

The Pennsylvania State University

The Graduate School

Ecosystem Science and Management

**MORPHOLOGICAL COMPARISON OF SOUTHERN
APPALACHIAN BROOK TROUT (*Salvelinus fontinalis*)
RELEGATED TO ALLOPATRIC HEADWATER STREAMS IN
GREAT SMOKY MOUNTAINS NATIONAL PARK**

A Thesis in

Wildlife and Fisheries Science

by

Thomas Casey Weathers

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The thesis of Thomas Casey Weathers was reviewed and approved* by the following:

Jay R. Stauffer, Jr.
Distinguished Professor of Ichthyology
Thesis Advisor

Matthew Hurteau
Assistant Professor of Forest Resources

Jeanette L. Schnars
Executive Director, Regional Science Consortium

Michael G. Messina
Head of Department of Ecosystem Science and Management

* Signatures are on file in the Graduate School

Abstract

Environmental Principle Components influencing variations in salmonid population traits are well documented among geographical isolated populations. Brook Trout (*Salvelinus fontinalis*) from geographically isolated headwater streams in Great Smoky Mountains National Park present an idealistic phylogenetic modeling opportunity to differentiate phenotypic relatedness. Through the configuration of a landmark truss network, shape analysis comprised of individual static landmarks allowed me to examine phenotypic variance of individual isolated Brook Trout populations.

For this investigation, I analyze the affects sex, elevation, and flow aspects have upon morphometrics and meristics to Brook Trout populations from the French Broad/Pigeon Watershed. Here I examined twenty-three morphometric and ten meristic characters, constructed a landmark truss network for multiple statistical examinations. Minimal Polygon Clusters were generated by plotting the retained largest contributing Principle Components of variance from to illustrate phenotypic variance amongst populations. Analysis of Variance (ANOVA) was utilized to compare covariate means of retained Principle Components. Populations that did not exceed critical alpha values under ANOVA testing conditions of $P < 0.05$, for morphometric and meristic characters, were considered unique phenotypic polymorphisms.

To further examine affects sex, elevation, aspect and locality had upon Brook Trout morphometrics and meristics; Nonmetric Multidimensional Scaling (NMDS) ordination plots were generated using PC-ORD™ 6 with greatest vectors of similarity influence. Lastly, phenotype characters where used to construct two cladograms used to disseminate phylogenetic relatedness of “southern Appalachian” Brook Trout populations from the French Broad/Pigeon Watershed.

My findings indicate high variation in Brook Trout shape analysis as represented by low p-values (<0.0001 to 0.1267) from all ANOVA results. Meristic counts displayed greater continuity of outward expression similarities as represented by p-values ranging from (<0.0001 to 0.669) across all ANOVA results. Here I provide significant evidence that the observed shape variation of unblocked Brook Trout analyzed is an artifact of sexual dimorphism coupled with phenotypic plasticity. Thus resulting in Brook Trout from geographically isolated streams retaining similar but measureable divergent phenotypes presumably derived from no more than two common ancestral forms.

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Introduction

Geographically isolated Brook Trout populations in the Great Smoky Mountains National Park (GRSM) are restricted to headwater lotic environments. Reproductive isolation (Mayr 1963) is presumed to play a dominant role in allopatric speciation events (Bush 1975, White 1978). It is thought that reproductive isolation is a by product of genetic divergence (Lande 1980); but that species extant in fragmented habitats are able to maintain phenotypic similarities irrespective of genetic isolation (Stebbins 1964, Ehrlich and Raven 1969). Salmonids experience seasonal sexual dimorphism (Young 2005, Kauser *et al.* 2003, Fleming 1994, Quinn 1994), thus difficulties in taxa descriptions using phenotypic characters is often challenging (Winston 1999).

Southern Appalachian Brook Trout (*Salvelinus fontinalis*) are located along the spine of the Appalachian Mountains, ranging south of the New River, West Virginia into northern Georgia (Besler 2007). Brook Trout of the Great Smoky Mountains (GRSM) inhabit well oxygenated, montane streams greater than 600 meters mean sea level (MSL) in elevation, that seldom exceed 25°C. Historically, anthropogenic perturbations lead to the extirpation of Brook Trout from lower elevations and thus limited successful migration between streams. Perturbations such as logging, settlement, fire and non-native salmonid mitigation stockings, anecdotally extirpated Brook Trout from approximately 70% of their historical range within Great Smoky Mountains National Park (Kelly *et al.* 1980).

It is assumed that given the logging and disturbance history of the park that all 19 headwater streams, examined within this investigation, have undergone similar anthropomorphic perturbation histories. Although mitigated stockings of both hatchery strain *S. fontinalis* and *O. mykiss* occurred, streams selected were presumed to have no stocking history of either species. The affects of extensive logging upon Brook Trout are well documented (Nislow and Lowe

2006; Nislow and Lowe 2003; Argent and Flebbe 1999; Marschall and Crowder 1996). Logging directly increases sediment load which in turn decreases abundance, recruitment rate, egg survivability, macro-invertebrate richness, available oxygen and pH. Conversely, increases in annual stream temperature ($> 25.0^{\circ}\text{C}$), flooding and substrate alterations create habitat not suitable for Brook Trout.

Unsuitable stream habitat at lower elevations, natural barriers and competitive exclusions limit effective migration of Brook Trout between fragmented streams and sub-watersheds. Sixteen sub-watersheds and three major watersheds are represented in the GRSM. Of those, this investigation contains specimens from four sub-watersheds (Cataloochee Creek, Middle Prong of the Little Pigeon River, West Prong of the Little Pigeon River and East Prong of the Pigeon River) and one major watershed (French Broad/Pigeon). Nineteen individual headwater streams were sampled for the purpose of this investigation, all within the French Broad/Pigeon watershed basin. All of the headwater streams sampled are considered allopatric for Brook Trout.

Loss of unremitting Brook Trout habitat has resulted in geographically isolated, headwater populations. Consequentially, each fragmented stream could possess unique genetic and phenotypic polymorphisms. Morphological variants commonly occur throughout Salmonidae (Currens et al., 1990; Beacham and Murray, 1983; Hendry and Quinn, 1997; Merz and Merz 2004), although few studies of morphological characters have been conducted. Willis King first noted that local Appalachian residents commented on the distinctive appearance of native Southern Appalachian Brook Trout versus hatchery stocked counterparts caught by local anglers (King 1939). Populations occurring in different geographic locations can be phenotypically differentiated in almost all species (Allendorf and Luikart 2007). Visual comparisons noted that Southern Appalachian Brook Trout possess one to seven red lateral spots,

larger dorsal fins highlighted by black stripes, while “Northern” fish have two to three rows of red lateral spots and are absent of black stripes on the dorsal fin (Williams 2002).

The precursor for differentiating phenotypic variations is morphometric and meristic character analysis. Species can be delineated by morphometric character landmark analysis and construction of truss networks, thereby determining the occurrence of unique morphotypes through shape analysis (Proulx and Magnan 2004, Stauffer 1994, Stauffer 1991). Stauffer and McKaye noted that the lack of morphological differentiation does not negate the presence of cichlid species status (Stauffer and McKaye 2001). Shape can be defined by omitting location, scale and rotational effects, what remains are the purest form of shape (Kendall 1977).

A major component influencing phenotypic polymorphism is exterior pressure exerted by environmental influences. Proulx and Magnan (2004) measured significant morphological character differences in Brook Trout males versus females in both littoral and pelagic environments. Darwin noted that conspecific individuals often vary in subtle traits such as shape, behavior or physiology and such variation could lead to altered ecological species interactions (Bolnick et al. 2011). McGlade and MacCrimmon (1979) observed morphometric differences among Brook Trout from three geographically isolated populations in Quebec following the brief geologically history post Pleistocene glaciation recolonization.

Same species which reside in diverse natural conditions show the ability to locally adapt to their environment, leading to the concept of phenotypic plasticity. Phenotypic plasticity can be the root premises of Evolutionary Significant Units as described by Waples (1991, 1998); whereas, “a unit represents a reservoir of phenotypic variation likely important for future evolutionary potential,” (Allendorf and Liukart 2007). Best management practices which forego the possibility of unique phenotypes and genotypes may experience reproductive isolating

mechanisms when multiple source stream stock introductions are utilized in founding newly restored populations.

Mate choice sorting mechanisms amongst same species derived from visual dissimilarities leads to the concept of positive assortative mating, which has resulted in speciation events among other groups (Stauffer and Gray, 2004). Phenotypic variation of Brook Trout might could cause sorting prior to and or during spawning periods thus, exhibiting positive pre-isolating spawning mechanisms. Fisheries biologists have sufficient evidence to show that to some degree Brook Trout in Leconte Creek, TN are exhibiting signs of reproductive isolation. GRSM fisheries biologists selected three isolated headwater populations of Brook Trout located at similar elevations within the same watershed (French Broad/Pigeon) to utilize as source stock to reestablish a Leconte Creek population. In 2010, eleven years post restoration; UGGS and GRSM biologists discovered that 84% of all fish sampled (n=30) were derived from same source stream pairings. Four years earlier, 2006, 77% of fish sampled (n=30) resulted from parents originating from same source stream pairings (King et al. 2010). This indicates the possibility of three separate unique populations functioning as biological species within Leconte Creek.

By examining 23 morphometric and 10 meristic characters from the 191 whole Brook Trout specimens collected by the National Park Service, researchers at Penn State were able to determine the likelihood of phenotypic similarities between populations in the French Broad/Pigeon Watershed. Critical evaluation of 23 morphometric and 10 meristic characters will aid fishery biologists in future Brook Trout management and restoration activities across their native range. I hypothesis that all Brook Trout will express similar phenotypes from populations within the French Broad/Pigeon Watershed and that elevation, stream flow aspect and sex have do not contribute to phenotype variability. This facet of the investigation will seek to meet the

objectives as followed pertaining to the French Broad/Pigeon watershed within Great Smoky Mountains National Park: 1) determine if Brook Trout in separate individual headwater streams exhibit variance in phenotype; 2) determine the effect of sex, elevation, and flow aspects have upon phenotypic variance; 3) determine if a restored Brook Trout population exhibits variance in phenotype when compared to source stock stream populations.

Study Area

The Great Smoky Mountains cover over 1,287 km² spanning the borders of Western North Carolina and Southeastern Tennessee. Over 60 species of fish, both native and non-native, live within the boundaries of the national park (Etnier and Starnes 1993). Brook Trout are the only native salmonid but both Rainbow Trout (*Oncorhynchus mykiss*) and Brown Trout (*Salmo trutta*) have been introduced and inhabit the clear, cool montane streams within GRSM. Historical stocking records indicate that *O. mykiss*, *S. trutta* and *S. fontinalis* were not translocated into the 19 study areas. The Great Smoky Mountains span in elevation from 266 to 2025 meters, annually receives 140 to 216 centimeters of precipitation, and being 95% forested provides an ideal ecosystem for Brook Trout to thrive.

Low buffer capacity and precipitation high in sulfides and nitrides constitute in annually low pH streams. Dominated by sedimentary geological formations formed during the Proterozoic Era (2,500 – 542 mya), the parks geology offers minimal buffering capacity of calcium carbonate. Low buffering capacities relates to low productivity of stream ecosystems and directly impacting aquatic richness. One adverse geological feature within the park is the presence of Anekeesta. Anekeesta or “hot rock” contains iron sulfide, when water leaches these sulfides the formation of acidic cations occur. The combination of acid precipitation and Anekeesta formations has led to a decline in annual stream pH of park waters. To date, twelve streams have been federally listed as imperiled 303D streams, which have an annual pH below 6.0. Of the twelve 303D streams within GRSM, nine (9) contain populations of native Brook Trout; four (4) of those nine populations have been extirpated (Kulp personal comm. 2012).

Thirteen of the nineteen headwater streams (Table 1) sampled lie within the Cataloochee sub-watershed. The Cataloochee sub-watershed lies with the southeast corner of GRSM, drains

into Waterville Lake, NC which drains into the Pigeon River, NC. The Pigeon River flows north along highway 40 before it joins the French Broad River approximately 7.25km north of Newport, TN.

Rock Creek (Table 1) a tributary to Cosby Creek joins Indian Camp Creek directly outside the GRSM boundary line. These two streams, Cosby Creek and Indian Camp form the confluence of the Pigeon River, TN. Rock Creek is not considered part of the Cataloochee sub-watershed, but part of the East Prong of the Pigeon sub-watershed. The remaining five streams (Table 1) are considered part of the greater Little Pigeon River sub-watershed. Both the Middle Prong and the West Prong of the Little Pigeon Rivers join in Sevierville, TN

Stream reach sampled varies for each collection locality. Sampling stopped when the required 31 Brook Trout were collected. Site data and locality were recorded using a Garmin eTrex®30 handheld geographic positioning system unit. Collection sites were imported into a geographic information system (Figure 1).

Table 1. Great Smoky Mountains National Park collection sites, locality, elevation and sampling dates for Brook Trout morphometric and meristic analysis at Penn State University Stauffer Lab.

Major Watershed	Sub-Watershed	Stream Name	Elevation (meters)	Flow Aspect	UTM Site Locality
French Broad	Cataloochee Creek	Little Cataloochee	881.79	091°	17 S 0310461 3949330
French Broad	Cataloochee Creek	Correll Branch	871.42	038°	17 S 0309858 3949337
French Broad	Cataloochee Creek	Bear Branch	1194.21	073°	17 S 304072 3941976
French Broad	Cataloochee Creek	Horse Creek	1178.05	123°	17 S 304120 3941945
French Broad	Cataloochee Creek	Hurricane Creek	944.58	006°	17 S 306973 3941658
French Broad	Cataloochee Creek	Messer Fork	1060.40	079°	17 S 305636 3943355
French Broad	Cataloochee Creek	Caldwell Fork	1075.03	038°	17 S 307371 3938551
French Broad	Cataloochee Creek	McKee Branch	979.63	003°	17 S 309869 3940968
French Broad	Cataloochee Creek	Onion Bed	1287.78	164°	17 S 3062427 3949655
French Broad	Cataloochee Creek	Pretty Hollow	1280.47	181°	17 S 306736 3949650
French Broad	Cataloochee Creek	Sag Branch	880.87	333°	17 S 310343 3943085
French Broad	Cataloochee Creek	Straight Creek	1051.26	039°	17 S 307329 3939042
French Broad	Cataloochee Creek	Winding Stair	800.00	324°	17 S 312349 3946477
French Broad	MP. Lt. Pigeon R	Buck Fork	882.09	269°	17 S 289945 3952617
French Broad	MP. Lt. Pigeon R	Chapman Prong	1206.09	254°	17 S 290438 3952240
French Broad	WP Lt. Pigeon R.	Road Prong	892.15	355°	17 S 275862 3946039
French Broad	EP Pigeon R.	Rock Creek	930.25	014°	17 S 299623 3958006
French Broad	WP Lt. Pigeon R.	Kephart Branch	978.71	261°	17 S 260746 3945442
French Broad	WP Lt. Pigeon R.	Walker Camp Pr.	1140.87	182°	17 S 280705 3944807

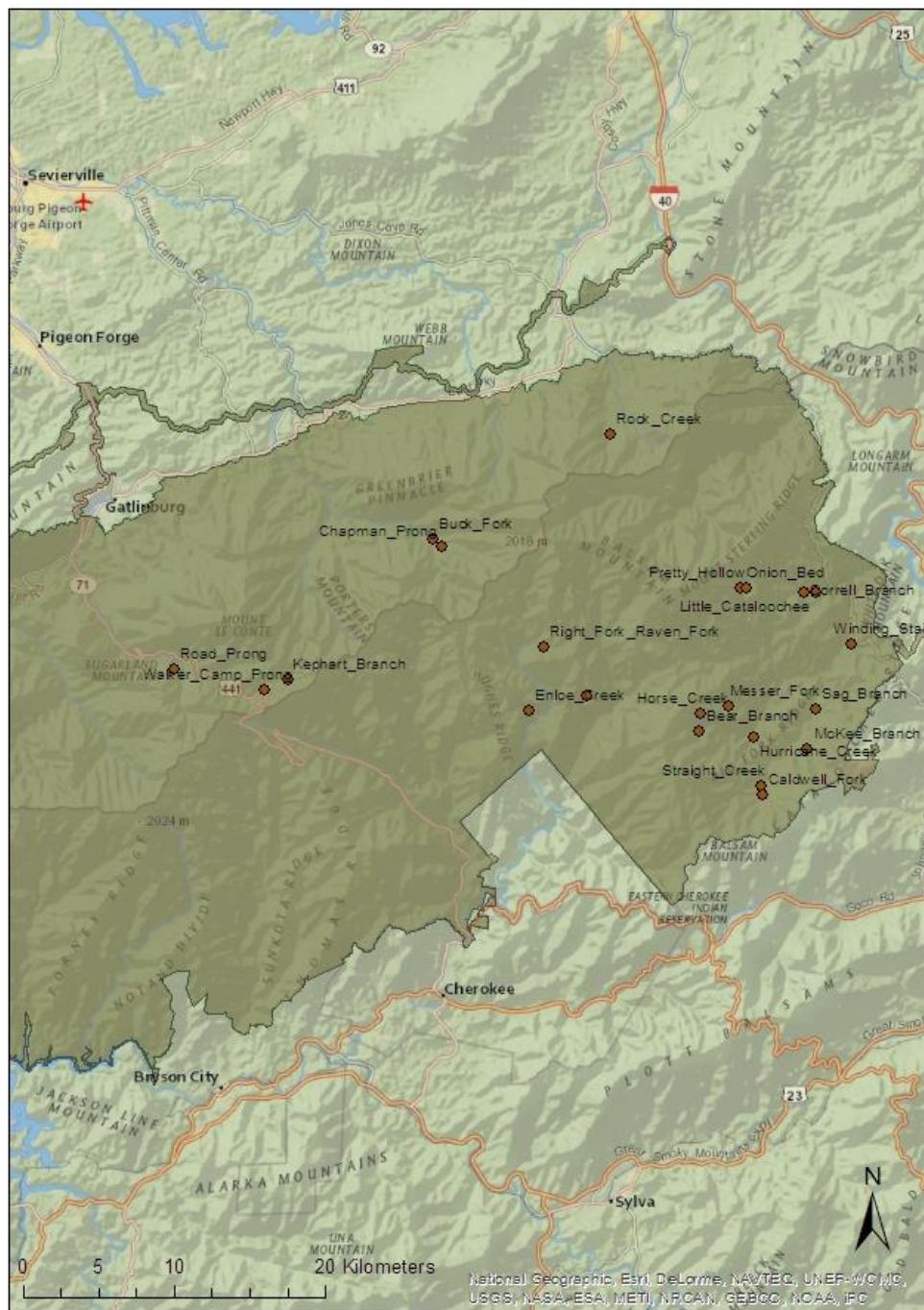


Figure 1. Collection sites for morphometric and meristic measurements of Brook Trout from Great Smoky Mountains National Park.

Methods

In order to determine the likelihood of genetic and phenotypic similarities of Brook Trout within the Great Smoky Mountains National Park, GRSM, USGS and PSU fisheries biologists collected Brook Trout from 19 study streams throughout the study area. Ten whole fish were collected and preserved from each study stream for morphometric and meristic analyses. Additionally, thirty tissue samples were collected from each study stream for microsatellite analyses. Stream reach sampled varied for each sampling locality. Sampling stopped when 31 Brook Trout were collected. Site data and locality were recorded using a Garmin eTrex® handheld geographic positioning system unit. Universal Transverse Mercator coordinates were obtained from each sample site, imported in ArcGIS and were used to acquire aspect and elevation.

In total, 19 streams were selected to provide data on 191 individual whole specimens and 570 individual tissue samples. All tissue samples were sent to the USGS Aquatic Ecology Lab in Leetown, W.V. for microsatellite assays whereas I retained all whole Brook Trout specimens for morphometric and meristic analysis at Penn State. These 19 populations were analyzed using sheared principle components analysis. Sheared Principle Component one relates to variance within sampled standard lengths (size) and was not retained for shape analysis of morphometric characters. Retained morphometric character loadings are subsequently used in sheared principle components. Meristic characters did not undergo shearing and were retained as covariate Principle Components for covariance matrix calculations.

All 19 populations were examined for grouping effects. Therefore, it was hypothesized that individual Brook Trout exhibit unique phenotypical shape variations that can thusly be grouped with individuals from the same population.

To further examine grouping effects, I hypothesized that variation in shape could be explained by phenotypic plasticity influenced by elevation and stream flow aspect. By blocking elevation into five 100 meter elevational treatment groups and flow aspect into 4 directional treatment groups, phenotypic plasticity could be inferred through groups with significantly different loaded shape characters.

Furthermore, analyses of Brook Trout parsed on the basis of sex were conducted to test for sexual dimorphism effects. I hypothesized that if significant variation in craniofacial characters within individual populations was observed it was attributed as an artifact to sexual dimorphism.

Prior to any analysis conducted, allometry had to be tested for. Allometric growth results in the differential enlargement of characters as an individual's standard length increases. Retained morphometric character loadings were regressed and slope calculated to examine the possibility of allometry.

Additionally, Non-metric Multidimensional Scaling (NMDS) was implemented to draw inference on the affects elevation and stream flow aspects would have upon the phenotype of Brook Trout. Two-dimensional and three- dimensional plots were constructed according to axis' accounting for significant variance within these ordinations. Therefore, NMDS was only utilized to draw inference into how environmental factors could account for observed phenotypic variance.

Collection

Ten whole Brook Trout specimens were collected from each study stream using one Appalachian Aquatics backpack unit set to output 600 volts of alternating current. In total, 191 Brook Trout were collected via backpack electrofishing protocol set-forth by Institutional

Animal Care and Use Committees (IACUC) approval guidelines. Backpack electrofishing gear included, variable wattage output (20w-700w) Appalachian Aquatics backpack unit, two probes serving as cathodes and anodes. Field technicians carried collection nets and buckets in order to capture stunned Brook Trout and retain them. Upon collection, fish were exposed to a concentration of 250 mg/L Tricaine methanesulfonate (MS222) for at least 10 minutes following cessation of respiratory movements. Tissue Samples were obtained from the right pectoral fin of nine morphometric and meristic specimens prior to exposure to formalin, placed into separate 0.5ml screw top vials filled with 95% ethyl-alcohol (ETOH) in preparation for microsatellite analyses. Ten percent formalin, a dissection kit, two dissection boards and dissection pins were utilized to display and set rigid all fins. Euthanized Brook Trout pinned to dissection trays were bathed in 10% formalin for a period of 15 minutes. After fins were set rigid, Brook Trout were placed into a one liter 10% formalin jar for a period of three weeks for preservation.. After three weeks specimens were washed of formalin and transferred into 70% ETOH for long-term storage and handling.

One Brook Trout remained unaltered to serve as the putative holotype for that individual headwater population. The remaining nine Brook Trout had their right pectoral fin clipped for nuclear DNA analysis at USGS Leetown Science Center West Virginia, under the supervision of Dr. Tim King. Post euthanasia, fish were pinned flat to a dissecting tray to display all fins for ray counts and exposed to a solution of 10% formalin for a period of 15 minutes to display and set rigid all fin rays. After a period of three weeks in preservation, Brook Trout were then transferred from 10% formalin into wash basins and rinsed for a period of three days. All used formalin was labeled accordingly and collected by Environmental Health and Safety Penn State. Once rinsed, Brook Trout were transferred to 70% ETOH for indefinite storage and considered

able for safe handling. Following the completion of preservation protocol, morphometric and meristic character analysis training transpired.

Training Protocol

One population (Correll Branch) containing ten Brook Trout specimens were arbitrarily selected for character measurement and counts training. Training was conducted at the USGS Aquatic Ecology Branch in Leetown, W.V. Fowler Tools Sylvac electronic calipers model S235 capable of measuring to the accuracy of one-hundredth of a millimeter (0.01mm) were used to collect distance measurement for all characters. Dr. Jay R. Stauffer, Jr (Penn State University) demonstrated, supervised and conducted a training seminar on the proper techniques and protocol for obtaining measurement data of 23 morphometric characters from Correll Branch Brook Trout. Training of meristics counts were conducted again under the guidance and supervision of Dr. Stauffer, counts were conducted visually under a 10x21 power Wild Heerbrugg stereo light microscope. Training measurements and counts were repeated three times over a span of three days. Training was concluded when standard deviations for each individual measurement and count adhered to benchmarks protocols not exceeding a standard deviation of 1.0 for any measurement or count with the exception of lateral lines (standev ≤ 3.0).

After training was conducted, data was reviewed and benchmark protocols for standard deviations were determined meet, I was then able to conduct the remaining measurements and counts to the 18 remnant populations. These measurements and counts were conducted at the Penn State University Stauffer Fisheries Laboratory in University Park, Pennsylvania.

Allometry

Allometric growth was examined by plotting retained morphometric character loadings divided by standard length data over standard length. Most significant retained morphometric

character loadings were snout length, horizontal eye diameter and lower jaw length, respectively. Slope of lines were calculated to examine the possibility of allometry. If allometry proved to influence shape Principle Component analysis the expected results would be shown through a positive linear relationship of shape Principle Component ratios over standard length or size. The calculated slope results and graph are as follows: Horizontal-Eye Diameter slope = -0.0878, Snout Length slope = 0.00024 and Lower Jaw Length slope = 0.00034. Based on these results I determined that allometric growth was not a Principle Component influencing shape variance.

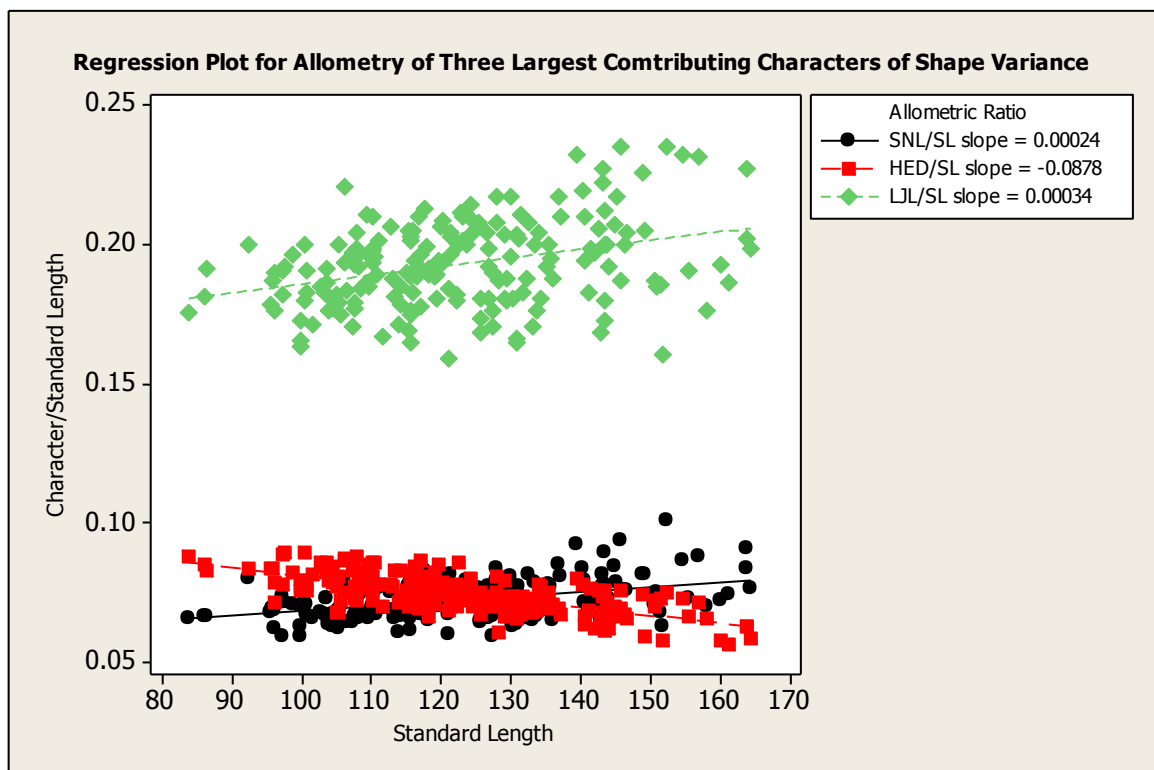


Figure 2. Brook Trout Allometric Growth Regression for the Three Shape Characters of Most Contributing Variance.

Data Collection

Twenty-three character component morphometric measurements were collected using FowlerTools Sylvac electronic calipers model S235 capable of measuring to the accuracy of one-hundredth of a millimeter (0.01mm). WinWedge Data Collection Software was used to import

caliper measurement data into Microsoft Excel and thus considered and treated as raw data. All measurements were obtained from the left side of Brook Trout specimens and adhered to methods outlined from Hubbs and Lagler (1958) and Stauffer (1991, 1994). Table 14 outlines all morphometric characters used as landmarks, character abbreviations and a brief description.

Prior to analysis, box plots were generated in Minitab for each measured morphometric character from each sample population. Box plots proved essential to examine errors in datum collection, reexamining any outlying datum points, and /or transfer and datum correction. If errors in the raw datum were discovered, measurements were then redone three times for each character, averaged, inputted and considered corrected.

Ten character component meristic counts were obtained visually aided by a 10x21 power Wild Heerbrugg stereo light microscope. Datum points collected were entered into Microsoft Excel manually. Table 14 outlines meristic characters counted, collected, character abbreviations and a brief description. As mentioned above, box plots were generated in Minitab for each meristic count, from each sample population and examined for errors in data collection and transfer. If errors in the raw datum were discovered, counts were then redone three times for each character, averaged, inputted and considered corrected. All raw measurement and count data (Appendix C) were assigned and stored into each representative group according to collection location.

Grouping Effects

Raw data were imported into SAS for SPCA, character loadings examined and covariance output scores plotted. Plotted output scores had minimal polygon clusters to encompass all individual points. Each plotted point represents individual Brook Trout collected. If determined that minimal polygon clusters could not be clearly established around individual

treatment groups, ANOVA was conducted. Thus, delineating populations expressing unique phenotypes could not be determined visually. Treatment groups were considered significantly different if all p-values did not exceeded critical alpha values of 0.05. Analysis of Variance (ANOVA) Duncan's Multiple Range Test groupings and means were examined in the case where treatment group p-values exceeded a critical alpha value (> 0.05), therefore similarities in analysis were inferred and minimal polygon clusters overlapped. In the above scenario, treatment groups proved to be statistical similar.

Blocked Elevation

Five treatment groups, containing all 19 sampled populations, were parsed at 100 meter elevational gains and blocked to examine the effects of elevation on phenotypes. Group one (800-899 meters) contained six populations; Buck Fork, Correll Branch, Little Cataloochee, Road Prong, Sag Branch and Winding Stair. Group two (900-999 meters) contained four populations; Hurricane Creek, Kephart Branch, McKee Branch and Rock Creek. Group three (1000-1099 meters) contained three populations; Caldwell Fork, Messer Fork and Straight Creek. Group four (1100-1199 meters) contained three populations; Bear Branch, Horse Creek and Walker Camp Prong. Group five (1200 meters plus) contained three populations; Chapman Prong, Onion Bed and Pretty Hollow. Raw data were imported into SAS for SPCA, character loadings examined and covariance output scores plotted. If determined that minimal polygon cluster could not be clearly established around individual treatment groups, ANOVA was conducted. Treatment groups were considered significantly different if all p-values did not exceeded critical alpha values of 0.05. Analysis of Variance (ANOVA) Duncan's Multiple Range Test groupings and means were examined in the case where treatment group p-values exceeded a

critical alpha value (> 0.05), therefore similarities in analysis were inferred and minimal polygon clusters overlapped.

Blocked Flow Aspect

Four treatment groups, containing all 19 sampled populations, were parsed at stream flow directional aspect at sample sites to examine the effects of photoperiod and temperature on phenotypes. Group one aspect (315° to 45° North) contained eight populations; Correll Branch, Caldwell Fork, Hurricane Creek, McKee Branch, Rock Creek, Road Prong, Sag Branch, Winding Stair. Group two (46° to 135° East) contained five populations; Bear Branch, Horse Creek, Little Cataloochee, Messer Fork and Straight Creek. Group three (136° to 225° South) contained three populations; Onion Bed, Pretty Hollow and Walker Camp Prong. Group four (226° to 314° West) contained three populations; Buck Fork, Chapman Prong and Kephart Branch. Raw data were imported into SAS for SPCA, character loadings examined and covariance output scores plotted. If determined that minimal polygon cluster could not be clearly established around individual treatment groups, ANOVA was conducted. Treatment groups were considered significantly different if all p-values did not exceeded critical alpha values of 0.05. Analysis of Variance (ANOVA) Duncan's Multiple Range Test groupings and means were examined in the case where treatment group p-values exceeded a critical alpha value (> 0.05), therefore similarities in analysis were inferred and minimal polygon clusters overlapped.

Parsed Sex

Brook Trout were parsed into two (2) treatment groups according to sex (females and males). Females were treated as group one and contained 99 individuals. Males were treated as group two (2) and contained 92 individuals. Sex was determined visually by craniofacial ratio

analysis. Individuals with relatively greater length measurement character ratios to standard length were considered group two (2) males. Conversely, relatively smaller length measurement character ratios were considered group one (1) females. Raw data were imported into SAS for SPCA, character loadings examined and covariance output scores plotted. If determined that minimal polygon cluster could not be clearly established around individual treatment groups, ANOVA was conducted. Treatment groups were considered significantly different if all p-values did not exceed critical alpha values of 0.05. Analysis of Variance (ANOVA) Duncan's Multiple Range Test groupings and means were examined in the case where treatment group p-values exceeded a critical alpha value (> 0.05), therefore similarities in analysis were inferred and minimal polygon clusters overlapped.

Winding Stair

Winding Stair allopatric Brook Trout population were restored utilizing source stocks from Caldwell Fork and Little Cataloochee. I analyzed these three (3) populations without blocking in order to determine if Winding Stair has phenotypically diverged from source stock populations. Thus, raw data were imported into SAS for SPCA, character loadings examined and covariance output scores plotted. If determined that minimal polygon cluster could not be clearly established around individual treatment groups, ANOVA was conducted. Treatment groups were considered significantly different if all p-values did not exceed critical alpha values of 0.05. Analysis of Variance (ANOVA) Duncan's Multiple Range Test groupings and means were examined in the case where treatment group p-values exceeded a critical alpha value (> 0.05), therefore similarities in analysis were inferred and minimal polygon clusters overlapped.

Phenotypic Similarity

Cluster analysis was then performed on French Broad/Pigeon Watershed populations' means measurements and mode counts in PC-ORD 6. Nearest neighbor group linkage and Euclidian distance measure criteria were selected for cluster analysis configurations. The addition of a Brook Trout sister group from Long Island, NY and an outgroup Spotted Gar (*Lepisosteus oculatus*) from Mingo Creek, Stoddard County, MO, aided in delineating differentiations to homology in morphometric and meristic characters. Chord distance measurements, node bifurcations and percent retained characters were examined and recorded to postulate phylogenetic relatedness of Brook Trout from the French Broad/Pigeon Watershed. Delimitation of divergent events could not be drawn upon, as the full history of individual streams does not exist.

NMDS

Following ANOVA, Non-metric Multidimensional Scaling (NMDS) ordinations were then conducted on a dual matrix derived formulation platform with the software package PC-ORD 6. Two-dimensional and three-dimensional graphs were then generated from derived axis output of ordination analysis (Appendix G). It is important to note that NMDS will rank groups or populations based on dissimilarities analysis and distance plot groups or populations and thus produces greater distances between data points from individual members with most dissimilar phenotypes. Multidimensional Scaling (NMS) ordination plots axis was determined within the software based on ranked-distance matrices. Final stress levels were multiplied by 100, levels below 0.20 were considered near flawless without the risk of any misinterpretations. Distance measures were conducted by selecting Euclidian measurements on three (3) axis ran 250 times for real data set at 100 iterations. Three (3) vectors of significant were loaded over

both plots. Visual examination of vectors accounting for variance was used to draw inference into extenuating environmental influences effecting phenotype.

Summary of Methods

Sheared Principle Component Analysis proved essential in eliminating data points that had minimal influence on Brook Trout shape (morphometrics) and outward appearance (meristics). This analysis was conducted on all stream populations contained within the French Broad/Pigeon watershed, Winding Stair and its two source streams (Little Cataloochee and Caldwell Fork), blocked elevation, blocked flow aspect and individuals parsed on the basis of sex.

Sheared Principle Component Analysis retained the three largest contributing Principle Components of variance for morphometrics during each assay. Eigenvalues, contributions and proportions gave rise to SPCA morphometric coordinates and meristic Principle Components of retention. Scree plots (Appendix D) were generated from each SPCA morphometric coordinate and meristic Principle Components. Scree plots justified proper retention of morphometric principle coordinate(s) and meristic Principle Component(s) for further statistical assays and analysis. Eigenvalue correlations and proportions, generated in SAS, were plotted and regressed in Minitab and drew inference to the three largest contributing Principle Components of variance from both morphometric and meristic characters.

I then plotted the largest contributing sheared principle component (SPCA2) of morphometric data against the first principle component (PC1) of meristic data, generated minimal polygon clusters (MPC) or convex hulls, to aid in delineating groups or populations with unique morphotypes. Minimal Polygon Clusters or Convex Hulls were not plotted if distinct groupings could not be confirmed and/or visual convolution occurred from plotting.

Minimal Polygon Clusters Plots (Appendix E) aided in drawing inference to phenotypic grouping similarities, or lack thereof, for each SAS variance assay within the scope of this investigation.

Following SPCA, Analysis of variation (ANOVA) of all groupings was performed in SAS, if overlapping occurred in minimal polygon clusters. Output results from SPCA contained the morphometric principle coordinates and meristic Principle Components of highest contributing variance for each assay. Critical alpha values set at 0.05 were established as the benchmark to examine significant variations in each population, blocked elevation, blocked stream flow aspect and parsed sex, of Brook Trout. P-values which exceeded the critical alpha value (> 0.05) were considered to be significant and could therefore represent unique phenotypic morphotypes. Output of retained sheared morphometric principle components and meristics Principle Components were analyzed for each individual assay under the aforementioned ANOVA criteria (Appendix F).

Cluster analysis was performed on all assays with the addition of a sister group and an out group. This enabled me to create a cladogram with distance measures and percent retention of homologous characters to examine phylogenetic relatedness of Brook Trout within the French Broad/Pigeon watershed.

Lastly, NMDS was conducted to visually examine vectors accounting for variance and used to draw inference into extenuating environmental influences effecting phenotype.

Results

Grouping Effects

Sheared principle component analysis of eigenvalue proportional values were examined and resulted in the elimination of morphometrics principle component one (Size/Standard Length) which accounted for 91.05 % of the variance explained in shape. Thus, morphometrics sheared principle component two (SPCA2) was retained and accounted for 2.395 % of the remaining shape variance. Morphometric characters within SPCA2 that accounted for the most variance were: Snout Length, Horizontal-Eye Diameter and Lower Jaw Length and had absolute contributing values of 0.38928, 0.38828 and 0.37443, respectively (Appendix D).

Meristic eigenvalue proportional principle component one (PC1) accounted for 15.87 % of all variation in meristic characters. Characters within meristic PC1 that accounted for the most variance were: Gill Rakers on First Ceratobranchial, Pored Scales Posterior to the Lateral Line and Dorsal Rays and had absolute contributing values of 0.60514, 0.60154 and 0.55461, respectively (Appendix D).

Morphometrics SPCA2 versus meristic PC1 output data results were then plotted in Minitab (Appendix E). Minimal polygon clusters (MPC) were not created as no population appeared to visually exhibit unique phenotypes. Approximately 23% of all individuals from groups or populations overlapped in phenotype. Given that 191 individuals were plotted this created problems in minimal polygon clusters construction of definitive clarity around each population.

Morphometrics SPCA2 and meristics PC1 data were then imported into SAS in preparation for ANOVA. Results for the ANOVA morphometrics SPCA2 model (Appendix F) had 18 degrees of freedom, a sum of squares value of 0.2996, a mean square of 0.0166, an F-

value of 13.81 and a P-value less than 0.0001. Results for the ANOVA meristics PC1 model (Appendix F) had 18 degree of freedom, a sum of squares value of 83.1994, a mean square value of 4.6222, an F-value of 7.44 and a P-value of less than 0.0001. Given that both p-values do not exceed my critical alpha value of 0.05, I would then reject my null hypothesis that Brook Trout from the French Broad/ Pigeon Watershed are similar in phenotypic expression

ANOVA Duncan's grouping results (Table 3) for morphometrics SPCA2 and meristics PC1 indicate significant similarities in means which correspond to similarities in morphometrics and meristics. Winding Stair, Onion Bed and Horse Creek draw inference to the three most similar populations when comparing morphometrics SPCA2 and meristics PC1 against each other.

Table 3. Duncan Grouping Results for Sheared Principle Component 2 (Morphometrics) from French Broad/Pigeon Watershed Brook Trout Populations.

Duncan's Multiple Range Test for spca2				
Duncan Grouping		Mean	N	grp
	A	0.07440	10	Straight Creek
B	A	0.04748	10	Kephart Branch
B	A	0.04328	10	Pretty Hollow
B	C	0.03449	10	Hurricane Creek
B	C	0.03329	10	Chapman Prong
B	C	0.03268	10	Correll Branch
B	C	0.02371	10	Onion Bed
B	E	0.01756	10	Bear Branch
F	E	0.00285	11	Sag Branch
F	E	-0.00182	10	Horse Creek
F	E	-0.00318	10	Winding Stair
F	E	-0.00920	10	Caldwell Fork
F	E	-0.01440	10	McKee Branch
F	G	-0.03002	10	Rock Creek
F	G	-0.03141	10	Buck Fork
	G	-0.03418	10	Little Cataloochee
	G	-0.03655	10	Messer Fork
	I	-0.06421	10	Road Prong
	I	-0.08505	10	Walker Camp Prong

Duncan's Multiple Range Test for PC1

Duncan Grouping		Mean	N	grp
	A	1.2551	11	Sag Branch
B	A	1.0908	10	Caldwell Fork
B	A	0.5809	10	Winding Stair *
B	D	0.4853	10	Onion Bed *
B	D	0.4675	10	Horse Creek *
B	E	0.3369	10	Walker Camp Prong
B	E	0.3051	10	Little Cataloochee
	E	0.2594	10	Chapman Prong
F	E	0.1202	10	McKee Branch
F	E	0.0599	10	Kephart Branch
F	E	-0.0731	10	Pretty Hollow
F	E	-0.2062	10	Hurricane Creek
F	E	-0.3222	10	Road Prong
F	E	-0.3558	10	Messer Fork
F	E	-0.3786	10	Straight Creek
F	G	-0.5760	10	Buck Fork
F	G	-0.6934	10	Bear Branch
	G	-1.2132	10	Correll Branch
	G	-1.2679	10	Rock Creek

Means with the same letter are not significantly different.

- Populations most similar with Sheared Principle Component 2

Blocked Elevation

Sheared principle component analysis of eigenvalue proportional values were examined and resulted in the elimination of morphometrics principle component one (Size/Standard Length) which accounted for 91.05 % of the variance explained in shape. Thus, morphometrics sheared principle component two (SPCA2) was retained and accounted for 2.395 % of the remaining shape variance. Morphometric characters within SPCA2 that accounted for the most variance were: Snout Length, Horizontal-Eye Diameter and Lower Jaw Length and had absolute contributing values of 0.40687, 0.39618 and 0.39073, respectively (Appendix D).

Meristic eigenvalue proportional principle component one (PC1) accounted for 15.87 % of all variation in meristic characters. Meristic characters within PC1 that accounted for the most variance were: Gill Rakers on First Ceratobranchial, Pored Scales Posterior to the Lateral Line and Dorsal Rays and had absolute contributing values of 0.60514, 0.60154 and 0.55461, respectively (Appendix D).

Morphometric SPCA2 versus meristic PC1 output data results were then plotted in Minitab (Appendix E). Minimal polygon clusters (MPC) were not created as no blocked elevational grouping appeared to visually exhibit unique phenotypes. Approximately 23% of all individuals from groups or populations overlapped in phenotype. Given that 191 individuals were plotted this created problems in minimal polygon clusters construction of definitive clarity around each blocked elevational grouping.

Morphometrics SPCA2 and meristics PC1 data were then imported into SAS in preparation for ANOVA. Results for the ANOVA SPCA2 model (Appendix F) had 4 degrees of freedom, a sum of squares value of 0.0938, a mean square of 0.02345, an F-value of 11.72 and a P-value less than 0.0001. Results for the ANOVA PC1 (meristics) model (Appendix F) had 4 degrees of freedom, a sum of squares value of 6.1932, a mean square value of 1.5483, an F-value of 1.57 and a P-value of 0.185. Due to the resultant p-value of 0.185 exceeding my critical alpha value of 0.05 for meristic analysis we would fail to reject my null hypothesis that Brook Trout from the French Broad/ Pigeon Watershed are similar in phenotypic expression and conclude that, when Brook Trout are blocked in similar elevations their shape is highly variable but their outward expression (meristics) are highly similar.

ANOVA Duncan's grouping results (Table 4) for SPCA2 and PC1 indicate significant similarities in means which correspond to similarities in morphometrics and meristics. Blocked elevations (800-899m and 1100-1199m) draw inference to the most similar populations when comparing morphometrics SPCA2 and meristics PC1 against each other. Populations sampled within the 800-899m and 1100-1199m elevational blocks are as follows: Buck Fork, Correll Branch, Little Cataloochee, Road Prong, Sag Branch, Winding Stair and Bear Branch, Horse Creek, Walker Prong, respectively.

Table 4. Duncan Grouping Results for Sheared Principle Component 2 (Morphometrics) from French Broad/Pigeon Watershed Brook Trout Blocked Elevation Populations.

Duncan's Multiple Range Test for spca2			
Duncan Grouping	Mean	N	grp
A	0.04069	30	1200m +
B	0.01187	30	1000-1099m
B	0.00702	40	900-999m
C	-0.02011	61	800-899m
C	-0.02102	30	1100-1199m

Duncan's Multiple Range Test for PC1			
Duncan Grouping	Mean	N	grp
A	0.2239	30	1200m +
B	0.1188	30	1000-1099m
B	0.0370	30	1100-1199m *
B	0.0254	61	800-899m *
B	-0.3235	40	900-999m

Means with the same letter are not significantly different.

* Populations most similar with Sheared Principle Component 2

Blocked Flow Aspect

Sheared principle component analysis of eigenvalue proportional values were examined and resulted in the elimination of morphometrics principle component one (Size/Standard Length) which accounted for 91.05 % of the variance explained in shape. Thus, morphometrics sheared principle component two (SPCA2) was retained and accounted for 2.395 % of the remaining shape variance. Morphometric characters within SPCA2 that accounted for the most variance were: Snout Length, Horizontal-Eye Diameter and Lower Jaw Length and had absolute contributing values of 0.40189, 0.39411 and 0.38612, respectively (Appendix D).

Meristic eigenvalue proportional principle component one (PC1) accounted for 15.87 % of all variation in meristic characters. Meristic characters within PC1 that accounted for the most variance were: Gill Rakers on First Ceratobranchial, Pored Scales Posterior to the Lateral Line and Dorsal Rays and had absolute contributing values of 0.60514, 0.60154 and 0.55461, respectively (Appendix D).

Morphometric SPCA2 versus meristic PC1 output data results were then plotted in Minitab (Appendix E). Minimal polygon clusters (MPC) were not created as no blocked flow aspect grouping appeared to visually exhibit unique phenotypes. Approximately 15.66% of all individuals from groups or populations overlapped in phenotype. Given that 191 individuals were plotted this created problems in minimal polygon clusters construction of definitive clarity around each blocked flow aspect grouping.

Morphometrics SPCA2 and meristics PC1 data were then imported into SAS for ANOVA. Results for the ANOVA morphometrics SPCA2 model (Appendix F) had 3 degrees of freedom, a sum of squares value of 0.0139, a mean square of 0.0046, an F-value of 1.93 and a P-value of 0.1267. Results for the ANOVA meristics PC1 model (Appendix F) had 3 degrees of freedom, a sum of squares value of 2.9819, a mean square value of 0.9939, an F-value of 0.99 and a P-value of 0.3969. Due to my resultant p-values exceeding my critical alpha value of 0.05 I would fail to reject my null hypothesis that Brook Trout from different populations have the same phenotypic expression.

ANOVA Duncan's grouping results (Table 5) for SPCA2 and PC1 indicate significant similarities in means which correspond to similarities in morphometrics and meristics. Blocked flow aspect (East, South and West) draw inference to the most similar populations when comparing morphometrics SPCA2 and meristics PC1 against each other. Populations sampled within the three most similar blocked flow aspects from East, South and West are as follows: Bear Branch, Horse Creek, Little Cataloochee, Messer Fork, Straight Creek and Onion Bed, Pretty Hollow, Walker Camp Prong and Buck Fork, Chapman Prong, Kephart Branch, respectively.

Table 5. Duncan Grouping Results for Sheared Principle Component 2 (Morphometrics) from French Broad/Pigeon Watershed Brook Trout Blocked Elevation Populations.

Duncan's Multiple Range Test for spca2			
Duncan Grouping	Mean	N	grp
A	0.01713	30	West
A	0.00183	30	West
A	0.00126	50	East
B	-0.00780	81	North

Duncan's Multiple Range Test for PC1			
Duncan Grouping	Mean	N	grp
A	0.2497	30	South *
A	0.0201	81	North
A	-0.0856	30	West *
A	-0.1311	50	East *

Means with the same letter are not significantly different.

* Populations most similar with Sheared Principle Component 2

Parsed Sex

Sheared principle component analysis of eigenvalue proportional values were examined and resulted in the elimination of morphometrics principle component one (Size/Standard Length) which accounted for 90.43 % of the variance explained in shape. Thus, morphometrics principle component two (SPCA2) was retained and accounted for 2.418 % of the remaining shape variance. Morphometric characters within PC2 that accounted for the most variance were: Snout Length, Horizontal-Eye Diameter and Lower Jaw Length and had absolute contributing values of 0.40378, 0.39242 and 0.39227, respectively (Appendix D).

Meristic eigenvalue proportional principle component one (PC1) accounted for 16.10 % of all variation in meristic characters. Meristic characters within PC1 that accounted for the most variance were: Gill Rakers on First Ceratobranchial, Pored Scales Posterior to the Lateral Line and Dorsal Rays and had absolute contributing values of 0.64051, 0.63391 and 0.54118, respectively (Appendix D).

Morphometric SPCA2 versus meristic PC1 output data results were then plotted in Minitab (Appendix E). Minimal polygon clusters (MPC) were not created as no parsed group appeared to exhibit unique morphotypes.

Morphometrics SPCA2 and meristics PC1 data were then imported into SAS for preparation for ANOVA. Results for the ANOVA morphometric SPCA2 model (Appendix F) had 1 degree of freedom, a sum of squares value of 0.0335, a mean square of 0.0335, an F-value of 14.12 and a P-value of 0.0002. Results for the ANOVA meristic PC1 (meristics) model (Appendix F) had 1 degree of freedom, a sum of squares value of 0.1841, a mean square value of 0.1841 an F-value of 0.18 and a P-value of 0.6690. Due to my resultant p-values exceeding my critical alpha value of 0.05 I would fail to reject my null hypothesis that Brook Trout of different sex have the same phenotypic expression.

ANOVA Duncan's grouping results (Table 6) for SPCA2 and PC1 indicate significant similarities in means which correspond to similarities in morphometrics and meristics. Significant similarities cannot be drawn between parsed sex morphometrics, which indicates the probability of sexual dimorphism occurring within Brook Trout in this investigation.

Table 6. Duncan Grouping Results for Sheared Principle Component 2 (morphometrics) and PC1 (meristics) from French Broad/Pigeon Watershed Brook Trout Blocked Elevation Populations.

Duncan's Multiple Range Test for spca2			
Duncan Grouping	Mean	N	grp
A	0.013727	92	Males
B	-0.012757	99	Females

Duncan's Multiple Range Test for PC1			
Duncan Grouping	Mean	N	grp
A	0.03221	92	Females
A	-0.02993	99	Males

Means with the same letter are not significantly different.

Winding Stair

Sheared principle component analysis of eigenvalue proportional values were examined and resulted in the elimination of morphometrics principle component one (Size/Standard Length) which accounted for 89.56 % of the variance explained in shape. Thus, morphometrics principle component two (SPCA2) was retained and accounted for 2.66 % of the remaining shape variance. Morphometric characters within SPCA2 that accounted for the most variance were: Snout Length, Caudal Peduncle Length and Posterior-Anal to Dorsal Caudal had absolute contributing values of 0.4583, 0.43216 and 0.32965, respectively (Appendix D).

Meristic eigenvalue proportional principle component one (PC1) accounted for 22.94 % of all variation in meristic characters. Meristic characters within PC1 that accounted for the most variance were: Anal Rays, Pored Scales Posterior to the Lateral Line and Gill Rakers on First Epibranchial had absolute contributing values of 0.68940, 0.59272 and 0.57949, respectively (Appendix D).

Morphometric SPCA2 versus meristic PC1 output data results were then plotted in Minitab (Appendix E). Minimal polygon clusters (MPC) were created and contained groupings which appeared to exhibit unique morphotypes.

Morphometrics SPCA2 and meristics PC1 data were then imported into SAS in preparation for ANOVA. Results for the ANOVA morphometric SPCA2 model (Appendix F) had 2 degrees of freedom, a sum of squares value of 0.0162, a mean square of 0.0081, an F-value of 7.07 and a P-value of 0.0081. Results for the ANOVA meristic PC1 (meristics) model (Appendix F) had 2 degrees of freedom, a sum of squares value of 17.6893, a mean square value of 8.8447 an F-value of 21.11 and a P-value of less than 0.0001. Due to my resultant p-values

exceeding my critical alpha value of 0.05 I would reject my null hypothesis that Brook Trout of different populations have the same phenotypic expression.

ANOVA Duncan's grouping results (Table 7) for SPCA2 and PC1 indicate significant similarities in means which correspond to similarities in morphometrics and meristics. Significant similarities could be drawn between morphometrics and meristics from Winding Stair and Caldwell Fork, which indicates the possibility that to some degree Caldwell Fork phenotypes are more represented among the ten Brook Trout sampled from Winding Stair.

Table 7. Duncan Grouping Results for SPCA 2 and PC1 from Winding Stair and Source Populations.

Duncan's Multiple Range Test for spca2			
Duncan Grouping	Mean	N	grp
A	0.03231	10	Little Cataloochee
B	-0.01120	10	Caldwell Fork
B	-0.02111	10	Winding Stair

Duncan's Multiple Range Test for PC1			
Duncan Grouping	Mean	N	grp
A	1.0405	10	Little Cataloochee
B	-0.2511	10	Caldwell Fork *
B	-0.7895	10	Winding Stair *

Means with the same letter are not significantly different.

* Populations most similar with Sheared Principle Component 2

Phenotypic Similarities

Brook Trout from the French Broad/Pigeon Watershed were analyzed for cluster groupings to create a cladograms/phylogenetic tree in PC-ORD 6. Hierarchical clustering analysis agglomerated populations based on two different linkage properties. Method one was formatted to run given the parameters flexible beta analysis of 0.75 linkage. This method allowed me to examine French Broad/Pigeon populations on a large scale view with a sister-group of Brook Trout added from Long Island, NY and an out-group of spotted gar. Under these criteria all Brook Trout fell under the genus node of *Salvelinus*. Under this node, two distinct

branches of Brook Trout formed with groups parsed by parr marks being less than and greater than eight.

Method two was formatted agglomerate nearest neighbor methodology, whereas Brook Trout of the highest similarity tend to form singular linkages. Again All Brook Trout were Properly assigned to the *Salvelinus* genus node and then parsed into four sub-branching nodes with distance linkage values all being retained to a level of greater than 90 % for all characters. This indicates that 10 % of all Brook Trout populations' characters within the French Broad/Pigeon Watershed are variable population wide. Therefore, approximately three (3) to four (4) phenotypic characters separate 19 populations. These characters are as follows: French Broad/Pigeon separated from Long Island Group by having greater than seven (7) dorsal rays, and having a measureable distance from the anterior dorsal fin origin to the posterior of the anal fin as less than 59.39mm in length. French Broad/Pigeon population can then be broken into two unique branches defined ray counts of the pectoral fin being less than 15 and then equal to or greater than 13.

NMDS

Nonmetric Multidimensional Scaling was used to draw inference into environmental variables (Elevation and Stream Flow Aspect) influences upon phenotypes of populations. Relative Euclidian distance measure was applied with a maximum of three axis selected with a maximum of 100 iteration produced a final stress of 0.0948. This low of value of stress is considered excellent with zero false inferences being drawn upon. Stress values in PC-ORD are automatically multiplied by 100, therefore respective stress value fall below 0.20. NMDS scores for each axis were then plotted two-dimensionally and three-dimensionally. Two-dimensional plots were used to visually compare two-dimensional plots from sheared principle component analysis outputs retained principle component two versus principle component one.

Table 8. NMDS Stress results to three dimensional relation of French Broad/Pigeon Brook Trout Parsed Sex Groups

STRESS IN RELATION TO DIMENSIONALITY (Number of Axes)							
Stress in real data				Stress in randomized data			
250 run(s)				Monte Carlo test, 250 runs			
Axes	Minimum	Mean	Maximum	Minimum	Mean	Maximum	p
3	0.345	0.788	2.050	1.282	1.564	4.995	0.0040
p = proportion of randomized runs with stress < or = observed stress i.e., $p = (1 + \text{no. permutations} \leq \text{observed}) / (1 + \text{no. permutations})$							

Conclusion: a 3-dimensional solution is recommended.

Similar results were show in both 2D and 3D NMDS plots, with high degrees of overlapping groups or populations. Stream flow aspect appears to separate North flowing streams, which indicates that environmental factors pertaining to aspect effect more northern flowing stream phenotypes. Elevation appears to be significant in that minimal polygon clusters are smaller at higher elevation populations versus larger in lower elevation populations. This

indicates greater variance in phenotype expressed in populations sampled at lower elevations. It can be speculated that at lower elevations, populations are more genetically heterogeneous, thus express more variance in phenotype.

Discussion

Brook Trout from the French Broad/Pigeon Watershed exhibit high variability in shape (morphometrics) but exhibit low variability in outward appearance (meristics). Here, I demonstrated that through thorough analysis of multiple blocking and parsing of testable criteria that individual Brook Trout populations possess shapes unique to their geographically isolated stream. The exception being, Brook Trout blocked elevation groups. Populations analyzed at blocked elevations exhibited high degrees of similarity and express near exact shape. Shape of Brook Trout populations differed between females and males, with head length, snout length and lower jaw length being the greatest contributing Principle Components of variance upon analysis. Males and females did not differ in their meristics.

Meristic analysis results indicate that Brook Trout populations are not different in their outward appearances. Brook Trout populations examined under no blocking criteria within the French Broad/Pigeon Watershed was the exception. Brook Trout groups from Winding Stair and its source stream populations differed only morphometrically.

Interestingly enough, two of the aforementioned characters, head length and lower jaw length, are observed as being highly variable across all assays. Thus, it can be implied that sexual dimorphism is a largest contributor of variance within this investigation. Secondly, horizontal eye diameter is the third largest contributor of variance in all assays with the exception being parsed sex and Winding Stair. Feduccia and Slaughter (1974) were able to attribute eye diameter of rays to sexual dimorphism, therefore it is plausible to assume that eye diameter of Brook Trout is directly correlated back to an artifact of sexual dimorphism in male specimens.

In regards to phenotypic plasticity, Winding Stair analysis showed that Snout Length, Caudal Peduncle Length and Posterior-Anal to Dorsal Caudal contributed the most to observed variance. I further analyzed ratios of the aforementioned contributors of variance means over standard length for each population to the nearest thousandth of a decimal. The following is an attempt to decipher morphometric variance as a result of phenotypic plasticity on Winding Stair and its Source Stream Populations:

Table 9. Winding Stair and Source Populations Character Ratio to Standard Length.

	Winding Stair Means	Caldwell Means	Little Cat. Means
CPL	18.129	20.425	19.913
PADC	23.157	26.525	25.677
SNL	8.445	9.883	8.617
SL	119.576	129.874	126.734
	Winding Stair Ratio	Caldwell Ratio	Little Cat. Ratio
CPL	0.152	0.157	0.157
PADC	0.194	0.204	0.203
SNL	0.071	0.076	0.080

Winding Stair Brook Trout sampled and analyzed for ratio comparisons indicated smaller ratio size in all categorizes. These results imply that Brook Trout from Winding Stair are less fusiform than those from Caldwell Fork; Caldwell Fork Brook less fusiform than those Brook Trout of Little Cataloochee, thus Winding Stair Brook Trout is the least fusiform of this analysis. Thus, I would deduce that Winding Stair has less stream velocity than both Caldwell Fork and Little Cataloochee; therefore they require a less stream-lined form. I would further imply that Winding Stair populations are and have adaptively radiated to their local environment.

In all cases Nonmetric Multidimensional Scaling validated visually, through the creation of three-dimensional ordination plots, high degrees of overlapping similarities. Upon inspecting NMDS ordination plots (Appendix H), and cross comparing them to Principle Component Minimal Polygon Cluster graphs it can be inferred that to some degree homogenization of phenotypes exists between Brook Trout within the French Broad/Pigeon Watershed. NMDS plots indicate that elevation appears to significantly contribute to phenotypic variance. Brook Trout within the French Broad/Pigeon Watershed of Great Smoky Mountains National Park have shown to be highly variable in shape, but highly similar in expressed outward appearance. Therefore, it is my conclusion that within this investigation, elevation and sexual dimorphism are the dominant contributors of shape variance; geographically isolated Brook Trout cannot be assigned back to stream origin based on meristic counts; and it can be inferred that these populations studied here probabilistically are derived from a common ancestor. It appears as though Brook Trout within the French Broad/Pigeon Watershed are/or have diverged phenotypically into two (2) distinct clades. This diversion appears to be related to phenotypic plasticity derived from adaptive radiation to local habitat at varying elevation clines; with sexual dimorphic character states being an artifact of sampling.

Recommendations

Given the results of this investigation, Biologists selecting Brook Trout source stock for founding populations should be cautious in selection criteria of stocks based on singular non-blocked morphometric and meristic analysis. Plausible source stocks should be analyzed to delineate genotype and phenotype configurations prior to translocation. I recommend that Brook Trout of both sexes within this investigation undergo computed topography (CT) scans for craniofacial analysis to examine the effects of sexual dimorphism. Results from CT scans could lead to further insight into inferring the exact phylogenetic relatedness of this species. In addition to, mitochondrial deoxyribonucleic acid (mDNA) should be obtained from Brook Trout tissue samples to delineate ancestral relatedness of geographically isolated populations. Combining morphometric, genomic and CT assays should generate sufficient data to conclude that to what degree Brook Trout from the French Broad/Pigeon Watershed are differentiating. Debates as to whether Brook Trout populations are diverging into subspecies or even newly arisen species classifications cannot be definitively settled until all three of the aforementioned assays are conducted. Therefore, further analysis of these populations needs to be conducted range wide to determine the current status of Brook Trout.

Further replicate studies of this kind conducted on allopatric Brook Trout streams that have been restored at variable time frames would be very beneficial to gather more insight into the evolutionary process of phenotypes.

More over, the focus of future studies should be relegated to determining which populations of Brook Trout have the best likelihood of persistence into the future. I would suggest that given recent advances in the field of genomics, that meta-populations be delineated and established as evolutionary protected reservoirs. Projects involving habitat restoration serve

their purpose, but we as biologists will never be able to create cold water habitat for the persistence of Brook Trout.

Phenotypes are dynamic in nature. Offspring of restoration founders might show greater plasticity in order to adapt to their local environment. Thus offspring could exhibit signs of evolution without changes in allelic frequency. Tracking phenotype and genotype dynamics in restored streams can be accomplished by obtaining subsamples prior to and at set intervals post restoration. This will allow biologists to draw inferences into how differentiation affects populations post restoration.

Appendix A

Morphometric Landmarks with Truss Network Schematic

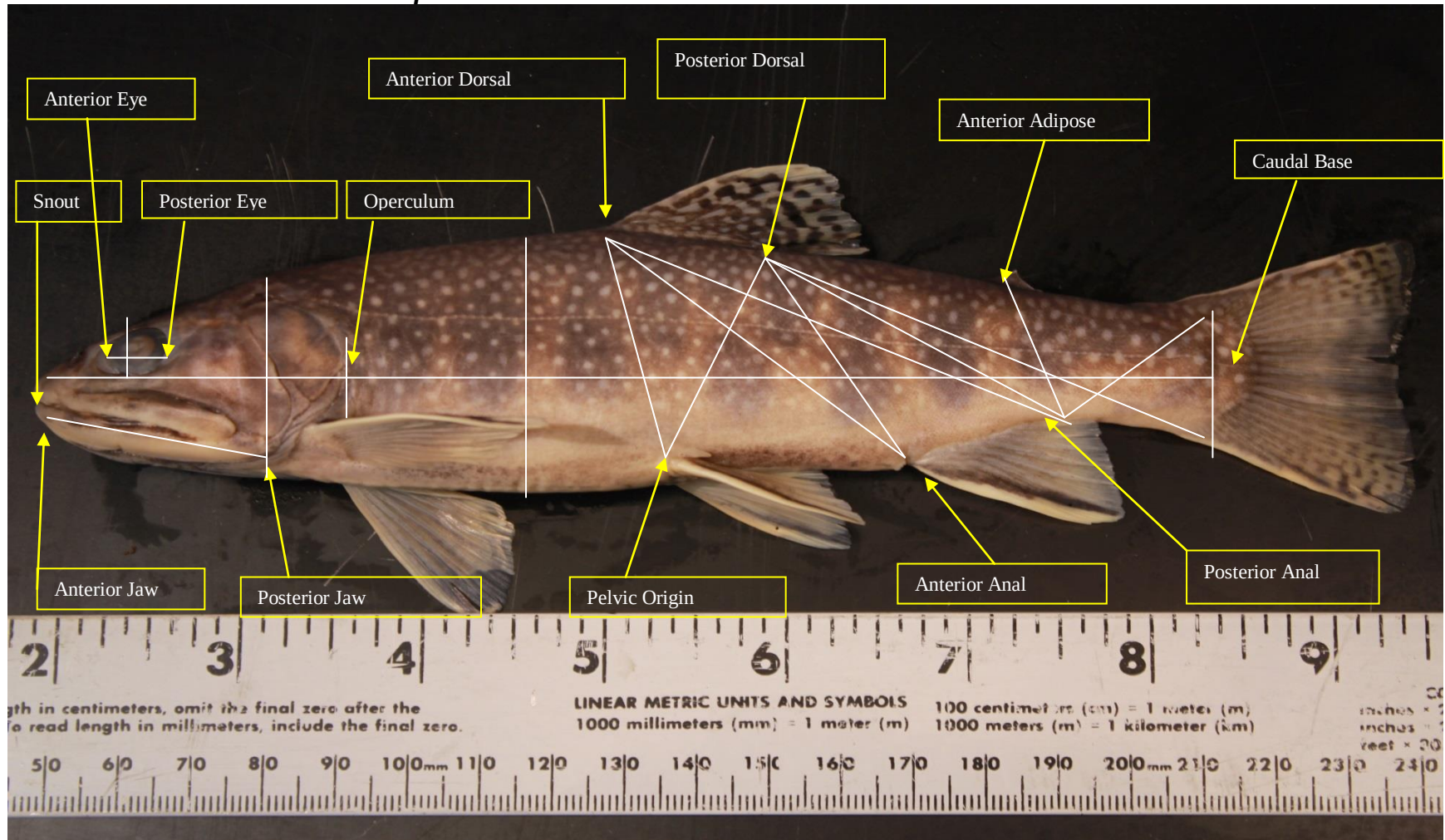


Figure 3. Brook Trout Morphometric Character Landmarks (measurements)

Table 10. Brook Trout morphometric measurement names, abbreviations and descriptions from Great Smoky Mountains, French Broad/Pigeon Watershed, Tennessee and North Carolina

		Morphometrics		
Measurement	Abbreviation	Mean Measurement (mm)	Range Measurements (mm)	Description
Standard Length	SL	122.61	83.86 - 164.49	Tip of Snout to Caudal Base
Head Length	HL	33.44	22.23 - 47.74	Tip of Snout to Operculum
Snout Length	SNL	8.92	5.48 - 15.35	Tip of Snout to Anterior Eye
Post Orbital Head Length	POHL	17.43	10.70 - 24.03	Posterior Eye to Operculum
Horizontal Eye Diameter	HED	9.06	6.87 - 12.52	Anterior Eye to Posterior Eye
Vertical Eye Diameter	VED	8.10	6.18 - 10.29	Ventral Eye to Dorsal Eye
Lower Jaw Length	LJL	23.72	14.68 - 37.23	Anterior Jaw Tip to Posterior Jaw Bone
Head Depth	HD	22.79	15.95 - 32.09	Dorsal Nape to Ventral Head (greatest depth)
Body Depth	BD	29.84	20.08 - 44.11	Anterior Dorsal-fin to Posterior Pelvic-fin Origin (greatest depth)
Snout to Dorsal Origin	SNDOR	59.61	40.19 - 84.48	Tip of Snout to Anterior Dorsal-fin Origin
Snout to Pelvic Origin	SNPEL	63.63	41.83 - 89.41	Tip of Snout to Pelvic-fin Origin
Dorsal-fin Base Length	DFBL	17.06	11.22 - 25.07	Anterior Dorsal-fin Origin to Posterior Dorsal-fin Insertion
Anterior Dorsal to Anterior Anal	ADAA	42.15	28.30 - 57.36	Anterior Dorsal-fin Origin to Anterior Anal-fin Origin
Anterior Dorsal to Posterior Anal	ADPA	50.56	34.70 - 67.05	Anterior Dorsal-fin Origin to Posterior Anal-fin Insertion
Posterior Dorsal to Anterior Anal	PDAA	27.79	18.08 - 37.84	Posterior Dorsal-fin Origin to Anterior Anal-fin Origin
Posterior Dorsal to Posterior Anal	PDPA	33.55	21.12 - 46.58	Posterior Dorsal-fin Origin to Posterior Anal-fin Insertion
Posterior Dorsal to Ventral Caudal	PDVC	50.47	34.05 - 43.86	Posterior Dorsal-fin Insertion to Base of Ventral Caudal-fin Origin
Posterior Anal to Dorsal Caudal	PADC	24.56	17.53 - 34.73	Posterior Anal-fin Insertion to Base of Dorsal Caudal-fin Origin
Anterior Adipose to	AADPAA	16.61	10.90 - 24.62	Anterior Adipose-fin

Posterior Anal				Origin to Posterior Anal-fin Origin
Anterior Dorsal to Pelvic	ADP2	29.14	19.51 - 43.23	Anterior Dorsal-fin Origin to Pelvic-fin Origin/Insertion
Posterior Dorsal to Pelvic	PDP2	27.26	18.43 - 39.50	Posterior Dorsal-fin to Pelvic-fin Origin/Insertion
Caudal Peduncle Length	CPL	19.02	13.11 - 27.40	Posterior Anal-fin Insertion to Ventral Caudal-fin Base
Caudal Peduncle Depth	LCPD	16.84	10.80 - 23.93	Depth Caudal-fin base
Meristics	Abbreviation	Mode (mm)	Range (mm)	Description
Dorsal-fin Rays	DRAYS	11	9 - 13	Soft Ray Counts on Dorsal-fin
Anal-fin Rays	ARAYS	11	9 - 13	Soft Ray Counts on Anal-fin
Pelvic-fin Rays	P2RAYS	9	8 - 11	Soft Ray Counts on Pelvic-fin
Pectoral-fin Rays	P1RAYS	13	12 - 15	Soft Ray Counts on Pectoral-fin
Lateral Line Scales	LLS	106	95 - 119	Scales on Lateral Line
Pored Scales Posterior to Lateral Line	PSPLL	4	0 - 7	Pored Scales Posterior to Caudal-fin Base
Gill Rakers on First Ceratobranchial	GRLOW	8	4 - 10	Gill Rakers on First Lower Gill Arch
Gill Rakers on First Epibranchial	GRUP	4	2 - 7	Gill Raker on First Upper Gill Arch
Total Lower Left Jaw Teeth	TORLLJ	13	10-15	Total Teeth Count on Lower Left Jaw
Parr Marks	prr mks	8	6 - 12	Total Vertical Bars on Left Lateral Side

Appendix B

Meristic Character Descriptions

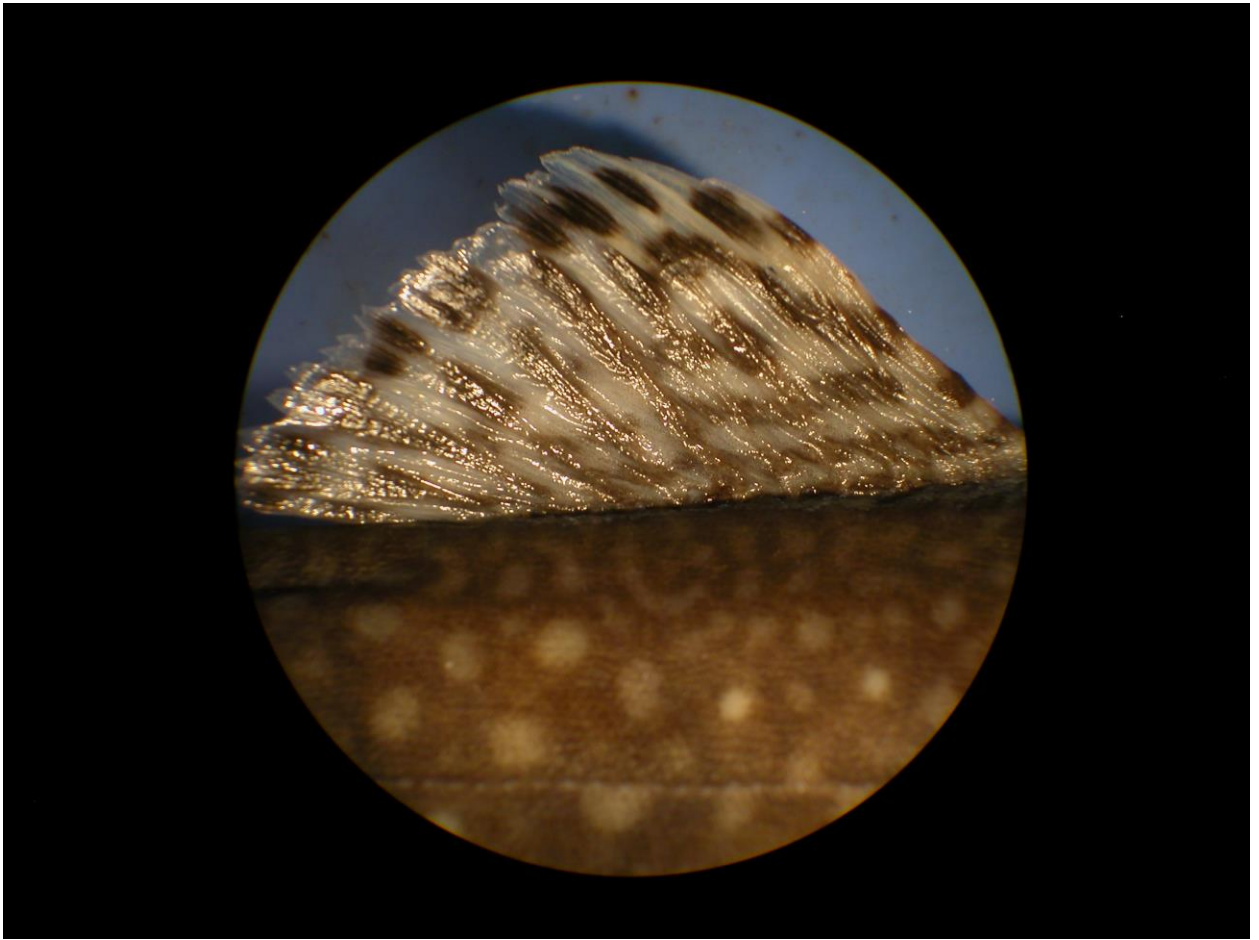


Figure 4. Dorsal Rays (DRAYS)

Dorsal rays are soft, branched supporting elements of the dorsal fin. Branching rays are never counted separately, but as whole elements. Often times rudimentary rays are located posterior, these are never counted.

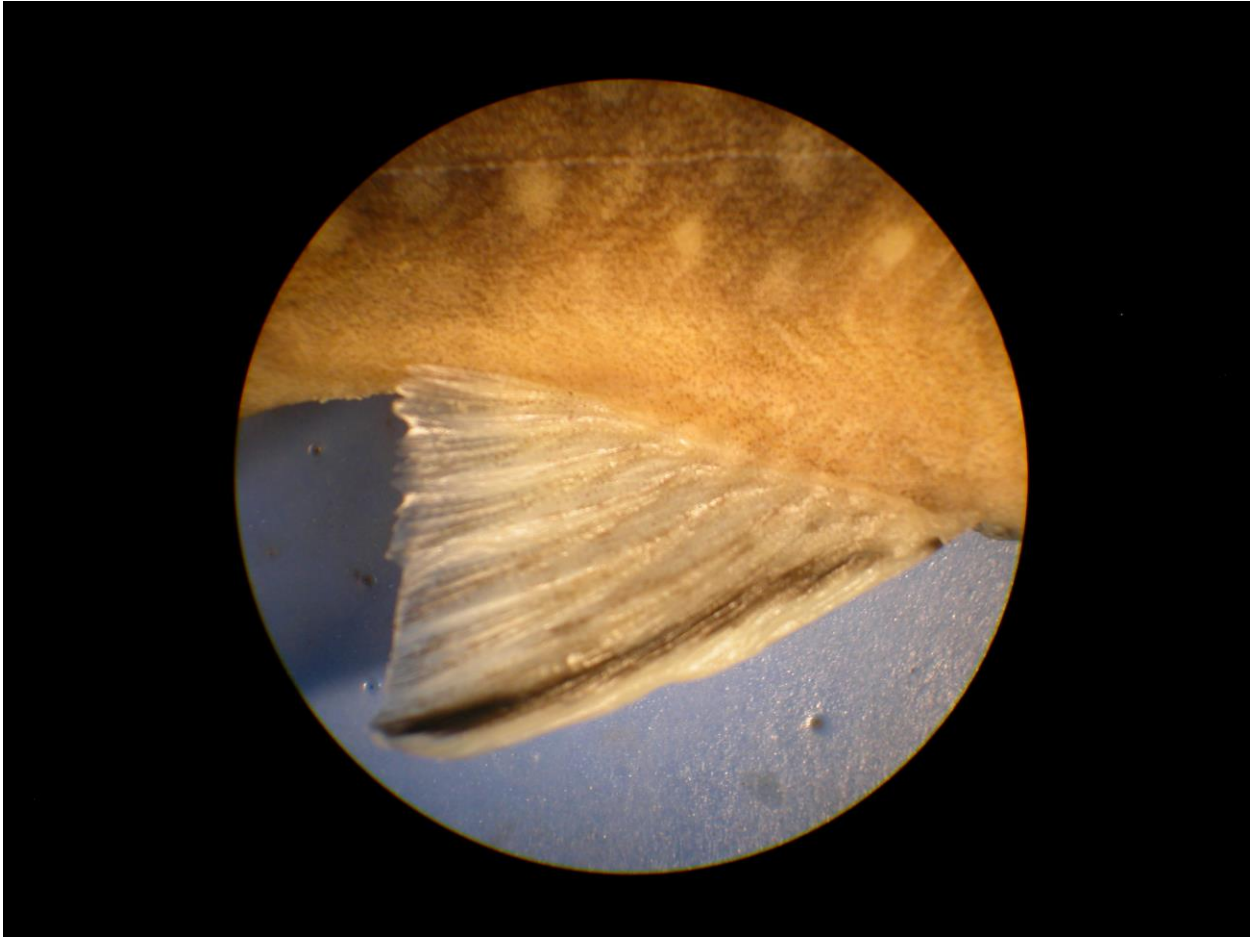


Figure 5. Anal Rays (ARAYS)

Anal rays are soft, branched supporting elements of the anal fin. Branching rays are never counted separately, but as whole elements. Often times rudimentary rays are located posterior, these are never counted.

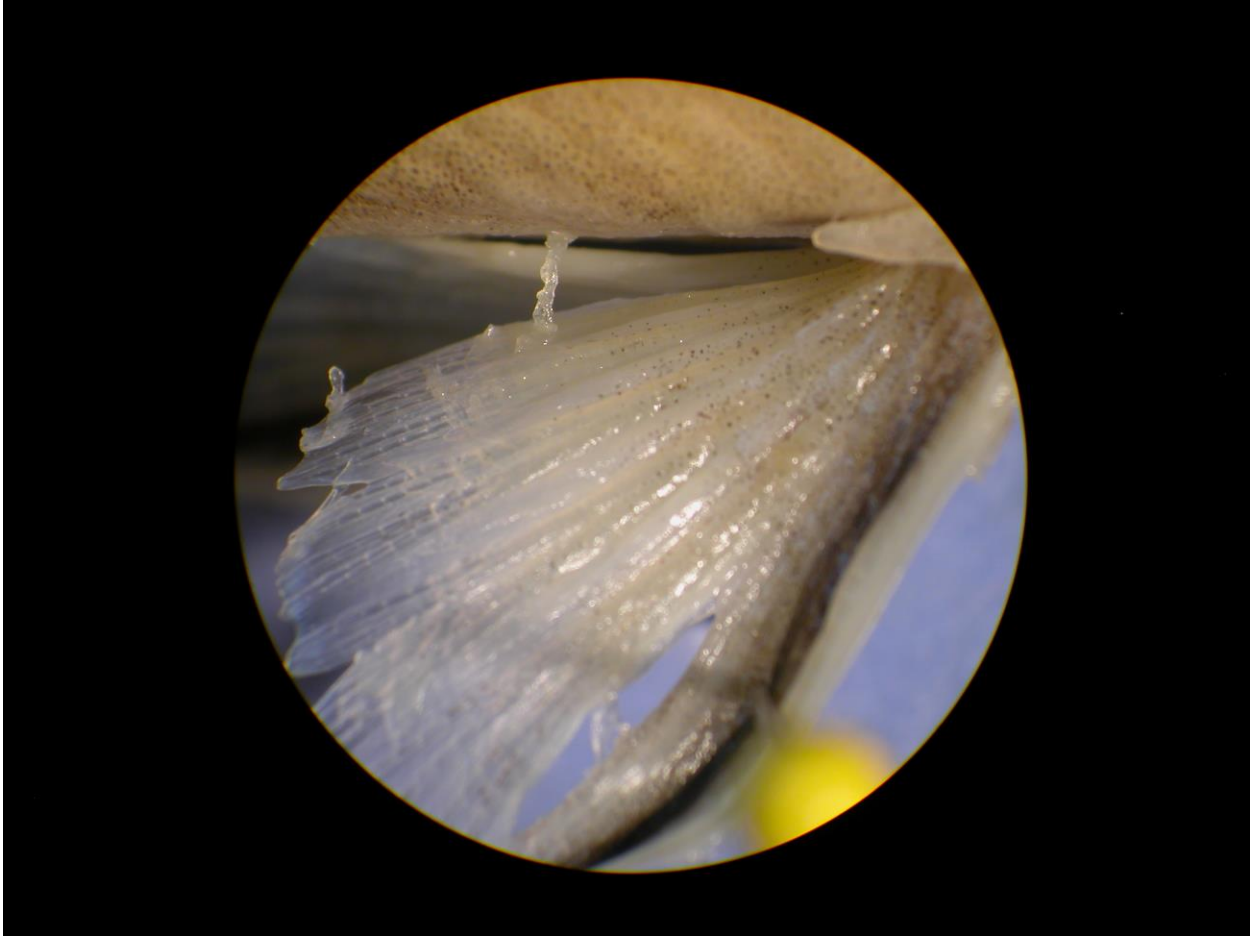


Figure 6. Pelvic Rays (P2RAYS)

Pelvic rays are soft, branched supporting elements of the pelvic fin. Branching rays are never counted separately, but as whole elements. Often times rudimentary rays are located posterior, these are never counted.



Figure 7. Pectoral Rays (P1RAYS)

Pectoral rays are soft, branched supporting elements of the pectoral fin. Branching rays are never counted separately, but as whole elements. Often times rudimentary rays are located posterior, these are never counted.

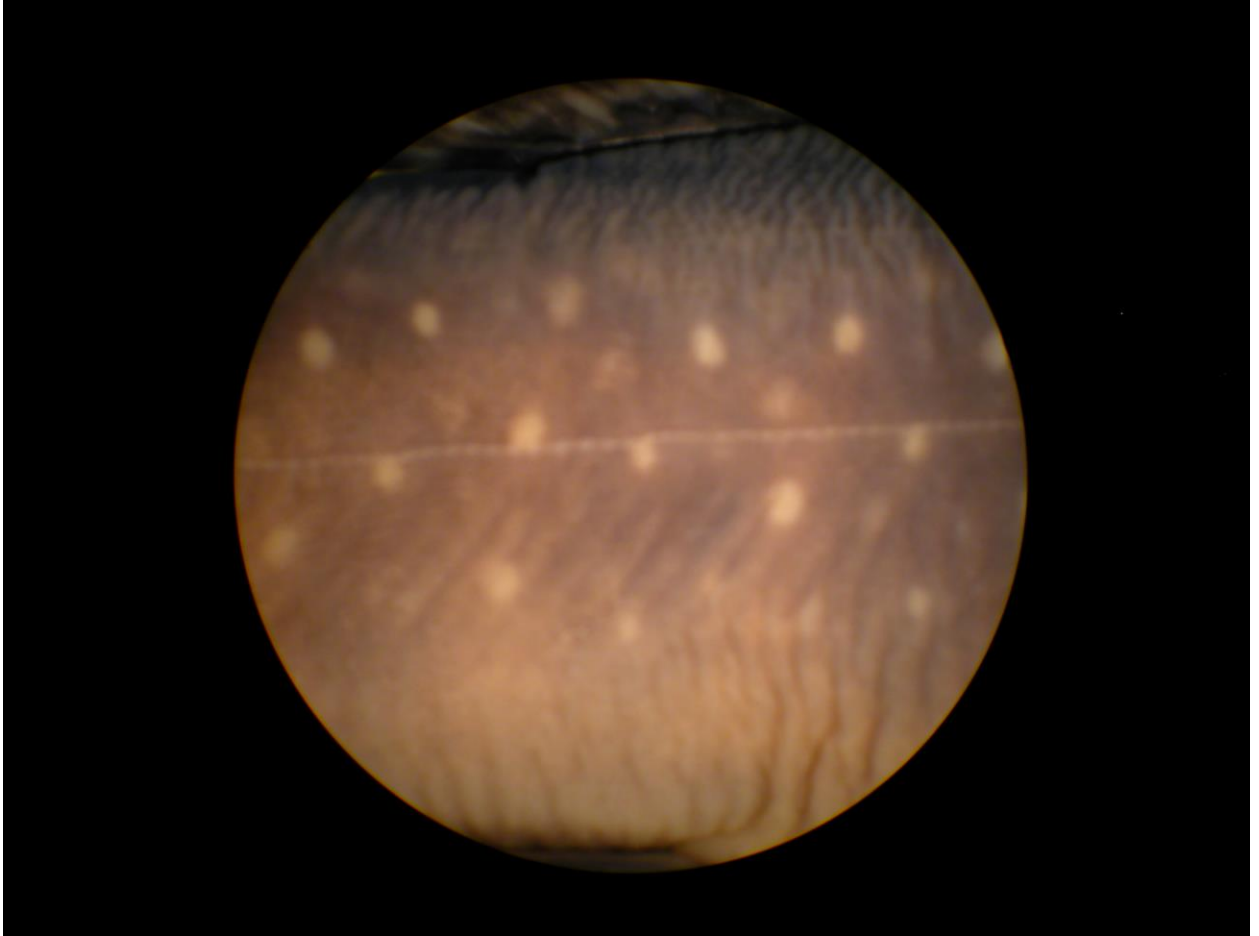


Figure 8. Lateral Line Scales (LLS)

Lateral line scales in Brook Trout are defined as pored cycloid scales along the lateral line of the fish. Counts begin at the shoulder origin and stop at the base of the caudal fin, determined by moving the caudal in order to develop a distinct crease (Hubbs and Lagler 1958). Lateral line scales that fall directly in the caudal crease are never counted.

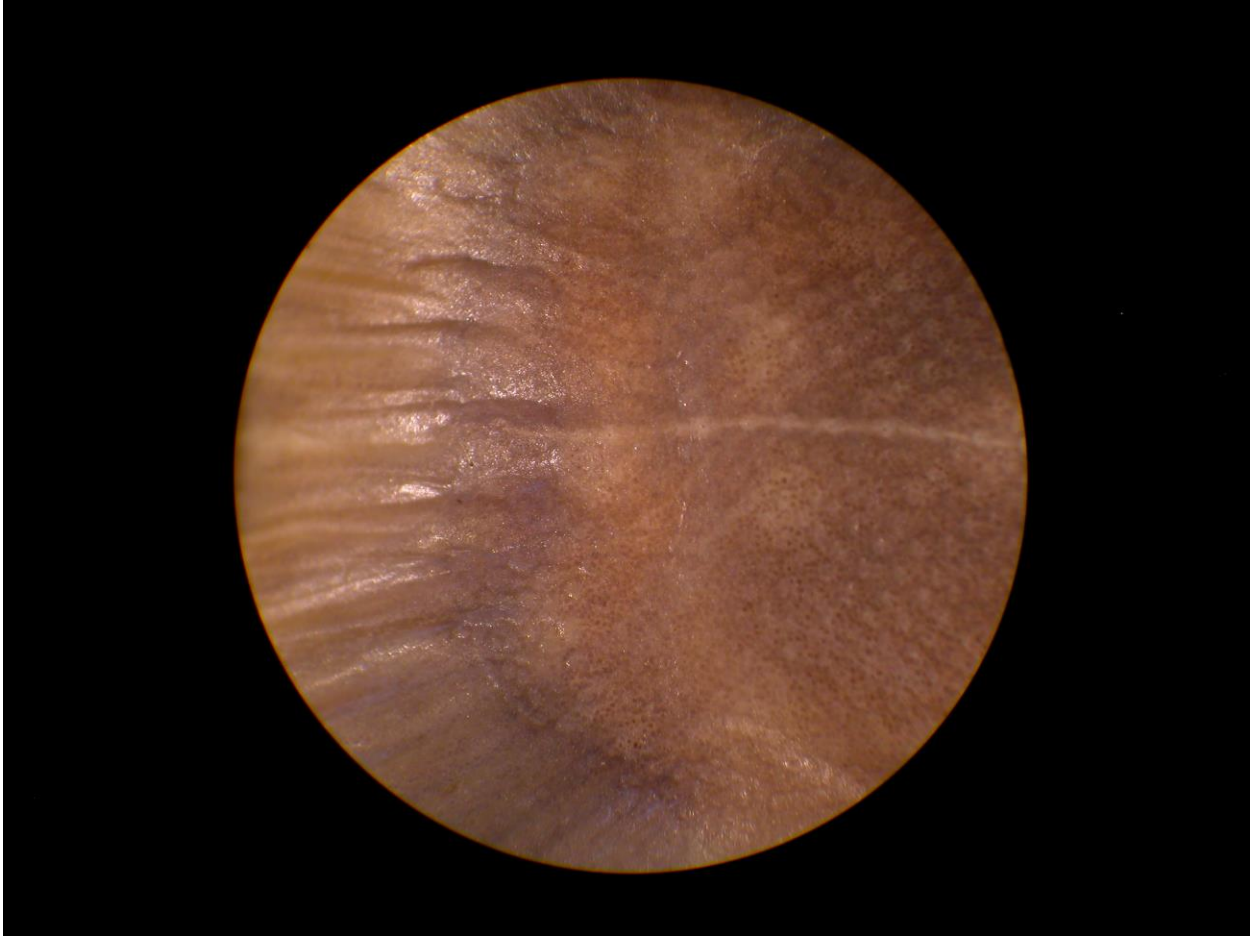


Figure 9. Pored Scales Posterior to Lateral Line (PSPLL)

Pored scales posterior to the lateral line are pored scales that are in line with the lateral line directly following that lateral line crease. In rare cases branching occurs. In which case all pored scales are counted and noted as being an anomaly.

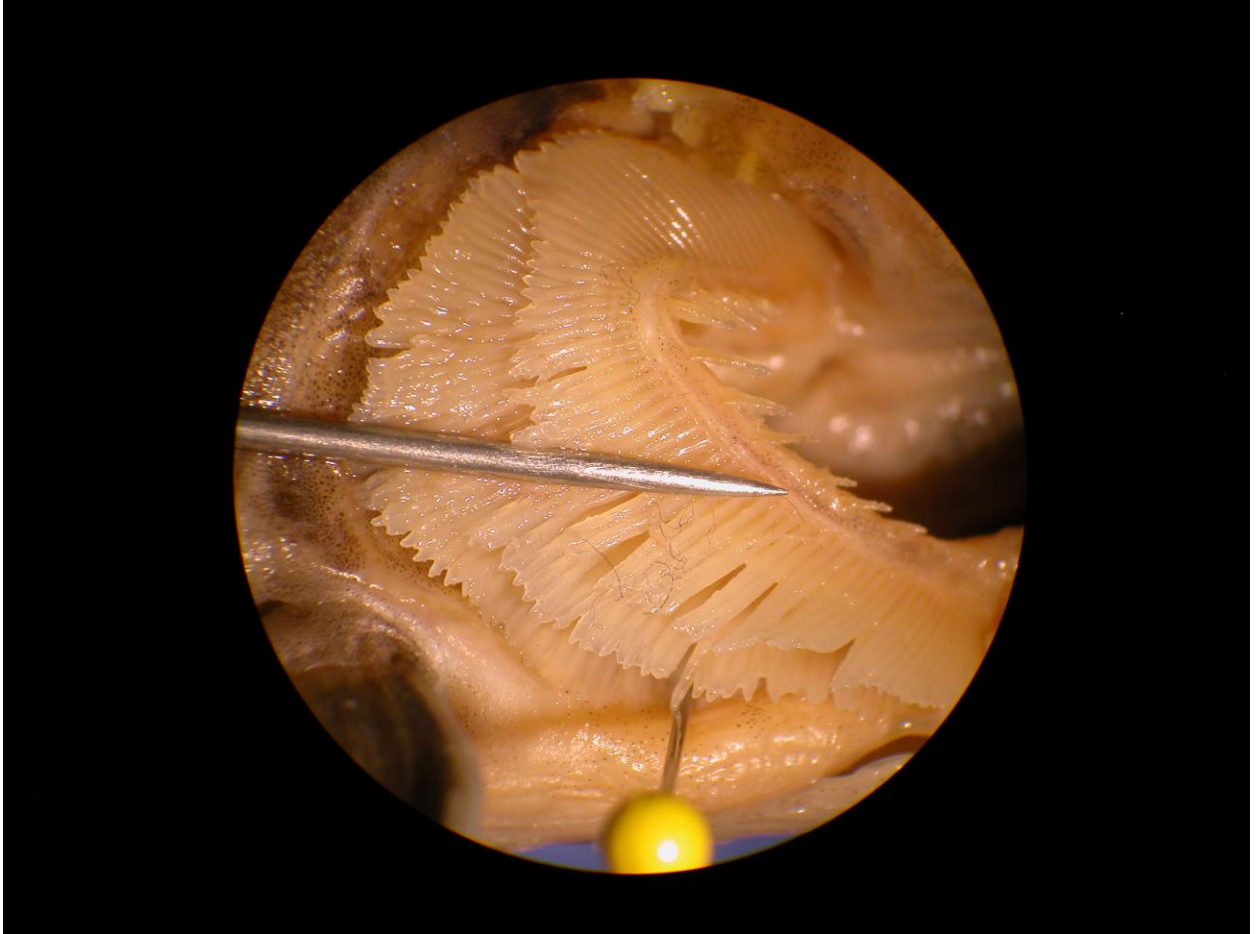


Figure 10. Gill Rakers on First Ceratobranchial (GRLOW)

Gill rakers on the first branchiostegal (lower) gill arch are filtering membranes used to retain prey item in the mouth to be directed toward the digestive system. All gill rakers are counted on the lower arch with the exception being the mid point gill raker.

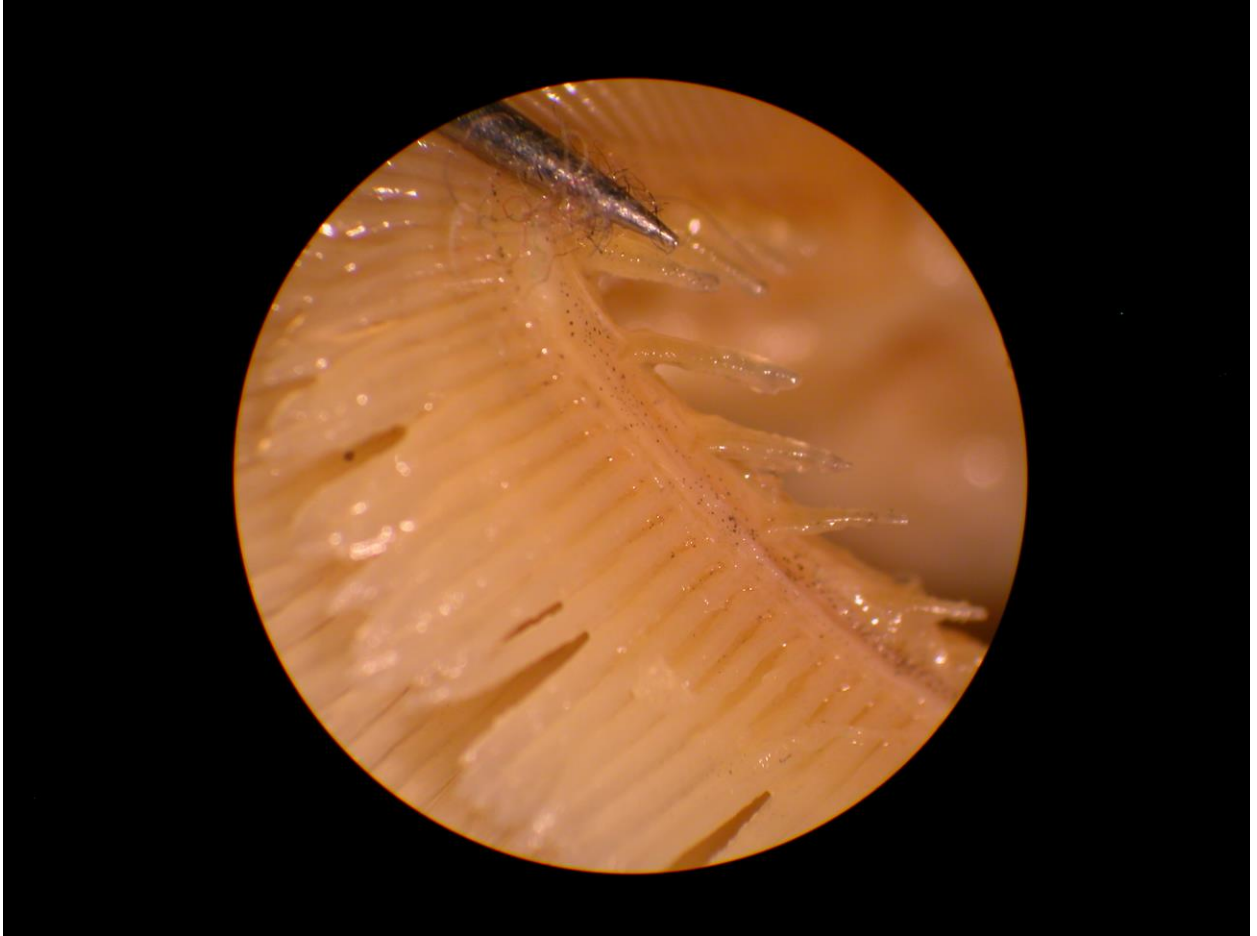


Figure 11. Gill Rakers on First Epibranchial (GRLOW)

Gill rakers on the first epibranchial (upper) gill arch are filtering membranes used to retain prey item in the mouth to be directed toward the digestive system. All gill rakers are counted on the upper arch, with the exception being the mid point gill raker.

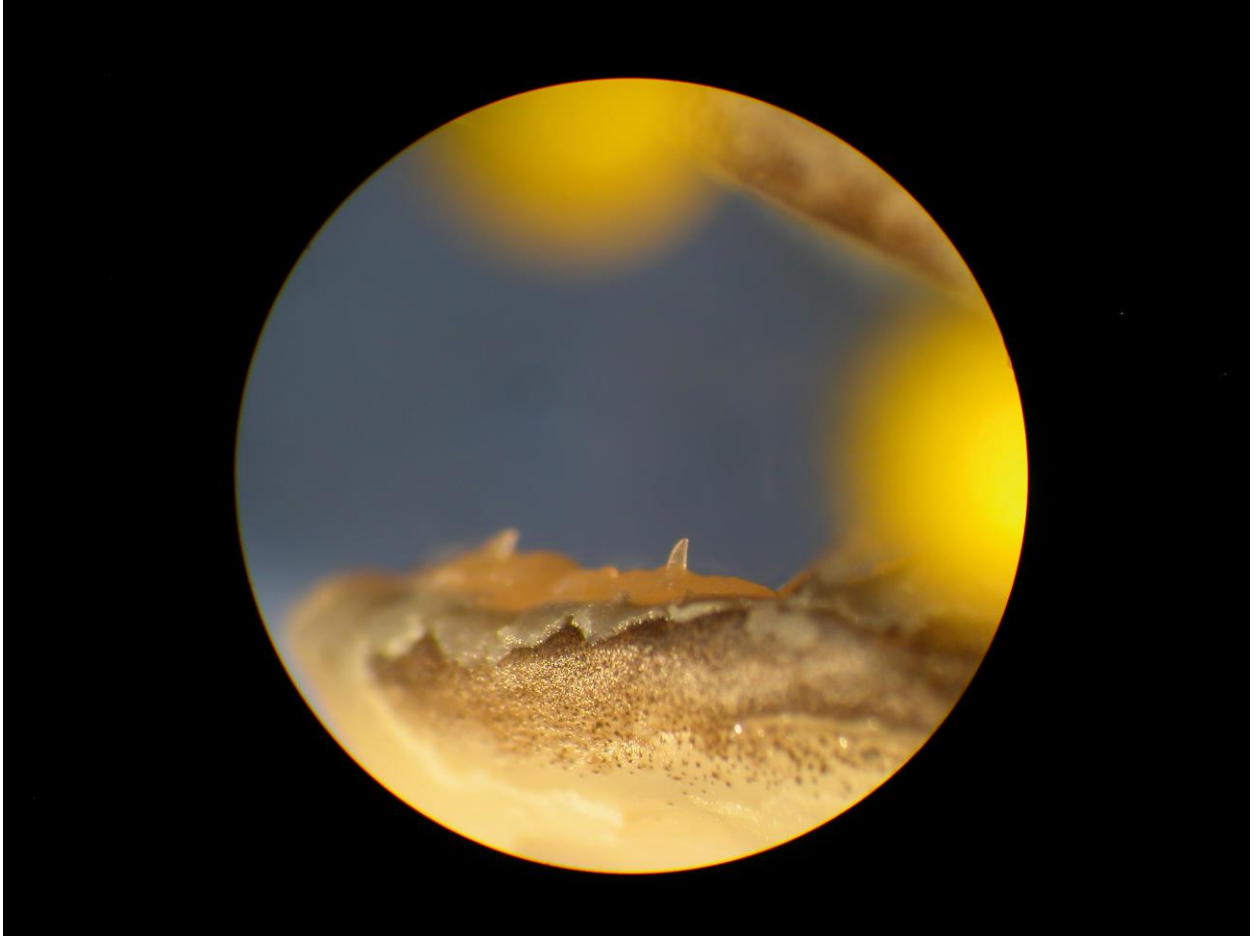


Figure 12. Lower Left Jaw Teeth (TORLLJ)

All visible and pored tooth sockets on the lower left portion of the jaw from the tip of the lower jaw to the posterior of the jaw.



Figure 13. Parr Marks (prk mks)

Parr marks are vertical bands originating from the dorsal that travel across the lateral line to the mid-belly on salmonid species. These marks typically fade and are not visible on adult fishes. Parr marks which do not travel to the mid-belly are not counted.

Appendix C

Raw Measurement Data

Table 11. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Bear Branch, Tennessee

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA	PDA
Bear_Branch	1	1	122.81	34.06	9.45	17.51	9.23	8.22	25.96	21.74	33.32	62.71	62.91	17.91	44.76	50.21	28.93
Bear_Branch	1	2	116.95	34.22	8.85	17.81	9.36	7.75	24.5	21.08	29.56	58.73	60.42	15.14	39.63	47.45	26.35
Bear_Branch	1	3	105.57	27.41	7.31	14.18	7.62	6.79	18.43	16.98	24.24	50.94	52.35	14.23	36.29	43.47	22.97
Bear_Branch	1	4	115.7	31.25	8.55	15.76	8.92	7.6	21.81	19.37	27.32	56.78	60.23	16.71	40.78	48.16	27.65
Bear_Branch	1	5	107.74	27.75	7.13	14.32	8.09	7.09	19.31	18.11	27.05	51.67	54.47	16.09	38.47	47.97	26.82
Bear_Branch	1	6	108	28.73	7.29	14.92	7.78	7.11	21.41	18.04	23.98	53.27	55.37	14.41	34.87	43.06	22.58
Bear_Branch	1	7	110.14	29.56	7.69	16.11	7.91	6.94	21.81	18.12	23.11	54.09	57.12	15.15	35.62	42.36	22.49
Bear_Branch	1	8	108.11	30.57	8.14	16.18	8.72	7.96	21.24	19.66	27.88	54.15	55.75	15.83	38.97	45.75	26.37
Bear_Branch	1	9	129.19	36.45	9.48	19.43	10.24	8.81	26.26	22.33	30.56	63.33	66.63	17.96	44.71	44.83	29.52
Bear_Branch	1	10	113.04	30.64	7.74	15.64	8.72	7.59	21.19	18.33	24.62	54.39	56.96	16.38	39.63	47.64	25.84
		Mean/Mode	113.73	31.06	8.16	16.19	8.66	7.59	22.19	19.38	27.16	56.01	58.22	15.98	39.37	46.09	25.95

	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	32.37	50.94	25.91	16.77	31.9	28.99	20.59	17.75	11	10	9	13	103	3	8	4	12	9
	30.97	48.03	22.32	14.25	28.82	25.49	18.35	16.67	11	11	9	13	104	4	8	3	12	9
	29.1	42.79	22.19	14.03	23.4	21.56	16.84	13.4	10	10	9	14	103	3	8	3	11	8
	31.29	47.39	22.26	14.66	26.92	24.72	16.64	15	11	10	8	13	105	4	8	3	12	8
	32.48	45.1	20.36	14.83	25.4	24.23	13.97	14.84	12	10	9	14	102	4	9	3	13	9
	27.78	42.9	19.52	14.02	23.23	22.91	16.59	13.9	10	10	9	13	104	5	8	3	11	8
	27.81	43.66	21.37	14.01	23.05	20.95	16.89	13.87	10	10	9	12	105	4	7	3	12	9
	29.87	45.58	22.33	15.37	26.91	24.82	17.65	15.52	11	10	8	14	104	5	9	3	12	10
	35.53	52.93	25.89	16.55	29.56	27.82	20.22	17.46	12	10	9	14	103	4	7	3	12	8
	33.05	48.22	22.21	14.59	24.57	23.55	17.26	14.53	10	10	8	13	103	4	8	4	13	9
Mean/Mode	31.03	46.75	22.44	14.91	26.38	24.50	17.50	15.29	11	10	9	13	103	4	8	3	12	9

Table 12. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Buck Fork Tennessee

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Buck_Fork	1	1	149.26	42.18	12.15	22.23	8.81	8.42	30.55	28.35	36.46	73.35	77.05	18.65	51.65	58.87
Buck_Fork	1	8	135.92	36.76	8.83	18.82	9.63	8.21	25.52	23.65	30.66	64.17	71.18	16.62	45.95	55.82
Buck_Fork	1	2	132.53	38.53	10.78	20.3	9	8.75	27.54	24.42	28.8	64.24	68.16	15.9	43.9	52.8
Buck_Fork	1	3	129.17	33.98	9.73	18.71	8.55	7.89	23.29	25.11	33.01	61.87	67.13	18.46	45.27	55.84
Buck_Fork	1	5	128.42	34.13	8.74	17.94	7.81	7.74	23.99	22.96	28.78	59.71	65.24	15.44	42.04	53.34
Buck_Fork	1	4	119.03	33.1	8.46	17.42	8.42	7.86	22.45	22.7	25.76	54.24	64.28	14.96	39.34	47.34
Buck_Fork	1	7	118.23	33.44	8.6	17.1	8.57	7.96	22.56	22.35	29.14	56.48	63.41	15.02	39.01	48.36
Buck_Fork	1	9	118.15	32.15	7.65	16.45	7.84	7.11	22.37	21.26	25.43	57.93	59.44	13.4	36.98	45.61
Buck_Fork	1	6	108.32	31.18	7.1	16.42	8.47	7.92	20.76	21.32	27.86	53.77	53.69	14.01	35.73	43.77
Buck_Fork	1	10	96.04	27.54	5.99	15.3	7.54	7.25	18.23	18.17	22.25	46.38	47.57	12.4	32.17	40.04
		Mean/Mode	123.51	34.30	8.80	18.07	8.46	7.91	23.73	23.03	28.82	59.21	63.72	15.49	41.20	50.18

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	34.34	40.14	61.39	30.16	19.38	37.93	33.81	25.36	22.02	11	11	9	14	116	4	8	3	12	7
	30.47	38.75	55.56	27.68	18.08	31.91	30.07	22.66	19.77	11	11	9	12	114	3	8	2	12	8
	30.36	36.25	55.51	27.58	17.8	29.53	26.98	21.08	19.13	10	10	10	14	115	5	6	3	12	8
	31.26	37.89	53.45	25.46	18.35	32.25	30.77	19.59	19.05	10	10	8	13	108	5	8	2	11	9
	28.73	37.22	55.08	26.37	16.13	28.46	26.77	19.42	18.46	12	12	9	15	109	4	9	2	12	8
	25.58	32.63	49.09	26.16	16.27	27.47	25.43	21.25	16.22	11	10	11	15	117	3	9	5	13	8
	26.12	31.93	47.14	24.25	15.87	28.91	25.61	18.25	16.32	11	11	9	14	116	5	8	2	10	8
	24.47	31.15	50.21	26.78	15.31	24.86	23.48	19.98	16.67	9	12	9	15	117	4	9	2	12	8
	24.25	30.08	46.96	24.34	14.95	26.49	25.12	18.1	14.92	12	11	10	14	111	4	6	4	10	8
	21.87	27.43	40.01	20.48	12.39	22.72	21.51	15.07	12.88	11	11	9	13	106	4	6	4	12	8
Mean/Mode	27.75	34.35	51.44	25.93	16.45	29.05	26.96	20.08	17.54	11	11	9	14	116	4	8	2	12	8

Table 13. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Caldwell Fork North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Caldwell_Fork	1	1	144.8	42.55	12.22	23.21	10.1	9.01	30	26.43	36.73	71.76	75.89	21.28	49.95	60.27
Caldwell_Fork	1	2	123.19	35.28	9.34	19.4	9.04	7.67	24.76	22.23	30.52	60.89	62.97	17.38	42.39	50.04
Caldwell_Fork	1	3	137.23	38.35	11.03	20.55	9.2	8.17	28.82	24.15	34.78	66.12	70.28	21.38	47.45	58.87
Caldwell_Fork	1	4	131.38	36.97	9.7	19.79	8.84	7.76	27.64	23.83	32.75	64.97	68.33	18.66	46.2	54.21
Caldwell_Fork	1	5	145.81	38.41	9.75	20.41	10.11	8.61	27.2	25.42	33.28	68.39	76.18	20.18	49.63	59.83
Caldwell_Fork	1	6	116.08	30.64	7.85	16.53	8.67	7.82	21.16	19.72	28.49	55.88	57.55	16.58	40.86	48.01
Caldwell_Fork	1	7	117.25	31.02	8.37	16.84	8.34	7.62	22.99	20.43	27.02	55.67	59.61	17.67	39.97	47.91
Caldwell_Fork	1	8	123.66	34.92	9.82	18.09	8.89	8.08	24.68	21.62	31.79	61.21	65.09	18.62	43.06	51.33
Caldwell_Fork	1	9	122.41	32.68	9.11	16.95	8.68	7.81	22.29	22.75	29.92	58.73	60.64	16.98	43.91	53.34
Caldwell_Fork	1	10	136.93	38.69	11.64	20.48	9.49	8.45	29.68	24.09	35.01	68.13	71.27	20.47	48.61	57.81
		Mean/Mode	129.87	35.95	9.88	19.23	9.14	8.10	25.92	23.07	32.03	63.18	66.78	18.92	45.20	54.16

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	32.72	39.45	58.57	28.1	19.49	35.27	32.92	21.36	19.59	12	12	10	14	107	6	8	4	14	8
	29.11	33.87	50.35	25.78	17.82	30.59	28.67	19.69	16.14	12	12	8	14	106	6	7	4	13	8
	29.91	37.31	56.49	28.31	18.9	33.75	31.72	20.12	19.24	13	11	9	14	105	6	9	4	13	7
	29.48	35.21	52.9	26.06	17.61	31.93	30.34	19.46	18.71	12	12	10	15	104	5	7	3	12	9
	32.46	40.79	61.43	29.42	17.63	33.13	31.44	23.16	18.45	12	12	9	13	107	6	9	4	12	7
	26.69	32.73	48.51	22.17	16.11	26.7	25.42	19.8	14.27	12	11	8	14	107	6	8	4	12	9
	26.76	33.05	48.77	25.76	15.22	26.94	24.96	17.95	15.11	11	11	8	12	109	7	7	4	13	9
	27.07	32.68	49.73	23.92	16.4	30.94	29.23	19.04	17.01	12	11	9	13	109	7	9	4	13	7
	28.94	36.2	53.74	24.63	16.88	29.03	27.48	18.41	17.12	11	11	10	13	110	6	7	3	13	8
	31.37	37.85	56.5	31.1	18.49	35.04	31.76	25.26	21.6	12	11	8	13	108	6	7	3	13	7
Mean/Mode	29.45	35.91	53.70	26.53	17.46	31.33	29.39	20.43	17.72	12	11	8	14	107	6	7	4	13	7

Table 14. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Chapman Prong Tennessee

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Chapman_Prong	1	1	152.3	47.74	15.35	24.03	11.46	10.29	35.77	32.09	41.7	72.19	84.61	21.62	53.83	62.65
Chapman_Prong	1	2	135.9	36.86	10.45	19.46	9.41	8.78	26.51	25.03	30.52	64.11	69.33	18.79	46.19	55.82
Chapman_Prong	1	3	145.92	45.59	13.7	23.54	11.06	10	34.29	28.44	37.43	73.33	80.31	21.2	49.13	56.16
Chapman_Prong	1	4	122.65	34.65	8.99	16.87	10.51	8.9	24.52	22.99	32.08	59.68	62.71	16.82	42.45	51.85
Chapman_Prong	1	5	120.23	32.93	8.65	17.01	8.93	8.18	23.27	21.9	32.44	57.38	60.2	17.27	43.35	52.27
Chapman_Prong	1	6	119.34	33.32	9.16	17.64	9.25	8.36	22.56	23.26	30.34	57.04	60.88	17.94	42.56	51.33
Chapman_Prong	1	7	133.54	36.3	10.46	18.84	9.66	8.47	26.7	24.21	32.9	62.36	68.57	18.64	49.12	57.33
Chapman_Prong	1	8	114.35	30.34	7.94	15.19	9.44	8.66	21.13	20.44	27.63	55.26	58.43	15.4	39.79	48.53
Chapman_Prong	1	9	143.38	43.09	12.84	22.05	10.89	9.89	30.42	30.11	40.64	69.45	80.39	21.14	54.36	62.98
Chapman_Prong	1	10	148.97	43.92	12.17	22.53	11.02	10.28	33.64	28.72	40.84	75.05	80.14	19.77	50.79	58.68
		Mean/Mode	133.66	38.47	10.97	19.72	10.16	9.18	27.88	25.72	34.65	64.59	70.56	18.86	47.16	55.76

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	35.16	42.14	60.68	31	20.68	39.73	36.08	23.13	22.36	11	11	9	14	102	5	8	4	14	8
	29.23	36.34	55.37	27.82	17.04	30.21	27.22	21.79	19.95	12	11	8	13	106	4	9	4	14	8
	33.12	34.92	54.31	29.09	20.15	37.72	34.31	22.42	22.43	10	11	8	14	102	4	6	4	13	8
	28.78	35.58	52.27	23.87	17.07	30.81	27.09	17.62	18.18	12	10	8	13	104	4	8	4	12	8
	29.26	34.39	51.47	25.22	17.16	28.86	28.94	19.01	18.08	11	11	9	13	106	6	8	4	14	9
	28.43	33.57	51.67	24.09	17.58	28.49	26.33	18.95	17.42	12	11	9	14	106	4	9	4	12	7
	32.24	38.73	57.86	25.73	17.66	32.65	27.74	19.53	18.35	11	11	9	14	108	5	9	4	13	10
	26.35	31.83	47.22	21.55	14.88	26.1	24.28	17.18	15.92	10	10	9	13	105	4	7	4	11	8
	35.57	41.01	59.51	27.89	20.72	40.03	34.52	22.93	22.31	12	10	9	14	104	5	8	4	13	9
	33.65	39.01	60.14	28.94	21.08	39.08	35.86	22.52	21.34	12	11	9	13	108	5	8	5	13	9
Mean/Mode	31.18	36.75	55.05	26.52	18.40	33.37	30.24	20.51	19.63	12	11	9	14	106	4	8	4	13	8

Table 15. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Correll Branch North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Correll Branch	1	1	115.41	34.13	8.87	17.47	8.42	8.24	23.65	22.37	29.8	55.17	61.61	17.13	37.97	46.9
Correll Branch	1	2	127.51	33.01	7.5	17.96	8.9	7.84	21.72	23.64	28.36	61.36	64.65	17.75	41.72	51.78
Correll Branch	1	3	115.15	31.56	8.44	16.35	8.68	8.28	21.86	20.96	24.06	55.76	61.71	15.01	36.86	46.82
Correll Branch	1	4	110.2	31.44	7.44	16.61	8.91	7.33	21.29	21.61	24.78	54.39	57.65	14.84	36.23	44.32
Correll Branch	1	5	104.51	28.32	6.58	14.48	8.23	7.9	18.49	19.59	23.82	50.08	53.36	15.16	36.28	43.5
Correll Branch	1	6	109.4	29.83	7.37	15.97	8.81	7.72	20.35	20.95	24.71	52.76	56.37	15.03	35.55	44.37
Correll Branch	1	7	107.75	30.35	8.07	15.36	8.29	7.41	20.76	21.14	24.52	51.18	56.55	15.42	35.51	43.52
Correll Branch	1	8	109.42	30.33	7.23	15.22	8.37	7.59	23.05	19.24	24.16	52.57	57.08	15.15	37.63	44.86
Correll Branch	1	9	105.32	30.19	7.2	15.85	8.46	7.29	21.04	20.42	21.81	51.7	55.63	13.87	33.65	41.94
Correll Branch	1	10	97.36	25.85	5.74	13.36	7.6	7.18	18.57	17.36	21.13	46.1	47.61	13.72	32.41	39.75
		Mean/Mode	110.20	30.50	7.44	15.86	8.47	7.68	21.08	20.73	24.72	53.11	57.22	15.31	36.38	44.78

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	SY235.00	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	23.57	30.03	47.37	23.67	13.73	29.08	25.71	20.15	14.65	12	11	9	14	107	5	6	5	12	8
	26.89	33.61	51.24	24.68	16.33	27.24	27.72	20.14	17	12	11	9	12	115	4	7	5	11	8
	23.28	31.07	46.32	22.15	13.21	24.01	23.06	17.08	13.96	11	11	9	14	114	0	5	4	11	10
	23.08	27.83	43.6	22.21	14.11	24.41	22.74	17.69	14.28	10	11	9	12	108	3	8	5	12	9
	22.23	28.39	42.97	20.96	14.35	23.65	22.42	17.43	14.54	12	12	9	13	116	3	8	5	13	8
	21.72	28.45	44.59	20.9	13.15	24.69	23.09	18.08	14.92	10	12	8	14	115	3	7	4	10	7
	21.8	27.83	44.15	21.79	13.58	24.2	22.07	18.5	14.4	12	11	8	14	119	1	4	3	13	9
	22.86	28.42	44.22	21.63	13.25	23.68	21.57	16.92	13.61	11	12	9	13	114	3	7	5	13	8
	21.17	27.42	43.48	21.24	13.07	21.64	20.87	17.07	14.22	11	10	9	13	117	5	8	6	12	9
	20.77	25.86	39.72	19.16	11.71	20.79	20.3	16.54	12.12	10	11	9	13	107	0	5	4	11	7
Mean/Mode	22.74	28.89	44.77	21.84	13.65	24.34	22.96	17.96	14.37	12	11	9	14	107	3	7	5	12	8

Table 16. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Horse Creek North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Horse_Creek	1	1	140.26	40.65	11.67	20.36	10.95	9.28	30.76	27.9	40.24	72.68	75.82	19.07	49.19	55.72
Horse_Creek	1	2	83.86	22.23	5.48	10.7	7.35	6.47	14.68	16.33	21.63	40.59	41.83	11.22	28.3	34.7
Horse_Creek	1	3	127.37	33.59	9.26	17.67	9.01	8.2	24.17	22.78	31.8	64.18	64.58	18	45.09	54.88
Horse_Creek	1	4	121.49	33.08	9.07	16.65	9.03	8.1	24.63	22.56	30.64	60.88	61.42	15.03	42.66	50.14
Horse_Creek	1	5	110.71	29.85	7.43	15.14	8.63	7.77	20.95	20.77	26.69	55.61	56.35	14.32	37.95	45.84
Horse_Creek	1	6	130.36	34.14	8.22	17.93	9.54	8.32	23.55	23.77	30.26	63.55	65.46	15.24	43.59	51.54
Horse_Creek	1	7	100.64	27.1	7.12	14.05	7.86	6.91	19.15	18.33	25.9	50.18	51.5	15.06	35.71	42.77
Horse_Creek	1	8	122.31	33.81	8.99	17.54	9.48	8.56	24.56	23.86	32.42	60.55	62.58	17.15	43.75	52.22
Horse_Creek	1	9	117.15	30.32	8.27	15.42	9.1	7.8	20.77	21.69	28.08	57.52	59.68	14.1	40.81	48.4
Horse_Creek	1	10	110.31	30.45	7.63	15.57	8.44	7.52	21.78	19.22	27.95	54.62	57.71	14	38.49	44.74
		Mean/Mode	116.45	31.52	8.31	16.10	8.94	7.89	22.50	21.72	29.56	58.04	59.69	15.32	40.55	48.10

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	33.42	38.6	57.64	26.69	18.61	37.49	34.51	22.33	19.21	12	10	9	12	104	2	8	4	15	8
	18.08	21.12	40.78	20.36	14.31	19.51	19.19	14.09	14.57	13	10	9	12	103	4	7	4	12	8
	31.04	37.75	54.33	22.23	16.6	29.78	27.91	18.69	17.23	13	10	9	14	105	4	8	4	14	9
	29.8	35.52	51.66	24.26	16.05	29.46	27.03	19.68	16.39	12	11	9	14	106	4	8	5	14	8
	25.97	31.64	47.39	20.14	14.03	25.18	24.16	16.6	14.46	13	10	9	13	104	4	7	5	13	9
	30.41	35.96	52.3	23.97	15.67	28.85	28.48	19.22	15.67	11	10	9	13	106	3	8	5	14	9
	24.23	27.77	41.87	23.11	14.52	25.14	23.83	16.6	14.76	13	10	9	13	106	4	7	5	15	9
	30.14	35.17	49.59	23.74	17.83	30.79	29.45	17.71	16.67	12	11	9	14	109	3	8	3	11	8
	28.15	33.81	51.11	24.96	16.38	27.22	25.69	18.52	15.77	12	11	9	13	108	5	7	4	14	8
	26.61	31.23	45.82	22.61	14.21	26.26	24.84	18.08	15.31	12	10	9	13	107	3	8	5	15	9
Mean/Mode	27.79	32.86	49.25	23.21	15.82	27.97	26.51	18.15	16.00	12	10	9	13	106	4	8	5	14	8

Table 17. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Hurricane Creek North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Hurricane_Creek	1	1	154.79	44.2	13.43	23.19	11.29	9.46	35.94	29.92	38.29	76.86	83.25	21.09	52.99	64.37
Hurricane_Creek	1	2	86.54	23.65	5.74	11.96	7.18	6.18	16.55	15.95	20.8	40.19	45.22	13.42	30.06	36.31
Hurricane_Creek	1	3	119.12	32.43	8.53	16.85	9.78	9.42	22.5	21.96	28.33	57.52	60.62	16.38	41.04	49.36
Hurricane_Creek	1	4	117.65	33.77	9.73	17.09	8.99	7.87	25.05	22.56	28.42	58.08	59.69	16.6	40.57	49.24
Hurricane_Creek	1	5	106.32	31.74	8.51	16.29	9.28	8.05	23.42	20.93	26.14	51.32	55.75	14.37	36.16	43.55
Hurricane_Creek	1	6	115.7	32.7	8.94	16.92	9.23	8.21	23.58	21.81	28.59	57.21	59.82	14.28	39.46	46.88
Hurricane_Creek	1	7	142.65	38.76	10.24	19.65	10.75	9.74	29.33	27.03	33.89	67.74	75.89	19.6	47.35	58.19
Hurricane_Creek	1	8	124.28	34.29	9.1	18.27	9.41	8.21	25.28	22.46	28.18	58.36	64.62	15.9	41.71	50.17
Hurricane_Creek	1	9	102.88	28.63	6.95	14.64	8.81	7.51	19	18.07	24.22	49.28	53.89	13.91	35.42	42.61
Hurricane_Creek	1	10	86.19	23.38	5.73	12.07	7.32	6.48	15.61	16.93	20.99	42.12	43.27	11.71	28.47	34.98
		Mean/Mode	115.61	32.36	8.69	16.69	9.20	8.11	23.63	21.76	27.79	55.87	60.20	15.73	39.32	47.57

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	34.71	43.42	67.13	31.35	22.11	38.41	34.32	24.74	22.21	10	11	8	14	106	3	6	3	15	8
	19.03	23.33	35.19	17.93	11.96	20.08	18.57	13.11	11.14	10	10	9	13	105	3	8	3	13	7
	27.59	33.34	50.86	24.07	17.06	27.82	26.04	18.05	16.5	11	10	9	13	108	4	7	3	13	7
	26.59	32.74	49.02	22.6	15.3	28.36	26.01	17.71	15.84	11	12	9	13	106	4	7	3	14	7
	23.48	29.19	44.33	21.85	14.03	25.6	23.29	17.21	16.57	12	11	9	14	106	6	9	3	13	9
	26.9	32.87	50.78	24.63	16.8	27.89	25.11	19.14	16.21	10	10	9	13	105	3	9	4	15	7
	30.82	39.13	59.04	27.52	18.51	33.56	31.66	20.6	19.02	11	10	9	13	106	4	9	4	14	8
	28.3	34.86	53.38	26.79	17.17	27.89	26.31	19.63	17.37	10	11	9	13	105	5	8	4	14	8
	22.81	28.89	43.17	20.62	13.44	23.67	21.49	15.25	12.38	11	11	8	13	107	4	9	4	12	8
	18.65	23.65	37.22	18.2	11.83	19.84	19.04	13.45	11.57	11	11	8	13	107	3	9	3	13	7
Mean/Mode	25.89	32.14	49.01	23.56	15.82	27.31	25.18	17.89	15.88	11	11	9	13	106	3	9	3	13	7

Table 18. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Kephart Prong Tennessee

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Kephart_Prong	1	1	134.15	37.7	9.74	19.86	10.45	9.04	27.4	25.85	32.19	67.94	71.88	17.96	46.53	56.14
Kephart_Prong	1	2	104.41	28.33	6.98	13.87	8.78	7.16	18.84	19.98	26.35	53.01	53.91	15.2	36.06	43.58
Kephart_Prong	1	3	103.57	27.35	6.88	14.48	8.87	7.71	18.81	19.27	24.32	50.41	52.59	14.76	33.96	41.09
Kephart_Prong	1	4	116.54	31.76	8.74	16.35	9.76	8.67	21.96	21.48	25.37	55.42	59.79	17.35	37.78	48.82
Kephart_Prong	1	5	115.71	33.7	7.63	17.27	9.45	8.53	23.31	22.72	26.36	58.25	62.77	16.06	38.44	45.64
Kephart_Prong	1	6	107.94	32.91	8.16	17.36	9.45	8.25	22	21.48	25.37	55.46	60.15	16.18	36.29	42.42
Kephart_Prong	1	7	107.49	28.34	6.87	15	8.91	8.03	18.33	21.36	27.69	52	54.1	15.14	36.85	44.53
Kephart_Prong	1	8	101.63	27.07	6.7	13.81	8.25	6.96	17.39	19.2	22.9	48.61	51.86	13.37	33.25	41.07
Kephart_Prong	1	9	100.39	27.7	7.56	14.29	8.95	7.8	18.07	17.69	21.27	48.81	52.93	13.3	33.59	40.73
Kephart_Prong	1	10	109.86	30.29	8.68	15.86	8.44	7.73	21.46	20.54	25.35	54.09	55.74	15.3	35.71	43.42
		Mean/Mode	110.17	30.52	7.79	15.82	9.13	7.99	20.76	20.96	25.72	54.40	57.57	15.46	36.85	44.74

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	30.03	36.73	53.57	24.89	19.06	30.96	28.82	19.12	17.67	12	10	9	14	105	4	9	4	13	8
	24.41	28.44	41.37	20.07	15.92	24.83	23.82	15.86	14.35	10	11	9	14	107	5	7	3	11	8
	22.39	26.61	41.53	20.18	14.6	22.71	21.58	17.36	15.45	11	10	10	14	102	3	8	3	11	9
	24.03	31.9	44.67	19.97	14.15	23.8	23.41	15.77	14.29	12	11	9	13	108	4	8	4	12	9
	24.68	30.01	45.87	24.24	14.2	25.85	23.99	19.59	15.76	11	11	9	13	104	4	8	4	13	8
	24.26	26.24	39.39	20.88	16.35	25.03	24.04	16.4	15.67	12	10	8	14	105	4	8	4	12	8
	24.87	29.38	42.59	22.71	15.6	26.29	24.86	17.76	14.04	12	11	8	14	104	4	9	4	11	8
	21.71	27.03	41.76	19.46	13.74	22.05	21.14	15.49	13.54	12	10	8	14	106	4	9	3	13	9
	23.15	28.29	38.54	19.05	12.07	20.39	18.43	15.73	12.7	11	10	9	14	105	4	9	3	12	8
	24.24	29.8	45.67	22.27	15.38	23.88	22.52	18.71	13.87	11	11	9	13	106	4	9	4	12	9
Mean/Mode	24.38	29.44	43.50	21.37	15.11	24.58	23.26	17.18	14.73	12	10	9	14	105	4	9	4	12	8

Table 19. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Little Cataloochee Creek North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Little_Cataloochee	1	1	140.5	39.52	11.11	20.58	9.31	8.65	29.46	28.98	39.14	69.93	74.4	18.99	49.48	58.49
Little_Cataloochee	1	2	126.9	33.47	8.31	18.91	8.87	8.27	22.87	23.38	29.85	59.43	65.09	17.44	42.58	51.88
Little_Cataloochee	1	3	129.45	34.24	8.73	18.03	8.61	8.27	24.29	24.67	30.65	62.1	68.01	17.55	43.89	52.21
Little_Cataloochee	1	4	115.75	30.19	7.07	16.06	8.31	7.88	19.07	20.82	25.93	54.66	60.27	13.87	39.59	48.04
Little_Cataloochee	1	5	130.74	35.08	9.8	18.25	8.54	8.26	26.6	25.81	32.2	61.87	69.19	16.57	45.27	53.67
Little_Cataloochee	1	6	125.82	32.22	8.05	17.22	8.43	7.94	21.75	21.86	27.92	59.45	64.37	17.35	43.37	52.65
Little_Cataloochee	1	7	125.84	32.64	8.18	17.62	8.8	8.32	21.2	23.64	28	59	66.49	16.2	42.36	50.93
Little_Cataloochee	1	8	121.13	33.13	8.15	17.85	9.37	8.58	22.3	23.07	29.49	59.14	62.14	15.78	41.5	49.39
Little_Cataloochee	1	9	107.71	28.42	7.03	14.9	7.84	7.57	19.02	19.45	23.74	50.07	54.67	15.39	36.25	43.59
Little_Cataloochee	1	10	143.5	38.93	9.74	20.76	8.75	8.25	25.81	26.08	35.08	69.75	75.21	20.59	48.78	58.68
		Mean/Mode	126.73	33.78	8.62	18.02	8.68	8.20	23.24	23.78	30.20	60.54	65.98	16.97	43.31	51.95

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	32.73	38.31	58.76	29.54	19.56	38.05	34.7	21.79	18.13	12	13	8	13	111	4	8	4	13	8
	27.01	32.8	51.99	25.81	16.44	30.52	27.63	19.97	15.98	11	12	8	13	114	5	8	2	13	9
	27.01	34.31	53.42	27.47	16.19	30.12	28.06	22.14	17.19	13	13	9	12	114	3	7	3	13	9
	26.41	32.31	49.35	24.58	14.2	25.62	24.51	17.58	14.42	12	12	9	14	100	4	7	4	13	8
	29.61	35.74	56.08	26.58	17.35	33.21	29.79	20.85	17.21	12	12	10	14	112	4	8	3	14	9
	28.32	35.33	53.09	26.25	15.97	27.83	26.61	20.13	16.4	12	13	9	14	111	3	8	3	11	8
	28.45	34.15	51.1	24.46	15.55	27.19	26.58	19.21	16.09	13	12	9	14	110	4	7	4	13	8
	27.71	33.08	49.33	23.62	15.78	29.3	26.64	18.8	16.95	12	11	8	14	110	3	8	4	12	8
	22.95	28.71	45.39	23.08	14.22	24.18	22.08	18.49	14.25	12	12	9	14	107	3	7	3	13	9
	29.85	37.38	57.3	25.38	16.9	34.94	32.84	20.17	17.49	12	12	9	14	104	5	7	4	11	8
Mean/Mode	28.01	34.21	52.58	25.68	16.22	30.10	27.94	19.91	16.41	12	12	9	14	111	4	8	4	13	8

Table 20. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, McKee Branch North Carolina

McKee_Branch	1	1	151.55	40.6	10.32	21.97	10.98	9.52	28.06	27.2	38.69	72.56	78.99	21.58	54.08	63.35
McKee_Branch	1	2	143.19	41.45	11.08	21.31	9.66	8.86	31.75	24.95	36.64	70.81	78.58	21.21	51.16	60.33
McKee_Branch	1	3	145.14	41.14	11.35	21.32	9.62	8.77	31.49	24.27	36.43	70.25	78.2	21.57	51.52	59.73
McKee_Branch	1	4	143.8	37.67	9.93	20.49	10.23	9.22	28.69	25.85	36.44	68.31	77	20.97	51.52	58.79
McKee_Branch	1	5	135.4	37.06	10.51	19.35	10.13	9.14	27.01	23.87	33.39	64	71.51	19.42	48.34	56.55
McKee_Branch	1	6	119.54	31.55	8.32	16.47	8.86	7.49	21.6	22.1	29.25	56.55	63.24	18.02	42.84	50.74
McKee_Branch	1	7	146.36	40.48	11.03	21.16	9.81	8.87	29.25	25.92	35.87	73.19	76.29	20.07	51.38	61.55
McKee_Branch	1	8	129.98	36.91	10.51	19.52	9.55	8.27	28.19	23.03	33.96	66.3	69.92	17.72	44.24	52.48
McKee_Branch	1	9	132.27	35.07	8.71	18.22	9.67	8.95	24.83	23.73	31.82	64.46	67.84	18.62	44.53	54.41
McKee_Branch	1	10	126.99	34.3	9.77	18.35	9.34	8.1	25.2	23.53	32.65	60.95	68.19	18.21	44.16	52.17
		Mean/Mode	137.42	37.62	10.15	19.82	9.79	8.72	27.61	24.45	34.51	66.74	72.98	19.74	48.38	57.01

	35.17	41.33	63.24	32.01	19.77	37.77	35.01	24.51	21.07	11	12	9	13	108	5	8	4	13	9
	32.74	38.83	59.1	29.15	20.66	36.58	32.82	20.9	19.75	11	12	8	13	104	5	8	4	13	8
	33.57	38.96	59.23	29.25	19.99	36.45	32.18	23.33	21.07	11	11	9	13	109	4	7	3	12	8
	34.26	39.3	58.25	28.95	19.61	36.17	33.2	21.83	19.19	12	12	8	13	106	5	9	4	14	8
	31.3	37.16	56.37	28.06	19.39	34.19	30.26	20.79	19.07	10	10	8	12	107	5	8	4	13	8
	28.23	33.1	49.48	24.39	16.85	29.55	27.44	17.94	16.79	10	11	9	13	106	5	8	4	13	7
	34.33	39.99	60.41	28.74	20.07	34.95	30.7	21.65	19.44	10	12	9	14	106	6	8	4	14	8
	30.11	34.44	53.1	25.94	18.64	33.47	30.05	20.57	17.93	12	10	9	13	106	4	8	4	12	9
	29.86	35.4	53.99	25.09	17.98	30.85	29.06	21.14	18.61	11	11	8	12	106	4	8	4	14	7
	28.75	34.55	51.6	25.55	17.13	32.61	29.99	19.51	18.29	11	10	8	12	111	5	8	4	15	8
Mean/Mode	31.83	37.31	56.48	27.71	19.01	34.26	31.07	21.22	19.12	11	12	9	13	106	5	8	4	13	8

Table 21. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Messer Fork North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Messer_Fork	1	1	156.9	46.45	13.82	23.61	11.17	9.89	36.26	31.94	44.11	79.01	84.07	24.61	57.36	67.05
Messer_Fork	1	2	158.17	40.68	11.01	21.29	10.37	9.45	27.85	28.74	36.58	76.12	81.79	20.41	54.81	66.44
Messer_Fork	1	3	143.59	37.64	11.17	19.4	9.46	8.4	28.69	26.52	33.76	66.61	74.25	20.47	49.08	59.05
Messer_Fork	1	4	124.64	33.88	9.51	17.85	8.72	7.42	25.47	23.53	31.39	60.79	64.66	17.5	45.47	52.94
Messer_Fork	1	5	134.29	36.21	10.13	18.53	10.37	9.2	24.23	25.4	31.54	64.33	68.55	18.91	45.4	54.53
Messer_Fork	1	6	150.85	39.1	11.28	20.79	10.91	9.73	27.88	27.15	34.63	71.36	75.95	19.9	51.04	61.92
Messer_Fork	1	7	111.74	27.57	7.74	14.95	7.85	6.81	18.65	19.88	24.88	51.5	56.33	16.54	38.55	47.11
Messer_Fork	1	8	131.2	35.53	10.15	18.52	9.32	8.13	26.48	25.07	33.22	62.98	67.31	19.61	45.06	54.74
Messer_Fork	1	9	115.44	29	7.7	15.39	8.07	7.18	19.48	20.22	27.18	52.84	57.62	16.45	41.54	48.83
Messer_Fork	1	10	116.86	30.8	8.4	16.24	8.11	7.03	22.42	22.02	27.87	55.27	60.02	18.3	41.17	49.92
		Mean/Mode	134.37	35.69	10.09	18.66	9.44	8.32	25.74	25.05	32.52	64.08	69.06	19.27	46.95	56.25

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	37.84	43.14	62.46	32.1	24.62	43.23	39.5	23.41	23.53	12	12	8	13	109	5	8	4	12	8
	37.03	45.72	68.03	28.92	21.19	36.74	34.4	23.27	21.04	10	11	8	13	109	5	7	3	13	7
	31.37	38.46	61.06	30.37	18.99	34.38	31.68	23.16	20.45	11	10	8	13	109	5	8	4	12	8
	31.03	36.3	53.68	26.3	18.6	31.89	29.49	18.99	18.67	10	11	8	13	107	4	8	3	11	9
	29.8	35.61	55.98	28.19	17.73	31.13	29.48	21.31	19.23	11	10	8	14	108	3	8	3	12	7
	33.98	42.11	64.71	30.13	20.42	34.3	32.84	22.69	20.66	10	10	9	13	108	5	9	4	12	8
	24.76	30.76	46.34	21.53	15.5	24.12	23.41	15.93	15.74	12	10	8	14	105	6	8	4	12	9
	29.28	35.11	54.08	25.81	18.38	32.77	30.75	21.02	19.48	10	10	8	13	107	4	8	4	14	7
	27.43	32.9	50.67	24.39	15.65	27.03	24.34	19.22	16.15	10	11	9	13	105	4	8	5	12	9
	26.05	31.42	49.54	24.23	16.8	28.45	25.33	18.39	16.7	11	10	9	14	105	4	8	5	11	8
Mean/Mode	30.86	37.15	56.66	27.20	18.79	32.40	30.12	20.74	19.17	10	10	8	13	109	5	8	4	12	8

Table 22. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Onion Bed North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Onion_Bed	1	1	130.11	35.63	10.3	19.15	9.29	8.29	25.4	25.59	35.49	64.37	70.37	21.58	47.87	56.43
Onion_Bed	1	2	135.29	35.08	9.3	18.54	9.96	8.7	26	25.43	29.75	64.46	67.93	19.6	46.92	56.39
Onion_Bed	1	3	125.5	35.03	9.6	18.2	9.34	8.81	26.06	24.19	32.23	62.04	66.64	19.93	43.84	52.29
Onion_Bed	1	4	128.01	36.63	10.67	17.85	10.35	9.23	27.78	24.31	33.82	62.75	68.26	19.01	45.95	54.58
Onion_Bed	1	5	116.11	31.53	7.98	16.48	9.76	8.82	22.53	22.17	28.59	57.81	58.91	17.39	39.6	48.84
Onion_Bed	1	6	115.79	29.56	7.64	15.43	8.7	7.59	20.35	20.93	27.24	57.32	57.83	16.28	39.25	48.22
Onion_Bed	1	7	123.24	34.39	9.3	17.74	9.39	8.35	25.86	24.07	32.14	59.36	66.62	18.88	43.78	51.68
Onion_Bed	1	8	117.13	31.76	7.85	16.21	10.16	8.85	22.29	22.27	27.91	57.88	58.64	17.65	39.99	48.15
Onion_Bed	1	9	112.72	31.61	8.45	16.09	8.77	7.68	23.24	21.86	30.48	55.73	60.51	17.16	40.62	47.64
Onion_Bed	1	10	111.05	30.91	8.45	16.09	8.68	7.81	22.31	21.99	28.05	52.65	58.25	17.35	39.29	45.75
		Mean/Mode	121.50	33.21	8.95	17.18	9.44	8.41	24.18	23.28	30.57	59.44	63.40	18.48	42.71	51.00

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	31.21	36.03	53.74	26.83	19.43	34.51	31.68	19.37	18.37	12	10	9	13	109	5	8	5	13	8
	30.49	36.77	57.55	27.61	16.37	29.49	28.4	21.37	18.11	12	12	8	14	109	4	9	4	14	8
	28.04	33.22	50.41	24.63	16.89	31.61	29.19	17.88	17.07	12	11	8	14	105	4	8	6	14	8
	29.97	36.04	52.31	24.14	16.08	32.62	29.16	18.38	16.24	11	10	9	13	106	3	8	5	14	8
	25.84	32	48.09	23.97	16.71	27.09	27.27	16.03	16	12	10	9	13	108	4	7	5	13	8
	25.66	32.23	49.43	24.13	15.11	25.26	25.7	17.84	15.96	13	11	8	13	109	6	9	4	14	9
	27.95	32.94	49.08	25.98	17.39	31.81	28.52	17.49	16.78	12	10	9	13	112	4	7	4	13	8
	26.43	32.17	47.04	23.97	15.84	26.58	26.95	18.42	15.61	11	11	8	13	106	3	7	4	13	8
	26.44	30.78	45.96	21.6	15.46	28.85	26.24	16.49	16.14	11	11	9	14	106	4	8	4	13	8
	25.07	29.76	44.26	24.11	15.2	27.32	25.78	16.35	15.72	13	10	9	13	106	5	8	4	14	8
Mean/Mode	27.71	33.19	49.79	24.70	16.45	29.51	27.89	17.96	16.60	12	10	9	13	106	4	8	4	13	8

Table 23. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Pretty Hollow North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Pretty_Hollow	1	1	143.21	40.96	11.64	21.69	10.54	9.46	32.48	28.43	39.16	72.8	76.04	20.83	51.01	60.69
Pretty_Hollow	1	2	119.55	33.89	8.37	17.76	10.18	8.96	23.21	22.28	29.59	59.74	62.72	17.33	42.02	50.83
Pretty_Hollow	1	3	139.43	42.53	12.82	21.63	11.18	10.03	32.32	28.53	35.65	70.55	76.77	19.03	45.83	54.86
Pretty_Hollow	1	4	128.07	35.43	10.16	17.76	9.61	8.5	26.58	24.87	33.4	64.47	69.36	19.49	44.76	52.4
Pretty_Hollow	1	5	120.27	33.33	9.13	17.37	9.47	7.93	25.1	22.74	29.64	60.12	61.96	17.83	41.59	49.52
Pretty_Hollow	1	6	117.91	32.35	8.37	16.52	9.52	8.42	23.48	22.75	28.16	57.64	59.35	17.26	43.3	50.63
Pretty_Hollow	1	7	124.4	35.72	9.88	18.31	9.59	8.42	26.63	23.87	30.77	62	65.95	18.61	42.44	51.06
Pretty_Hollow	1	8	126.66	33.62	9.05	17.18	9.02	7.87	25.87	23.44	31.62	62.24	66.42	18.54	43.61	53.1
Pretty_Hollow	1	9	108.38	29.24	8.03	15.25	8.94	8.12	19.92	20.99	26.37	53.92	54.7	15.38	37.37	45.5
Pretty_Hollow	1	10	103.52	28.83	7.52	14.75	8.65	7.68	19.77	20.39	25.45	52.98	54.04	14.99	35.96	43.05
		Mean/Mode	123.14	34.59	9.50	17.82	9.67	8.54	25.54	23.83	30.98	61.65	64.73	17.93	42.79	51.16

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	33.78	38.82	59.81	29.09	19.63	38.45	36.75	21.7	19.25	11	11	9	14	106	5	7	4	15	8
	28.45	33.39	48.93	22.23	16.64	27.98	28.22	16.32	15.63	12	10	8	12	104	4	7	4	14	7
	30.04	36.29	56.52	28.7	18.89	36.05	33.48	22.36	17.82	11	10	8	14	106	5	8	4	14	7
	29.3	34.19	52.24	24.73	17.55	32.75	30.43	19.89	17.55	11	11	9	13	107	4	8	4	13	8
	27.64	31.32	48.62	23.26	16.42	28.54	27.02	19.58	16.31	12	11	9	12	104	4	8	4	14	9
	29.04	33.69	50.05	23.74	16.27	27.29	26.76	17.12	16.25	12	10	8	13	105	3	7	4	14	8
	28.25	33.74	49.07	23.3	16.65	29.03	27.38	18.75	17.17	11	10	8	13	105	5	9	4	13	9
	28.24	34.07	52.22	26.31	16.18	30.98	28.31	20.73	16.89	11	11	8	13	108	3	8	4	13	8
	25.03	29.29	42.67	19.91	15.56	24.76	25.06	15.66	14.2	11	10	9	13	105	5	8	4	12	9
	23.73	28.65	41.99	20.97	14.23	24.17	23.7	15.21	14.32	10	10	8	13	105	5	8	4	14	9
Mean/Mode	28.35	33.35	50.21	24.22	16.80	30.00	28.71	18.73	16.54	11	10	8	13	105	5	8	4	14	8

Table 24. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Road Prong Tennessee

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Road_Prong	1	1	164.49	44.58	12.56	23.67	9.65	9.19	32.66	31.28	41.93	81.54	87.61	21.51	57.31	66.08
Road_Prong	1	2	115.58	32.65	9.08	17.14	8.16	7.8	23.44	23.9	31.59	59.5	61.74	14.03	39.94	45.52
Road_Prong	1	3	113.93	29.92	6.9	15.47	8.11	7.44	19.46	21.63	27.41	53.94	58.37	15.99	38.01	46.86
Road_Prong	1	4	121	29.15	7.24	14.88	8.26	7.23	19.25	23.2	30.49	57.43	60.08	16.57	40.33	47.61
Road_Prong	1	5	133.19	33.93	8.69	18.1	9.07	8.08	22.7	23.8	31.77	66.56	70.08	17.96	46.47	54.4
Road_Prong	1	6	130.77	33.33	9.28	17.38	9.17	8.38	21.71	24.67	32.2	61.29	64.78	16.5	45.65	54.41
Road_Prong	1	7	155.59	41.65	11.27	22.16	10.3	9.4	29.58	29.92	41.61	76.68	81.69	18.77	53.26	62.29
Road_Prong	1	8	163.87	44.18	13.68	23.22	10.25	9.11	33.08	31.4	40.33	79.38	85.31	22.14	54.63	64.94
Road_Prong	1	9	130.97	32.41	8.29	17.62	8.6	7.74	21.55	23.91	31.29	65.53	66.61	17.08	43.95	55.47
Road_Prong	1	10	140.59	37.58	10.04	19.98	8.96	8.01	27.27	27.77	34.4	67.5	71.65	17.93	46.77	56.04
		Mean/Mode	137.00	35.94	9.70	18.96	9.05	8.24	25.07	26.15	34.30	66.94	70.79	17.85	46.63	55.36

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	37.67	46.58	65.82	32.54	23.05	41.36	38.29	27.16	23.93	10	10	9	14	118	2	8	5	13	9
	27.89	31.08	46.99	24.27	17.82	31.12	28.88	19.22	17.39	10	11	9	14	109	4	8	4	14	8
	25.95	32.78	48.05	21.79	15.02	26.35	24.9	15.87	15.67	10	11	9	14	104	3	8	5	14	8
	27.21	33.41	48.69	23.41	17.5	28.3	28.26	19.29	16.42	11	12	10	14	101	3	7	4	14	9
	30.78	36.98	51.17	25.22	18.62	32.01	30.09	19.44	17.94	11	11	9	12	107	3	7	5	13	8
	30.58	36.77	55.17	25.3	16.68	30.49	29.16	19.83	18.1	12	11	9	14	108	3	8	4	13	8
	36.6	42.37	64.52	32.16	21.38	39.61	37.38	24.91	22.5	10	12	9	12	112	3	9	4	14	8
	34.86	42.61	66.23	33.09	22.01	38.72	37.57	26.53	23.71	10	11	9	13	108	4	7	3	15	8
	30.92	37.57	56.61	27.02	18.01	31.33	31.29	21.34	17.18	12	11	10	13	104	3	6	4	14	8
	30.94	38.14	57.17	28.43	18.46	34.12	32.14	21.69	20.36	12	11	9	13	107	2	7	5	13	9
Mean/Mode	31.34	37.83	56.04	27.32	18.86	33.34	31.80	21.53	19.32	10	11	9	14	104	3	8	4	14	8

Table 25. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Rock Creek Tennessee

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Rock_Creek	1	1	150.78	38	10.66	19.69	10.57	9.3	28.16	28.69	37.11	69.55	79.69	20.34	52.92	63.61
Rock_Creek	1	2	141.25	35.39	9.53	18.21	9.72	8.53	25.79	26.64	33.99	66.22	70.06	18.76	51.04	60.77
Rock_Creek	1	3	121.44	32.4	8.93	16.51	8.5	7.57	23.85	23.15	29.8	58.35	62.09	16.62	42.26	50.04
Rock_Creek	1	4	121.29	33.82	9.85	17.59	8.78	7.83	24.71	24.32	31.72	59.04	63.69	16.62	42.49	49.76
Rock_Creek	1	5	96.05	24.29	6.57	12.28	6.87	6.55	16.88	16.59	23.44	44.09	46.14	13.63	32.32	39.06
Rock_Creek	1	6	113.41	29.56	7.43	15.05	9.37	8.12	20.5	20.92	27.39	52.6	56.72	15.76	39.39	47.52
Rock_Creek	1	7	105.06	26.15	7.03	13.48	7.14	6.7	18.47	19.33	25.27	48.83	50.82	14.74	37.54	43.98
Rock_Creek	1	8	109.52	29.54	7.16	14.94	9.29	7.93	20.23	20.53	23.97	50.32	53.93	13.72	35.11	43.82
Rock_Creek	1	9	105.38	25.93	6.55	13	7.11	6.31	18.87	18.07	23.27	49.35	51.13	13.97	34.18	42.73
Rock_Creek	1	10	131.78	33.91	8.98	17.4	9.68	8.42	24.1	23.03	30.33	62.19	66.71	18.76	46.07	55.85
		Mean/Mode	119.60	30.90	8.27	15.82	8.70	7.73	22.16	22.13	28.63	56.05	60.10	16.29	41.33	49.71

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	35.59	44.17	64.26	29.9	20.7	36.76	34	22.59	20.12	11	10	9	13	113	4	7	3	14	10
	34.39	42.17	60.14	27.95	19.99	32.72	31.22	20.52	18.81	11	11	8	13	110	4	8	3	13	10
	27.57	33.95	48.85	24.62	17.19	28.86	26.85	18.98	17.59	11	10	9	13	111	5	7	3	13	10
	28.51	33.1	50.11	23.89	18.26	30.13	28.26	19.09	17.42	11	10	9	13	109	4	7	3	13	9
	20.76	26.95	40.37	19.72	13.22	21.24	20.49	15.18	12.61	11	11	9	13	113	4	8	3	12	8
	25.89	32.13	47.69	22.5	15.16	26.26	23.84	15.74	15.83	11	10	8	13	109	4	7	2	11	9
	24.97	30.29	43.78	19.93	14.62	24.08	22.82	15.3	13.48	10	10	9	13	113	4	8	2	12	9
	23.11	31.5	45.25	21.56	13.96	23.16	22.26	16.39	13.66	11	11	8	12	112	3	7	2	12	10
	22.69	28.18	43.81	21.57	14.04	22.49	21.53	16.22	13.47	11	11	9	12	113	5	8	3	12	10
	29.73	36.76	55.51	24.63	17.75	29.43	27.2	19.07	16.98	11	9	9	13	108	3	7	3	12	10
Mean/Mode	27.32	33.92	49.98	23.63	16.49	27.51	25.85	17.91	16.00	11	10	9	13	113	4	7	3	12	10

Table 26. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Sag Branch North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Sag_Branch	1	1	141.57	38.59	10.03	20.63	10.79	9.16	28.05	24.42	32.76	67.13	75.62	20.67	48.49	57.54
Sag_Branch	1	2	100.7	26.78	6.76	14.09	7.61	6.51	18.36	17.6	24.57	49.87	50.48	15.07	35.16	42.47
Sag_Branch	1	3	100.5	28.1	7.15	15.22	8	7	20.07	17.36	24.37	50.94	51.99	13.69	32.98	39.59
Sag_Branch	1	4	99.99	25.67	6.28	13.41	7.68	7.02	16.52	16.68	24.82	48.53	50.99	14.46	34.38	41.35
Sag_Branch	1	5	95.64	26.69	6.47	14.44	7.98	6.95	17.07	16.35	23.58	46.65	47.6	13.23	31.45	38.78
Sag_Branch	1	6	114.35	29.85	7.6	15.58	8.4	7.4	20.39	19.12	28.67	54.42	59.45	17.61	39.01	46.69
Sag_Branch	1	7	106.54	28.76	6.85	15.1	8.02	7.07	19.52	17.84	24.56	51.6	56.2	14.73	34.82	43.23
Sag_Branch	1	8	98.77	27.63	6.96	14.54	8.12	7.07	19.36	17.53	26.24	47.56	52.19	14.14	33.83	40.62
Sag_Branch	1	9	99.97	25.17	5.89	12.95	7.91	6.83	16.31	16.82	23.45	46.81	51.94	15.09	33.94	42
Sag_Branch	1	10	105.13	28.61	6.92	15.02	8.09	7.06	19.1	17.76	24.71	51.25	54	15.4	35.59	43.09
Sag_Branch	1	11	99.97	26.39	6.97	13.64	7.58	6.93	17.23	16.65	22.99	47.91	50.79	14.8	32.85	41.58
		Mean/Mode	105.74	28.39	7.08	14.97	8.20	7.18	19.27	18.01	25.52	51.15	54.66	15.35	35.68	43.36

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	prr mks
	31.01	37.9	57.51	27.22	19.59	32.84	29.55	20.57	18.59	12	11	9	13	107	6	8	4	14	8
	22.39	27.16	41.63	19.72	14.58	23	21.6	16.71	13.83	12	12	9	14	109	7	9	5	13	8
	23.24	25.6	39.78	20.55	14.19	23.29	22.99	15.58	14.78	11	11	9	13	109	6	8	3	12	8
	22.78	27.28	41.17	19.92	13.98	24.21	22.67	14.96	13.19	12	12	9	14	106	5	8	4	13	8
	20.97	24.8	41.43	19.23	13.36	21.94	20.93	16.11	13.64	12	11	9	14	109	6	8	4	12	8
	24.61	28.95	45.61	23.97	15.44	26.49	26.28	17.09	16.3	12	11	9	13	107	5	8	4	13	8
	21.88	27.66	42.97	22.65	13.53	24.11	22.31	15.94	14.69	12	11	9	14	109	7	9	3	13	9
	22.56	26.62	38.72	19.82	14.39	24.49	23.81	15.09	14.91	13	12	10	14	107	6	9	3	12	8
	21.83	27.44	41.45	20.54	14.2	22.73	21.66	14.73	14.35	12	11	9	14	108	4	8	4	12	8
	22.57	28.21	44.13	21.83	14.25	24.12	22.63	15.85	14.36	13	12	9	14	107	6	8	3	12	8
	21.32	26.67	40.97	20.18	13.74	22.66	20.89	14.79	13.9	12	11	9	13	107	6	8	3	12	8
Mean/Mode	23.20	28.03	43.22	21.42	14.66	24.53	23.21	16.13	14.78	12	11	9	14	107	6	8	4	12	8

Table 27. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Straight Fork North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Straight_Fork	1	1	124.32	34.81	9.2	17.4	9.97	8.52	25.99	23.61	31.57	61.48	68.39	16.72	42.96	50.41
Straight_Fork	1	2	119.97	34.1	9.74	16.92	9.3	8.43	24.77	21.61	29.07	57.22	63.35	18.41	41.35	49.04
Straight_Fork	1	3	115.89	33.39	9.31	16.69	9.38	8.29	23.77	22.36	28.82	56.8	60.66	16.26	40.66	48.21
Straight_Fork	1	4	110.31	32.53	8.92	16.34	9.45	8.29	23.12	21.2	26.93	55.52	56.63	17.12	38.03	45.02
Straight_Fork	1	5	97.51	27.4	6.99	13.77	8.72	7.42	18.69	18.28	22.84	47.26	48.84	13.6	33.12	40.31
Straight_Fork	1	6	110.38	31.26	8.5	16.05	9.46	8.38	21.55	21.19	28.42	54.09	55.55	17.13	37.97	45.04
Straight_Fork	1	7	107.3	31.75	8.16	16.68	9.28	8.06	21.09	20.22	26.79	54.75	55.71	14.34	36.73	43.88
Straight_Fork	1	8	95.75	26.24	6.62	12.57	8.03	7.17	17.91	17.6	22.51	45.49	48.11	13.61	31.45	38.83
Straight_Fork	1	9	92.36	26.33	7.41	13.5	7.69	6.85	18.45	19.2	24.58	47.45	47.66	13.36	32.57	37.38
Straight_Fork	1	10	97.33	26.52	7.18	13.2	8.59	7.44	17.73	18.17	22.29	47.83	49.86	14.45	31.95	40.07
		Mean/Mode	107.11	30.43	8.20	15.31	8.99	7.89	21.31	20.34	26.38	52.79	55.48	15.50	36.68	43.82

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	27.96	33.52	49.71	22.41	17.01	31.65	28.04	16.42	16.55	11	10	9	13	103	4	7	3	12	8
	25.06	30.75	46.2	22.3	15.83	28.47	26.16	17.86	16.53	12	10	9	13	104	4	8	4	11	9
	27.5	32.89	46.97	22.09	15.36	28.55	25.72	17.64	16.49	11	10	9	13	101	4	8	4	12	8
	24.38	28.77	44.23	21.86	15.13	26.22	24.89	17.47	15.61	11	10	9	13	99	4	8	4	11	8
	21.83	26.66	40.82	19.03	12.05	21.75	21.61	14.88	12.4	11	11	9	12	103	4	8	4	12	8
	23.09	27.42	43.61	22.49	14.67	26.53	25.41	19.08	15.37	11	10	9	12	103	4	8	3	12	8
	25.04	29.8	42.77	20.8	15.62	26.33	25.29	16.08	15.42	11	11	8	13	102	5	8	4	13	7
	20.76	25.63	39.39	19.39	12.39	20.78	20.44	17.17	13.03	12	11	8	12	103	5	8	3	11	7
	21.91	24.55	36.39	18.1	13.69	23.35	21.7	13.81	13.56	11	9	9	14	105	5	7	4	12	9
	20.51	26	39.25	19.32	12.09	21.12	20.89	15.76	12.49	11	10	9	13	107	5	8	4	13	9
Mean/Mode	23.80	28.60	42.93	20.78	14.38	25.48	24.02	16.62	14.75	11	10	9	13	103	4	8	4	12	8

Table 28. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Walker Camp Prong North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Walker_Camp_Prong	1	1	161.23	42.35	12.02	23.6	9.07	9.21	30.04	30.5	39	72.9	89.23	21.68	55.79	65.75
Walker_Camp_Prong	1	2	126.93	35.33	9.51	17.96	9.09	8.01	24.33	25.23	33.76	64.39	65.06	15.88	43.92	52.93
Walker_Camp_Prong	1	3	122.37	33.63	8.68	18	8.56	7.78	22	23.84	28.27	58.39	63.08	16.73	41.48	51.34
Walker_Camp_Prong	1	4	144.08	39.2	10.52	21.3	8.9	8.23	27.67	29.34	36.17	70.17	77.98	18.13	50.89	60.28
Walker_Camp_Prong	1	5	151.84	36.79	9.54	20.04	8.8	8.13	24.29	26.35	32.24	71.66	76.47	16.86	49.69	61.77
Walker_Camp_Prong	1	6	163.89	46.91	14.91	23.78	10.26	9.34	37.23	31.55	38.39	84.48	89.41	20.87	54.36	65.77
Walker_Camp_Prong	1	7	142.83	37.23	9.38	20.41	9.05	8.33	24	27.71	34.28	68.77	77.25	19.41	51.71	59.11
Walker_Camp_Prong	1	8	143.56	36.63	9.32	20.27	8.77	8.06	24.81	26.47	31.63	68.54	73.04	17.88	47.09	58.14
Walker_Camp_Prong	1	9	160.24	41.91	11.57	22.46	9.23	8.47	30.82	28.65	37.07	77.61	83.55	20.52	53.86	64.04
Walker_Camp_Prong	1	10	142.06	38.95	10.54	19.98	8.82	8.17	28	29.92	35.28	75.24	76.81	15.16	46.89	54.72
		Mean/Mode	145.90	38.89	10.60	20.78	9.06	8.37	27.32	27.96	34.61	71.22	77.19	18.31	49.57	59.39

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	prr mks
	37.3	43.86	70.13	34.73	22.58	37.31	35.97	27.4	22.97	9	10	9	15	109	3	9	5	14	7
	30.61	37.52	51.58	28.18	19.22	32.15	29.06	18.95	18.85	11	11	10	15	118	5	8	7	11	6
	28.61	34.56	49.35	24.58	17.1	28.75	27.77	19.29	17.48	12	12	9	15	110	5	8	5	13	7
	34.79	40.38	58.68	29.2	21.51	36.37	32.7	20.5	21.71	10	10	9	14	112	5	8	5	13	8
	34.28	44.22	65.1	30.61	20.4	32.26	30.16	24.16	19.42	10	11	10	14	115	4	8	5	12	6
	37.56	44.63	68.32	33.98	22.7	38.82	36.92	26.05	23.15	10	12	9	15	114	4	7	4	15	7
	33.58	40.31	59.67	29.71	21.38	34.47	31.72	22.03	20.24	12	10	9	14	109	5	9	4	12	8
	31.59	39.88	60.25	30.13	19.18	31.62	30.02	23.79	20.39	10	9	10	13	115	3	8	4	13	8
	35.22	43.35	65.94	32.79	20.94	36.3	33.66	26.61	22.84	10	9	9	15	116	5	7	5	14	9
	33.49	38.52	58.87	28.89	19.67	34.29	31.25	22.29	19.73	11	10	9	13	116	4	8	7	12	7
Mean/Mode	33.70	40.72	60.79	30.28	20.47	34.23	31.92	23.11	20.68	10	10	9	15	109	5	8	5	13	7

Table 29. Brook Trout morphometric and meristic values from Great Smoky Mountains, French Broad/Pigeon Watershed, Winding Stair North Carolina

loc	Group #	Fish #	SL	HL	SNL	POHL	HED	VED	LJL	HD	BD	SNDOR	SNPEL	DFBL	ADAA	ADPA
Winding_Stair	1	1	146.59	40.52	11.07	20.66	9.63	8.85	29.95	28.35	38.49	73.25	76.39	22.34	52.83	61.49
Winding_Stair	1	2	106.15	29.88	8	15.21	9.18	7.8	20.5	19.98	26.37	52.98	53.53	14.7	35.66	43.53
Winding_Stair	1	3	103.24	27.79	6.95	14.01	8.68	8.05	18.81	18.34	24.75	51.29	52.59	14.81	35.5	43.83
Winding_Stair	1	4	127.47	33.24	8.47	17.11	9.35	8.42	22.46	23.84	31.54	62.82	65.15	18.56	45.55	54.87
Winding_Stair	1	5	103.65	27.11	7.51	13.72	8.52	7.41	19.29	20.04	25.61	51.54	52.28	13.62	35.38	42.65
Winding_Stair	1	6	133.8	34.19	8.87	17.85	9.14	8.18	23.53	23.78	30.45	64.07	67.01	21.29	46.27	57.55
Winding_Stair	1	7	103.84	28.2	6.61	14.84	8.24	7.48	18.29	19.41	23.19	48.86	52.29	14.23	34.12	42.06
Winding_Stair	1	8	129.48	33.7	9.46	18.17	9.14	7.95	23.22	23.97	31.77	63.23	68.31	19.25	46.12	54.28
Winding_Stair	1	9	125.86	32.99	8.97	16.82	9.41	8.11	22.71	21.91	29.42	60.81	65.08	17.84	42.9	51.74
Winding_Stair	1	10	115.68	29.94	7.84	15.3	8.36	7.24	20.19	20.85	26.32	55.44	61.01	17.28	40.26	48.06
		Mean/Mode	119.58	31.76	8.38	16.37	8.97	7.95	21.90	22.05	28.79	58.43	61.36	17.39	41.46	50.01

	PDAA	PDPA	PDVC	PADC	AADPAA	ADP2	PDP2	CPL	LCPD	DRAYS	ARAYS	P2RAYS	P1RAYS	LLS	PSPLL	GRLOW	GRUP	TORLLJ	pr mks
	34.18	38.26	59.47	29.2	21.12	38.23	36.53	22.98	20.69	11	11	9	13	104	5	10	6	14	9
	23.56	28.56	43.13	21.07	14.23	24.51	23.85	17.2	14.67	12	11	9	13	106	5	7	5	13	9
	23.44	28.52	40.93	19.42	14.12	23.5	22.88	15.83	13.71	11	11	8	13	108	5	8	4	13	7
	29.97	36.6	51.26	24.77	18.13	30.85	29.53	18.82	16.45	12	11	9	13	108	5	8	3	13	8
	24.09	27.87	41.85	21.21	14.89	24.95	23.57	15.83	13.99	11	12	8	13	105	5	7	4	13	7
	29.54	36.91	55.24	25.35	17.53	30.65	28.76	21.2	17.28	11	12	9	13	104	4	8	4	14	8
	22.57	27.97	42.94	20.28	12.66	22.63	21.26	16.96	13.47	11	11	9	14	106	6	8	4	12	8
	30.38	34.54	52.2	25.09	18.46	31.6	29.76	18.26	16.8	11	11	9	12	106	5	8	3	14	9
	27.99	33.83	49.82	22.95	16.72	29.05	27.86	16.4	16.59	11	12	9	13	111	4	9	5	14	8
	25.9	30.52	45.59	22.23	15.16	26.88	24.54	17.81	15.12	12	10	9	13	112	4	9	5	12	9
Mean/Mode	27.16	32.36	48.24	23.16	16.30	28.29	26.85	18.13	15.88	11	11	9	13	106	5	8	4	14	9

Appendix D

Scree Plots, Eigenvalues and Three Retained Principle Components

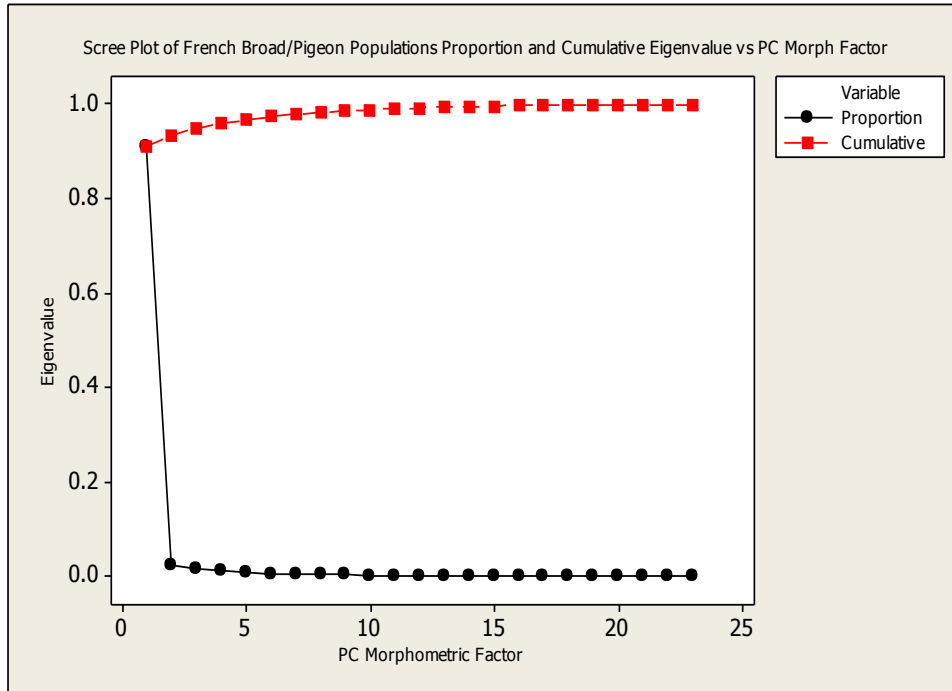


Figure 14. French Broad/Pigeon Watershed Brook Trout Headwater Stream Populations Scree Plot Illustrating Morphometric Variance

PC	Eigenvalue	Proportion	Cumulative	Sheared PC_2
1	0.09281	0.91050	0.91050	sl -0.13327
2	0.00244	0.02395	0.93445	hl 0.20446
3	0.00150	0.01472	0.94917	snl 0.38928
4	0.00112	0.01095	0.96012	pohl 0.11480
5	0.00088	0.00867	0.96879	hed 0.38828
6	0.00063	0.00616	0.97495	ved 0.30207
7	0.00046	0.00448	0.97943	ljl 0.37443
8	0.00039	0.00384	0.98326	hd 0.00942
9	0.00035	0.00343	0.98669	bd 0.02249
10	0.00025	0.00249	0.98918	sndor -0.02609
11	0.00023	0.00225	0.99143	snpel -0.02811
12	0.00019	0.00190	0.99333	dfbl 0.07814
13	0.00014	0.00134	0.99467	adaa -0.13976
14	0.00011	0.00112	0.99579	adpa -0.16946
15	0.00011	0.00105	0.99684	pdaa -0.19787
16	0.00009	0.00089	0.99772	pdpa -0.28102
17	0.00006	0.00059	0.99831	pdvc -0.26317
18	0.00005	0.00051	0.99882	padc -0.25117
19	0.00004	0.00038	0.99920	aadpaa -0.16928
20	0.00003	0.00031	0.99952	adp2 -0.00516
21	0.00002	0.00020	0.99972	pdp2 -0.05492
22	0.00002	0.00016	0.99988	cpl -0.20137
23	0.00001	0.00012	1.00000	lcpd -0.11011

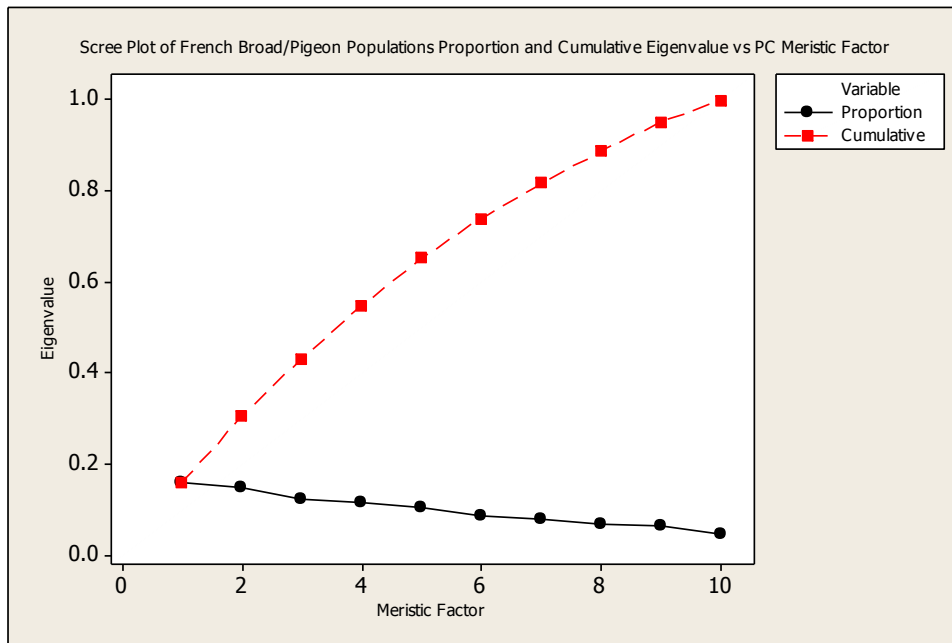


Figure 15. French Broad/Pigeon Watershed Brook Trout Headwater Stream Populations Scree Plot Illustrating Meristic Variance

Principle Component	Eigenvalue	Proportion	Cumulative	PC1
1	1.58724	0.1587	0.1587	drays 0.55461
2	1.47816	0.1478	0.3065	arrays 0.36466
3	1.24453	0.1245	0.4310	p2rays 0.17409
4	1.17233	0.1172	0.5482	p1rays 0.34951
5	1.04998	0.1050	0.6532	lls -0.13318
6	0.86304	0.0863	0.7395	pspll 0.60154
7	0.78451	0.0785	0.8180	grlow 0.60514
8	0.69655	0.0697	0.8876	grup 0.36229
9	0.64017	0.0640	0.9517	torllj 0.33096
10	0.48349	0.0483	1.0000	prrmks -0.08741

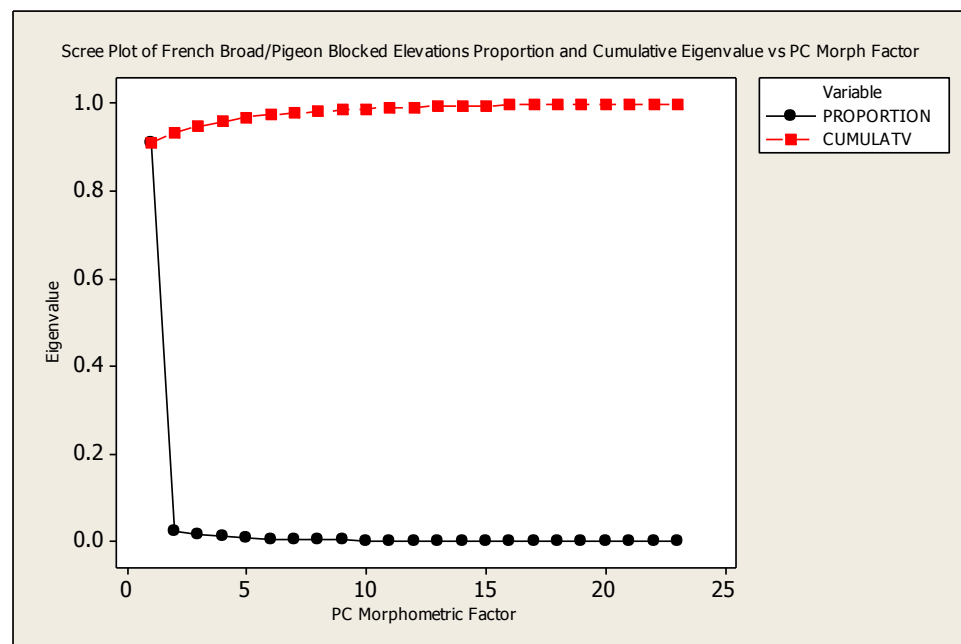


Figure 16. French Broad/Pigeon Watershed Blocked Elevation Brook Trout Scree Plot Illustrating Morphometric Variance

PC	Eigenvalue	Proportion	Cumulative	Sheared PC_2
1	0.09281	0.91050	0.91050	sl -0.12133
2	0.00244	0.02395	0.93445	hl 0.21787
3	0.00150	0.01472	0.94917	snl 0.40687
4	0.00112	0.01095	0.96012	pohl 0.12863
5	0.00088	0.00867	0.96879	hed 0.39618
6	0.00063	0.00616	0.97495	ved 0.31021
7	0.00046	0.00448	0.97943	ljl 0.39073
8	0.00039	0.00384	0.98326	hd 0.02294
9	0.00035	0.00343	0.98669	bd 0.03679
10	0.00025	0.00249	0.98918	sndor -0.01361
11	0.00023	0.00225	0.99143	snpel -0.01461
12	0.00019	0.00190	0.99333	dfbl 0.08996
13	0.00014	0.00134	0.99467	adaa -0.12681
14	0.00011	0.00112	0.99579	adpa -0.15748
15	0.00011	0.00105	0.99684	pdad -0.18468
16	0.00009	0.00089	0.99772	pdpa -0.26890
17	0.00006	0.00059	0.99831	pdvc -0.25128
18	0.00005	0.00051	0.99882	padc -0.23939
19	0.00004	0.00038	0.99920	aadpaa -0.15648
20	0.00003	0.00031	0.99952	adp2 0.00999
21	0.00002	0.00020	0.99972	pdp2 -0.04087
22	0.00002	0.00016	0.99988	cpl -0.18986
23	0.00001	0.00012	1.00000	lcpd -0.09656

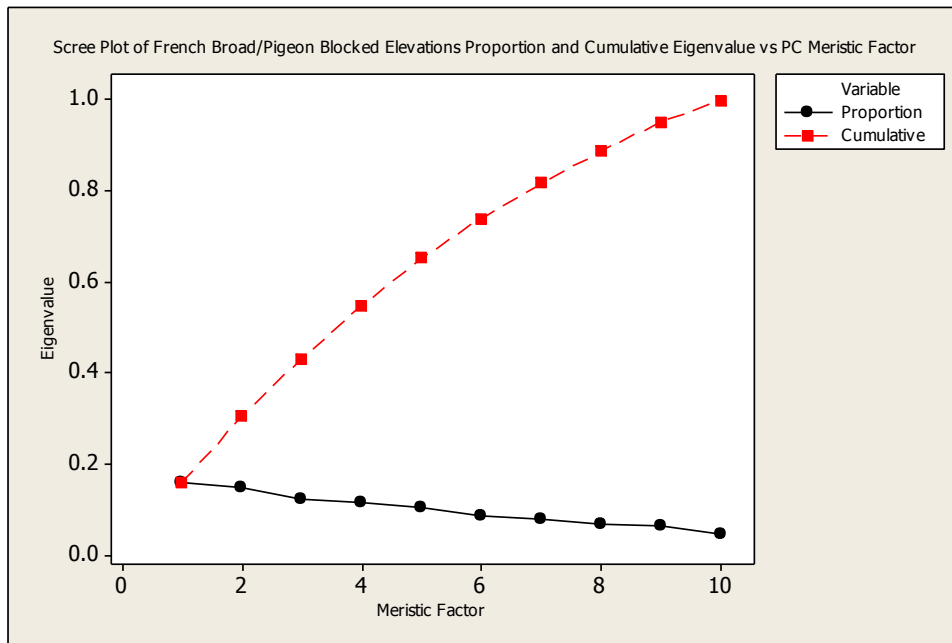


Figure 17. French Broad/Pigeon Watershed Blocked Elevation Brook Trout Scree Plot Illustrating Meristic Variance

Principle Component	Eigenvalue	Proportion	Cumulative	PC1 (meristics)
1	1.58724	0.1587	0.1587	drays 0.55461
2	1.47816	0.1478	0.3065	arays 0.36466
3	1.24453	0.1245	0.4310	p2rays 0.17409
4	1.17233	0.1172	0.5482	p1rays 0.34951
5	1.04998	0.1050	0.6532	lls -0.13318
6	0.86304	0.0863	0.7395	pspll 0.60154
7	0.78451	0.0785	0.8180	grlow 0.60514
8	0.69655	0.0697	0.8876	grup 0.36229
9	0.64017	0.0640	0.9517	torllj 0.33096
10	0.48349	0.0483	1.0000	prrmks -0.08741

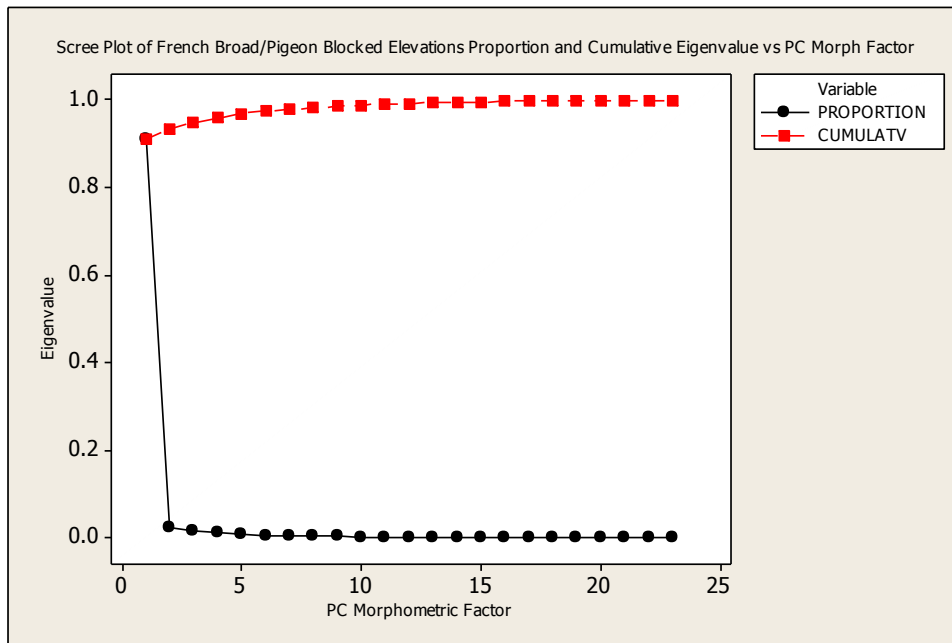


Figure 18. French Broad/Pigeon Watershed Blocked Flow Aspect of Brook Trout Scree Plots Illustrating Morphometric Variance

PC	Eigenvalue	Proportion	Cumulative	Sheared PC_2
1	0.09281	0.91050	0.91050	sl -0.1233
2	0.00244	0.02395	0.93445	hl 0.21584
3	0.00150	0.01472	0.94917	snl 0.40426
4	0.00112	0.01095	0.96012	pohl 0.12648
5	0.00088	0.00867	0.96879	hed 0.39511
6	0.00063	0.00616	0.97495	ved 0.30906
7	0.00046	0.00448	0.97943	ljl 0.38832
8	0.00039	0.00384	0.98326	hd 0.02079
9	0.00035	0.00343	0.98669	bd 0.03452
10	0.00025	0.00249	0.98918	sndor -0.01561
11	0.00023	0.00225	0.99143	snpel -0.01678
12	0.00019	0.00190	0.99333	dfbl 0.08811
13	0.00014	0.00134	0.99467	adaa -0.12894
14	0.00011	0.00112	0.99579	adpa -0.15947
15	0.00011	0.00105	0.99684	pdaa -0.18688
16	0.00009	0.00089	0.99772	pdpa -0.27097
17	0.00006	0.00059	0.99831	pdvc -0.25330
18	0.00005	0.00051	0.99882	padc -0.24139
19	0.00004	0.00038	0.99920	aadpaa -0.15861
20	0.00003	0.00031	0.99952	adp2 0.00757
21	0.00002	0.00020	0.99972	pdp2 -0.04314
22	0.00002	0.00016	0.99988	cpl -0.19179
23	0.00001	0.00012	1.00000	lcpd -0.09877

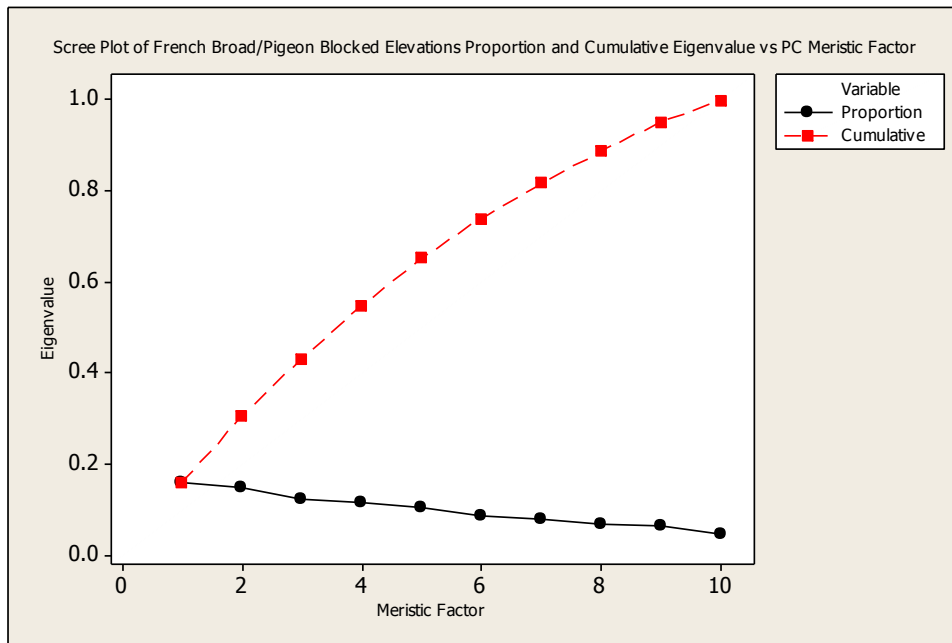


Figure 19. French Broad/Pigeon Watershed Blocked Flow Aspect of Brook Trout Scree Plots Illustrating Morphometric Variance

Principle Component	Eigenvalue	Proportion	Cumulative	PC1 (meristics)
1	1.58724	0.1587	0.1587	drays 0.55461
2	1.47816	0.1478	0.3065	arays 0.36466
3	1.24453	0.1245	0.4310	p2rays 0.17409
4	1.17233	0.1172	0.5482	p1rays 0.34951
5	1.04998	0.1050	0.6532	lls -0.13318
6	0.86304	0.0863	0.7395	pspll 0.60154
7	0.78451	0.0785	0.8180	grlow 0.60514
8	0.69655	0.0697	0.8876	grup 0.36229
9	0.64017	0.0640	0.9517	torllj 0.33096
10	0.48349	0.0483	1.0000	prrmks -0.08741

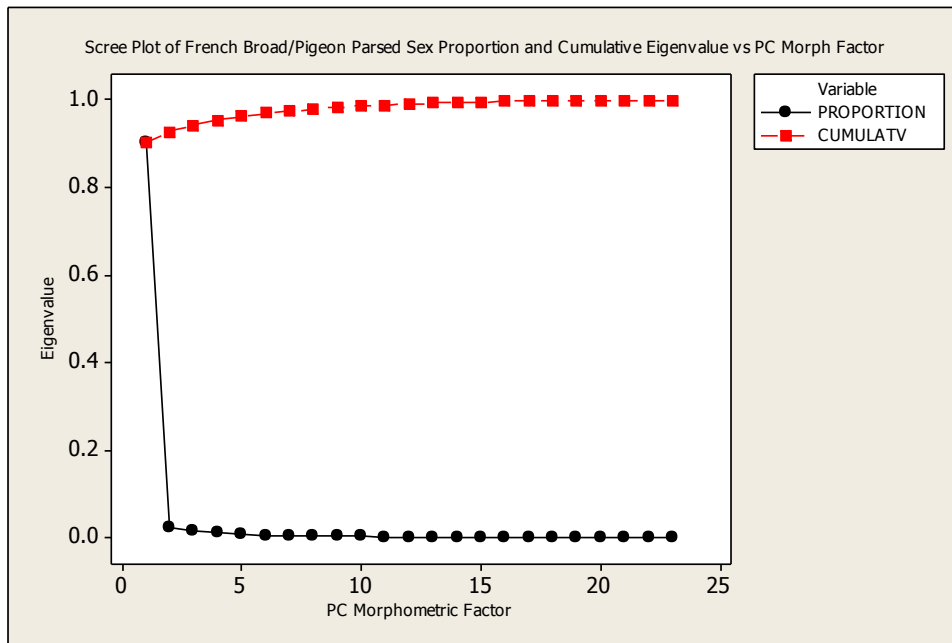


Figure 20. French Broad/Pigeon Watershed Parsed Sex of Brook Trout Scree Plots Illustrating Morphometric Variance

PC	Eigenvalue	Proportion	Cumulative	Sheared PC_2
1	0.09368	0.90430	0.90430	sl -0.10789
2	0.00250	0.02418	0.92848	hl 0.22563
3	0.00158	0.01526	0.94375	snl 0.40378
4	0.00114	0.01098	0.95473	pohl 0.13968
5	0.00094	0.00905	0.96378	hed 0.39242
6	0.00070	0.00674	0.97052	ved 0.31286
7	0.00054	0.00520	0.97572	ljl 0.39227
8	0.00043	0.00420	0.97992	hd 0.03709
9	0.00038	0.00369	0.98361	bd 0.03956
10	0.00034	0.00330	0.98691	sndor -0.00430
11	0.00027	0.00257	0.98948	snpel -0.00497
12	0.00025	0.00240	0.99188	dfbl 0.08574
13	0.00019	0.00186	0.99374	adaa -0.15639
14	0.00014	0.00137	0.99511	adpa -0.20603
15	0.00011	0.00107	0.99618	pdaa -0.17597
16	0.00011	0.00104	0.99721	pdpa -0.25848
17	0.00009	0.00085	0.99807	pdvc -0.23501
18	0.00006	0.00058	0.99864	padc -0.22067
19	0.00005	0.00051	0.99915	aadpaa -0.15512
20	0.00004	0.00035	0.99951	adp2 0.01545
21	0.00002	0.00019	0.99970	pdp2 -0.03265
22	0.00002	0.00018	0.99987	cpl -0.16159
23	0.00001	0.00013	1.00000	lcpd -0.13592

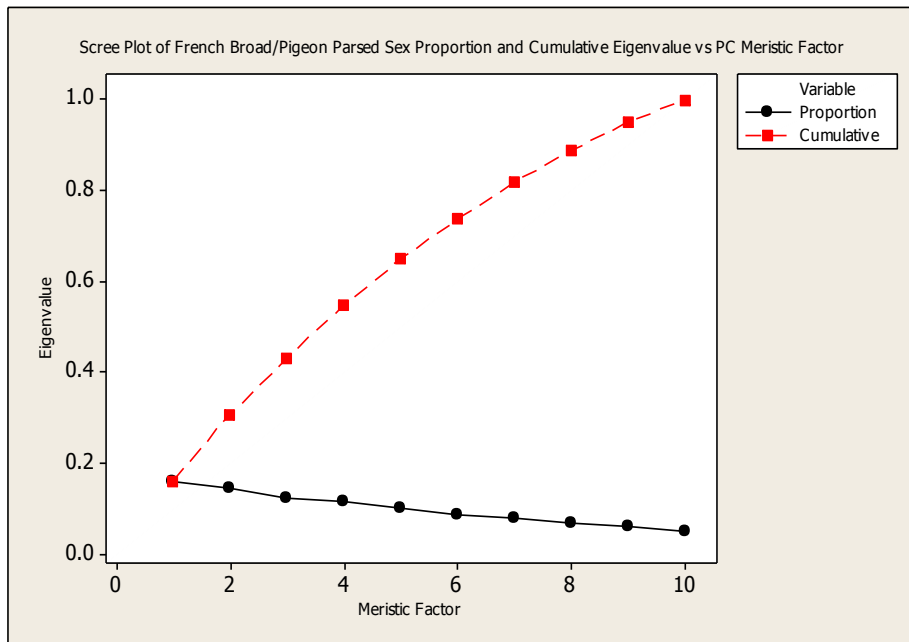


Figure 21. French Broad/Pigeon Watershed Parsed Sex of Brook Trout Scree Plots Illustrating Meristic Variance

Principle Component	Eigenvalue	Proportion	Cumulative	PC1 (meristics)
1	1.61006	0.1610	0.1610	drays 0.54118
2	1.47525	0.1475	0.3085	arrays 0.31951
3	1.22485	0.1225	0.4310	p2rays 0.11254
4	1.16663	0.1167	0.5477	p1rays 0.28045
5	1.02384	0.1024	0.6501	lls -0.20523
6	0.87128	0.0871	0.7372	pspll 0.63391
7	0.80638	0.0806	0.8178	grlow 0.64051
8	0.69590	0.0696	0.8874	grup 0.36153
9	0.62983	0.0630	0.9504	torllj 0.36670
10	0.49598	0.0496	1.0000	prrmks -0.06622

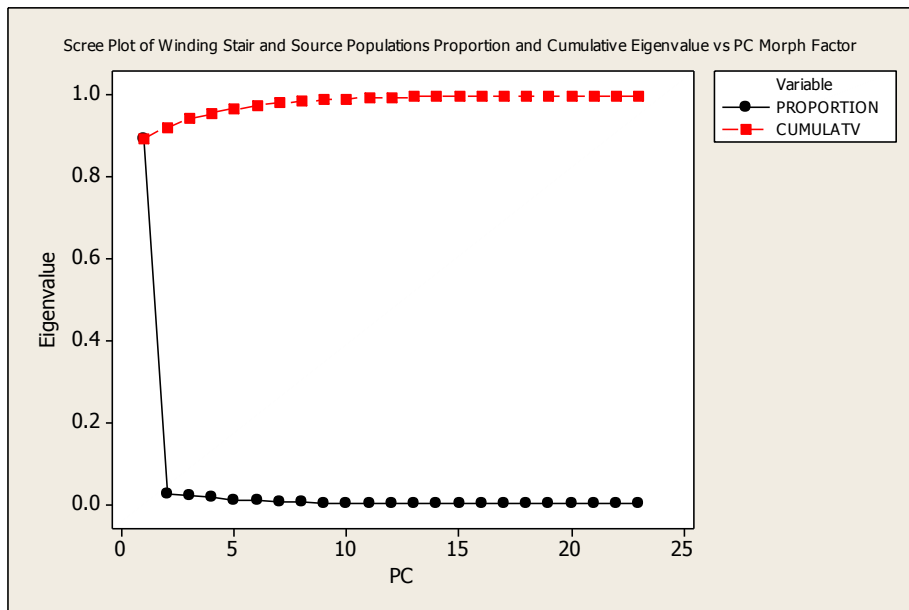


Figure 22. Winding Stair and Source Streams Populations Brook Trout Scree Plots Illustrating Morphometric Variance

PC	Eigenvalue	Proportion	Cumulative	Sheared PC_2
1	0.05445	0.89564	0.89564	sl 0.17031
2	0.00162	0.02662	0.92226	hl -0.05669
3	0.00121	0.01996	0.94221	snl -0.45383
4	0.00093	0.01535	0.95757	pohl 0.04235
5	0.00056	0.00929	0.96686	hed -0.16376
6	0.00048	0.00782	0.97467	ved 0.05344
7	0.00042	0.00694	0.98161	ljl -0.24436
8	0.00030	0.00486	0.98647	hd 0.12968
9	0.00017	0.00280	0.98926	bd -0.21812
10	0.00014	0.00232	0.99159	sndor -0.01875
11	0.00012	0.00191	0.99349	snpel 0.18215
12	0.00010	0.00169	0.99518	dfbl -0.07025
13	0.00009	0.00147	0.99665	adaa 0.11317
14	0.00006	0.00099	0.99764	adpa 0.13188
15	0.00004	0.00070	0.99835	pdaa 0.07238
16	0.00004	0.00061	0.99895	pdpa 0.23827
17	0.00002	0.00033	0.99928	pdvc 0.31759
18	0.00001	0.00024	0.99952	padc 0.32965
19	0.00001	0.00018	0.99970	aadpaa -0.21033
20	0.00001	0.00015	0.99985	adp2 -0.10867
21	0.00001	0.00010	0.99996	pdp2 -0.13768
22	0.00000	0.00003	0.99999	cpl 0.43216
23	0.00000	0.00001	1.00000	lcpd -0.06522

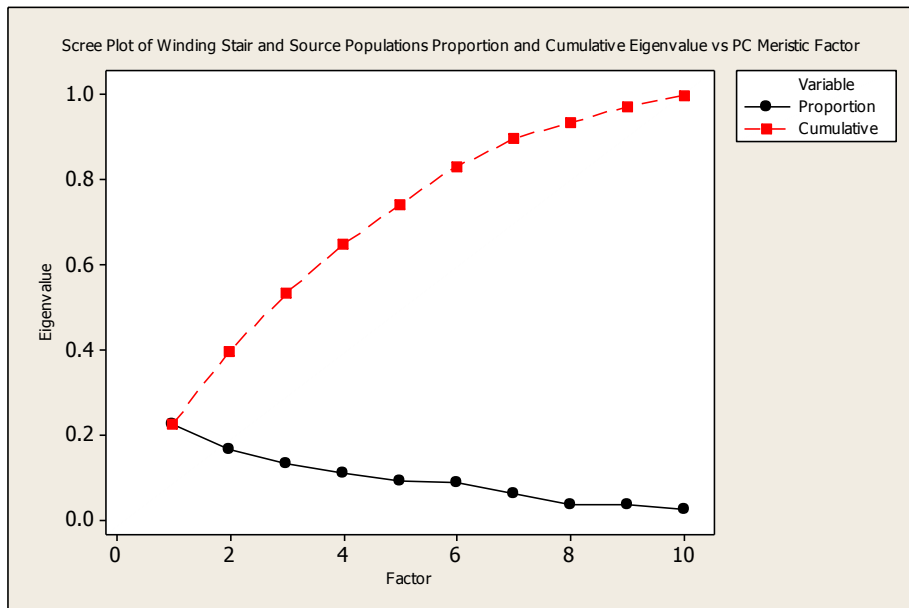


Figure 23. Winding Stair and Source Populations Brook Trout Scree Plots Illustrating Meristic Variance

Principle Component	Eigenvalue	Proportion	Cumulative	PC1 (meristics)
1	2.29386	0.2294	0.2294	drays 0.57458
2	1.69835	0.1698	0.3992	arays 0.68940
3	1.36733	0.1367	0.5360	p2rays 0.20829
4	1.14214	0.1142	0.6502	p1rays 0.45682
5	0.93540	0.0935	0.7437	lls 0.24919
6	0.89929	0.0899	0.8336	pspll -0.59272
7	0.63702	0.0637	0.8973	grlow -0.54503
8	0.39128	0.0391	0.9365	grup -0.57949
9	0.36929	0.0369	0.9734	torllj -0.38224
10	0.26603	0.0266	1.0000	prrmks 0.20977

Appendix E

Sheared Principle Component Analysis Plots and Associated Data

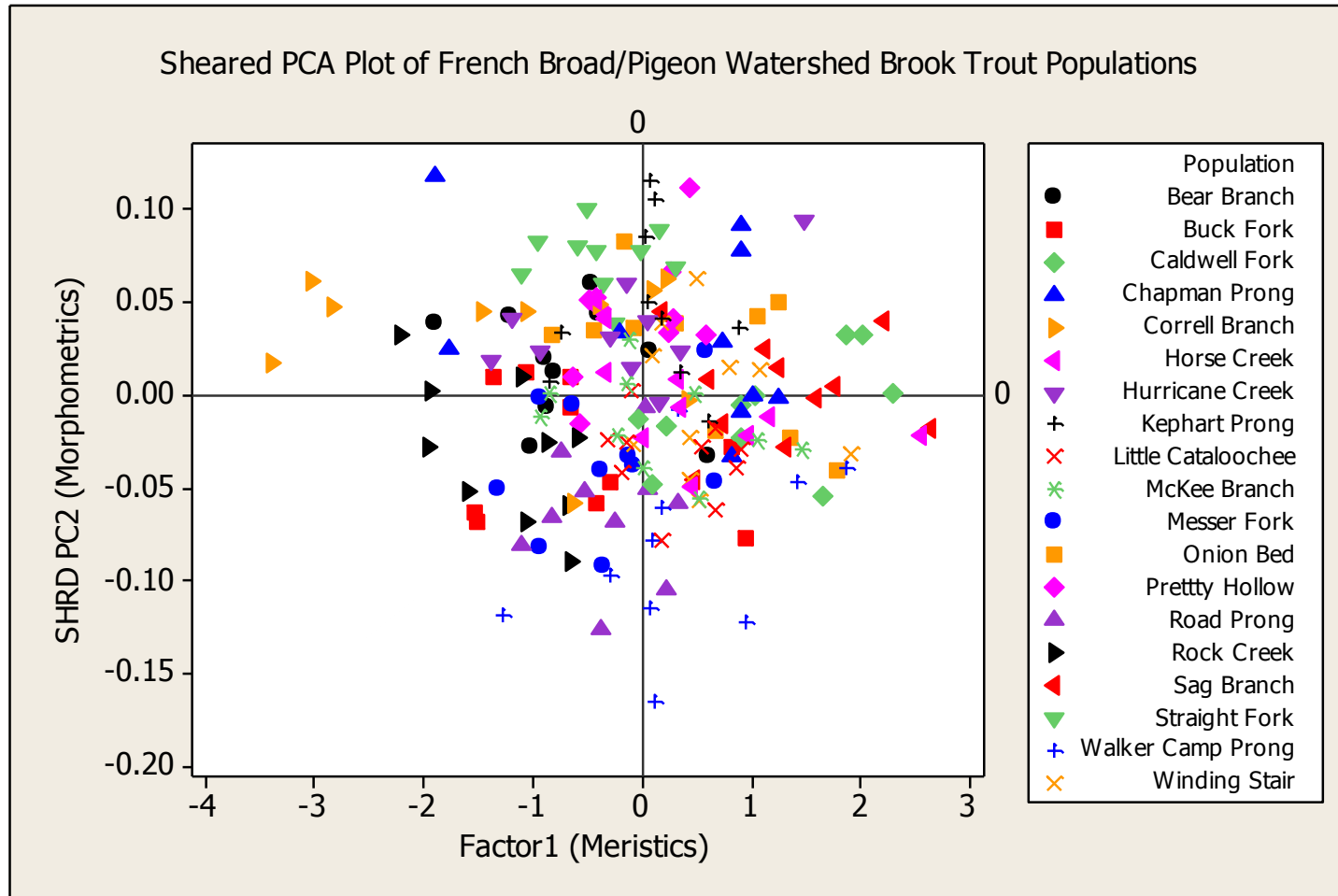


Figure 24. French Broad/Pigeon Watershed Brook Trout Headwater Stream Populations Sheared PCA Minimal Polygon Plots Illustrating Phenotypic Grouping

Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1
1	1	0.01220	-0.80913	49	5	0.05692	0.09649	97	10	-0.02435	1.04497	145	15	-0.02318	-0.5929
2	1	0.06097	-0.47241	50	5	0.01815	-3.38766	98	10	0.02998	-0.13431	146	15	0.00208	-1.93408
3	1	-0.02779	-1.01947	51	6	0.05163	-0.42286	99	10	-0.02158	-0.22411	147	15	-0.05243	-1.59948
4	1	0.02067	-0.89836	52	6	0.04159	-0.33536	100	10	0.00562	-0.14581	148	15	0.03301	-2.22294
5	1	-0.03312	0.60825	53	6	-0.02156	0.96194	101	11	0.02379	0.57682	149	15	-0.05972	-0.68187
6	1	0.04287	-1.21963	54	6	-0.01182	1.14877	102	11	-0.08239	-0.94062	150	15	-0.02724	-1.95493
7	1	0.03923	-1.90196	55	6	0.00890	0.32316	103	11	-0.04061	-0.38327	151	16	0.01517	1.24877
8	1	0.02352	0.05657	56	6	-0.02315	-0.00059	104	11	-0.05008	-1.31625	152	16	-0.01752	2.62369
9	1	0.04343	-0.40722	57	6	-0.02103	2.54904	105	11	-0.00154	-0.93799	153	16	0.04582	0.16531
10	1	-0.00641	-0.87105	58	6	0.01219	-0.34511	106	11	-0.03243	-0.13589	154	16	-0.02762	1.31524
11	2	-0.04735	-0.29499	59	6	-0.04907	0.45540	107	11	-0.04676	0.66465	155	16	0.02468	1.11928
12	2	-0.06819	-1.50590	60	6	-0.00591	0.34078	108	11	-0.00540	-0.63060	156	16	-0.01571	0.72013
13	2	0.01044	-1.36145	61	7	0.01927	-1.37879	109	11	-0.09226	-0.37167	157	16	0.00462	1.75618
14	2	-0.06279	-1.54016	62	7	0.04189	-1.18710	110	11	-0.03786	-0.08326	158	16	0.04083	2.20617
15	2	-0.07690	0.93239	63	7	0.02344	-0.94726	111	12	-0.01908	0.65877	159	16	-0.04566	0.46477
16	2	-0.02736	0.82324	64	7	0.06001	-0.15410	112	12	-0.02287	1.35020	160	16	-0.00151	1.58010
17	2	0.00947	-0.66607	65	7	0.09440	1.48082	113	12	0.05097	1.23890	161	16	0.00830	0.60628
18	2	-0.05756	-0.43204	66	7	0.01493	-0.10964	114	12	0.08280	-0.16268	162	17	0.06556	-1.10071
19	2	-0.00625	-0.65835	67	7	0.02399	0.34945	115	12	0.03651	-0.09308	163	17	0.09002	0.15117
20	2	0.01235	-1.05716	68	7	-0.00413	0.15373	116	12	-0.04089	1.78434	164	17	0.05988	-0.36374
21	3	0.03262	2.01423	69	7	0.03986	0.03590	117	12	0.03560	-0.43659	165	17	0.10018	-0.51323
22	3	0.00025	1.02680	70	7	0.03121	-0.30497	118	12	0.03252	-0.83538	166	17	0.07841	-0.41898
23	3	0.00115	2.29398	71	8	0.03612	0.87270	119	12	0.03918	0.29783	167	17	0.08269	-0.95977
24	3	-0.00500	0.88921	72	8	0.00696	-0.86220	120	12	0.04237	1.05102	168	17	0.06977	0.29959
25	3	-0.05412	1.64829	73	8	0.03408	-0.75471	121	13	0.03217	0.58250	169	17	0.03845	-0.25823
26	3	-0.02332	0.90346	74	8	0.10528	0.10449	122	13	0.05135	-0.49843	170	17	0.08120	-0.59663
27	3	-0.01256	-0.03192	75	8	0.04989	0.04531	123	13	0.11277	0.42128	171	17	0.07783	-0.02589
28	3	0.03316	1.85510	76	8	0.11625	0.05561	124	13	0.03351	0.24351	172	18	-0.11482	0.06542
29	3	-0.04747	0.09169	77	8	-0.01339	0.60066	125	13	0.04140	0.27549	173	18	-0.04660	1.40342
30	3	-0.01668	0.21669	78	8	0.01232	0.33412	126	13	0.01016	-0.62903	174	18	-0.03973	1.85297
31	4	0.09223	0.90950	79	8	0.08568	0.02176	127	13	0.06636	0.25950	175	18	-0.07771	0.09163
32	4	-0.00124	1.23757	80	8	0.04163	0.18152	128	13	-0.01493	-0.56646	176	18	-0.16480	0.10461
33	4	0.11908	-1.90076	81	9	-0.01788	0.66899	129	13	0.05322	-0.43585	177	18	-0.00822	0.31994
34	4	0.03351	-0.21767	82	9	-0.02374	-0.32261	130	13	0.04675	-0.38393	178	18	-0.12187	0.93630
35	4	-0.03282	0.80383	83	9	-0.04190	-0.19608	131	14	-0.08084	-1.11207	179	18	-0.11906	-1.28965
36	4	-0.00029	1.00749	84	9	-0.06245	0.66717	132	14	-0.00643	0.02711	180	18	-0.09694	-0.28789
37	4	-0.00948	0.89645	85	9	-0.02868	0.90845	133	14	-0.04995	0.05373	181	18	-0.06077	0.17257
38	4	0.02483	-1.76624	86	9	-0.07800	0.17402	134	14	-0.10473	0.22519	182	19	-0.03192	1.89861
39	4	0.02865	0.72988	87	9	-0.03935	0.85906	135	14	-0.06576	-0.82314	183	19	0.06316	0.50015
40	4	0.07839	0.89361	88	9	0.00296	-0.10549	136	14	-0.05837	0.31813	184	19	0.03842	0.17505
41	5	0.06284	0.21369	89	9	-0.02520	-0.14248	137	14	-0.06765	-0.24559	185	19	-0.04542	0.43889
42	5	-0.05782	-0.63411	90	9	-0.02759	0.53978	138	14	-0.02992	-0.75062	186	19	0.02082	0.08267
43	5	0.06156	-3.03818	91	10	-0.05610	0.51400	139	14	-0.12623	-0.38072	187	19	-0.05710	0.51663
44	5	0.04569	-1.06562	92	10	0.00153	0.47216	140	14	-0.05217	-0.53352	188	19	0.01521	0.78210
45	5	-0.00315	0.39883	93	10	-0.01134	-0.94493	141	15	-0.06819	-1.05875	189	19	-0.02615	-0.08832
46	5	0.04478	-1.47861	94	10	-0.02925	1.45608	142	15	-0.08954	-0.66330	190	19	0.01359	1.06678
47	5	0.04823	-2.84319	95	10	0.00099	-0.84425	143	15	-0.02476	-0.87060	191	19	-0.02236	0.43659
48	5	0.04962	-0.39408	96	10	-0.03947	0.00821	144	15	0.00976	-1.10049				

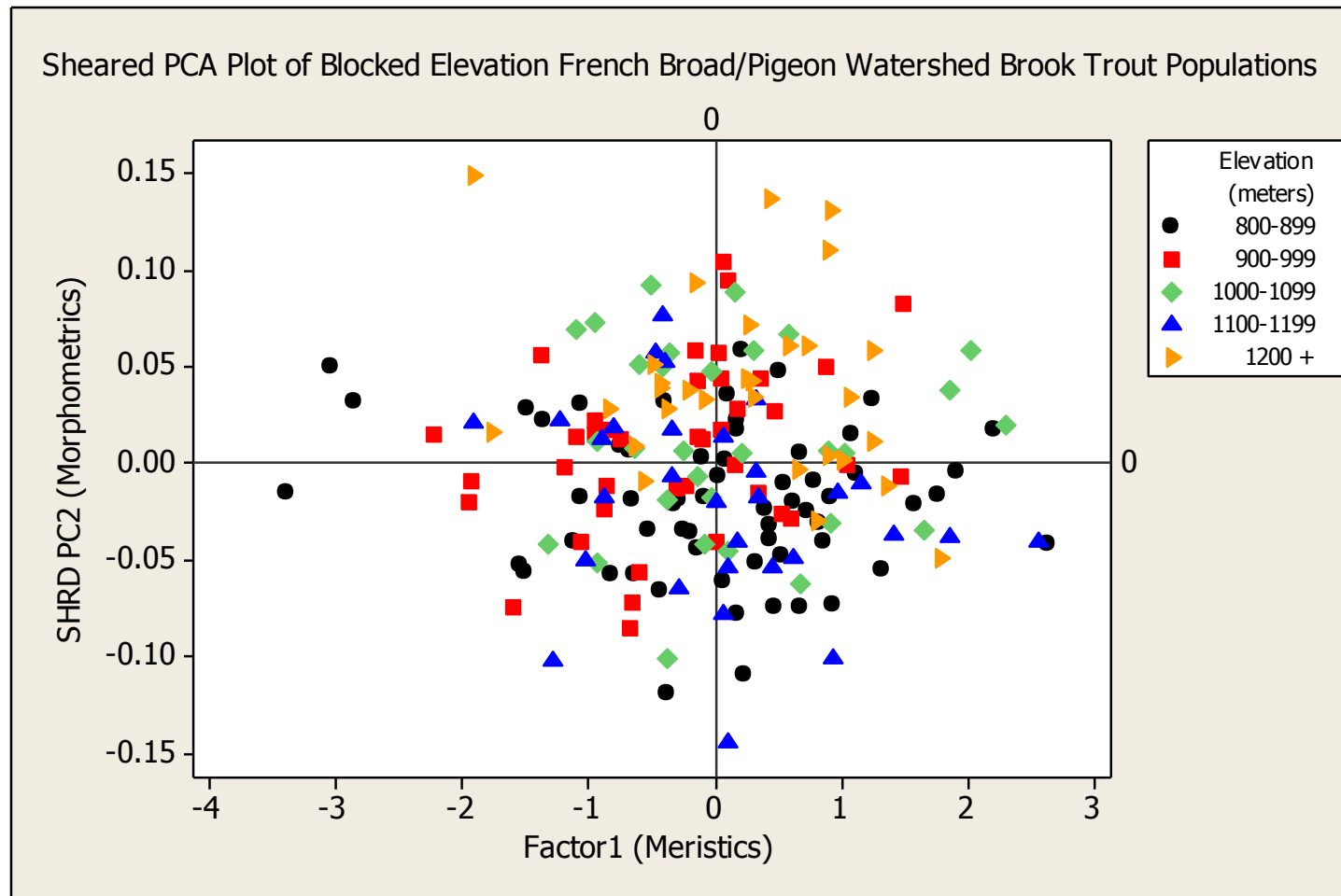


Figure 25. French Broad/Pigeon Watershed Blocked Elevation Brook Trout Headwater Stream Populations Sheared PCA Minimal Polygon Plots Illustrating Phenotypic Grouping

Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1
1	1	-0.01945	-0.29499	49	1	-0.07458	0.46477	97	2	-0.00886	-1.93408	145	4	-0.01028	1.14877
2	1	-0.05619	-1.50590	50	1	-0.02210	1.58010	98	2	-0.07465	-1.59948	146	4	-0.00473	0.32316
3	1	0.02166	-1.36145	51	1	-0.02000	0.60628	99	2	0.01449	-2.22294	147	4	-0.02038	-0.00059
4	1	-0.05253	-1.54016	52	1	-0.00406	1.89861	100	2	-0.08583	-0.68187	148	4	-0.04112	2.54904
5	1	-0.07406	0.93239	53	1	0.04736	0.50015	101	2	-0.02067	-1.95493	149	4	0.01693	-0.34511
6	1	-0.03099	0.82324	54	1	0.01656	0.17505	102	3	0.05820	2.01423	150	4	-0.05445	0.45540
7	1	0.00584	-0.66607	55	1	-0.03983	0.43889	103	3	0.00486	1.02680	151	4	-0.01752	0.34078
8	1	-0.06670	-0.43204	56	1	0.00085	0.08267	104	3	0.01919	2.29398	152	4	-0.07837	0.06542
9	1	-0.01859	-0.65835	57	1	-0.04830	0.51663	105	3	0.00627	0.88921	153	4	-0.03725	1.40342
10	1	-0.01779	-1.05716	58	1	-0.00914	0.78210	106	3	-0.03446	1.64829	154	4	-0.03869	1.85297
11	1	0.05828	0.21369	59	1	-0.01845	-0.08832	107	3	-0.03063	0.90346	155	4	-0.05399	0.09163
12	1	-0.05782	-0.63411	60	1	0.01423	1.06678	108	3	-0.01818	-0.03192	156	4	-0.14526	0.10461
13	1	0.04923	-3.03818	61	1	-0.03230	0.43659	109	3	0.03751	1.85510	157	4	0.03330	0.31994
14	1	0.03086	-1.06562	62	2	0.05560	-1.37879	110	3	-0.04562	0.09169	158	4	-0.10169	0.93630
15	1	-0.02397	0.39883	63	2	-0.00209	-1.18710	111	3	0.00509	2.01669	159	4	-0.10254	-1.28965
16	1	0.02832	-1.47861	64	2	0.02210	-0.94726	112	3	0.06661	0.57682	160	4	-0.06476	-0.28789
17	1	0.03167	-2.84319	65	2	0.05826	-0.15410	113	3	-0.05190	-0.94062	161	4	-0.04095	0.17257
18	1	0.03220	-0.39408	66	2	0.08239	1.48082	114	3	-0.01943	-0.38327	162	5	0.13044	0.90950
19	1	0.03539	0.09649	67	2	0.01202	-0.10964	115	3	-0.04214	-1.31625	163	5	0.01149	1.23757
20	1	-0.01553	-3.38766	68	2	0.04369	0.34945	116	3	0.01112	-0.93799	164	5	0.14934	-1.90076
21	1	0.00561	0.66899	69	2	-0.00115	0.15373	117	3	-0.00659	-0.13589	165	5	0.03784	-0.21767
22	1	-0.02134	-0.32261	70	2	0.01661	0.03590	118	3	-0.06216	0.66465	166	5	-0.03027	0.80383
23	1	-0.03607	-0.19608	71	2	-0.01311	-0.30497	119	3	0.00704	-0.63060	167	5	0.00162	1.00749
24	1	-0.07414	0.66717	72	2	0.04986	0.87270	120	3	-0.10080	-0.37167	168	5	0.00391	0.89645
25	1	-0.01849	0.90845	73	2	-0.01172	-0.86220	121	3	-0.04204	-0.08326	169	5	0.01575	-1.76624
26	1	-0.07802	0.17402	74	2	0.01208	-0.75471	122	3	0.06944	-1.10071	170	5	0.06055	0.72988
27	1	-0.04029	0.85906	75	2	0.09502	0.10449	123	3	0.08892	0.15117	171	5	0.11018	0.89361
28	1	0.00213	-0.10549	76	2	0.04329	0.04531	124	3	0.05736	-0.36374	172	5	-0.00345	0.65877
29	1	-0.04393	-0.14248	77	2	0.10473	0.05561	125	3	0.09192	-0.51323	173	5	-0.01174	1.35020
30	1	-0.01112	0.53978	78	2	-0.02846	0.60066	126	3	0.04961	-0.41898	174	5	0.05815	1.23890
31	1	-0.04052	-1.11207	79	2	-0.01505	0.33412	127	3	0.07324	-0.95977	175	5	0.09345	-0.16268
32	1	-0.00665	0.02711	80	2	0.05737	0.02176	128	3	0.05787	0.29959	176	5	0.03234	-0.09308
33	1	-0.06185	0.05373	81	2	0.02840	0.18152	129	3	0.00648	-0.25823	177	5	-0.04977	1.78434
34	1	-0.11012	0.22519	82	2	-0.02686	0.51400	130	3	0.05155	-0.59663	178	5	0.04125	-0.43659
35	1	-0.05733	-0.82314	83	2	0.02637	0.47216	131	3	0.04778	-0.02589	179	5	0.02830	-0.83538
36	1	-0.05181	0.31813	84	2	0.01421	-0.94493	132	4	0.01837	-0.80913	180	5	0.03385	0.29783
37	1	-0.03457	-0.24559	85	2	-0.00672	1.45608	133	4	0.05745	-0.47241	181	5	0.03434	1.05102
38	1	0.00863	-0.75062	86	2	0.01753	-0.84425	134	4	-0.05048	-1.01947	182	5	0.06018	0.58250
39	1	-0.11919	-0.38072	87	2	-0.04072	0.00821	135	4	0.01272	-0.89836	183	5	0.05111	-0.49843
40	1	-0.03471	-0.53352	88	2	-0.00051	1.04497	136	4	-0.04970	0.60825	184	5	0.13678	0.42128
41	1	0.03318	1.24877	89	2	0.04253	-0.13431	137	4	0.02180	-1.21963	185	5	0.04410	0.24351
42	1	-0.04244	2.62369	90	2	-0.01231	-0.22411	138	4	0.02024	-1.90196	186	5	0.04220	0.27549
43	1	0.02230	0.16531	91	2	0.01386	-0.14581	139	4	0.01355	0.05657	187	5	0.00868	-0.62903
44	1	-0.05527	1.31524	92	2	-0.04111	-1.05875	140	4	0.05249	-0.40722	188	5	0.07180	0.25950
45	1	-0.00625	1.11928	93	2	-0.07210	-0.66330	141	4	-0.01849	-0.87105	189	5	-0.00912	-0.56646
46	1	-0.02568	0.72013	94	2	-0.02437	-0.87060	142	4	0.07651	-0.42286	190	5	0.03887	-0.43585
47	1	-0.01631	1.75618	95	2	0.01383	-1.10049	143	4	-0.00750	-0.33536	191	5	0.02848	-0.38393
48	1	0.01730	2.20617	96	2	-0.05718	-0.59299	144	4	-0.01583	0.96194				

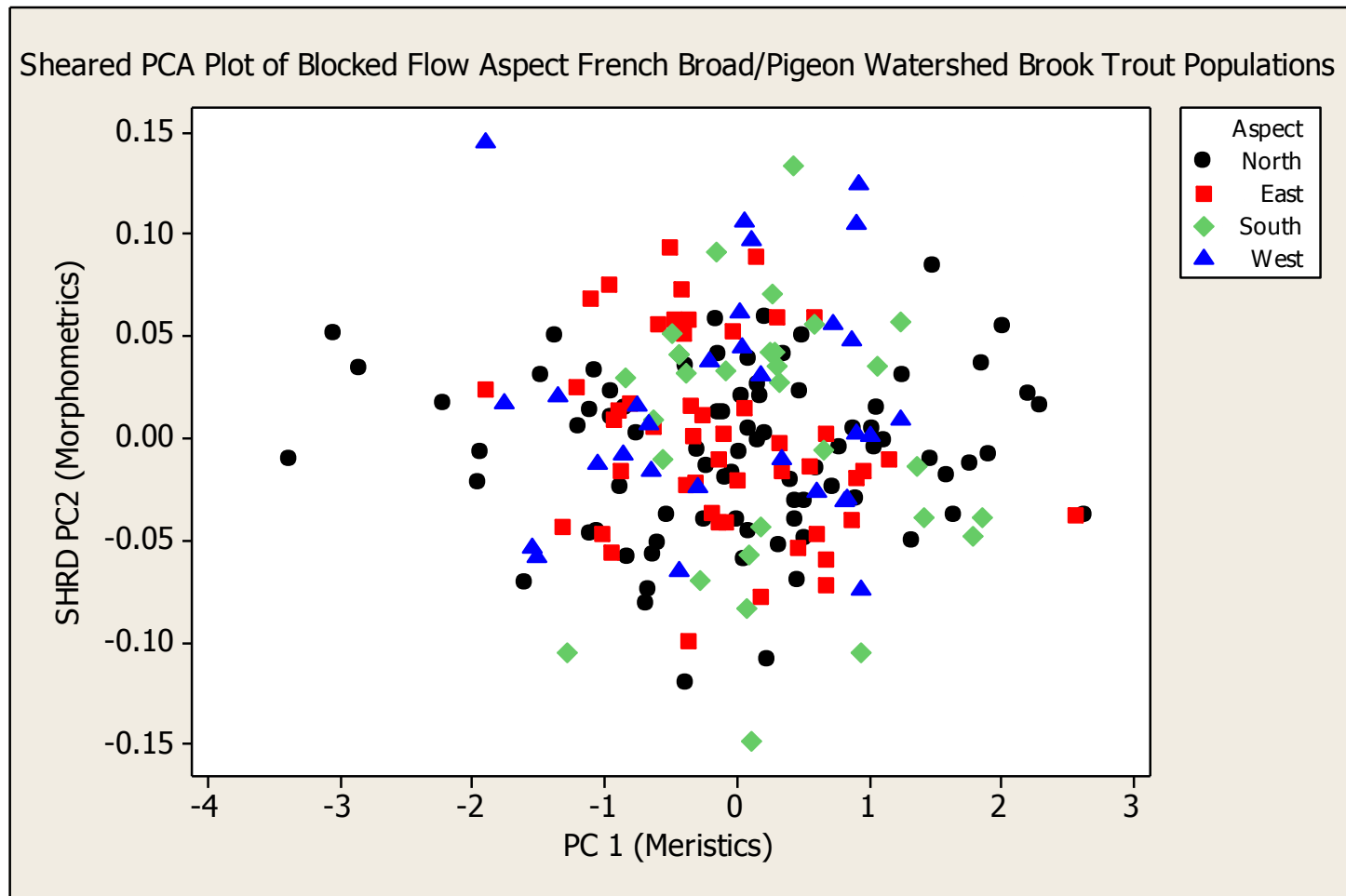


Figure 26. French Broad/Pigeon Watershed Blocked Flow Aspect of Brook Trout Headwater Stream Populations Sheared PCA Minimal Polygon Plots Illustrating Phenotypic Grouping

Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1
1	1	0.054140	2.01423	48	1	0.002470	-0.75062	96	2	-0.002552	0.32316	144	3	0.133010	0.42128
2	1	0.004130	1.02680	49	1	-0.120370	-0.38072	97	2	-0.020833	-0.00059	145	3	0.042430	0.24351
3	1	0.016320	2.29398	50	1	-0.037520	-0.53352	98	2	-0.037923	2.54904	146	3	0.042090	0.27549
4	1	0.004470	0.88921	51	1	-0.045465	-1.05875	99	2	0.016183	-0.34511	147	3	0.008920	-0.62903
5	1	-0.037620	1.64829	52	1	-0.074928	-0.66330	100	2	-0.053616	0.45540	148	3	0.070960	0.25950
6	1	-0.029470	0.90346	53	1	-0.024442	-0.87060	101	2	-0.015670	0.34078	149	3	-0.010060	-0.56646
7	1	-0.017290	-0.03192	54	1	0.013186	-1.10049	102	2	0.001850	0.66899	150	3	0.041190	-0.43585
8	1	0.036830	1.85510	55	1	-0.051770	-0.59299	103	2	-0.021730	-0.32261	151	3	0.031420	-0.38393
9	1	-0.045940	0.09169	56	1	-0.007114	-1.93408	104	2	-0.037020	-0.19608	152	3	-0.084240	0.06542
10	1	0.001610	0.21669	57	1	-0.071134	-1.59948	105	2	-0.072300	0.66717	153	3	-0.038760	1.40342
11	1	0.059040	0.21369	58	1	0.017460	-2.22294	106	2	-0.020130	0.90845	154	3	-0.038870	1.85297
12	1	-0.057850	-0.63411	59	1	-0.081697	-0.68187	107	2	-0.078050	0.17402	155	3	-0.057810	0.09163
13	1	0.051230	-3.03818	60	1	-0.021728	-1.95493	108	2	-0.040160	0.85906	156	3	-0.148460	0.10461
14	1	0.033250	-1.06562	61	1	0.030314	1.24877	109	2	0.002270	-0.10549	157	3	0.026680	0.31994
15	1	-0.020650	0.39883	62	1	-0.038472	2.62369	110	2	-0.040960	-0.14248	158	3	-0.104970	0.93630
16	1	0.030970	-1.47861	63	1	0.026070	0.16531	111	2	-0.013760	0.53978	159	3	-0.105240	-1.28965
17	1	0.034330	-2.84319	64	1	-0.050870	1.31524	112	2	0.059790	0.57682	160	3	-0.069940	-0.28789
18	1	0.035000	-0.39408	65	1	-0.001306	1.11928	113	2	-0.056800	-0.94062	161	3	-0.044140	0.17257
19	1	0.038850	0.09649	66	1	-0.024096	0.72013	114	2	-0.022830	-0.38327	162	4	-0.023930	-0.29499
20	1	-0.010150	-3.38766	67	1	-0.012967	1.75618	115	2	-0.043430	-1.31625	163	4	-0.058140	-1.50590
21	1	0.049810	-1.37879	68	1	0.021070	2.20617	116	2	0.009100	-0.93799	164	4	0.019880	-1.36145
22	1	0.004940	-1.18710	69	1	-0.069991	0.46477	117	2	-0.010730	-0.13589	165	4	-0.054190	-1.54016
23	1	0.022320	-0.94726	70	1	-0.018819	1.58010	118	2	-0.059720	0.66465	166	4	-0.074550	0.93239
24	1	0.058570	-0.15410	71	1	-0.015486	0.60628	119	2	0.005050	-0.63060	167	4	-0.030420	0.82324
25	1	0.084350	1.48082	72	1	-0.008520	1.89861	120	2	-0.099480	-0.37167	168	4	0.006420	-0.66607
26	1	0.012490	-0.10964	73	1	0.049910	0.50015	121	2	-0.041390	-0.08326	169	4	-0.065270	-0.43204
27	1	0.040560	0.34945	74	1	0.020065	0.17505	122	2	0.068860	-1.10071	170	4	-0.016630	-0.65835
28	1	-0.001630	0.15373	75	1	-0.040744	0.43889	123	2	0.089140	0.15117	171	4	-0.012980	-1.05716
29	1	0.020330	0.03590	76	1	0.004042	0.08267	124	2	0.057790	-0.36374	172	4	0.124390	0.90950
30	1	-0.006030	-0.30497	77	1	-0.049731	0.51663	125	2	0.093290	-0.51323	173	4	0.009460	1.23757
31	1	-0.031550	0.51400	78	1	-0.005247	0.78210	126	2	0.054240	-0.41898	174	4	0.144570	-1.90076
32	1	0.022410	0.47216	79	1	-0.019688	-0.08832	127	2	0.074780	-0.95977	175	4	0.037170	-0.21767
33	1	0.010130	-0.94493	80	1	0.014136	1.06678	128	2	0.059800	0.29959	176	4	-0.030700	0.80383
34	1	-0.010330	1.45608	81	1	-0.030729	0.43659	129	2	0.011600	-0.25823	177	4	0.001320	1.00749
35	1	0.014900	-0.84425	82	2	0.017393	-0.80913	130	2	0.056310	-0.59663	178	4	0.001770	0.89645
36	1	-0.040540	0.00821	83	2	0.058041	-0.47241	131	2	0.052610	-0.02589	179	4	0.017210	-1.76624
37	1	-0.004330	1.04497	84	2	-0.046873	-1.01947	132	3	-0.005950	0.65877	180	4	0.055480	0.72988
38	1	0.040550	-0.13431	85	2	0.013999	-0.89836	133	3	-0.013520	1.35020	181	4	0.105150	0.89361
39	1	-0.013790	-0.22411	86	2	-0.047074	0.60825	134	3	0.057030	1.23890	182	4	0.047680	0.87270
40	1	0.012550	-0.14581	87	2	0.025178	-1.21963	135	3	0.091790	-0.16268	183	4	-0.008740	-0.86220
41	1	-0.046990	-1.11207	88	2	0.023288	-1.90196	136	3	0.033020	-0.09308	184	4	0.015600	-0.75471
42	1	-0.006620	0.02711	89	2	0.015155	0.05657	137	3	-0.048370	1.78434	185	4	0.096710	0.10449
43	1	-0.059980	0.05373	90	2	0.051064	-0.40722	138	3	0.040370	-0.43659	186	4	0.044370	0.04531
44	1	-0.109310	0.22519	91	2	-0.016562	-0.87105	139	3	0.028990	-0.83538	187	4	0.106630	0.05561
45	1	-0.058710	-0.82314	92	2	0.072570	-0.42286	140	3	0.034720	0.29783	188	4	-0.026070	0.60066
46	1	-0.052880	0.31813	93	2	0.000352	-0.33536	141	3	0.035640	1.05102	189	4	-0.010680	0.33412
47	1	-0.039880	-0.24559	94	2	-0.016757	0.96194	142	3	0.055730	0.58250	190	4	0.061920	0.02176
				95	2	-0.010529	1.14877	143	3	0.051170	-0.49843	191	4	0.030530	0.18152

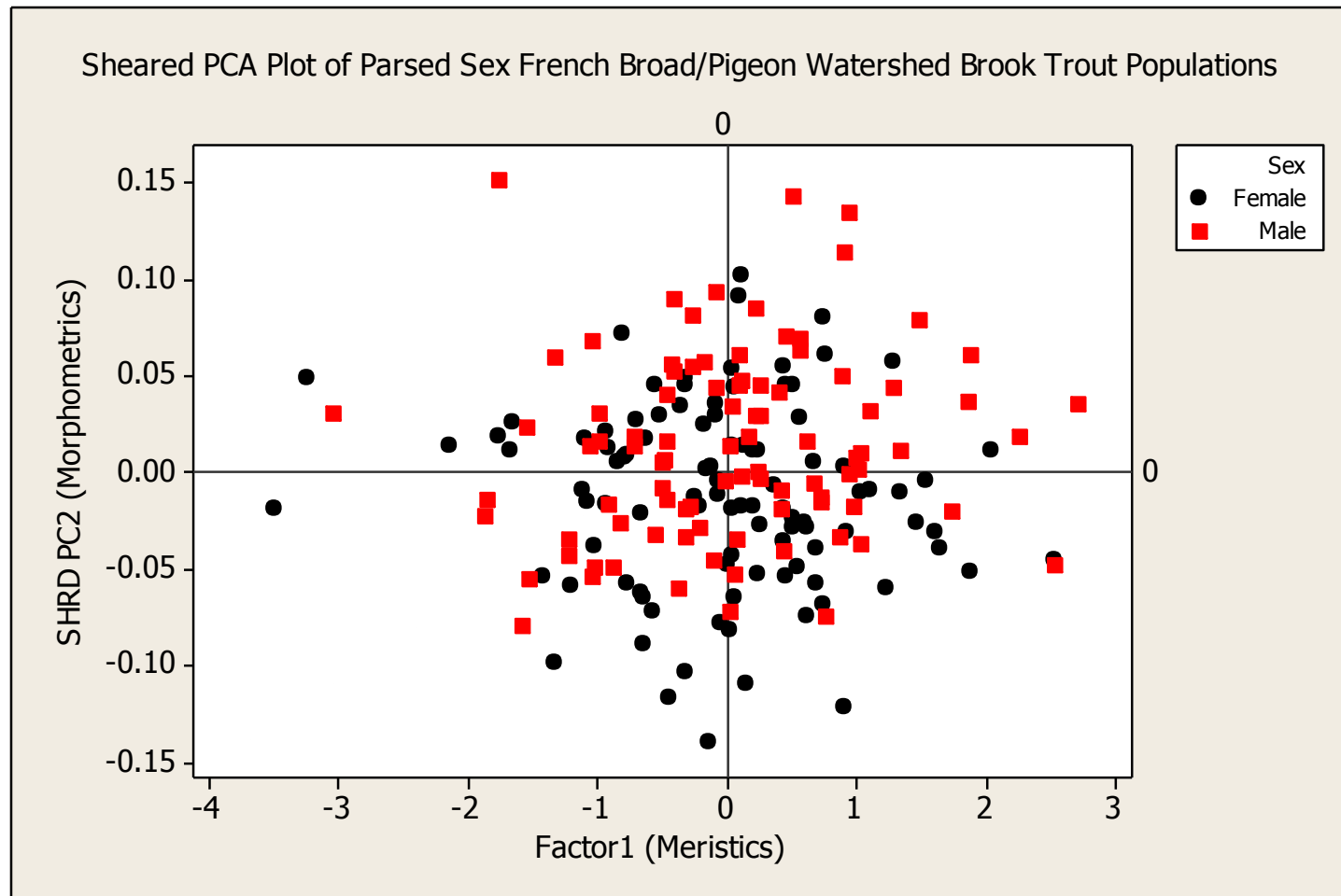
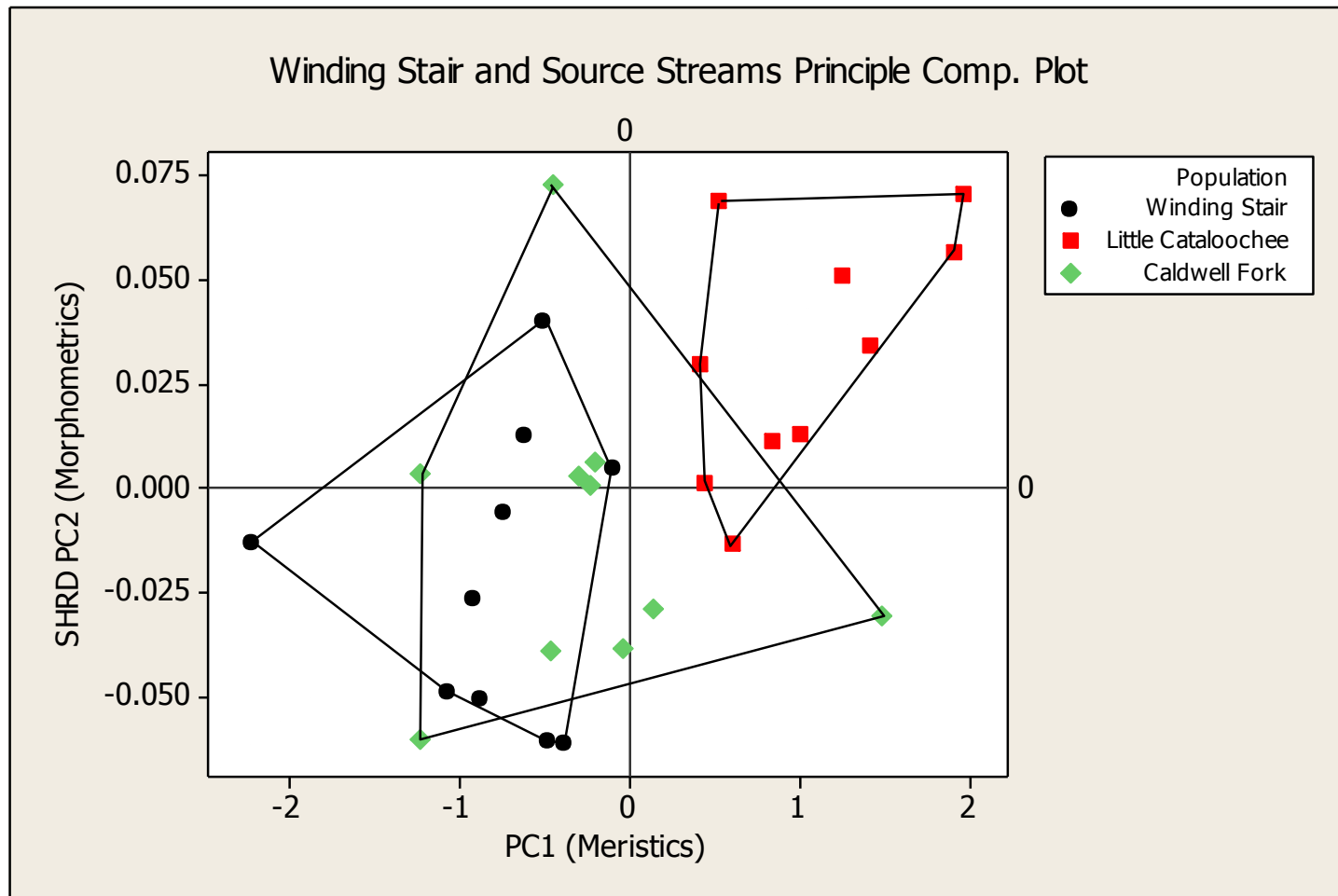


Figure 27. French Broad/Pigeon Watershed Parsed Sex Brook Trout Headwater Stream Populations Sheared PCA Minimal Polygon Plots Illustrating Phenotypic Grouping

Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1	Obs	grp	SHRD_PC2	PC1
1	1	-0.14051	-0.13525	50	1	0.09074	0.09220	99	1	0.01140	0.23983	148	2	-0.01561	0.72067
2	1	-0.09912	-1.33755	51	1	0.10197	0.10787	100	2	0.04736	0.11260	149	2	-0.03317	-0.31452
3	1	-0.12162	0.90213	52	1	-0.02911	0.62386	101	2	-0.07196	0.01961	150	2	-0.01954	-0.32161
4	1	-0.03930	1.64209	53	1	-0.01618	-0.93398	102	2	-0.05985	-0.37470	151	2	-0.04885	-1.01644
5	1	0.07146	-0.81159	54	1	0.00787	-0.79590	103	2	-0.05301	0.05277	152	2	0.05014	0.89217
6	1	0.05495	0.42903	55	1	-0.01911	0.43312	104	2	-0.03475	0.08553	153	2	0.04468	0.09356
7	1	0.04565	-0.31614	56	1	0.05314	0.04441	105	2	-0.03677	1.03423	154	2	0.02962	0.22626
8	1	0.04388	0.05500	57	1	0.04572	0.45378	106	2	0.06761	-1.03287	155	2	0.06016	-1.33305
9	1	0.00310	-0.12572	58	1	0.02080	-0.93244	107	2	0.08546	0.22437	156	2	-0.00006	0.23249
10	1	0.04544	-0.55104	59	1	0.01407	0.12240	108	2	0.05486	-0.25968	157	2	0.05669	-0.18232
11	1	-0.02604	1.46110	60	1	-0.00920	-1.11157	109	2	0.08931	-0.40524	158	2	0.01315	0.01581
12	1	-0.06031	1.22990	61	1	-0.01791	-0.22047	110	2	0.04405	1.27992	159	2	0.07910	1.48357
13	1	-0.08196	0.02954	62	1	-0.01808	0.20883	111	2	-0.01255	0.72656	160	2	0.08098	-0.26756
14	1	-0.02650	0.60641	63	1	-0.00948	1.11085	112	2	-0.02007	1.73369	161	2	-0.01811	0.98033
15	1	0.01132	2.03676	64	1	-0.05456	0.44978	113	2	-0.04751	2.53487	162	2	0.01556	-0.46687
16	1	-0.01033	1.03219	65	1	-0.00697	0.37301	114	2	0.01845	0.16046	163	2	-0.01860	0.42193
17	1	-0.03843	-1.02990	66	1	-0.04502	2.52739	115	2	-0.02242	-1.87342	164	2	0.06090	0.09904
18	1	-0.07200	-0.57264	67	1	-0.01322	-0.24345	116	2	-0.02614	-0.83073	165	2	0.03039	-0.99464
19	1	0.01334	-2.13178	68	1	-0.05880	-1.19633	117	2	0.01346	-1.06292	166	2	0.03065	-3.04116
20	1	-0.08921	-0.64195	69	1	0.04861	-3.24591	118	2	-0.01376	-1.85821	167	2	0.03401	0.04352
21	1	-0.06220	-0.65513	70	1	0.02960	-0.52493	119	2	-0.07966	-1.58294	168	2	0.13429	0.94258
22	1	-0.05785	-0.77599	71	1	0.02638	-1.66120	120	2	-0.03473	-1.22009	169	2	0.11423	0.90180
23	1	-0.11657	-0.44561	72	1	-0.02768	0.24876	121	2	0.01385	-0.70833	170	2	0.15219	-1.75786
24	1	-0.05252	0.23817	73	1	-0.01858	-3.49223	122	2	-0.02905	-0.21721	171	2	0.01124	1.33696
25	1	-0.11017	0.14231	74	1	0.06118	0.76508	123	2	-0.03219	-0.55471	172	2	-0.03296	0.87910
26	1	-0.06487	0.06342	75	1	0.00235	0.89967	124	2	-0.00502	-0.00577	173	2	-0.00048	0.94068
27	1	0.04875	-0.31293	76	1	0.03496	-0.09319	125	2	0.06379	0.57120	174	2	0.06045	1.87351
28	1	0.03477	-0.34681	77	1	0.01131	-1.66380	126	2	0.14361	0.50492	175	2	0.01875	2.25318
29	1	0.02454	-0.17798	78	1	-0.03068	1.60521	127	2	0.04471	0.25520	176	2	-0.00285	0.25732
30	1	-0.01095	1.33128	79	1	0.00569	0.67914	128	2	-0.00830	-0.49910	177	2	0.03619	1.85629
31	1	0.05693	1.27684	80	1	-0.04799	0.00547	129	2	0.07087	0.45015	178	2	0.00710	0.99896
32	1	0.02755	-0.70070	81	1	-0.01830	0.11233	130	2	0.04167	0.40300	179	2	-0.01468	-0.46766
33	1	0.02955	-0.08653	82	1	-0.03048	0.92399	131	2	0.00565	-0.50606	180	2	-0.05487	-1.52024
34	1	-0.05194	1.88234	83	1	-0.05378	-1.41096	132	2	-0.00556	0.68053	181	2	0.02385	-1.54892
35	1	-0.00406	-0.06470	84	1	-0.02813	0.51858	133	2	0.09295	-0.08857	182	2	-0.07432	0.75592
36	1	0.01208	-0.92111	85	1	0.00562	-0.84591	134	2	0.04002	-0.46891	183	2	-0.01685	-0.92354
37	1	-0.10332	-0.32271	86	1	-0.06463	-0.64500	135	2	0.02982	0.26309	184	2	0.05261	-0.41739
38	1	-0.06855	0.74785	87	1	-0.01490	-1.08589	136	2	0.03139	1.11040	185	2	0.01822	-0.71695
39	1	-0.02339	0.50188	88	1	0.00922	-0.76385	137	2	-0.04915	-0.88471	186	2	0.05605	-0.42080
40	1	-0.00433	1.53801	89	1	-0.02161	-0.66827	138	2	0.06931	0.57228	187	2	-0.05380	-1.04343
41	1	0.02768	0.55570	90	1	0.01852	-1.76089	139	2	-0.01743	-0.28902	188	2	0.03504	2.70713
42	1	0.01770	-0.63280	91	1	0.01076	0.19993	140	2	0.00647	-0.48682	189	2	-0.04081	0.43878
43	1	-0.01226	-0.06580	92	1	0.01791	-1.09652	141	2	-0.04351	-1.22870	190	2	0.01062	1.03077
44	1	0.01333	0.04120	93	1	-0.05775	0.68105	142	2	-0.04515	-0.10560	191	2	-0.00247	0.11977
45	1	-0.04349	0.04181	94	1	-0.04885	0.54139	143	2	0.00128	1.01749				
46	1	-0.03955	0.68805	95	1	-0.01950	0.04552	144	2	0.01569	-0.98286				
47	1	-0.07779	-0.05152	96	1	-0.03542	0.43697	145	2	0.04451	-0.08394				
48	1	0.00159	-0.15532	97	1	0.04482	0.51100	146	2	-0.00924	0.42184				
49	1	-0.07408	0.62051	98	1	0.07996	0.74391	147	2	0.01573	0.61232				



Obs (meristics)	grp	SHRD_PC2	PC1
1	1	-0.038676	-0.03636
2	1	-0.029268	0.13837
3	1	-0.038966	-0.46204
4	1	-0.030692	1.49282
5	1	0.072603	-0.45440
6	1	0.006180	-0.20260
7	1	0.003496	-1.23283
8	1	-0.060192	-1.23015
9	1	0.000459	-0.22706
10	1	0.003055	-0.29626
11	2	-0.013200	0.60479
12	2	0.029775	0.41554
13	2	0.056825	1.91236
14	2	0.068912	0.52660
15	2	0.012719	1.01332
16	2	0.070696	1.96640
17	2	0.050805	1.25887
18	2	0.001324	0.44560
19	2	0.034217	1.41904
20	2	0.011062	0.84257
21	3	-0.013171	-2.21985
22	3	-0.061241	-0.38139
23	3	-0.049141	-1.07137
24	3	0.004792	-0.09484
25	3	-0.060956	-0.47096
26	3	0.039905	-0.50615
27	3	0.012249	-0.61821
28	3	-0.026865	-0.91949
29	3	-0.050676	-0.87232
30	3	-0.006031	-0.74000

Appendix F

ANOVA Output

Table 30. SAS ANOVA output from retained PCA Principle Components for French Broad/Pigeon Brook Trout Populations.

Dependent Variable: spca2

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	18	0.29961570	0.01664532	13.81	<.0001
Error	172	0.20728884	0.00120517		
Corrected Total	190	0.50690455			

R-Square 0.591069
 Coeff Var -66306653
 Root MSE 0.034716
 spca2 Mean -0.000000

Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	18	0.29961570	0.01664532	13.81	<.0001

Dependent Variable: PC1

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	18	83.1994034	4.6221891	7.44	<.0001
Error	172	106.8005959	0.6209337		
Corrected Total	190	189.9999993			

R-Square 0.437892
 Coeff Var 1505067507
 Root MSE 0.787993
 PC1 Mean 5.2356E-8

Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	18	83.19940343	4.62218908	7.44	<.0001

Table 31. SAS ANOVA output from retained PCA Principle Components for French Broad/Pigeon Brook Trout Grouped Elevation Populations.

Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	4	6.19317130	1.54829283	1.57	0.1849

Dependent Variable: spca2

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	4	0.09379618	0.02344905	11.72	<.0001
Error	186	0.37229144	0.00200157		
Corrected Total	190	0.46608762			

R-Square	Coeff Var	Root MSE	spca2 Mean
0.201242	28483750	0.044739	1.57068E-7

Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	4	0.09379618	0.02344905	11.72	<.0001

Dependent Variable: PC1

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	4	6.1931713	1.5482928	1.57	0.1849
Error	186	183.8068280	0.9882088		
Corrected Total	190	189.9999993			

R-Square	Coeff Var	Root MSE	PC1 Mean
0.032596	1898705965	0.994087	5.2356E-8

Table 32. SAS ANOVA output from retained PCA Principle Components for French Broad/Pigeon Brook Trout Grouped Aspect Populations.

Dependent Variable: spca2

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	3	0.01390878	0.00463626	1.93	0.1267
Error	187	0.44992770	0.00240603		
Corrected Total	190	0.46383648			

R-Square	Coeff Var	Root MSE	spca2 Mean
0.029986	21787905	0.049051	2.25131E-7

Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	3	0.01390878	0.00463626	1.93	0.1267

Dependent Variable: PC1

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	3	2.9819548	0.9939849	0.99	0.3969
Error	187	187.0180444	1.0000965		
Corrected Total	190	189.9999993			

R-Square	Coeff Var	Root MSE	PC1 Mean
0.015694	1910092161	1.000048	5.2356E-8

Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	3	2.98195485	0.99398495	0.99	0.3969

Table 33. SAS ANOVA output from retained PCA Principle Components for French Broad/Pigeon Brook Trout Parsed Sex Populations.

Dependent Variable: spca2

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	1	0.03344790	0.03344790	14.12	0.0002
Error	189	0.44780614	0.00236934		
Corrected Total	190	0.48125405			

	R-Square	Coeff Var	Root MSE	spca2 Mean	
	0.069502	3.38347E17	0.048676	1.4386E-17	
Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	1	0.03344790	0.03344790	14.12	0.0002

Dependent Variable: PC1

		Sum of			
	DF	Squares	Mean Square	F Value	Pr > F
Model	1	0.1841147	0.1841147	0.18	0.6690
Error	189	189.8158622	1.0043167		
Corrected Total	190	189.9999769			

	R-Square	Coeff Var	Root MSE	PC1 Mean	
	0.000969	957059021	1.002156	1.04712E-7	
Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	1	0.18411468	0.18411468	0.18	0.6690

Table 34. SAS ANOVA output from retained PCA Principle Components for Winding Stair and Source Populations of Brook Trout.

Corrected Total 29 0.04698751

Dependent Variable: spca2

						R-Square	Coeff Var	Root MSE	spca2 Mean	
						0.343790	-101379918	0.033793	-0.000000	
Source	DF	Sum of Squares	Mean Square	F Value	Pr > F					
Model	2	0.01615384	0.00807692	7.07	0.0034	Source	DF	Type I SS	Mean Square	F Value
Error	27	0.03083366	0.00114199			grp	2	0.01615384	0.00807692	7.07
										0.0034

Dependent Variable: PC1

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	2	17.68929517	8.84464759	21.11	<.0001
Error	27	11.31068719	0.41891434		
Corrected Total	29	28.99998236			

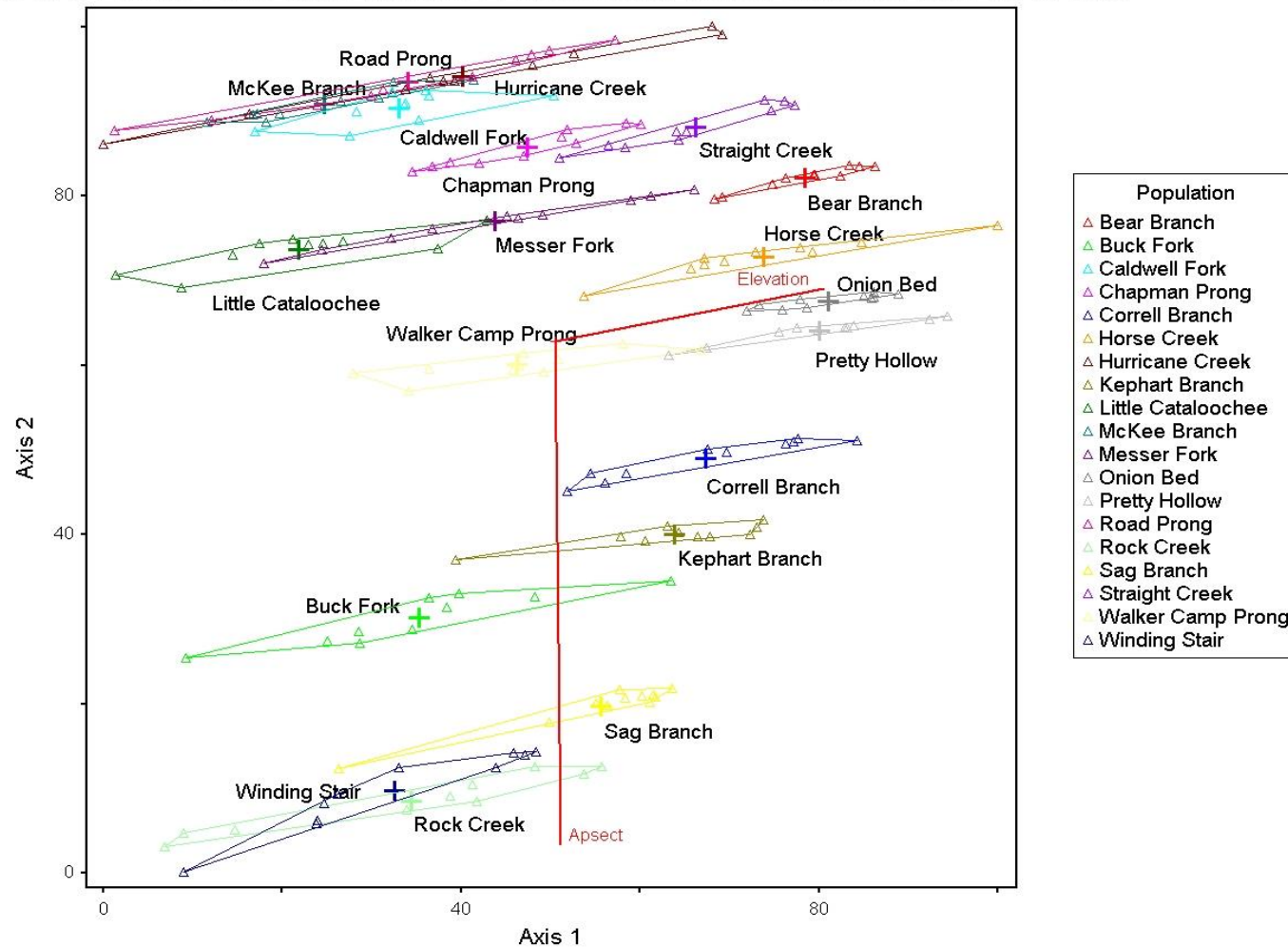
R-Square 0.609976
 Coeff Var -2.4985E18
 Root MSE 0.647236
 PC1 Mean -0.000000

Source	DF	Type I SS	Mean Square	F Value	Pr > F
grp	2	17.68929517	8.84464759	21.11	<.0001

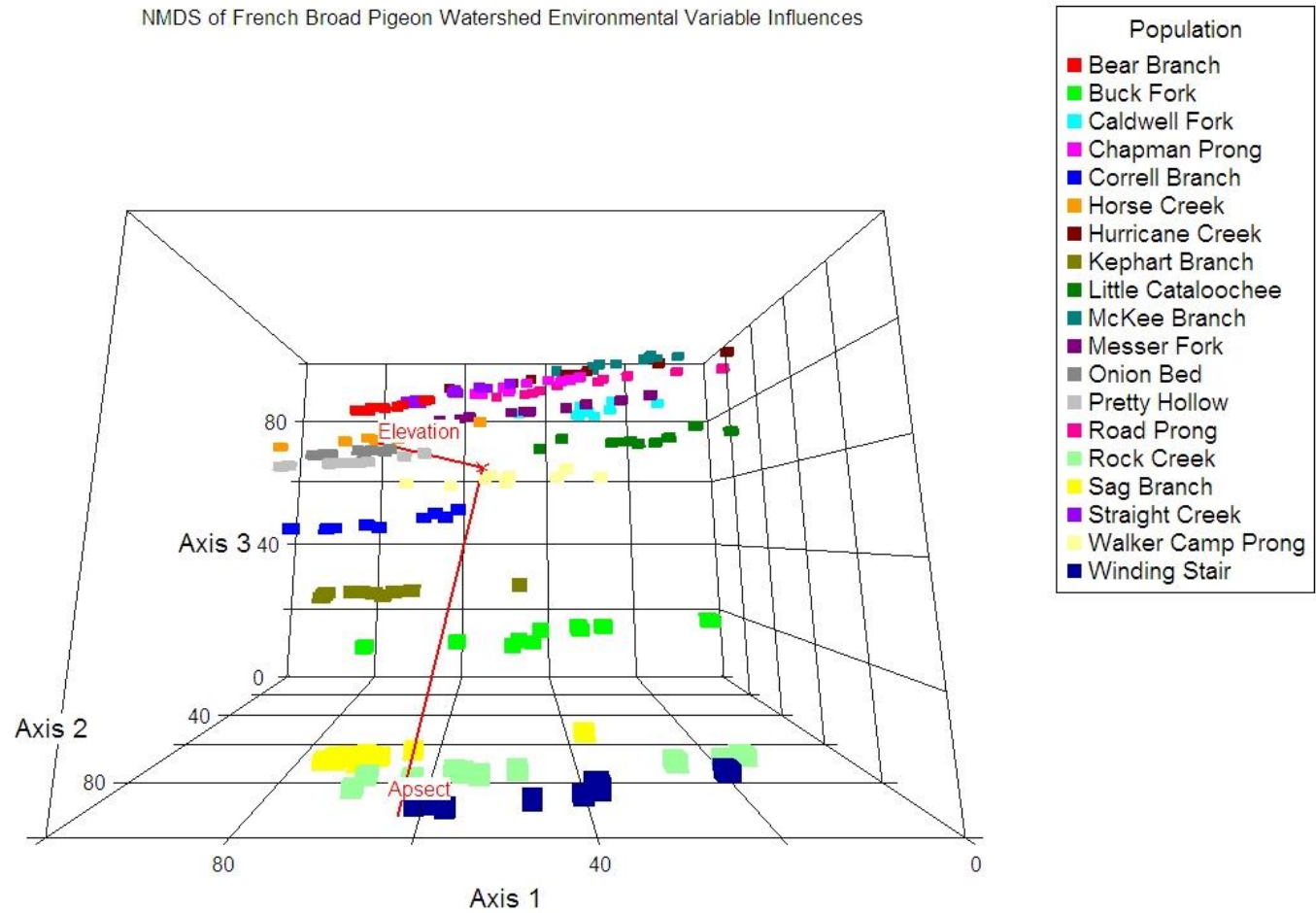
Appendix G

Nonmetric Multidimensional Scaling (NMDS)

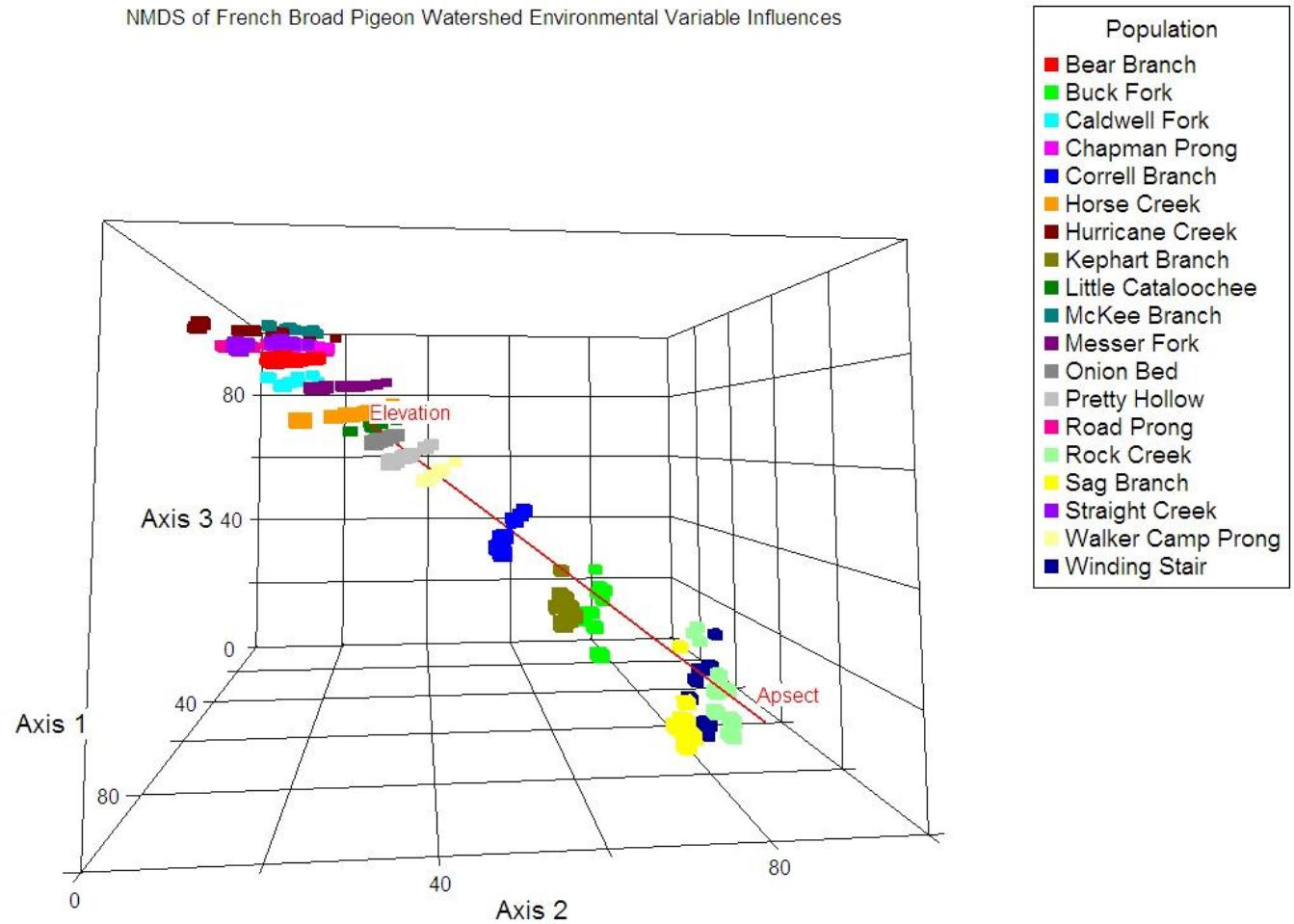
IMDS of French Broad Pigeon Watershed Environmental Variable Influences Upon Brook Trout



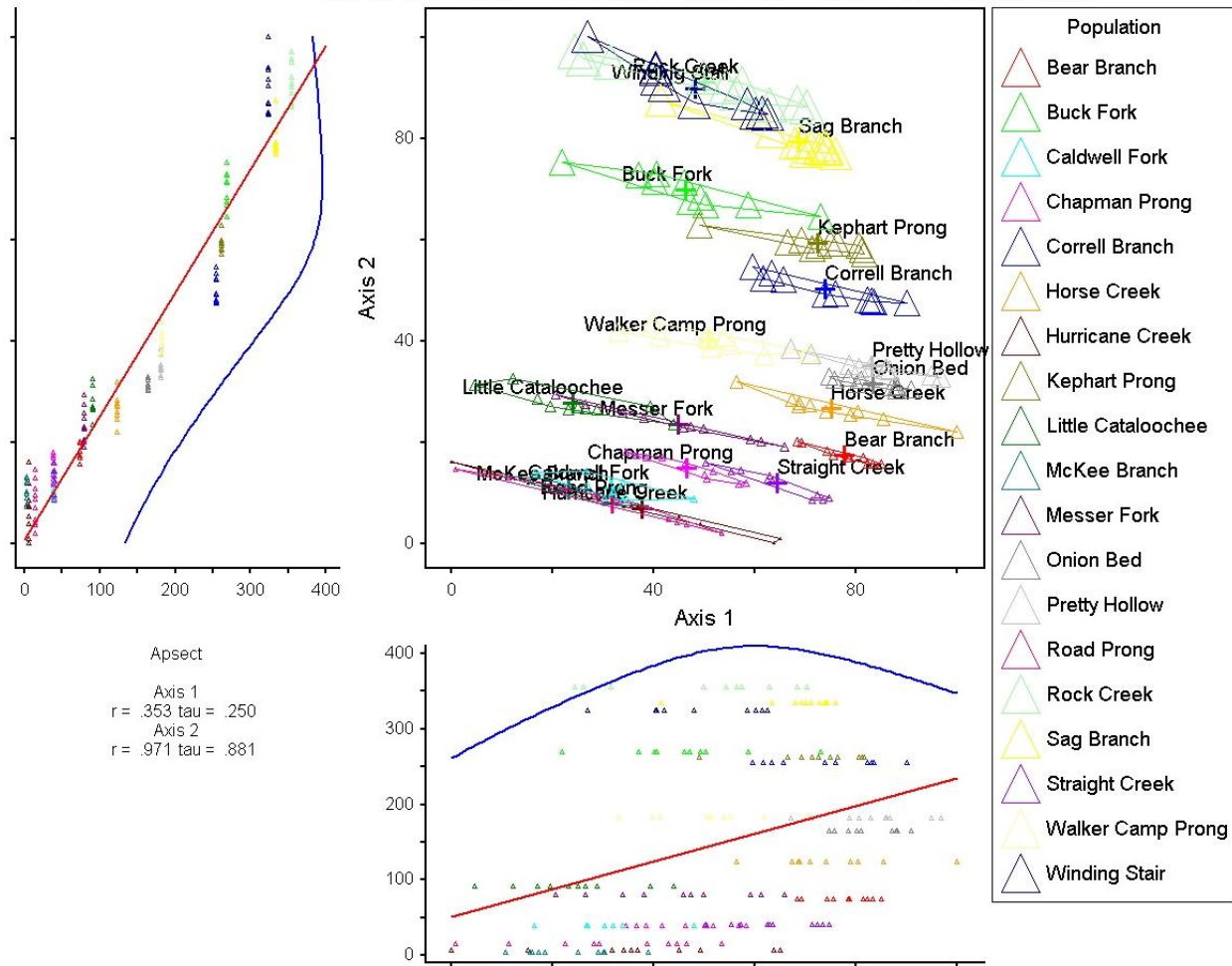
NMDS of French Broad Pigeon Watershed Environmental Variable Influences



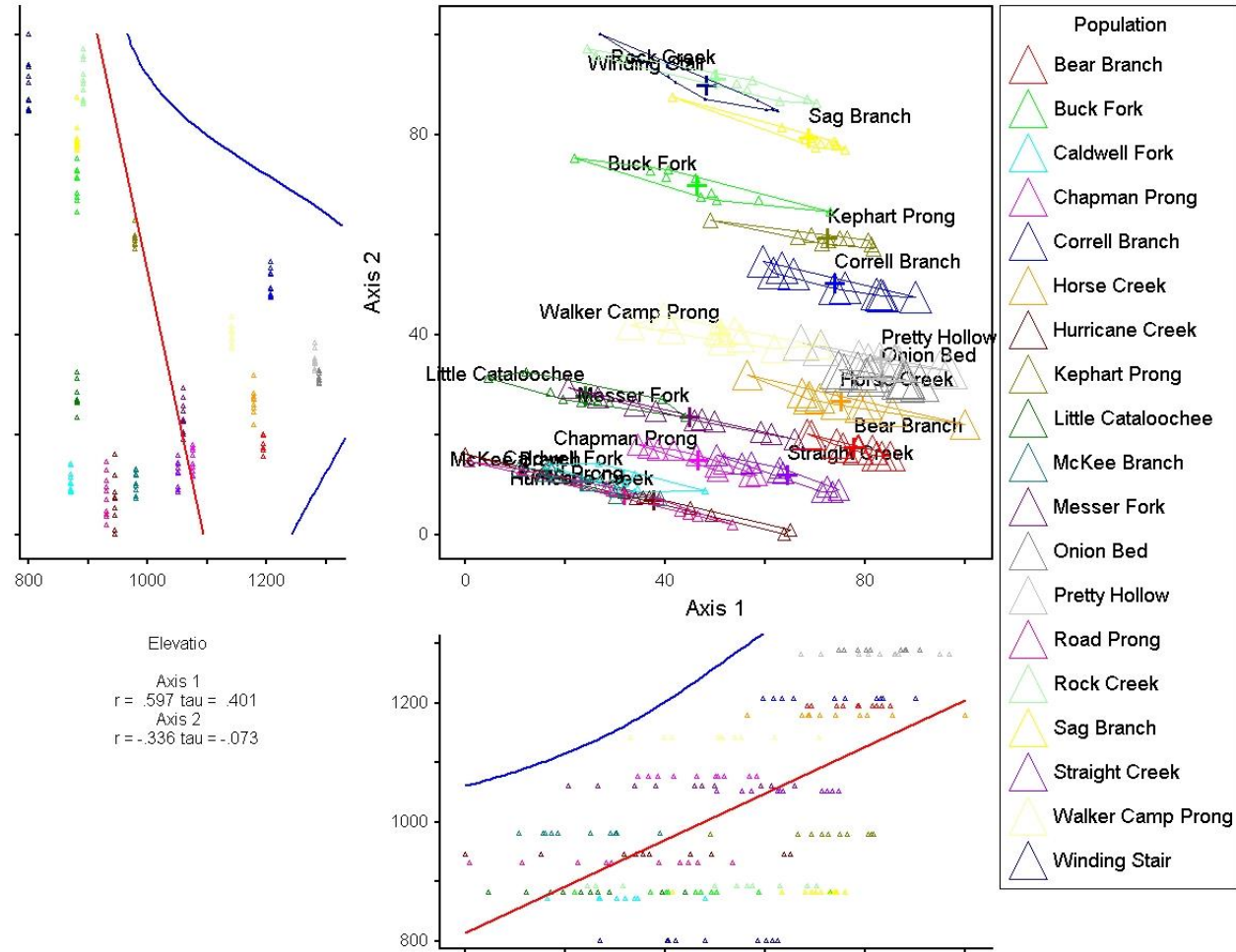
NMDS of French Broad Pigeon Watershed Environmental Variable Influences



NMDS of French Broad Pigeon Watershed Apect Effect Brook Trout



NMDS of French Broad Pigeon Watershed Elevation Effect Brook Trout



Appendix H

Cladistic Tree Derived from Morphometric and Meristic Characters

Cladogram of French Broad Pigeon Watershed Brook Trout with Sister & Outgroup

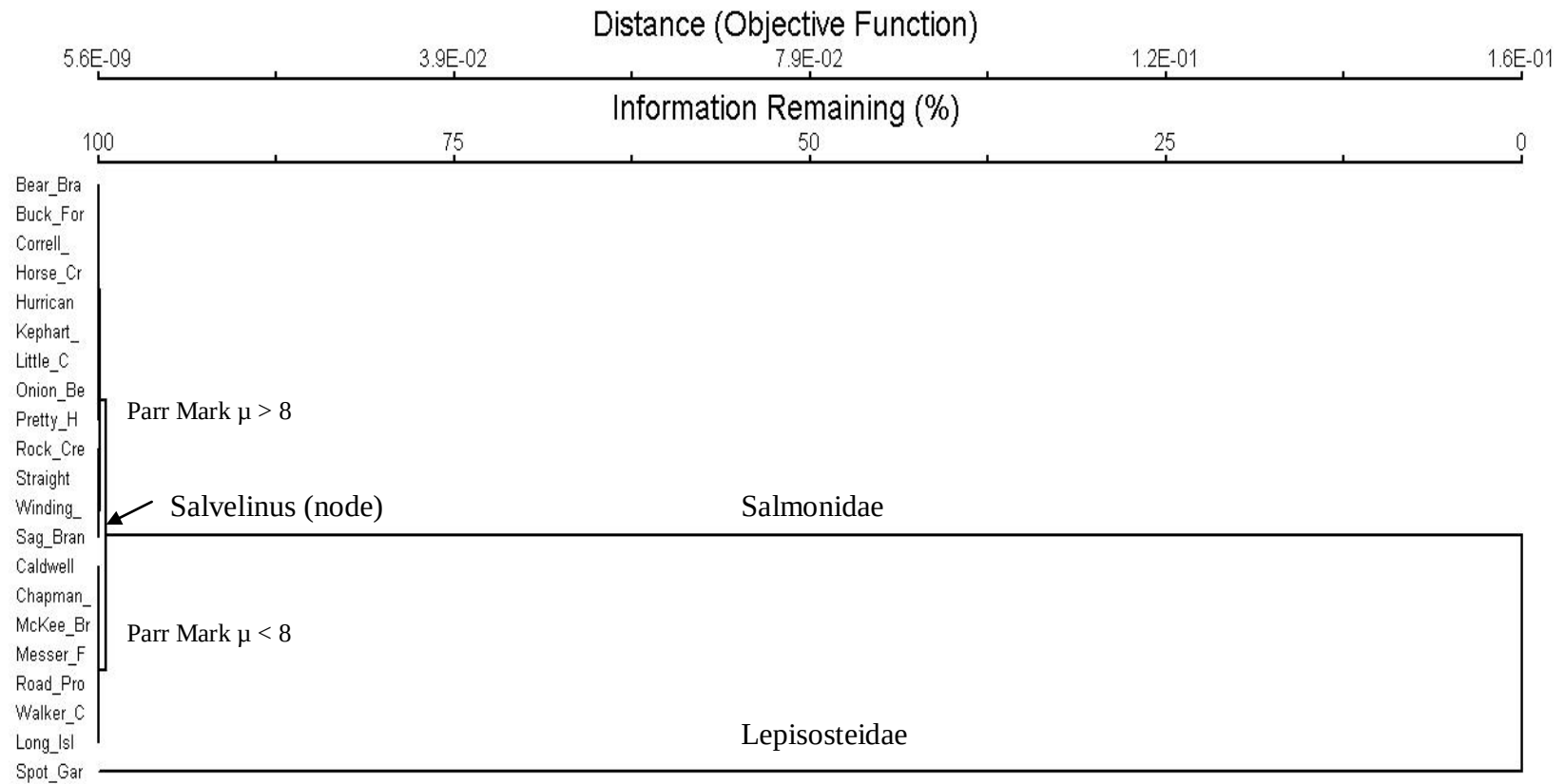


Figure 29. French Broad/Pigeon Watershed Brook Trout Headwater Cladogram used to Illustrate Phylogenetic Relatedness with Long Island, NY Brook Trout added as sister-group and Spotted Gar (*Lepisosteus oculatus*) added to function as an out-group.

Cladogram of French Broad Pigeon Watershed Brook Trout Minimized Distance Function

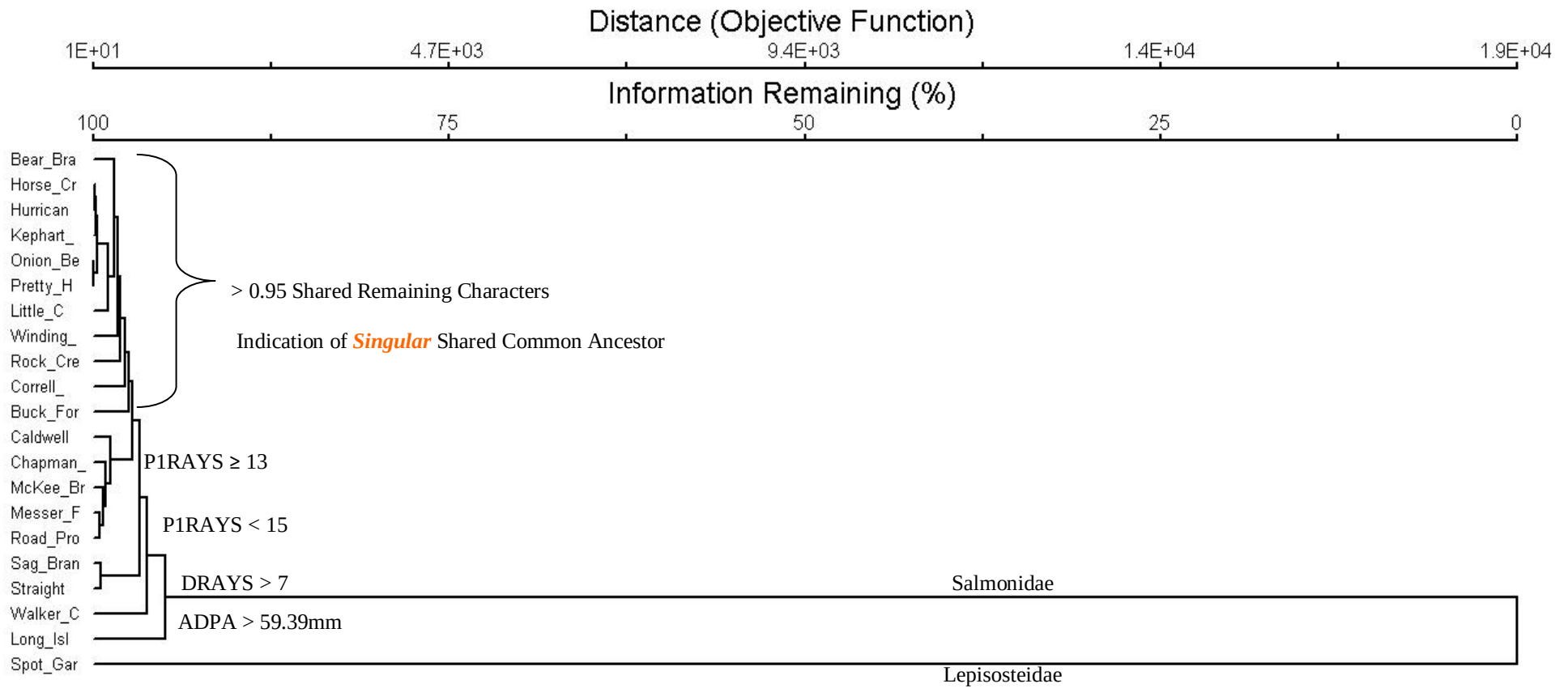


Figure 30. French Broad/Pigeon Watershed Brook Trout Headwater Cladogram used to Illustrate Phylogenetic Relatedness highlighted by synapamorphic character node breaks with Long Island, NY Brook Trout added as sister-group and Spotted Gar (*Lepisosteus oculatus*) added to function as an out-group.

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