resources to adapt and persist (Hoffman et al. 2017). Moreover, demographic and genetic population parameters are often uncorrelated (Belmar-Lucero et al. 2012), further highlighting the need for population genetic information to support management and to disseminate case studies to demonstrate its utility.

Management Need: Strategic consideration of genetic diversity in conservation planning is critical to ensure the best outcomes are achieved and progress is made towards CBP objectives. Conserving genetic diversity of wild Brook Trout populations is one of the Eastern Brook Trout Joint Venture (EBTJV) key conservation actions listed in their Conservation Roadmap and Action Strategies. It is critically important that managers and conservation practitioners understand how genetic diversity relates to conservation outcomes and how currently available information can support their activities. The importance of this is reflected in the current BTWG Action Plan and Logic Table and this proposal addresses the following aspects of that Plan:

Gap: *“Better understanding of population genetics and functional genomics, and their role in informing conservation and restoration decisions”*

Actions: *“Work with EBJTV to host brook trout genetics workshop for managers.”*
“Develop online genetics portal”

This workshop is needed to fully address factors impeding our ability to achieve the Brook Trout Outcome. It will also address relevant management needs in the Fish Passage Work Group and Healthy Watersheds Action and Logic Plans.

Rationale for STAC Workshop: Communicating the relevance of genetic and genomics to Brook Trout managers has proved challenging. This is in part due the highly technical nature of genetics data, which is falls outside of the training of many resource managers. There is a critical need to provide training to conservation practitioners (typically state agencies and NGOs) so that Brook Trout management and restoration efforts are implemented in a manner consistent with our genetic understanding. The STAC workshop framework is the perfect setting to bring together scientists and managers to discuss this topic. The BTWG has previously identified that members and other fishery managers in the Chesapeake Bay Watershed typically have limited resources to support meeting attendance, so the STAC funding is an essential need to complete our objectives.

Anticipated Speakers, Topics, and Specific Questions:

We have already confirmed the following speakers and have a list of others who have expressed interest pending final details:

Dr. David Kazyak (USGS), Dr. Amy Welsh (WVU), Dr. Shannon White (PSU) , Dr. Jay Stauffer (PSU)

Speakers will address the following major topics:

- (1) Patterns of genetic diversity across the landscape
- (2) Genetic drift and effective population size
- (3) Introgression of stocked hatchery lineages into wild populations
- (4) Reintroductions

- (5) Genetic rescue: state of the science
- (6) Monitoring using environmental DNA (eDNA)
- (7) Case studies demonstrating the utility of genetic information in conservation

Additional anticipated participants include:

Brook Trout genetics and genomics researchers (e.g., USGS, USFWS, and university scientists)

Brook Trout managers (e.g., state agency staff, National Park Service Staff)

Brook Trout conservation practitioners (e.g., Trout Unlimited, National Fish and Wildlife Foundation, The Nature Conservancy)

The workshop will address the following questions:

- (1) What key genetic issues should managers consider when developing conservation strategies for Brook Trout?
- (2) How can available population genetic data support efforts to conserve and restore wild Brook Trout populations?
- (3) What opportunities exist to further develop genetics information within the Chesapeake Bay watershed?

Workshop Outcomes/Products: A workshop report will be produced which summarizes the topics covered during the workshop, including: (1) key considerations for the genetic management of wild Brook Trout, (2) how available data can be leveraged to improve outcomes, and (3) what can be done to further develop the science in the future. Key information and conclusions from the report will be presented to CBP Goal Teams and the EBTJV partners and will be incorporated in the next BTWG Action Plan and Logic Table. The EBTJV is a Fish Habitat Partnership comprised of a diverse group of partners, including state fish and wildlife agencies, federal resource agencies, Indian tribes, academic institutions and non-governmental organizations. This network will be a valuable resource in helping communicate the results of the workshop to the fish management community. The BTWG has not previously applied for STAC workshop funds.

Logistics and Budget: The exact timing for the proposed workshop is flexible. In order to allow time for outreach and preparation, we anticipate a two-day workshop in late 2020 or early 2021. A meeting during this time frame would minimize conflicts with the field season for most participants. Workshop participation will be by invitation only and target ~30 participants. Estimated costs for venue, catering and travel are included below:

Venue - \$3,000 Catering - \$2,000 Travel for participants - \$5,000 Total - \$10,000



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From: Jay R. Stauffer, Jr

Subject: Workshop

I recommend and will support a workshop on Understanding Genetics for Successful Conservation and Restoration of Resilient Chesapeake Bay Brook Trout Populations. Salmonid fishes inhabiting lower latitudes in North America present significant challenges to conservation biologists that attempt to identify and maintain ecological and evolutionary processes within and among populations. To date, Brook Trout (*Salvelinus fontinalis*) functions as a keystone species in some headwater streams. Brook Trout populations are threatened by changes in land use patterns, reduced canopy, temperature changes in head water streams, and introduced populations. They are used by management agencies as keystone species throughout their range. The initial step in preserving the adaptive potential of a trust resource is to delineate the fundamental unit of management (e.g., species, metapopulation, population). As noted by Behnke (1972) and others, every effort should be made to protect the genetic diversity of these postglacial salmonid populations, which are fragile and susceptible to extirpation by introductions. In effect, resource managers must plan for an evolutionary future for trust species, as such, ecological and evolutionary processes—those that maintain genetic diversity and provide the raw material for evolution and adaptation of populations—must be explicitly identified. The current paradigm for conservation of species and associated habitats emphasizes the recognition and protection of irreplaceable evolutionarily distinct lineages; in effect, we must be able to recognize and identify distinct species. Thus, we need to document unique populations and determine both the census and effective population sizes of this important species.

