

Patch Metrics: A cost effective method for short and long term monitoring of Chesapeake Bay wild brook trout populations?

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The wild brook trout resource in the Chesapeake Bay has been significantly reduced over the last 150 years and faces ongoing and future threats from climate change, land use changes, invasive species and loss of genetic integrity (Hudy et al. 2008). Monitoring both short and long term trends on individual brook trout (*Salvelinus fontinalis*) populations and the resource as a whole are important needs of managers.

Past assessments on the 1,443 subwatersheds in the Chesapeake Bay found that 226 had healthy brook trout (intact); 542 had reduced populations and 290 were extirpated (Hudy et al. 2008). However, the subwatershed scale assessment was not fine scale enough to efficiently monitor trends on the ground of interest to many managers. Standard population estimates using mark-recapture and depletion removal estimates are also not viable for large scale monitoring because of expense, inability to detect trend (i.e. large coefficient in variation), and problems expanding the sample to the entire population. However, fine scale occupancy data (at the catchment level) exist for the majority of the brook trout resource in the Chesapeake Bay. Currently (not counting New York, not completed yet), there are 3,003 catchments containing allopatric brook trout populations; 1,716 catchments containing sympatric populations (with brown or rainbow trout); and 1,966 catchments containing only exotic trout species. We used this fine scale catchment data to identify unique “patches” of brook trout. We define a “patch” as a group of contiguous catchments occupied by wild brook trout (Figure 1). Patches are not connected physically (separated by a dam, unoccupied warm water habitat, downstream invasive species, etc) and are generally assumed to be genetically isolated. In the Chesapeake Bay there are 868 patches of brook trout habitat with an average patch size of 2,800 ha.

Recent developments have made genetic sampling a cost effective surrogate for population estimates (Tallmon et al. 2010). Genetic monitoring is used to quantify temporal changes in population genetic metrics, as opposed to a snapshot assessment of population genetic characteristic at a single point in time (Schwartz et al. 2007). Snapshots of genetic diversity

themselves can be highly useful. Genetic diversity within a patch provides information about past population size because larger populations retain more genetic diversity. Within-patch genetic diversity also provides information about resilience to future environmental change because populations with greater genetic diversity are more likely to be able to adapt to future environmental change.

Added benefit from genetic sampling comes from samples collected from the same population at different points in time (genetic monitoring). We recommend two genetic monitoring metrics. First, multiple estimates of the amount of genetic diversity within a patch can be used to evaluate changes in relative abundance. This metric is sensitive to relative changes in population size but does not quantify it. Second, estimates of N_b (defined as the number of individual brook trout (regardless of age) contributing to a year class; Whiteley et al. 2012) serve as a surrogate for estimates of census population size (N) and can be used to directly test for changes in population size (Tallmon et al 2010). Increasing trends in N_b are generally a positive response from improved habitat or increasing populations. Decreasing trends in N_b suggest loss of habitat and decreasing populations. N_b is related to effective population size (N_e), however N_e is harder to accurately calculate for iteroparous species such as brook trout because of the lack of detailed life history information. Furthermore, N_b is a more intuitive measure as it directly relates to annual recruitment. While the ratio of N_b/N is considered by most a good indicator of resilience and risk it is hard to get reliable estimates of N and relatively easy to get reliable estimates of N_b . Cost-benefit suggests that N_b alone can be a very valuable surrogate for risk. In a pilot study in Virginia, we found that the number of breeders (N_b) was often very low (less than 100) indicating that many of the existing small patches may be at risk. Monitoring N_b at five-year intervals has the potential to be a more useful and less expensive method than monitoring population levels (N).

Monitoring changes in patch metrics (number, size, genetic diversity, and N_b) in a monitoring design combining fixed annual “sentinel” patches and a rotating panel design for other patches has potential to be a cost effective tool for managers to detect trends in wild brook trout populations.

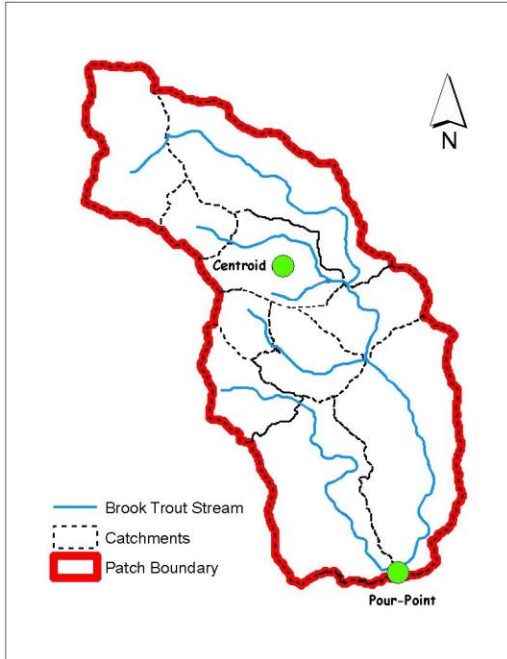


Figure 1. Nine contiguous catchments containing brook trout are combined into one “patch” of reproducing brook trout habitat. Habitat below pour point does not contain brook trout. Recommended patch metrics for large scale monitoring include: number of patches with allopatric populations (brook trout only), number of patches with sympatric populations (brook trout with rainbow and/or brown trout), average size of patches, number of patches increasing in size (connectivity), number of patches decreasing in size, number of patches with decreasing or stable genetic diversity, and number of patches with increasing, decreasing or stable number of effective breeders (N_b).

Proposed Monitoring Design and Methods

1. Use cluster analysis to subsample the existing 868 “patches” of brook trout
 - a. Develop a panel design where “x” patches are sampled every year (sentinel samples) and others are sampled every 5 years. Sentinel samples capture year to year and fast changes while the once every five year samples captures long term trends. For example 250 sites are selected by cluster analysis for monitoring (cluster based on patch size, elevation, climate vulnerability, eco-region, invasive species, regional interest, etc). A total of 25 of the 250 sites are designated as sentinel sites and are sampled every year. An additional 45 of the remaining sites are sampled every year on a rotating panel so each site is visited once every 5 years. This equals 70 sites monitored Chesapeake Bay wide each year.
2. Monitor individual brook trout populations and the Chesapeake Bay’s brook trout resource by several “patch” or population metrics. These metrics (a-e) can be calculated using standard electrofishing occupancy sampling already being used by the staff. Metric (f) would require taking fin clips from young of the year brook trout collected during electrofishing samples using methods in Whiteley et al. 2012. Briefly, we recommend sampling 75 young-of-the-year individuals from three equally-spaced sampling starting locations in the patch.
 - a. Number of patches
 - b. Number of patches with increasing size/connectivity (i.e. additional downstream/upstream catchments occupied by reproducing brook trout)
 - c. Number of patches decreasing in size (loss of occupancy of downstream/upstream catchments)
 - d. Average patch size of the entire resource
 - e. Number of patches with allopatric or sympatric (with rainbow or brown trout) populations
 - f. Genetic diversity contained within patches. This metric is defined as either heterozygosity or allelic diversity (number of alternate copies of a given gene).
 - g. The effective number of individual brook trout (regardless of age) contributing to a year class or cohort. This metric is defined as N_b or the effective number of breeders. The effective number of breeders may be lower than the actual number of breeders (parents) for a given cohort if family sizes resulting from successful breeders are highly variable. N_b is related to effective population size (N_e), however N_e is harder to accurately calculate for iteroparous species such as brook trout because of the lack of detailed life history information. Furthermore, N_b is a more intuitive measure as it directly relates to annual recruitment. Genetic processing (to obtain metrics described in f. and g.) would cost between \$750 and \$1,500 per patch or between \$52,500 and \$105,000 per year using the panel numbers described above.
3. Standard quantifiable population estimates for brook trout such as mark recapture and depletion estimations on representative reach samples have little utility or statistical power to detect population changes because of the high variability in brook trout populations. The coefficient of variation (CV) in Virginia (long term studies on Fridley

Gap and Staunton River) exceeds 50% on adult brook trout and 121% on young of the year complicating trend analysis.

4. N_b estimates appear to have several advantages for statewide monitoring.
 - h. The estimate represents the entire “patch” or population and not just the representative reach.
 - i. N_b values for a patch are always less than N (typically 10%-50%), and thus require fewer samples for accurate estimation than estimates of N using depletion or mark-recapture estimates (Tallmon et al, 2010) making them better suited for determining trends for numerous sites.
 - j. N_b will provide a reliable ‘at risk’ evaluation that integrates year-to-year variation in N
 - k. Bonus information from genetic data – genetic diversity within a patch itself as an indication of past population size and population resilience to future environmental change, population structure, some information on sibship, archiving data for future genomics analyses

Selected Literature:

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