

Proceedings

Exploring differences between fine-spotted and large-spotted Yellowstone cutthroat trout

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Upper Snake River Cutthroats

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Preface

The historic range of the Yellowstone cutthroat trout *Oncorhynchus clarkii bouvieri* consists of the Snake River drainage upstream of Shoshone Falls (near the present day city of Twin Falls, Idaho, Fig. 1) and the Yellowstone River drainage downstream to the Tongue River. A morphologically distinct cutthroat trout, the Snake River fine-spotted cutthroat trout, is found within that range, specifically in the Snake River and its tributaries between Jackson Lake and Palisades Reservoir. The downstream extent of the fine-spotted cutthroat trout prior to the construction of Palisades Reservoir in the mid-1950s is not known with certainty; however, the large-spotted variety is native to the Snake River and its tributaries from the Henry's Fork downstream, including the entire Henry's Fork drainage. The historic spatial distribution of cutthroat trout was determined by drainage basin evolution and climatic changes, most notably warming and drying of the climate in western North America over the past 10,000 years. These processes have acted to isolate cutthroat trout into basin-scale geographic units, which have generally been used as the basis for taxonomic distinction among cutthroat trout subspecies. However, the consideration of the fine-spotted Snake River cutthroat trout as taxonomically distinct from the Yellowstone subspecies is based primarily on morphology, in particular the much smaller size and larger numbers of spots in the fine-spotted variety, rather than on geographic isolation.

Behnke (2002) lists a 1970 edition of the *Wyoming Game and Fish Bulletin: Wyoming Fishes* as the first publication of which he was aware that distinguished between the Yellowstone (large-spotted) and Snake River (fine-spotted) cutthroat trout. Because of its importance as a sport fish and its apparent ability to remain morphologically distinct in sympatry with the large-spotted variety, the fine-spotted cutthroat trout has received a great deal of attention from researchers, managers, and anglers since the 1970s. Kiefling (1978) published the first definitive work on the biology and management of the Snake River cutthroat, which he called *Salmo clarki* spp. In the first edition of his angling classic, *Trout*, Schweibert (1978) referred to the Snake River cutthroat as *Salmo clarki carmichaeli*, after a Jackson Hole fly fishing shop owner. The subspecies name *carmichaeli* is still used by some authors (e.g., Benson et al. 2004). Trotter (1987) and Behnke (1992) list the Snake River fine-spotted cutthroat trout as a distinct subspecies, but neither assigned a Latin subspecies name to the subspecies. Citing Behnke's (1992) description of the fine-spotted Snake River cutthroat trout, Montgomery (1995) listed the fish as a distinct subspecies with the name *Oncorhynchus clarki behnkei*. Behnke (2002) subsequently adopted the subspecies name *behnkei* for the Snake River finespotted cutthroat trout. Without quibbling over whether correct nomenclatural procedure was followed by the various authors in establishing either of the proposed subspecies names (*carmichaeli* and *behnkei*), it is clear that more than a few scientists, managers, and anglers consider the Snake River fine-spotted cutthroat as a distinct subspecies of cutthroat trout. On the other hand, some federal natural resource agencies do not consider the fine-spotted variety as distinct subspecies (e.g., Duff 1996, USFWS 2006), which has potentially important consequences for cutthroat trout management.

We therefore convened this symposium to address the questions: 1) Are differences between fine-spotted and large-spotted Yellowstone cutthroat trout sufficient for them to be considered separate subspecies? and 2) Is management dependent upon designation of one versus two subspecies?

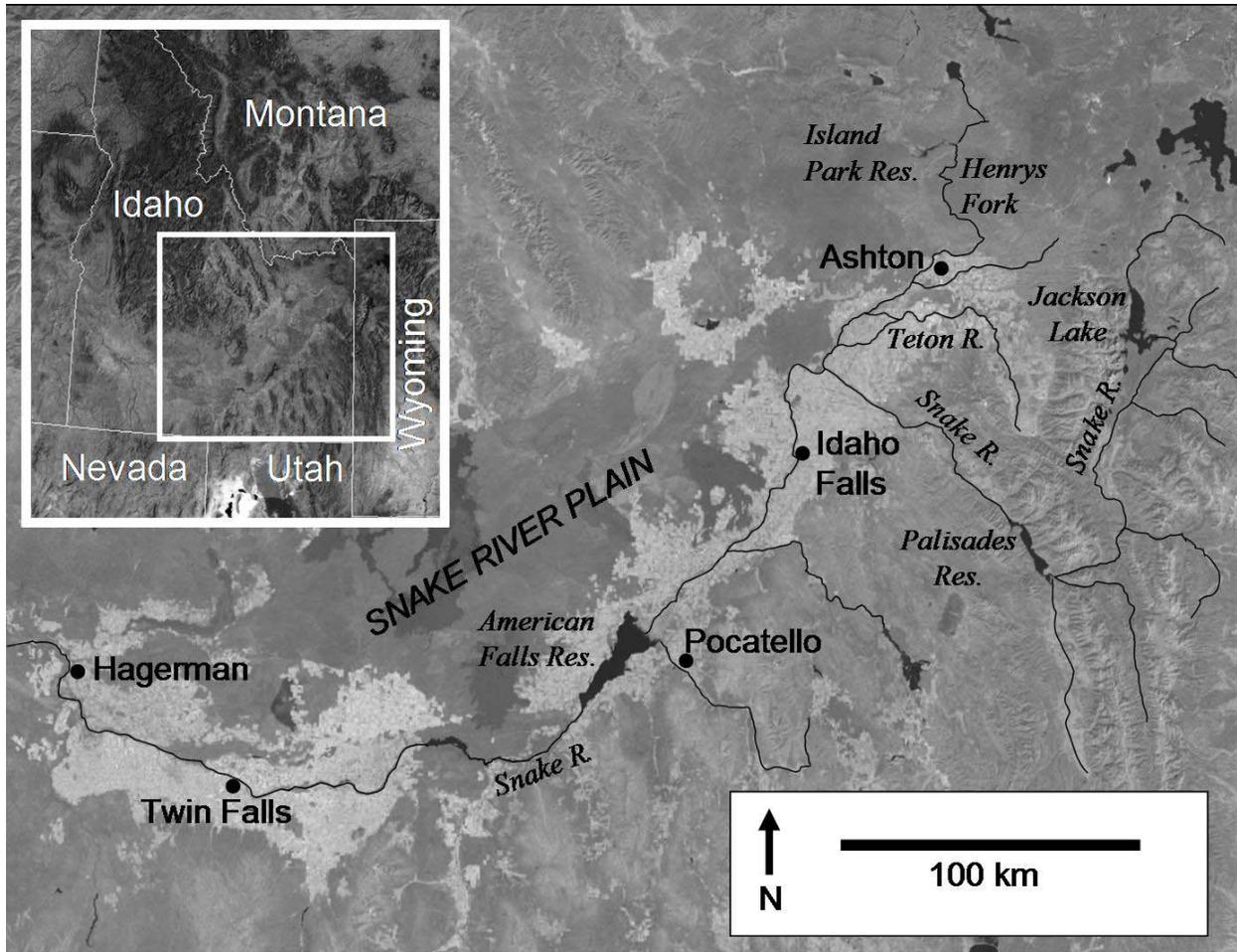


Figure 1. Upper Snake River.

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The Yellowstone Hotspot, drainage evolution, and fish distribution in the Greater Yellowstone Area

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Physical factors affecting historic and modern fish distribution in the Greater Yellowstone area (GYA) include changes in stream courses, stream altitudes, and stream gradients, as well as orographically enhanced precipitation patterns and glaciation. Three surface geologic processes associated with the track of the Yellowstone hotspot are volcanism, faulting, and uplift. The history of these processes is well explained by southwest migration of the North American Plate above a thermal mantle plume over the last 16 million years. The Yellowstone volcanic field started about 2.1 million years ago. The next older field along the hotspot track centered north of Idaho Falls and was active from about 6.6 to 4.5 million years ago. Northeast migrating uplift on the leading margin and subsidence on the trailing margin of the hotspot has had the largest effect on drainages. Uplift of the Yellowstone area is estimated to be about 3000 feet over about the last 5 million years. Also reflecting uplift is the radial drainage pattern of the GYA that centers on Yellowstone National Park. Biographic and mineral indicators suggest the Continental Divide and other divides along the hotspot track have progressively migrated northeastward compatible with a mantle plume driving the hotspot process. The high elevation of the GYA combined with the atmospheric moisture conduit provided by the lowland trough of the adjacent eastern Snake River Plain (hotspot track) result in large orographic snow accumulations and enhanced stream flow in the GYA.

About 140,000 years ago during the Bull Lake glaciation, much of the GYA and essentially all of Yellowstone National Park, Jackson Hole, and the West Yellowstone basin were covered by ice. Later, 15,000 to 20,000 years ago during the Pinedale Glaciation, nearly as much of the GYA was covered by glacial ice, although outlet glaciers were shorter to the west, southwest, and south. Habitability of streams by trout would have been limited by presence of glacial meltwater (glacial “milk”) downstream from glaciers. During and after deglaciation in the last 12,000-15,000 years, fish re-colonized this glaciated area to produce the historic pattern of fish distribution. Colonization of Yellowstone Lake by cutthroat trout probably occurred from the Snake River drainage northward by way of Two Ocean Pass

Evolution, Distribution and Historical Management of Yellowstone Cutthroat Trout

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Environmental factors, determined primarily by geomorphology and climate, have driven the evolution of *Oncorhynchus* in the Greater Yellowstone/Great Basin region of North America. The fossil record shows evidence of *Salvelinus* presence in the region as early as the mid-Miocene (about 10 million years ago), pre-dating *Oncorhynchus*. Recent work (see Shiozawa below) indicates that the cutthroat trout (*O. clarki*) lineage diverged from the rainbow trout (*O. mykiss*) lineage about 8 million years ago, with subsequent major divergences occurring between groups (Bonneville, Yellowstone, Westslope, Lahontan) 2 and 4 million years ago and within

these groups over the past 1 million years or less. Extinction due to climatic changes has driven this evolution more than has speciation; trout persisted in high-elevation streams during warm, dry periods and in large, low-elevation lakes during wet, cool periods. Over a continuum of decreasing temporal and spatial scales, environmental conditions have differentiated *Oncorhynchus* into species, *Oncorhynchus clarki* into subspecies, subspecies into metapopulations, and metapopulations into populations. As evidenced by differences in spawn timing, size and other life history parameters in Yellowstone Lake cutthroat trout, this differentiation can occur on very small spatial scales due to subtle environmental differences such as drainage area and aspect among individual spawning tributaries. Differentiation of fine- and large-spotted cutthroat trout in the Snake River drainage falls along the differentiation continuum somewhere in the subspecies to metapopulation range. Since European settlement of the Yellowstone region, the historic distribution of cutthroat trout and its various subgroups has been greatly altered by land, water, and fisheries management activities, including legal and illicit introductions of nonnative fish and other aquatic species.

What is a subspecies? An introduction to subspecies and Evolutionarily Significant Unit definitions (with an emphasis on genetic criteria)

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“Subspecies” is a taxonomic term used to define geographically isolated, morphologically distinct groups of populations within a species and was not originally defined for conservation or management purposes. Despite a well-defined procedure (the International Code for Zoological Nomenclature) for naming subspecies, there is no “international code of zoological taxonomy” for defining them. One criterion that has been proposed for defining a subspecies based on morphological characteristics is the “75% rule,” which considers a population as a distinct subspecies if 75% of the population lies outside 99% of the range of all other populations within the species for a given defining morphological character or set of characters. This definition has been sporadically applied in the literature and does not assess reproductive isolation or place any value on the defining character(s) with respect to phylogenetic history or evolutionary importance. A more recently proposed definition based on phylogeny and geography requires that members of a subspecies share a unique geographic locale, a set of phylogenetically concordant phenotypic traits, a unique natural history relative to other subspecies, and an exclusive common ancestry. These criteria emphasize reproductive isolation and adaptive genetic variation. From a conservation and management perspective, however, a more relevant question than “what is a subspecies?” is “what is an evolutionarily significant unit (ESU)?,” because the latter is used to define distinct population segments for protection under the Endangered Species Act. The most well known definition of an ESU is a population or group of populations that is substantially reproductively isolated from other conspecific population units and represents an important component of the evolutionary legacy of the species. Hence, “ESU” and “subspecies” are very similar concepts, and usage is determined primarily by context, with “subspecies” being used in the taxonomic context and “ESU” in the legal/management context. Although genetic characters by themselves do not denote evolutionary significance, they are useful as indicators of how long populations have been reproductively isolated. Genetic analysis has been used recently to inform taxonomic distinctions at the subspecies level in a variety of

organisms, including some involved in high-profile conservation cases such as the northern spotted owl and jumping mouse. Subspecific classification will always be difficult and subjective to some degree, but the phylogeographic definition provides a framework for considering subspecies designation based on evolution of the subspecies relative to that of other components of the species.

Status and Conservation of Yellowstone Cutthroat Trout in Montana

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Westslope cutthroat trout (*O. c. lewisi*) and large-spotted Yellowstone cutthroat trout are native to Montana. Of the 12,100 stream km currently occupied by Yellowstone cutthroat trout, 2,195 km lie in Montana, all within the Yellowstone River drainage. The goal of interagency cutthroat trout conservation Memorandum of Understanding (MOU) in Montana is to conserve the two native cutthroat trout subspecies in the state by protecting existing populations and ensuring their long-term persistence within their historical ranges. Objectives are to secure and/or enhance all designated conservation populations, continue surveys to find additional populations, restore and expand populations, monitor distribution and abundance, and conduct outreach, collaborative, and fundraising activities to accomplish these objectives. “Core” populations are defined as those with no evidence of genetic introgression, and “conservation” populations are defined as those that may have some introgression but are deemed to have a high conservation value. All other cutthroat trout or hybrid populations are defined as “recreational.” There are currently 29 core and 225 conservation populations of Yellowstone cutthroat trout in Montana. Of particular importance in cutthroat conservation and restoration is careful consideration of whether to isolate or connect populations. Isolation of a population within its aquatic habitat provides short-term protection from introgression, competition, and disease, but places the isolated population at risk of extinction over the long-term. Connectivity allows metapopulation processes to operate, but increases risk of introgression, competition, and disease. In some cases, such as that of rainbow and cutthroat trout in spawning tributaries of the Yellowstone River, spatial isolation may not be required to avoid introgression because of temporal segregation of spawners. In other cases, spatial isolation may be required to protect core and conservation populations.

Historical and Current Influences of Genetic Population Structure in Yellowstone Cutthroat Trout

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We used mitochondrial and microsatellite DNA analyses to assess factors that shape genetic diversity in Yellowstone cutthroat trout. Mitochondrial DNA is maternally inherited, has a uniform mutation rate of about 1% per million years, and is useful for evaluating evolutionary

history and lineages over long time scales. Microsatellite DNA is bi-parentally inherited, has a high mutation rate, can discriminate among individuals, and is useful for quantifying gene flow, identifying sources of immigrants, and for assessing effects of environmental changes (e.g., migration barriers) over the past 100 years. Mitochondrial DNA was obtained from cutthroat trout collected from 48 sites in Yellowstone Lake, Bear Lake, and streams in the Snake, Beaver-Camas and Bear watersheds. Of 15 haplotypes observed throughout the range of the sub-species, one haplotype was present in 32 of the 48 sites and nine of the 15 haplotypes were observed at frequencies of 5% or greater. The mitochondrial DNA results showed a high degree of diversity in Yellowstone cutthroat trout across the upper Snake basin. The geographic discontinuities in the distribution of haplotypes indicated that many of the drainages have been isolated from one another for a long period of time. The mtDNA results are consistent with the geologic history. The Bonneville cutthroat clade diverged from the Yellowstone clade by about 1.5% to 1.8%, but the Bear Lake and Bear River fish clustered in the Yellowstone clade. Geologic history shows that the Bear River was a tributary to the Snake River until about 500,000 years ago, at which time its course changed to flow into the Bonneville basin. Furthermore, haplotypes from both clades were found in the Portneuf River, consistent with exchange between the Bonneville and Portneuf drainages as a result of the Bonneville flood about 14,000 years ago. Almost all of the Wyoming samples, which included individuals from both the Snake and Yellowstone drainages, show much lower levels of variation, and a continuous pattern of haplotype distribution, consistent with recolonization of higher elevation streams following glacial retreat 10,000 to 14,000 years ago. Microsatellite DNA was also collected from 45 populations distributed among 11 major drainages in the upper Snake River Basin. We found strong partitioning of populations at the drainage level, and a wide range of genetic differentiation within drainages. For example, each of the seven populations sampled in the Portneuf drainage comprised of genetically distinct population units, whereas all eight populations sampled in the Salt River drainage fell within the same population unit. At the drainage scale, genetic differentiation was not a function of geographic distance but was more reflective of habitat conditions. We conclude that present-day genetic variation in Yellowstone cutthroat trout is a product of both geologic history (volcanism, drainage basin changes, and glaciation) and modern environmental habitat conditions (habitat alterations, migration barriers).

Evolution, distribution and phylogeny of cutthroat trout in Utah and Wyoming

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The evolutionary history of cutthroat trout in eastern Idaho, western Wyoming, and northern Utah is strongly influenced by geologic history. The capture of the Bear River into the Bonneville Basin has been considered to have been instrumental in the introduction of cutthroat trout into the Bonneville Basin. The Bear River was a tributary of the Snake River until the late Pleistocene, when basalt flows in the Soda Springs area dammed the Bear River and formed Lake Thatcher. Lake Thatcher eventually drained into the Bonneville Basin. This is hypothesized to have allowed the dispersal of Bear River/upper Snake River fish throughout most of western Utah. The subsequent Bonneville flood also provided a temporary connection

between the Bonneville Basin and the Snake River. Concurrent glacial recession allowed recolonization of streams on the Yellowstone Plateau and adjacent mountains.

We examined mitochondrial DNA from 61 populations of cutthroat trout from the Yellowstone, Snake, and Bear rivers and the Bonneville Basin in Utah and Wyoming. Sequence divergence was 0.4% between Yellowstone cutthroat trout and Bonneville cutthroat trout from the Bear River drainage of the Bonneville Basin. However sequence divergence between the Bonneville cutthroat trout in the Bear River drainage and those from the main Bonneville Basin was 2.2% and the sequence divergence between the main basin Bonneville cutthroat trout and Yellowstone cutthroat trout was 2.1%. Other cutthroat trout subspecies differed from each other by approximately 2% to 3% sequence divergence. All cutthroat trout subspecies diverged from rainbow trout by 7.5% to 8.5%.

Two dominant Yellowstone cutthroat trout haplotypes occurred in both the Yellowstone and Snake River drainages. The first of these occurred with 43% frequency in the Yellowstone River Basin and 3% frequency in the upper Snake River Basin. The second occurred with 25% frequency in the Yellowstone River Basin and 48% frequency in the Snake River Basin. Twenty-four other minor, but closely related, Yellowstone cutthroat trout haplotypes were found in this study. Of those, 12 were occurred only in the Yellowstone River Drainage and 10 were only found in the Snake River drainage. The remaining two were shared between the two basins.

Three additional haplotypes were also unique to the Snake River Drainage, occurring in Jackson Lake tributaries at frequencies of 6% to 8%, in North Horse Creek (Hoback Junction) at a frequency of 11.5%, in a Greys River tributary at 26.1%, and in a Salt River tributary at 3.7%. In a TCS phylogenetic network, these three haplotypes were most closely associated with, and most likely derived from, haplotypes common in the Bear River Drainage of the Bonneville Basin. The main Bonneville Basin Bonneville cutthroat trout were too divergent to connect with the Yellowstone River-Snake River-Bear River TCS network.

We conclude that two mitochondrial DNA lineages exist in the Snake River. The dominant mitochondrial lineage in the Snake River system is shared with the Yellowstone River drainage, but the TCS network gives strong evidence of a founder effect. This is related to colonization of the Yellowstone River Drainage from the Snake River after the recession of the Pinedale glaciation. Fixation indices also show significant genetic structure between the Snake River and Yellowstone River drainages. The minor mitochondrial lineage reflects relationships between the cutthroat trout in the Snake River and Bear River while the Bear River was still connected to the Snake River system. The main basin Bonneville cutthroat trout are separated from the Bear River Bonneville cutthroat trout by sequence divergences equivalent to those seen between subspecies.

Morphological differences among Yellowstone cutthroat trout and its close relatives in the Greater Yellowstone region

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Although cutthroat trout have been recognized as a complex of distinct species, very few studies have provided quantitative evidence that morphological differences exist between them. We conducted a study of Yellowstone cutthroat trout to determine if there is any evidence that separates fine-spotted Yellowstone cutthroat trout from the upper Snake River and Yellowstone cutthroat trout found in other areas of the species range. We compared a suite of 39 external morphological characteristics measured from digital photographs of 1244 individual trout collected from 25 sampling localities in southeastern Idaho or western Wyoming. For comparative purposes, we also tested the power of our morphological measurements to discriminate closely and more distantly related salmonids species by comparing Yellowstone cutthroat to Bonneville cutthroat trout and to rainbow trout as well as hybrid individuals of Yellowstone cutthroat trout and rainbow trout. Our data indicate that morphological measures provide good discriminating ability of some the groups we compared. We suggest that morphological characteristics measured from digital photographs may be a useful tool for biologists in documenting important variation in fish species of conservation concern.

Patterns of landscape distribution and morphological and genetic variability in cutthroat trout of the Snake River headwaters

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We used a landscape scale approach to facilitate the synthesis of geomorphic, ecological, and genetic information regarding the distribution and organization of Yellowstone cutthroat trout, *Oncorhynchus clarkii bouvieri*, and finespotted Snake River cutthroat trout, *Oncorhynchus clarkii* subspecies, in the Snake River headwaters of northwest Wyoming. Selection criteria allowed us to hierarchically analyze for morphological or geographic structuring from the basin scale, to the stream reach scale. Multivariate analyses of spotting patterns can discriminate between the large and fine-spotted morphotypes when assessing fish that represent the extremes, although enough overlap in spotting patterns exist within the respective morphotypes to confound any clear cut distinction. We were unable to genetically differentiate between the morphotypes using an 1,150 bp region of the ND2 mitochondrial genome. Genetic differences among drainages were apparent, and two distinct clades were present in the mtDNA dataset. Clade 1 haplotypes were more common in two northern geographic areas, and clade 2 haplotypes were more common in three southern areas. Morphological and genetic differences were observed in rainbow-cutthroat hybrids that distinguished them from cutthroat trout, and hybridization was limited. Further work is recommended using the existing samples and nuclear markers, combined with additional collections from the main stem Snake River.

Taxonomic and Genetic Considerations in the Context of Management and Conservation

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For proper management and conservation of biodiversity, the limitations of taxonomy and genetic data to define units of diversity should be understood. Significant and rapid divergences can come about in some populations resulting in different life histories and ecologies that are unrelated to taxonomy or degrees of genetic similarity. The preservation of intraspecific diversity produced by adaptive radiation is the basis for recognizing Evolutionarily Significant Units (or Distinct Population Segments) for listings under the Endangered Species Act.

Management Implications

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On August 18, 1998, the U.S. Fish and Wildlife Service (FWS) received a formal petition to list the Yellowstone cutthroat trout *Oncorhynchus clarkii bouvieri* (YCT) as a threatened “species.” In their petition, the petitioners considered the finespotted Snake River cutthroat trout to be a morphological form of YCT. Although Behnke (1992) considered the YCT and finespotted Snake River cutthroat trout distinct taxa (but the latter an unnamed subspecies), for purposes of the subsequent Endangered Species Act listing decision (*Federal Register* February 23, 2001) FWS followed the position taken in the petition and considered the YCT and finespotted Snake River cutthroat trout a single taxon, *O. c. bouvieri*. The FWS also stated at that time that our position did not represent the opinion of the Federal government with regard to the taxonomic validity of the finespotted Snake River cutthroat trout. Instead, such validation remained the responsibility of taxonomists, geneticists, and other qualified scientists. Subsequent litigation and a Court order compelled FWS to revisit its “not substantial” petition assessment in 2005. In the interim, Behnke (2002) referred the finespotted Snake River subspecies to a new taxon, *O. c. behnkei*. I will summarize the process followed by FWS in assessing the present taxonomic status of finespotted Snake River cutthroat trout in the context of our forthcoming listing decision, which will be detailed in a *Federal Register* notice in February 2006.

Editors’ note: The *Federal Register* notice of the FWS finding on the Yellowstone cutthroat trout listing petition appeared on February 21, 2006. The finding explicitly stated that the FWS considered the large- and fine-spotted form as a single entity, as petitioned. The FWS found that listing of Yellowstone cutthroat trout as either threatened or as endangered was not warranted.

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The Intermountain Region of the Forest Service manages aquatic habitat for six cutthroat trout subspecies. These include Westslope, Yellowstone, Colorado River, Bonneville, Paiute and Lahontan cutthroat trout. As a land management agency, one of the goals of the Forest Service is to maintain quality cold-water habitat for all native and non-native trout species. In addition to

this goal, the Forest Service places a high priority on maintaining quality cold-water habitat for native cutthroat trout, regardless of the subspecies. The Forest Service has and will continue to work cooperatively with the States and other partners to conserve native cutthroat trout through habitat management, removal or construction of fish barriers, and cooperative implementation of piscicide projects for non-native trout removal.

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The Snake River watershed is the third largest in Yellowstone National Park. Historically, Yellowstone cutthroat trout (*Oncorhynchus clarkii bouvieri*), Snake River finespotted cutthroat trout (*O. clarkii behnkei*), and several other native fish species occupied the main stem river and its tributaries. Much of this basin has not been previously surveyed because of its remote location and difficult access to pre-selected study areas. In 2004 and 2005, National Park Service fisheries personnel conducted a native fishes inventory of the Snake River in order to describe the distribution of cutthroat trout subspecies in the remote headwaters region within the park. A primary objective of the survey is detection of areas where the two cutthroat trout subspecies may coexist. Equally important is documenting the relative abundance and distribution of other native fishes and potentially harmful nonnative species, including brown (*Salmo trutta*), brook (*Salvelinus fontinalis*), and lake (*Salvelinus namaycush*) trout in this watershed. Complete surveys of two of the most remote tributaries (Forest Creek and Sickle Creek) were accomplished in 2005.

The Forest Creek basin was most likely historically fishless due to the presence of a large waterfall located about 1 km upstream from the confluence with the Snake River main stem. This waterfall is estimated to be over 20 feet tall and undoubtedly acts as a permanent barrier to upstream fish passage. According to official Yellowstone Park records, about 100,000 eyed Yellowstone cutthroat trout eggs from the Yellowstone Lake hatchery were stocked annually into Forest Creek between 1939 and 1943. In 2005, the survey team captured only cutthroat trout in the upper sections of Forest Creek. The relatively high abundance and widespread distribution of cutthroat trout there suggests that the historical transplants of cutthroat trout from Yellowstone Lake were highly successful. Much of the Forest Creek watershed was intensely burned during the 1988 wildfires. The stream channel now contains abundant deadfall and other woody debris from the riparian areas and adjacent uplands. The cutthroat trout population sampled this year throughout Forest Creek contains numerous size groups representing several year classes. Abundance, distribution, and utilization of a variety of habitat types by the cutthroat trout all suggest that wildfire effects on this isolated population were negligible

Sickle Creek flows out of a steep canyon into the Snake River approximately halfway between the headwaters of the river and the South Entrance of the park. In 2004, two sections near the confluence with the Snake River were sampled. All but one of the cutthroat trout caught in the high gradient areas characterized by bedrock pools and unstable stream channel were less than

150 mm total length. In 2005, the inventory team completed the survey of Sickie Creek, which contains large low-gradient meadows in its headwater sections. Again, only cutthroat trout were caught with the electrofishing equipment, but their relative abundance in the upper reaches was one of the highest of any section yet sampled in the Snake River watershed. Most of the sampled trout had typical Yellowstone cutthroat trout spotting patterns; however, several fish were captured had small to intermediate-size spots distributed in a pattern similar to that characteristic of fine-spotted cutthroat trout. Several size classes of cutthroat trout were captured throughout the stream and young of the year were very abundant. The largest cutthroat was captured in the headwater section.

In 2005, we also were able to initiate an inventory of a large unnamed tributary that flows north from Big Game Ridge into the Snake River just slightly upstream from Crooked Creek. For mapping purposes, we unofficially titled this tributary Big Game Creek. This tributary appears to comprise a substantial amount of the total main stem flow. The cutthroat trout captured in the tributary typically were smaller than those caught in the nearby main stem section in 2004. The unnamed tributary is the only location where mottled sculpins were collected in 2005.

A secondary objective of the survey was to collect additional cutthroat trout from previously sampled streams in order to obtain an adequate number of tissue samples for stream-specific genetic analyses. With the collection of additional fish this year, we now have enough genetic samples to examine subspecific differences (if any) among the Heart River, Sickie Creek, Crooked Creek, and Forest Creek populations. Only Red Creek (which may have permanent barriers located near the mouth) and Basin Creek (which does have an occasional angler report of cutthroat trout) remain to be surveyed.

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Trout Unlimited is a non-profit conservation group dedicated to the protection and restoration of North America's salmonid fisheries and their watersheds. Our most significant contribution to the conservation of Yellowstone cutthroat trout is our Home Rivers Initiative on the South Fork of the Snake River. Initiated in early 2002, the South Fork Project is a collaborative multi-year effort to restore native cutthroat trout through rainbow trout harvest, tributary restoration and fish migration management, and ecologically-based flow management at Palisades Dam. Yellowstone and Snake River finespotted cutthroat trout face essentially the same threats and benefit from similar restoration efforts, so our conservation approach will not be affected by a one or two-subspecies designation.

We already recognize the Yellowstone and Snake River finespotted cutthroat trout as distinct forms based on their phenotypic, ecological, and geographic differences. Management and conservation of salmonids is often based on a unit other than "species" or "subspecies" (e.g., Geographic Management Unit, Distinct Population Segment, Evolutionarily Significant Unit, unique genetic strain), so their formal taxonomic designation is not our highest priority. Our expectation is that both forms persist and flourish in their historical range and evolutionary context, and we will continue to support conservation efforts with that goal.

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For management purposes, the Wyoming Game and Fish Department has always treated the Snake River and Yellowstone forms distinctly. Cutthroat trout in the Snake River drainage are managed as Snake River cutthroat trout and cutthroat trout in the Missouri River drainage are managed as Yellowstone cutthroat trout. Similarly, the culture system utilizes two distinct brood sources. Only Yellowstone cutthroat trout are stocked in historic Yellowstone cutthroat trout waters and only Snake River cutthroat trout are stocked in the Snake River drainage. Since the two forms cannot be genetically separated with existing methods, the next best option is to manage for phenotype. Managing the two phenotypic forms separately allows for future management options if the two forms are someday genetically separated.

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Idaho Department and Fish and Game manages Yellowstone cutthroat trout by geographic management units, in which fish within a given unit interact with each other more than with individuals from other units. These units are usually defined and managed at the watershed level. Therefore, Idaho Fish and Game does not manage Yellowstone cutthroat trout based on any taxonomic or morphological distinction and does not consider the fine- and large-spotted forms to be distinct subspecies.

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Montana does not have both morphs of Yellowstone cutthroat trout in its waters, only the large-spotted phenotype. Montana believes that these two phenotypes, fine- and large-spotted, do not warrant separate taxonomic categorization. Rather, Montana believes that the YCT's two phenotypes reflect the genetic variability present in the Yellowstone cutthroat trout (*Oncorhynchus clarkii bouvieri*). As such, management of *Oncorhynchus clarkii bouvieri* must conserve both of these morphs, including naturally sympatric populations, in order to fully conserve the genetic and morphological diversity remaining in the species.

Conclusion

Although no consensus was reached among the symposium participants on whether the fine-spotted Snake River cutthroat trout deserves recognition as a distinct subspecies, everyone agreed that the Snake River cutthroat trout represents an evolutionarily and ecologically important group of individuals that lies somewhere in the range of metapopulation to subspecies. The Snake River cutthroat trout therefore is deserving of management and protection aimed at preserving its distinct morphological and ecological features.