

this status review is not the definition of “species” under the Act, but rather, the scientific criteria used by professional zoologists and field biologists to taxonomically classify individuals, and populations of interbreeding individuals, as members of a particular species or subspecies.

The scientific criteria for describing and formally recognizing taxonomic species of fish are based almost entirely on morphological characters (Behnke 1992; Bond 1996; Moyle and Cech 1996). Indeed, the scientific basis for distinguishing rainbow trout and cutthroat trout (*O. clarki*) as distinct species are well-established differences in the number of scales in the lateral-line series, spotting patterns on the sides of the body, and the presence of: (a) Basibranchial teeth (*i.e.*, teeth on a series of bones behind the tongue and between the gills) and (b) a distinctive red or orange slash mark that occurs just below both sides of the lower jaw in cutthroat trout but not in rainbow trout (Miller 1950). Morphological differences, particularly external spotting patterns, also distinguish subspecies of cutthroat trout (Behnke 1992). These morphological differences among cutthroat trout subspecies are consistent with their distinct, geographic distributions (*e.g.*, Yellowstone [River] vs. Lahontan [basin] cutthroat trout [*O. c. henshawi*]). In addition, the common names of the various species of trout clearly reflect their distinctive morphological appearances, *e.g.*, rainbow trout, redband trout (*O. m. gairdneri*), cutthroat trout, and golden trout (*O. m. aguabonita*) (Behnke 2002).

The advent of molecular genetic techniques in the mid-1960s added an additional set of biological characters that can be used to distinguish species and subspecies of native trouts (*Oncorhynchus* spp.) in the western United States. In most cases, the new molecular genetic data simply confirmed the evolutionary distinctness of species and subspecies that had already been described taxonomically on the basis of morphology (Behnke 1992). One notable exception was the failure of molecular genetic techniques to distinguish fine-spotted Snake River cutthroat trout (*O. c. subsp.*) and YCT as two evolutionarily distinct forms (Loudenslager and Kitchen 1979).

Although molecular genetic data have had little impact on the taxonomic recognition of rainbow trout, cutthroat trout, and their respective subspecies, molecular genetic markers are very sensitive tools for detecting natural hybridization and small amounts of genetic introgression. For example,

Campton and Utter (1985) used allozymes (proteins) to first document the incidence of natural hybridization between naturally sympatric populations of coastal cutthroat trout (*O. c. clarki*) and rainbow trout/steelhead (*O. mykiss*), although earlier morphological descriptions had suggested such interbreeding was occurring (DeWitt 1954; Hartman and Gill 1968). The sensitivity of the molecular genetic data simply provided compelling evidence that interbreeding was indeed occurring.

In general, molecular genetic methods are capable of detecting extremely small amounts of genetic introgression (*e.g.*, <1 percent) undetectable by other methods (Weigel *et al.* 2002; *see also* Fig. 2 of Kanda *et al.* 2002). For example, a large number of situations exist in the scientific literature where the mitochondrial DNA (mtDNA) from one species appears to have introgressed via hybridization into the nuclear genetic background of a closely related species (*e.g.*, Ferris *et al.* 1983; Bernatchez *et al.* 1995; Glemet *et al.* 1998; Wilson and Bernatchez 1998; Redenbach and Taylor 2002). This ability to detect very low levels of introgression raises fundamental questions regarding the criteria by which introgressed populations, and individuals in those populations, should be included with, or excluded from, their parental or morphological species. In the mtDNA situations cited above, the scientific community considers the “introgressed” individuals to be legitimate members of their morphological species despite the presence of mtDNA from another species. Similarly, individuals of a particular “species” may possess nuclear genes from another taxon detectable only by molecular genetic methods, yet those individuals may still conform morphologically, behaviorally, and ecologically to the scientific taxonomic description of the parental or native species (*e.g.*, Busack and Gall 1981; Weigel *et al.* 2002).

Previous Service positions regarding hybridization, based upon interpretations in a series of opinions by the U.S. Department of the Interior, Office of the Solicitor, generally precluded conservation efforts under the authorities of the Act for progeny, or their descendants, produced by matings between taxonomic species or subspecies (O'Brien and Mayr 1991). However, advances in biological understanding of natural hybridization (*e.g.*, Arnold 1997) prompted withdrawal of those opinions. The reasons for that action were summarized in two sentences in the withdrawal

memorandum (Memorandum from Assistant Solicitor for Fish and Wildlife, U.S. Department of the Interior, to Director, U.S. Fish and Wildlife Service, dated December 14, 1990): “New scientific information concerning genetic introgression has convinced us that the rigid standards set out in those previous opinions should be revisited. In our view, the issue of “hybrids” is more properly a biological issue than a legal one.”

Our increasing understanding of the wide range of possible outcomes resulting from exchanges of genetic material between taxonomically distinct species, and between entities within taxonomic species that also can be listed under the Act (*i.e.*, subspecies, DPSs), requires the Service to address these situations on a case-by-case basis. In some cases, introgressive hybridization may be considered a natural evolutionary process reflecting active speciation or simple gene exchange between naturally sympatric species. In other cases, hybridization may be threatening the continued existence of a taxon due to anthropogenic factors or natural environmental events. In many cases, introgressed populations may contain unique or appreciable portions of the genetic resources of an imperiled or listed species. For example, populations with genes from another taxon at very low frequencies may still express important behavioral, life-history, or ecological adaptations of the indigenous population or species within a particular geographic area. Consequently, the Service plans to carefully evaluate the long-term conservation implications for each taxon separately on a case-by-case basis where introgressive hybridization may have occurred. The Service shall perform these evaluations objectively based on the best scientific and commercial information available consistent with the intent and purpose of the Act.

For example, the Service may recognize that small amounts of genetic introgression do not disqualify individuals or populations from “species membership” or the Act’s protections if those individuals or populations conform to the scientific taxonomic description of that species. A natural population of a particular species that possesses genes from another taxon at low frequency, yet retains the distinguishing morphological, behavioral, and ecological characters of the native species, may remain very valuable to the overall conservation and survival of that species.