



**STATE OF CONNECTICUT
DEPARTMENT OF ENERGY AND
ENVIRONMENTAL PROTECTION**

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**Among Headwaters Conservation Genetics of Brook
Trout: Occurrence of Meta-Populations and
Landscape Scale Fragmentation**

**Bureau of Natural Resources
Inland Fisheries Division
79 Elm Street, Hartford, CT 06106**

Project Update March 2015

Project title: Among Headwaters Conservation Genetics of Brook Trout: Occurrence of Meta-Populations and Landscape Scale Fragmentation

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Background

The project entitled “Among Headwaters Conservation Genetics of Brook Trout: Occurrence of Meta-Populations and Landscape Scale Fragmentation” is funded by the Connecticut Department of Energy and the Environment (DEEP) through the State and Tribal Wildlife Grants program. The goal of the project is to collect information on population fragmentation and gene flow among Connecticut’s headwater brook trout populations to better inform future management actions. The objectives of this study are to investigate 1) the contemporary level of population fragmentation, asking specifically if each headwater drainage network represents isolated populations or if meta-population dynamics are present, 2) document how often, if at all, dispersal among headwater populations has occurred over the past several generations, 3) use these results to model extinction risk for isolated populations, highlight what stream network scenarios represent barriers to gene flow, and recommend areas of conservation opportunity in the state of Connecticut, 4) scan for evidence of introgression with stocked and hatchery fish, and 5) determine if any watersheds appear to be particularly unique in genetic composition. This project update represents the progress that has been made from December 2014 to March 2015 and future directions.

Field Collection and Genetic Methods

To begin objectives 1-3, brook trout tissue samples were collected from July-November 2014. Headwater streams were selected for sampling based on historical collection data and predicted population boundaries. Sampling in 2014 focused on Eastern Connecticut, specifically streams east of the Connecticut River. Region wide sampling was conducted in an effort to include at least one sample location per regional watershed, as per the U.S. Geological Survey (USGS) Watershed Boundary Dataset. Additionally, a focal region was identified to investigate finer scale genetic questions. For the eastern half of the state, the combined Hop, Willimantic, Fenton, Mt. Hope, and Natchaug River watersheds (i.e. upper Shetucket River) were selected as the focal area. Sites were selected in an effort to distribute them in such a way that, on average, sites were located no more than five river km apart. Additionally, specific sites were selected for objectives 4 and 5 to search for potential introgression between stocked and wild individuals and for unique ‘heritage’ strains, respectively. At each site brook trout were captured using single pass backpack electrofishing. A minimum of 200 meters were sampled, with a target sample size of $N > 30$ at each site. Tissue samples were obtained in the form of a small fin clip and were immediately stored in 95% ethanol until processing. Genetic samples were extracted using a Promega plate based DNA extraction kit and genotyped using a Beckman Coulter sequence analyzer. Lab work was conducted at the Wild Genomics Laboratory at West Virginia University under the direction of Dr. Amy Welsh (co-advisor of L. Nathan).

Objective 1: Determine contemporary level of population fragmentation

In total, 2,688 brook trout fin clips were collected from 71 field sites spanning 16 regional watersheds during the 2014 sampling year (Fig. 1; Table 1). These samples will serve as the genetic material from the eastern half of the state for objectives 1-5. As of March 2015, 400 samples have been extracted and genotyped from sites 1-20. These sites make up the western half of the first focal area, which includes the Hop and Willimantic watersheds. Data is currently undergoing checks for genotyping errors and quality control. Upon completion of these preliminary assessments, further analyses will be conducted to make progress towards addressing specific research questions.

Objective 2: Document how often dispersal among headwater populations has occurred over the past several generations

Objective two will be addressed using the same genetic data as gathered as part of objective one. See above for most current update.

Objective 3: Model extinction risk for isolated populations, highlight what stream network scenarios represent barriers to gene flow, and recommend areas of conservation opportunity in the state of Connecticut

Objective three will be addressed using the same genetic data as gathered as part of objective one. See above for most current update.

Objective 4: Scan for evidence of introgression with stocked and hatchery fish

Of the 71 sites that were sampled in 2014, 36 were identified as potential sites for introgression between stocked and wild individuals (Table 1). These sites were identified based on overlapping distribution or near proximity of wild trout and documented stocking events. Samples from seven of these sites were included in the initial sample processing in January 2015 and are awaiting results. Although some sites were specifically targeted as potential introgression sites, all processed samples will be analyzed for evidence of recent introgression. Additionally, 13 trout collected during the 2014 field season that were identified as stocked individuals based on morphological characteristics were genotyped to provide a source of genetic comparison to wild individuals.

Objective 5: Determine if any watersheds appear to be particularly unique in genetic composition

Of the 71 sites that were sampled in 2014, 15 were identified as potential 'heritage' sites and will be examined to identify any rare genetic populations in the state (Table 1). These sites were identified by those that had no historical stocked records, or those that are isolated from streams that have been stocked historically. Streams that have not received direct stocking historically, but are in close proximity of streams that have been stocked in recent years are considered for both objectives four and five, and are identified as such in Table 1. Samples from ten of these sites were included in the initial sample processing in January 2015 and are awaiting results. Similar to objective four, all sites will be analyzed for potential 'heritage strains', despite not being designated as such a priori.

Future Work

Upon completion of data quality control checks, genotyping data from the first 400 individuals (sites 1-20) will be analyzed using a suite of genetic metrics and analytical techniques to address objectives one,

two, four, and five. Additional samples collected during the 2014 sampling season will be genotyped and analyzed in 2015. From July to September 2016 sampling will take place on the Western side of Connecticut using the sampling protocol outlined above. State wide sampling will be continued using the USGS Watershed Boundary Dataset and an additional focal area will be identified to allow for finer scale genetic analyses.

Table 1. Brook trout fin clips collected from Connecticut stream sites from July to November 2014. Site number corresponds to Figure 1. (i) = site identified as potential introgression between wild and stocked individuals for objective 4. (h) = site identified as potential heritage strain population for objective 5. N = number of fin clips collected from each site.

Site	Stream Name	N
1	Delphi Brook	38
2	Diamond Ledge Brook (i)	39
3	Aborn Brook (h)	12
4	Stickney Hill Brook (h)	19
5	Roaring Brook (i)	1
6	Ruby Brook	32
7	Bonemill Brook (h)	109
8	Clark Brook (h/i)	54
9	Bonemill Brook (h)	21
10	Grapevine Brook	39
11	Clough Brook (h)	90
12	Spice Brook (h)	23
13	Olson's Brook (h/i)	17
14	Hop River (i)	14
15	Brigham Tavern Brook (h/i)	25
16	Burnap Brook	28
17	Rufus Brook (h)	28
18	Clarks Brook	35
19	Gifford Brook (i)	26
20	Sawmill Brook	46
21	Wells Brook	19
22	Scranton/Bush Meadow Brook (i)	93
23	Lead Mine Brook (h/i)	18
24	Stiles Brook (h)	7
25	Fenton River/Curtis Brook (h/i)	34
26	Eldridge Brook (i)	67
27	Branch Brook (i)	30
28	Bosworth/Bungee Brook	94
29	Fenton River/Conant Brook (i)	89
30	Knowlton Brook (i)	27
31	Gardner Brook (i)	43
32	Mt. Hope River	38
33	Eagleville Brook (i)	33
34	Stones Brook	9
35	Goodwin Brook (i)	40
36	Mt. Hope River	42

Site	Stream Name	N
37	Bebbington Brook	2
38	Stonehouse Brook	21
39	Gulf Stream (i)	40
40	Abbey Brook (i)	41
41	Broad Brook (i)	52
42	Pease Brook	83
43	Tankerhousen River	72
44	Mohegan Brook	19
45	Latimer Brook (i)	17
46	Merrick Brook	19
47	Dark Hollow Brook/Mott Hill (i)	154
48	Muddy Brook	36
49	Culver Brook (h)	44
50	Mashentuck Brook (i)	23
51	Hop Brook (h)	24
52	Reservoir Brook	28
53	Little River (i)	40
54	Lyman Brook	35
55	Eightmile River	106
56	Flat Brook (i)	11
57	Mashamoquet Brook (i)	40
58	Sugar Brook (i)	34
59	Wood Brook (i)	35
60	Dennison Brook (i)	46
61	Mt Kinney Brook (i)	4
62	Lisbon Brook/Sheep Barn Brook (i)	67
63	Stony Brook (i)	19
64	Joe Clark Brook	26
65	Thompson Brook	28
66	Bindloss Brook	35
67	Charters Brook	30
68	Roberts Brook (i)	9
69	Bundys Brook (i)	23
70	Moses Brook (i)	13
71	Labonite Brook (i)	33

Figure 1. Locations of brook trout tissue collection sites from July to November 2014. Site ID Corresponds to site number in table 1.

