**UNITED STATES DEPARTMENT OF COMMERCE**
**National Oceanic and Atmospheric Administration**
National Marine Fisheries Service
Southwest Fisheries Science Center
Fisheries Ecology Division
110 Shaffer Road
Santa Cruz, California 95060

June 14, 2007

Dear Interested Party:

The Technical Recovery Team (TRT) for the North-Central California Coast Recovery Domain has recently completed a draft report titled "A framework for assessing the viability of threatened and endangered salmon and steelhead in the North-Central California Coast Recovery Domain." We seek comment from interested parties regarding the scientific content and analysis that underlie the recommendations made in this report.

Biological viability criteria specify those biological conditions that, if met, would indicate that populations and Evolutionarily Significant Units (ESUs) are at low risk of extinction. Ideally, viability criteria for salmonid populations would be tailored to each population, taking into account specific biological characteristics of populations and differences in the inherent productive capacities of the habitats that underlie those attributes. However, the data required for such population-specific analyses are lacking throughout the entire recovery domain. We therefore have adopted population-level criteria that are general to salmonids, with the expectation that these criteria can provide preliminary guidance on targets for viability, but may eventually be replaced with population-specific criteria as more information becomes available. Proposed ESU-level criteria are similarly derived from fundamental principles of conservation biology, providing guidance on configurations of viable populations (the units that constitute an ESU) that lead to a high probability of ESU persistence by ensuring representation of diversity within an ESU across most of its historical range, redundancy of viable populations to guard against large-scale catastrophic risk, and ensuring connectivity among populations in order to maintain longer-term ecological and evolutionary processes.

We emphasize that the conclusions in this document are technical recommendations and do not represent policy decisions. Throughout the report, we have discussed assumptions underlying the proposed criteria and associated scientific uncertainties. Where those uncertainties are great, we generally adhere to the precautionary principle of conservation biology, which calls for erring on the side of conservation to ameliorate/mitigate the risk arising from such uncertainty.

We invite comment on the scientific content and analysis presented in this report. The report is available in electronic form on the website of the Fisheries Ecology Division of the NOAA Southwest Fisheries Science Center (http://swfsc.noaa.gov/textblock.aspx?Division=FED&id=2266). Comments should be sent via email to Brian Spence (Brian.Spence@noaa.gov) with "Draft NCCC Viability Comments" in the subject line, or by regular mail to the address shown above. We ask that reviewers please submit comments by July 15, 2007.

Sincerely,

Brian C. Spence

Brian C. Spence, Ph.D.
Research Fishery Biologist
Chair, North-Central California Coast TRT

# A Framework for Assessing the Viability of Threatened and Endangered Salmon and Steelhead in North-Central California Coast Recovery Domain

Brian Spence, NOAA NMFS SWFSC Fisheries Ecology Division
Eric Bjorkstedt, NOAA NMFS SWFSC Fisheries Ecology Division
John Carlos Garza, NOAA NMFS SWFSC Fisheries Ecology Division
David Hankin, Department of Fisheries Biology, Humboldt State University
Jerry Smith, Department of Biological Sciences, San Jose State University
David Fuller, Bureau of Land Management
Weldon Jones, California Department of Fish and Game (retired)
Richard Macedo, California Department of Fish and Game, Central Coast Region
Thomas H. Williams, NOAA NMFS SWFSC Fisheries Ecology Division
Ethan Mora, NOAA NMFS SWFSC Fisheries Ecology Division

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# 1 Introduction

## 1.1 Background

Since 1989, the National Marine Fisheries Service (NMFS) has listed twenty-seven Evolutionarily Significant Units (ESUs) or Distinct Population Segments (DPSs)[1] of coho salmon, Chinook salmon, sockeye salmon, chum salmon, and steelhead in the states of Idaho, Washington, Oregon, and California as threatened or endangered under the federal Endangered Species Act (ESA). Among the provisions of the ESA, as amended in 1988, are requirements that NMFS develop recovery plans for listed species and that these recovery plans contain "*objective, measurable criteria which, when met, would result in a determination… that the species* [or ESU] *be removed from the list*." (ESA Sec 4(f)(1)(B)(ii)). The ESA, however, provides no detailed guidance on how to define these recovery criteria.

In 2000, NMFS organized recovery planning for listed salmonid ESUs[2] into geographically coherent units termed "recovery domains." Subsequently, Technical Recovery Teams (TRTs) consisting of scientists from NOAA Fisheries; other federal, tribal, state, and local agencies; academic institutions; and private consulting firms were convened for each recovery domain to provide technical guidance in the recovery planning process. Among their responsibilities, the TRTs have been charged with developing biological viability criteria for each listed ESU within their respective domains. The North-Central California Coast (NCCC) Recovery Domain, which is the focus of this report, encompasses four ESA-listed ESUs and DPSs of anadromous salmon and steelhead: California Coastal Chinook salmon (CC-Chinook salmon ESU), listed as threatened in 1999; Central California Coast coho salmon (CCC-Coho salmon ESU), listed as threatened in 1996 and revised to endangered in 2005; Northern California steelhead (NC-Steelhead DPS), listed as threatened in 1997; and Central California Coastal steelhead (CCC-Steelhead DPS), also listed as threatened in 1997. These ESUs cover a geographic area extending from the Redwood Creek watershed (Humboldt County) in the north, to tributaries of northern Monterey Bay in

[1] The ESA allows listing not only of species, but also "distinct population segments" of species. Policies developed by NMFS have defined distinct population segments as populations or groups of populations that are reproductively isolated from other conspecific population units and that are an important component in the evolutionary legacy of the species. NMFS has termed these distinct population segments "Evolutionarily Significant Units" or ESUs (Waples 1991). More recently, NMFS revisited the distinct population segment question as it pertains to populations of *O. mykiss*, which may have both resident and anadromous forms living sympatrically. Although at the time of the original listings of Central California Coast and Northern California steelhead, both resident and anadromous forms were considered part of these ESUs, only the anadromous forms were listed (62 FR 43937, at 43591). A court ruling (Alsea Valley Alliance v. Evans, 161 F. Supp. 2d 1154 (D. Or. 2001)) concluded that listing a subset of a delineated group, such as the anadromous form of an ESU, was not allowed under ESA. Thus, existing federal policy regarding DPSs (61 FR 4722) was applied to delineate resident and anadromous forms of *O. mykiss* as separate DPSs. Subsequently, the CCC and NC steelhead DPSs were listed as threatened under ESA (71 FR 834).

[2] Throughout this document, we frequently use the term ESU to encompass both ESUs and DPSs when speaking in general terms about listed salmonid units in order to avoid awkward or cumbersome language. When referring to a specific ESU or DPS, we use the appropriate term.

the south, inclusive of the San Francisco Bay estuary east to the confluence of the Sacramento and San Joaquin rivers (Figure 1)[3].

The first step in the development of viability criteria was to define the historical population structure for each ESU within the domain. The biological organization of salmonid species is hierarchical, from species and ESUs down to local breeding groups or subpopulations, reflecting differing degrees of reproductive isolation. For example, by virtue of their close proximity and shared migratory pathways, subpopulations within the same watershed are likely to exchange individuals through the process of straying on a regular basis (i.e., annually), whereas for populations or larger groups (i.e., diversity strata) such interactions may occur much less frequently. The level of exchange of individuals among spawning aggregations can have significant bearing on the population dynamics and extinction risk of such groups, which in turn may influence the persistence of higher-level groups, on up to ESUs. For recovery planning purposes, it is particularly important to identify the minimum population units that would be expected to persist in isolation of other such populations, as recovery strategies focused solely on smaller units would have a high likelihood of failure. Additionally, over the spatial scale typical of an ESU, reproductive isolation of populations and exposure of these reproductively isolated populations to unique environmental conditions are likely to result in local adaptations and genetic diversity. This diversity, coupled with spatial structure at levels above the population, is important to the long-term persistence of the ESU. Development of appropriate viability criteria and recovery goals requires some understanding of and accounting for this hierarchical structure, and it was therefore necessary to explore probable historical relationships among various spawning groups of salmonids within each ESU. The NCCC TRT (Bjorkstedt et al. 2005) has provided the foundation for viability criteria at these spatial scales by defining both population units and diversity strata (i.e., groups of populations that likely exhibit genotypic and phenotypic similarity due to exposure to similar environmental conditions or common evolutionary history) important to consider in the development of ESU viability criteria. Further consideration by the TRT has led to some modifications to the structures proposed in Bjorkstedt et al. (2005); revised summaries for each ESU and DPS are presented in Appendix A of this report.

This *Population Viability Report* is the outcome of the second step in development of viability criteria for ESUs and DPSs within the NCCC Recovery Domain. Specifically, we develop a framework for assessing viability using criteria representing three levels of biological organization and processes that are

[3] A fifth listed ESU, the Southern Oregon-Northern California Coast coho salmon ESU, extends into the geographic region of the NCCC Recovery Domain; however, viability criteria for this ESU are being developed by the Southern Oregon-Northern California Coast workgroup of the Oregon-Northern California Coast Technical Recovery Team.

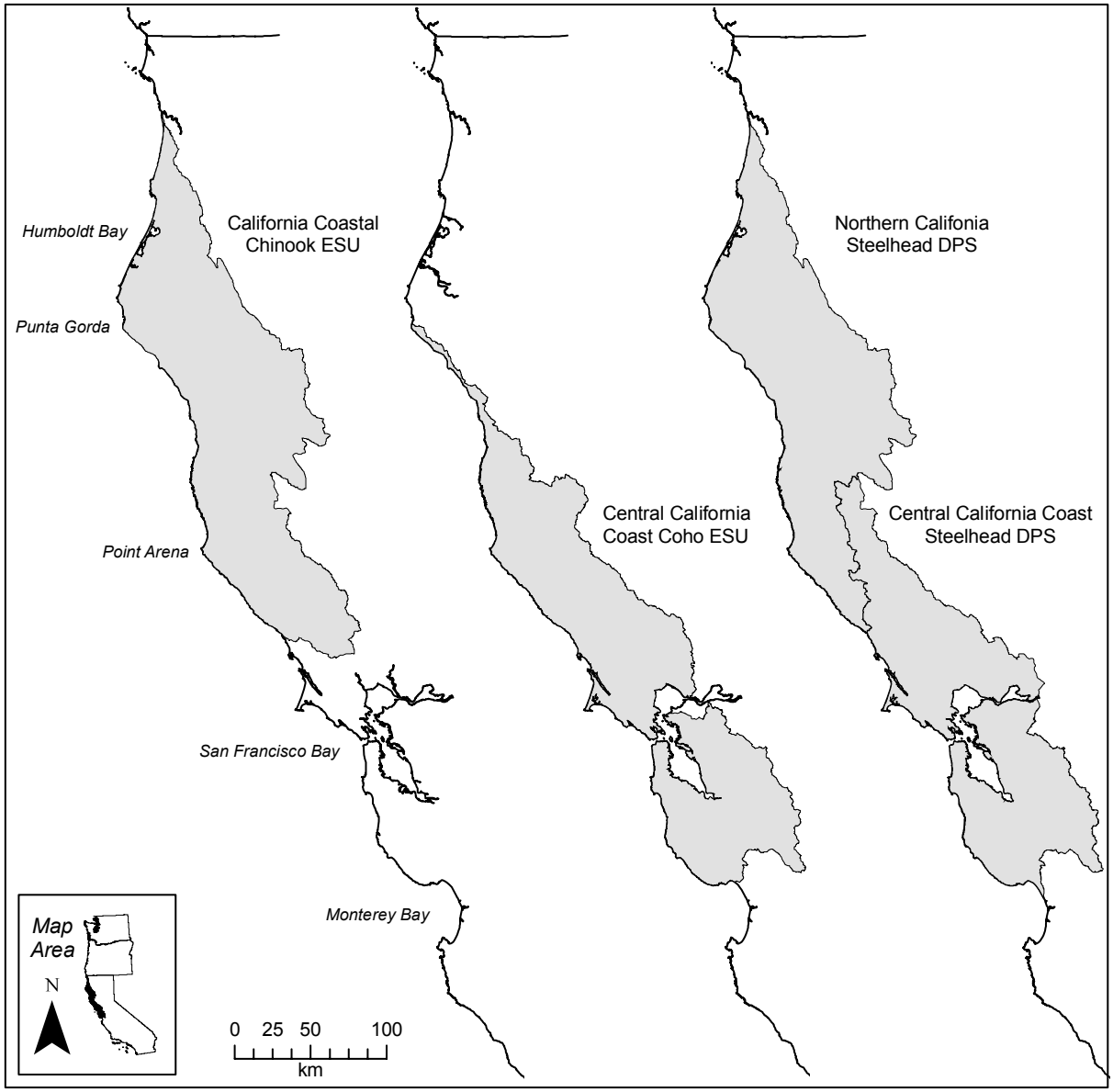


**Figure 1.** Approximate historical geographic boundaries of ESA-listed salmon and steelhead ESUs and DPSs in the North-Central California Coast Recovery Domain.

important to persistence and sustainability: populations, diversity strata, and the ESU as a whole. Ideally, population-level criteria would be tailored to each population, taking into account specific biological characteristics of populations, and differences in the inherent productive capacities of the habitats that may underlie these biological differences. However, in most cases, such population-specific information is not currently available, and likely will not be available in the foreseeable future. In the absence of

extensive quantitative population data, the Recovery Science Review Panel[4] (RSRP 2002) and Shaffer et al. (2002) have recommended using general, objective population-based criteria such as those used by the IUCN (IUCN 2001). In response to both data limitations and recommendations by the RSRP, we have adopted (with modifications) the conceptual approach of Allendorf et al. (1997), who proposed a series of general criteria for assessing extinction risk and prioritizing the conservation of populations of Pacific salmonids. The Allendorf et al. approach includes criteria related to population size (effective and total) and recent trends in abundance (catastrophic and longer term), to which we have added criteria related to population density and hatchery effects. Other TRTs within the Pacific Northwest have likewise adopted the Allendorf et al. (1997) framework, with various modifications (Lindley et al. 2007; Boughton et al., in prep; Williams et al., in prep.). Our criteria for diversity strata emphasize the need for within-strata redundancy in viable populations so as to minimize the risks of losing a significant component of the overall genetic diversity of an ESU due to a single catastrophic disturbance. At the ESU level, criteria are intended to ensure that the range of genetic diversity of the ESU is adequately represented and to foster connectivity among the constituent populations and diversity strata. For diversity strata and ESU-level criteria, we draw heavily from the work of the Puget Sound (PSTRT), Willamette and Lower Columbia (WLCTRT), Interior Columbia (ICTRT), Oregon/Northern California Coast (ONCC TRT) technical recovery teams, all of which have published or are producing criteria incorporating similar, though not identical, elements (PSTRT 2002; WLCTRT 2003; ICTRT 2005; Wainwright et al., in prep.; Williams et al., in prep.).

The primary intent of our framework for assessing population and ESU viability is to guide future determinations of when populations and ESUs are no longer at risk of extinction. To implement the framework, it is necessary to have fairly lengthy time-series of adult abundance (at least 10-12 years to evaluate the general criteria and even longer time series to conduct credible population viability analyses) at appropriate spatial scales (i.e., population-level estimates for most historically independent populations that have been identified within each ESU). The practical reality in California is that almost no such datasets exist. Although there are a number of ongoing salmonid monitoring activities, few are designed to generate estimates of abundance at the population level; thus, there is an urgent need to initiate monitoring programs that will generate data of sufficient quality to rigorously assess progress toward population and ESU recovery. Development of a comprehensive coastal monitoring plan for salmonids has been underway for several years by the California Department of Fish and Game, with input from NMFS; however, datasets that will allow assessment of status using the criteria described herein are likely

[4] The Recovery Science Review Panel was convened by NMFS to provide guidance on technical aspects of recovery planning.

more than a decade away. Consequently, the present values of the criteria put forth in this document are both to inform the development of such a monitoring plan and to provide preliminary targets for recovery planners to aim towards.

## 1.2 Relationship Between Biological Viability Criteria and Delisting Criteria

Before elaborating on our approach to developing biological viability criteria, it is important to distinguish *biological viability criteria* proposed herein from the *recovery criteria* that will ultimately be put forth in a recovery plan. Although the ESA provides no detailed guidance for defining recovery criteria, subsequent NMFS publications including *Recovery Planning Guidance for Technical Recovery Teams* (NMFS 2000), and *Interim Endangered and Threatened Species Recovery Planning Guidance* (NMFS 2006) have elaborated on the nature of recovery criteria and underlying goals and objectives. NMFS (2006) clearly affirms that the primary purpose of the Federal Endangered Species Act is to *"...provide a means by whereby the ecosystems upon which endangered species and threatened species depend may be conserved*" (16 U.S.C. 1531 et sec., section 2(a)), noting that "*in keeping with the ESA's directive, this guidance focuses not only on the listed species themselves, but also on restoring their habitats as functioning ecosystems*". To this end, NMFS (2006) directs that recovery criteria must address not only the biological status of populations and ESUs, but also the specific threats and risk factors that contributed to the listing of the ESU. These threats and risks can include (a) current or threatened destruction, modification or curtailment of the ESU's habitat or range; (b) overutilization for commercial, recreational, scientific or educational purposes; (c) disease or predation; (d) the inadequacy of existing regulatory mechanisms; (e) other natural or manmade factors affecting the ESU's continued existence (16 USC 1533). Thus, formal recovery or delisting criteria for Pacific salmonids will at a minimum likely include at least two distinct elements: (1) criteria related to the number, sizes, trends, structure, recruitment rates, and distribution of populations, as well as the minimum time frames for sustaining specified biological conditions; and (2) criteria to measure whether threats to the ESU have been ameliorated (NMFS 2006)[5]. The latter criteria have been referred to as "administrative delisting criteria" (NMFS 2000), and may require that management actions be taken to address specific threats before a change in listing status would be considered (NMFS 2006). Recovery plans may also set recovery goals higher than those needed to achieve delisting of the species under ESA in order to allow for other uses (e.g., commercial, recreational, or tribal harvest) or to provide ecological benefits (e.g.,

[5] The need to address each listing factor when developing delisting criteria has been affirmed in Court, which concluded that "since the same five statutory factors must be considered in delisting as in listing…in designing objective, measurable criteria, the FWS must address each of the five delisting factors and measure whether threats to the [species] have been ameliorated." (Fund for Animals v. Babbitt, 903 F. Supp. 96 (D.D.C 1995), Appendix B).

maintenance of ecosystem productivity). These additional goals have been termed "broad-sense" recovery goals (NMFS 2000). Where such recovery goals are established, NMFS (2006) indicates that they should be clearly distinguished from ESA-specific recovery goals.

The *biological viability criteria* proposed in this document represent the NCCC TRT's recommendations as to the minimum population and ESU characteristics indicative of an ESU having a high probability of long-term (> 100 years) persistence. Population viability criteria define sets of conditions or rules that, if satisfied, we believe would suggest that the population is at low risk of extinction. ESU viability criteria define sets of conditions or rules related to the number and configuration of viable populations across a landscape that would be indicative of low extinction risk for the ESU as a whole. The ESU criteria do not explicitly specify which populations must be viable for the ESU to be viable (though in some cases, certain populations will likely be critical for achieving viability, given their current status or functional role), but rather they establish a framework within which there may be several ways by which ESU viability may be achieved.

The biological viability criteria can be viewed as indicators of biological status and thus are likely to be directly related to the biological delisting criteria that will be defined in a recovery plan. However, the criteria are independent of specific sources of mortality (natural or human-caused) or specific threats to populations and ESUs that led to their listing under ESA; thus, the criteria should not be construed as sufficient, by themselves, for determining the ESA status of ESUs. These threats, and associated administrative delisting criteria, are to be addressed through a formal "threats assessment" process in the second phase of recovery planning. Likewise, development of "broad-sense" recovery goals is to occur during phase two of recovery planning. These latter processes will provide the basis for determining which populations have the highest likelihood of being recovered to viable levels (based on current status, practicality and cost of restoring habitat or otherwise ameliorating threats) or to levels that will achieve broad-sense recovery goals. Thus, formal biological delisting criteria contained in a recovery plan are likely to have greater specificity about which populations may need to be viable before the ESU is considered so.

NMFS (2006) recovery planning guidance document highlights a number of objectives that are relevant to the TRT's task of developing biological viability criteria. Recovery and long-term sustainability of endangered or threatened species depends on the following:

- Ensuring adequate reproduction for replacement of losses due to natural mortality factors (including disease and stochastic events)
- Maintaining sufficient genetic robustness to avoid inbreeding depression and to allow adaptation
- Providing sufficient habitat (type, amount, and quality) for long-term population maintenance
- Elimination or control of threats (which may include having adequate regulatory mechanisms in place).

The NMFS interim guidance document further states that, in order to meet these general objectives, recovery criteria should at a minimum address three major issues related to long-term persistence of populations and ESUs: representation, resiliency, and redundancy (NMFS 2006). Representation involves conserving the breadth of the biological diversity of the ESU to conserve its adaptive capabilities. Resiliency involves ensuring that populations are sufficiently large and/or productive to withstand both natural and human-caused stochastic stressor events. Redundancy involves ensuring a sufficient number of populations to provide a margin of safety for the ESU to withstand catastrophic events (NMFS 2006). Each of these issues may be relevant at more than one spatial scale. For example, genetic representation may be important both within populations (i.e., maintaining genetic diversity at the population level, which allows for the expression of phenotypic diversity and hence buffers against environmental variation) and among populations across an ESU (i.e., preserving genetic adaptations to local or regional environmental conditions to maintain evolutionary potential in the face of large-scale environmental change). The NCCC TRT has attempted to develop viability criteria that encompass these primary principles and objectives.

It is not practical for the TRT, which must necessarily focus on ESU-scale analysis, to address various threats and risk factors that contributed to the ESA listing of ESUs within the NCCC Recovery Domain or to develop criteria related to those threats and risks at the resolution and detail required for effective recovery. Nevertheless, it is important to understand the primary factors that have contributed to salmonid declines within these areas so that the proposed viability criteria can be viewed in an appropriate context. Each listed ESU within the domain has undergone one or more status reviews prior to listing, in which a number of general factors for decline were identified. Federal Register notices containing the final listing determinations likewise have identified factors contributing to the declines of listed species [6]. All of these reviews have identified habitat loss and degradation associated with land-use practices as a primary cause of population declines within the listed salmon and steelhead ESUs (Weitkamp et al. 1995;

[6] For the most part, published status reviews and Federal Register Notices have provided only general lists of factors that affect multiple populations within an ESU or DPS; they typically do not provide details on population-specific risk factors.

Busby et al. 1996; Myers et al. 1998; NMFS 1999; Good et al. 2005). Almost all watersheds within the domain have experienced extensive logging and associated road building, which have wide-reaching effects on hydrology, sediment delivery, riparian functions (e.g., large wood recruitment, fine organic inputs, bank stabilization, stream temperature regulation), and channel morphology. Activities such as splash damming and "stream cleaning", though no longer practiced, have had substantial effects on channel morphology that continue to affect the ability of streams and rivers to support salmonids. Impacts of agricultural practices on aquatic habitats, though spatially perhaps not as widespread as those associated with forest practices, are often more severe since they typically involve repeated disturbance to the landscape, often occur in historical floodplains or otherwise in close proximity to streams, commonly involve diversion of water in addition to the land disturbance, and frequently involve intensive use of chemical fertilizers and pesticides that degrade water quality. Urbanization has severely impacted streams, particularly in the San Francisco Bay area, portions of the Russian River basin, and the Monterey Bay area, often involving stream channelization, modification of hydrologic regime, and degradation of water quality, among other adverse effects. Hard rock (mineral) and aggregate (gravel) mining practices have also substantially altered salmonid habitats in certain portions of the domain. For example, gravel extraction in the Russian River has substantially altered channel morphology both in the mainstem, and in tributaries entering the mainstem (Kondolf 1997). Loss and degradation of estuarine and lagoon habitats—which are important juvenile rearing and feeding habitats (Smith 1990; Bond 2006; Hayes et al. in review), as well as being critical areas of acclimation while smolts make the transition from fresh to salt water—have likely also contributed to declines of salmon and steelhead in the region. Published status reviews have also noted that many of the impacts associated with land use have been exacerbated by severe floods such as the 1964 flood (Busby et al. 1996; Myers et al. 1998).

In certain watersheds and regions (e.g., Mad River, Eel River, Russian River, and many San Francisco Bay tributaries), dams have blocked access to historical spawning and rearing habitats (Busby et al. 1996), though compared with other regions, such as California's Central Valley and the Columbia Basin, the fraction of historical habitat lost behinds dams is relatively small in most of the NCCC Recovery Domain. In addition to preventing access to historical spawning and rearing habitats, dams disrupt natural hydrologic patterns, sediment transport dynamics, channel morphology, substrate composition, temperature regimes, and dissolved gas concentrations in reaches downstream, potentially affecting the suitability of these reaches to salmonids. Water withdrawals for agricultural, industrial, and domestic use have resulted in reduced stream flows, increased water temperatures, and otherwise diminished water quality. Water diversions are widespread throughout the domain, but are a particularly acute problem in portions of the domain with intense agriculture or urbanization, such as portions of the Russian River,

upper Navarro River, tributaries of San Francisco and Monterey bays, and the lower reaches of many coastal watersheds.

Excessive commercial and sport harvest of salmonids is also believed to have contributed to the declines of populations within the region, though little information on harvest rates is provided in published status reviews for ESUs or DPSs within the NCCC Recovery Domain. In addition to affecting the number of adults that return to their natal streams to spawn, harvest can also have a substantial effect on the age- and size-structure of returning adults through selective harvest of older individuals, which are vulnerable to fishing for a longer period, or size-selective fishing gear (Ricker 1981). This selectivity usually results in a reduction in the proportion of larger, older individuals in a population, particularly for Chinook salmon, which are vulnerable to ocean fisheries for several years. Selection on size- and age-at-maturity can result not only in immediate demographic consequences (e.g., reductions in spawner abundance and average fecundity of spawners), but may potentially result in genetic selection for early maturation (Hankin et al. 1993). Such changes in population attributes may have longer-term demographic consequences. Though directed commercial and sport harvest of listed salmonids in the NCCC Recovery Domain has decreased since populations were first listed in the mid-1990s, incidental take of listed ESUs continues to occur in fisheries targeting non-listed ESUs, including Central Valley and Klamath River fall Chinook salmon. Although no direct estimates of harvest rates are currently available for listed ESUs or DPSs in the NCCC Recovery Domain, it seems unlikely that harvest rate of CC-Chinook salmon stocks is less than that for Klamath River Chinook, and it is possible that some of these populations (e.g., Eel River Chinook salmon) are harvested at very high rates in the Central California fishery.

Status reviews have identified hatchery practices, including out-of-basin transfers of stocks, as important risk factors in all four listed ESUs (Weitkamp 1995; Busby et al. 1996; Myers et al. 1998; Good et al. 2005). While the status reviews emphasize potential genetic risks associated with hatcheries, there are demographic and ecological risks as well (see Section 2.2 of this report for further discussion). Additionally, the introduction or invasion of nonnative fishes may also pose a significant threat to salmonids within the domain. Busby e al. (1996) identified the introduction of nonnative species (e.g. Sacramento pikeminnow) as a significant threat to NC steelhead populations in the Eel River, and it is likely a threat to Chinook and coho salmon populations in this basin as well (CDFG 2002). Numerous other nonnative species, including various cyprinids, centrarchids, ictalurids, and clupeids, have been introduced into coastal watersheds within the domain and may influence listed populations through predation or competition. The Redwood Creek, Mad River, Eel River, Russian River, and Tomales Bay systems may be the most likely systems affected by such introductions, as nonnative fishes currently

make up 30% or more of the total fish species present in these watersheds (Moyle 2002). Many tributaries of San Francisco Bay likewise have a high percentage of nonnative fishes (Leidy et al. 2007).

All of the factors listed above have likely contributed to declines in the abundance and distribution of listed salmon and steelhead within the NCCC Recovery Domain and will need to be addressed in the development of recovery plans. Although attainment of the biological criteria proposed herein would suggest that some of the conditions that led to listing have been ameliorated, natural variation in environmental conditions in both the freshwater and marine environments can produce substantial changes in abundance of salmon and steelhead, even without fundamental improvement in habitat quality (Lawson 1993). Consequently, complementary analyses of both biological status and existing or future threats will need to form the basis of future status assessments.

## 1.3 Population Delineations and Biological Viability Criteria

Scientists from NMFS' Northwest Fisheries Science Center and Southwest Fisheries Science Center developed a series of guidelines for setting viability objectives in a document titled "*Viable Salmonid Populations and the Recovery of Evolutionarily Significant Units*" (McElhany et al. 2000). The so-called viable salmonid population (VSP) concept developed in McElhany et al. (2000) forms the foundation upon which the draft viability criteria proposed here rests. McElhany et al. (2000) defined a viable salmonid population as "*an independent population of any Pacific salmonid (genus* Oncorhynchus*) that has a negligible risk of extinction due to threats from demographic variation (random or directional), local environmental variation, and genetic diversity changes (random or directional) over a 100-year time frame*." They defined an independent population to be "*any collection of one or more breeding units whose population dynamics or extinction risk over a 100-year time period is not substantially altered by exchanges of individuals with other populations*." Their conceptualization thus distinguishes between independent populations, as defined above, and dependent populations, whose dynamics and extinction risk *are* substantially affected by neighboring populations.

For our purposes, we found it useful to further distinguish among independent populations based on both their viability in isolation and their degree of self-recruitment (i.e., the proportion of spawners of natal origin), which assists in identifying the functional role different populations historically played in ESU persistence (Bjorkstedt et al. 2005). We defined *functionally independent* populations as "those with a high likelihood of persisting over 100-year time scales and [that] conform to the definition of independent 'viable salmonid populations' offered by McElhany et al. (2000, p. 3)". We defined *potentially*

*independent populations* as those that "have a high likelihood of persisting in isolation over 100-year time scales, but are too strongly influenced by immigration from other populations to exhibit independent dynamics." Thus, whereas the McElhany et al. definition of independence explicitly requires sufficient isolation for demographic independence, the NCCCTRT definition of independence encompasses populations that could conceivably persist in isolation in the absence of adjacent populations that at one time may have substantially influenced their extinction risk (Bjorkstedt et al. 2005). We also define dependent populations as those that have a substantial likelihood of going extinct within a 100-year time period in isolation, but that receive sufficient immigration to alter their dynamics and reduce their extinction risk (Bjorkstedt et al. 2005).

These distinctions are important to consider in developing a recovery strategy for two reasons. First, certain historical functionally independent populations likely had disproportionate influence on ESU persistence. By definition, functionally independent populations are net sources of strays that influence the dynamics of neighboring populations. Loss or reduction of such populations thus may have greater impact on ESU persistence, since associated potentially independent and dependent populations are also negatively affected. Second, recovery planners will need to consider the functional role a population is playing or might play in the future, relative to its historical role. For example, dams that block access to a significant proportion of a population's habitat might preclude that population from behaving as a functionally independent population. While such a population may continue to persist, it should not be viewed as providing the same contribution to ESU viability as the historical population. Conversely, there may be certain circumstances where functionally or potentially independent populations have been lost or severely depleted, but neighboring dependent populations continue to persist. In these instances, dependent populations, while not expected to persist indefinitely in isolation, may provide the only reasonable opportunity for recovering nearby populations classified as functionally or potentially independent under historical conditions. Dependent populations may also provide reservoirs of genetic diversity that has been lost from depleted independent populations. And finally, dependent populations may provide connectivity among independent populations that is important for long-term ESU viability. Thus, when prioritizing recovery efforts among watersheds, recovery planners will need to evaluate the full context of the historical and current population structure.

## 1.4 Report Organization

In the remaining sections of this report, we present both the general framework for assessing population and ESU viability, and application of the framework to the four listed ESUs within the NCCC Recovery

Domain. Section 2 describes an approach for categorizing populations according to extinction risk that extends the framework proposed by Allendorf et al. (1997). Extinction risk is evaluated based on six metrics intended to address issues of abundance, productivity, spatial structure, and diversity identified in McElhany et al. (2000). We briefly summarize the rationale for inclusion of each viability criterion and then discuss some assumptions and caveats associated with each. The NCCC TRT augmented the Allendorf et al. (1997) criteria by adding criteria related to spawner densities and hatchery contributions. In these two instances, we provide somewhat more detailed rationale for these criteria. These modifications to the Allendorf et al. (1997) approach have been done in coordination with other TRTs in NMFS' Southwest Region; thus, there is substantial overlap in approaches used (see e.g., Lindley et al. 2007; Williams et al. in prep.; Boughton et al., in prep.).

Section 3 puts forth viability criteria at the levels of diversity strata and entire ESUs. Diversity strata were identified in the *Population Structure Report* (Bjorkstedt et al. 2005), and have subsequently been revised by the TRT (see Appendix A). These strata represent regional population groupings that have evolved under similar environmental conditions, as well as life-history diversity expressed within a particular watershed (e.g., spring- and fall-run Chinook salmon). Criteria at the level of diversity strata and ESUs are directed toward increasing the likelihood that a full suite of genetic and phenotypic diversity is represented across the ESU, that there is redundancy in viable populations within diversity strata to reduce the risk that an entire diversity stratum is affected by a single catastrophic event, and that connectivity among populations necessary for maintenance of long-term demographic and genetic processes is maintained.

In Section 4, we apply the methods described in the preceding two sections to the four ESUs within the NCCC Recovery Domain. As noted earlier, the NCCC Recovery Domain suffers from an almost complete lack of appropriate data that can inform the risk analysis. This paucity of data precludes us from drawing firm conclusions about population or ESU status based on our framework; however, the exercise is instructive both in identifying important information gaps that need to be filled, and in establishing preliminary numeric targets that can assist planners in developing recovery strategies.

# 2 Population Viability Criteria

## 2.1 Key Characteristics of Viable Populations

McElhany et al. (2000) propose a conceptual framework for both defining a viable salmonid population (VSP) and the critical parameters that should be evaluated when assessing viability of both populations and ESUs. The issue of defining populations for the NCCC Recovery Domain has been treated at length in Bjorkstedt et al. (2005). Here, we turn our attention to defining appropriate parameters to be measured when assessing viability, and the development of specific metrics and criteria that would enable classification of populations according to their extinction risk.

McElhany et al. (2000) propose that four general population parameters are key to evaluating population status: abundance, population growth rate, population spatial structure, and diversity. Abundance—the number of individuals within the population at a given life stage—is of obvious importance. Other factors being equal, small populations are at greater risk of extinction than larger populations due to the fact that several deterministic and stochastic processes operate differently in small versus large populations. As discussed by McElhany et al. (2000), to be viable, a population needs to be large enough 1) to have a high probability of surviving environmental variation of the patterns and magnitude observed in the past and expected in the future; 2) to allow compensatory processes to provide resilience to natural environmental and anthropogenic disturbances; 3) to maintain its genetic diversity over the long term (i.e., avoiding inbreeding depression, fixation of deleterious alleles, genetic drift, and loss of long-term adaptive potential); and 4) to provide important ecological functions (e.g., provision of marine-derived nutrients to maintain productivity, physical modification of habitats such as spawning gravels) throughout its life cycle.

Population growth rate refers to the actual or expected ratio of abundances in successive generations, and provides information about how well the population is performing in its environment over its entire life cycle. Populations that consistently fail to replace themselves over extended periods are at greater risk of extinction than those that are consistently at or above replacement. Additionally, populations with higher intrinsic productivity (i.e., recruits per spawner when spawner densities are low, compensation is not reducing per capita productivity, and depensatory effects are absent) recover more rapidly following a decline in abundance than do those with lower intrinsic productivity. Thus, a population with lower abundance but higher intrinsic productivity may be less prone to extinction than one with greater mean abundance but lower productivity. Additionally, when comparing populations with equal mean

abundance and intrinsic productivities, populations that exhibit more variability in abundance and growth rate are likewise more vulnerable to extinction than less variable populations.

Spatial structure refers to the distribution of members in the population at a given life stage among the potentially available habitats, and the processes that give rise to that structure (McElhany et al. 2000). Populations may organize themselves in a variety of ways across a watershed or landscape depending on the spatial arrangement and quality of habitats, and the dispersal characteristics of individuals within the population. Under natural conditions, the distribution of favorable habitats may shift over time in response to environmental disturbances, such as fires, floods, or landslides. Consequently, local breeding groups with differing relative productivities may populate the landscape. Populations that exhibit such structure may be less vulnerable to disturbances such as fires, floods, landslides, and toxic spills that typically occur at relatively small scales (reach to subwatershed) than populations with more restricted distributions. Portions of the landscape unaffected by the disturbance may assume increased importance as disturbed areas recover, and provide sources of colonizers as habitat conditions improve, imparting greater resilience to the population. Maintenance of this spatial structure requires that high quality habitat patches, and suitable corridors connecting these patches to one another and the marine environment, be consistently present.

Diversity is the variety of life histories, sizes, ages, fecundity, run timing, and other traits expressed by individuals within a population, and the genetic variation that in part underlies these differences. In many respects, diversity is tied closely to spatial structure. Diversity results from the interaction of genetic and environmental factors, and it imparts several attributes to populations that influence persistence by spreading of risk through both space and time. First, natural genetic diversity potentially allows a population to use a wider range of habitats than it could with lower diversity; thus, loss of this diversity may diminish the productive capacity and spatial extent of a population. Additionally, distribution of populations across a heterogeneous watershed may lead to phenotypic variation in characteristics such as length of freshwater residence, resulting in more complicated age-structures. Such diversity can buffer populations against poor environmental conditions in either the freshwater or marine environment, effectively spreading risk across both time and space and thereby increasing population resilience in the face of environmental stochasticity. And finally, the underlying genetic diversity of a population determines its ability to adapt to long-term changes in environmental conditions.

Although it is clear that each of the parameters described by McElhany et al. (2000) is important to assessing viability, selecting specific metrics by which to assess viability in relation to these parameters is

less straightforward, and defining criteria for each of these metrics proves even more challenging. For abundance and productivity parameters, relationships between various metrics and extinction risk are more fully developed in the scientific literature. For spatial structure and diversity, the theoretical basis underlying the importance of these parameters is clear, but there is substantially more uncertainty regarding quantitative relationships between these attributes and population viability. Nevertheless, the TRT felt strongly that the our approach needed to address each of these issues, since failing to do so would leave a substantial gap between our approach and both the conceptual framework proposed in McElhany et al. (2000) and interim NMFS guidance on viability criteria (NMFS 2006). We also note that although the VSP framework proposed by McElhany et al. (2000) has intuitive appeal, we found it difficult to develop individual metrics that correspond to the VSP parameters in one-to-one fashion. Thus, several of the metrics we propose directly or indirectly address multiple VSP parameters.

In the VSP framework, the concept of population viability can be viewed from two distinct but equally important perspectives. The first perspective relates to the goal of defining the minimum viable population size (MVP) for which a population can be expected with some specified probability to persist over a specified period of time (Soule 1987; Nunney and Campbell 1993). In one sense, the minimum viable population size can be thought of as identifying the approximate lower bounds for a population at which risks associated with demographic stochasticity, environmental stochasticity, severe inbreeding, and long-term genetic losses are negligible (Soule 1987). This conceptualization of viability asks where a population is likely going in the future, but not necessarily where it has been in the past. For example, with respect to genetic diversity, criteria related to a fixed MVP size are intended to guard against further erosion of genetic diversity, but do not necessarily consider diversity that may have already been lost.

A second way in which viability can be considered is in terms of how a population is currently functioning in relation to its historical viability. From this perspective, historical patterns of abundance, productivity, spatial structure, and diversity form the reference conditions about which (at least for independent populations) we have high confidence that the population had a high probability of persisting (i.e. low risk of extinction) over long periods of time. This broader (and longer term) view asks how a population functioned in its historical context (e.g., what roles did spatial structure and diversity play in population persistence?), and what functional role the population played in relation to other populations within an ESU (e.g., was the population likely a key source of dispersers that contributed to the persistence of other independent or dependent populations?). As populations depart from these historical conditions, their probability of persistence likely declines and their functional role with respect to ESU viability may be diminished.

The criteria we propose in this document encompass both of these perspectives, addressing both immediate demographic and genetic risks, as well longer-term risks associated with loss of spatial structure and diversity that are important both for population resilience (and hence persistence) and the ability of populations to fulfill their roles within the ESU and thus to contribute to ESU viability. Given the technical difficulties associated with developing accurate population viability analyses that focus on a strict definition of viability (e.g., MVP), the second perspective is especially useful in that it embodies a precautionary approach through which increasing departure from historical characteristics logically requires a greater degree of proof that a population is indeed viable. Likewise, this second perspective links directly to viability criteria for higher levels of biological organization.

## 2.2 Population-Level Criteria

The approach we use seeks to classify populations into various extinction risk categories based on a set of quantitative criteria. Both the approach and the specific criteria employed have their roots in the IUCN (1994) red list criteria (derived in part from Mace and Lande 1991) and subsequent modifications made by Allendorf et al. (1997) to specifically deal with populations of Pacific salmon. The Allendorf et al. (1997) framework defines four levels of extinction risk according to the probability of extinction over a specified time frame:

Very high: 50% probability of extinction within 5 years
High: 20% probability of extinction within 20 years
Moderate: 5% probability of extinction within 100 years
Special concern: Historically present, believed to still exist, but no current data

Evaluation of extinction risk is then done either based on population viability analysis (PVA) or, in the absence of sufficient data to construct a credible PVA model, using four surrogate criteria related to population size and trend in abundance. These surrogate criteria address effective population size per generation (or, in the absence of data on effective population size, total population size), population declines, and the effects of recent catastrophes on abundance (see Table 1 in Allendorf et al. 1997).

For our purposes, we make several modifications to the Allendorf et al. (1997) approach—both the risk categories and the metrics used to evaluate risk—to deal with our specific needs in recovery planning (Table 1). First, we add a “low risk” category, which is implicit in Allendorf et al. (1997), defining criteria we believe are indicative of a high likelihood (>95%) of persistence over a 100-year time frame.

**Table 1.** Criteria for assessing the level of risk of extinction for populations of Pacific salmonids. Overall risk is determined by the highest risk score for any category. See Table 2 for definitions of $N_g$, $N_e$, *and* $N_a$. Modified from Allendorf et al. (1997).

| Population Characteristic | Extinction Risk | | |
|---|---|---|---|
| | **High** | **Moderate** | **Low** |
| Extinction risk from population viability analysis (PVA) | ≥ 20% within 20 yrs | ≥ 5% within 100 yrs but < 20% within 20 yrs | < 5% within 100 yrs |
| | - or any ONE of the following - | - or any ONE of the following - | - or ALL of the following - |
| Effective population size per generation | $N_e \leq 50$ | $50 \leq N_e \leq 500$ | $N_e \geq 500$ |
| *-or-* | *-or-* | *-or-* | *-or-* |
| Total population size per generation | $N_g \leq 250$ | $250 \leq N_g \leq 2500$ | $N_g \geq 2500$ |
| Population decline | Precipitous decline[a] | Chronic decline or depression[b] | No decline apparent or probable |
| Catastrophe | Order of magnitude decline within one generation | Smaller but significant decline[c] | Not apparent |
| Spawner density | $N_a/IP\text{-}km$[d] < 1 | 1 < $N_a/IP\text{-}km$ < MRD[e] | $N_a/IP\text{-}km$ > MRD[e] |
| Hatchery influence[f] | Evidence of adverse genetic, demographic, or ecological effects of hatcheries on wild population | | No evidence of adverse genetic, demographic, or ecological effects of hatchery fish on wild population |

[a] Population has declined within the last two generations or is projected to decline within the next two generations (if current trends continue) to annual run size $N_a \leq 500$ spawners (historically small but stable populations not included) <u>*or*</u> $N_a > 500$ but declining at a rate of ≥10% per year over the last two-to-four generations.
[b] Annual run size $N_a$ has declined to ≤ 500 spawners, but is now stable *or* run size $N_a > 500$ but continued downward trend is evident.
[c] Annual run size decline in one generation < 90% but biologically significant (e.g., loss of year class).
[d] *IP-km* = the estimated aggregate intrinsic habitat potential for a population inhabiting a particular watershed (i.e., total accessible km weighted by reach-level estimates of intrinsic potential; see Bjorkstedt et al. [2005]for greater elaboration).
[e] MRD = minimum required spawner density and is dependent on species and the amount of potential habitat available. Figure 5 summarizes the relationship between spawner density and risk for each species.
[f] Risk from hatchery interactions depend on multiple factors related to the level of hatchery influence, the origin of hatchery fish, and the specific hatchery practices employed.

Second, we collapse the "very high risk" and "high risk" categories of Allendorf et al. (1997) into a single "high risk" category. Whereas discriminating between "high risk" and "very high risk" was critical to Allendorf et al.'s emphasis on prioritizing stocks for conservation, the distinction is less important for our purposes, since either categorization would clearly indicate populations that should not be considered viable over short-to-moderate time frames.

The practical effects of collapsing these two categories are relatively minor, though lead to a configuration and implementation of the viability criteria table that differs somewhat from that of Allendorf et al. (1997). Foremost, we adopt a rule that the assignment of risk to the population is based on the highest risk category for any individual risk metric. For example, a population rated at "high risk" based on effective population size, but moderate or low risk for the other metrics would receive the "high risk" rating. Allendorf et al. (1997) employ a similar strategy, but have an additional rule whereby populations that rank at a certain risk level for more than one metric get elevated to the next highest risk level when categorizing the population (e.g., a population rated at moderate risk for two metrics is considered at high risk overall). For this reason, the criteria listed in our "high risk" and "moderate risk" categories superficially align themselves with the "very high risk" and "high risk" categories, respectively, in Allendorf et al. (1997). In actual application, a population that satisfies a single criterion (as opposed to two or more) receives the same ranking using either the Allendorf et al. (1997) or the NCCCTRT approach. We viewed our configuration of the risk matrix to be somewhat simpler to apply and understand, but note that populations that rank at a given level for multiple metrics should be considered more vulnerable to extinction than populations that rank at that level for a single metric. Finally, we define as "data deficient" populations that are believed to still persist, but where data for evaluating risk are partially or entirely lacking. This category equates to the "special concern" category of Allendorf et al. (1997).

Two extensions we made to the Allendorf et al. (1997) approach were the addition of criteria related to spawner density and to the potential effects of hatchery activities on wild populations. The density criteria are intended to address aspects of spatial structure and diversity that are important to population viability (McElhany et al. 2000), but are not explicitly addressed by the Allendorf et al. metrics. We believe there is a compelling theoretical basis for including these criteria, though acknowledge that, as with other metrics, there is considerable uncertainty surrounding the relationship between the specific metrics and extinction risk. The hatchery criteria consider potential genetic, demographic, and ecological risks associated with the interaction between hatchery and wild fish. Here, the NCCC TRT concluded that simple numerical criteria relating hatchery influence to risk were inappropriate given the substantial variation in how individual hatcheries are operated and the fact that impacts associated with hatcheries are often highly context-dependent. Instead, we propose general narrative criteria related to hatcheries under assumption that each case will require independent analysis of risks. Allendorf et al. (1997) address the issue of hatchery influence in a separate analysis that evaluates the biological consequences of extinction

**Table 2.** Description of variables used to describe population size in the population viability criteria. All expressions of population size refer to naturally spawning adults, inclusive of jacks but exclusive of hatchery fish.

| Population Variable | Description |
|---|---|
| $N_a$ | Total abundance of adult spawners in a year. Related forms that appear in this report include $N_{a(t)}$ = the number of adult spawners in year $t$; and $\overline{N}_{a(geom)}$ = the geometric mean of adult spawner abundance over a specified period (see equation 3, pg. 26) |
| $N_e$ | Effective population size per generation. |
| $N_g$ | Total number of spawners for the generation. Related forms that appear in this report include $N_{g(t)}$ = the running sum of adult abundance at time $t$ for a period equal to one generation (rounded to nearest whole year; see equation 2, pg. 24); and $\overline{N}_{g(harm)}$ = the harmonic mean of the running sums of abundance, $N_{g(t)}$, calculated over a specified period (see equation 1, pg. 24). |

for populations that have been free from such introductions, but do not attempt to develop criteria linking hatchery influence to risk.

Several points of clarification regarding terminology used in this report are required before beginning our discussion of the population viability criteria. First, we use the term "risk category" to describe the possible status (i.e., extinct, high risk, moderate risk, low risk, or data deficient) of a population in relation to either a particular population characteristic or the full suite of characteristics. We use the term "risk metric" to mean those attributes of a population that are measured in order to evaluate risk, and the term "risk criteria" to indicate the specific values of a metric that are used to place a population into a particular risk category for that metric. We also note that in describing population size, our criteria use three different terms: $N_a$, which is number of annual spawners; $N_g$, the number of spawners per generation; and $N_e$, the effective population size per generation (Table 2). The inclusion of population size metrics expressed as functions of both annual run size and the numbers of spawners per generation creates some potential for confusion; however, it is necessary both to provide a generalized table that can be used across all three species (each with a unique mean generation time) within our domain, and to reflect the different time scales over which the specific processes addressed by these criteria occur (e.g., demographic processes that operate at an annual time scale versus genetic processes where generational time scales are more relevant). Table 2 summarizes these different terms for population abundance.
In the sections that follow, we provide a discussion of each criterion listed in the modified Allendorf et al. (1997) table, including the rationale for inclusion of the criteria, the specific criteria associated with low-,

moderate-, and high-risk populations, and guidance on metrics and estimators used in application of the criteria. We also discuss additional considerations that need to be made in evaluating viability using this generalized framework.

### *Extinction Risk Based on Population Viability Analysis (PVA)*

**Rationale:** The first set of criteria in Table 1 follow directly from Allendorf et al. (1997) and deal with direct estimates of extinction risk over a specified time frame based on population viability models. If PVAs are available and considered reasonable, then such analyses may be sufficient for assessing risk. In fact, Allendorf et al. (1997) intended the remaining criteria in the table to be used as surrogates if models for estimating extinction probability were not available, or if parameters required in such models could not be estimated with acceptable accuracy. A number of models for population viability analysis have been proposed (e.g., Samson et al. 1985; Simberloff 1988; Ferson et al. 1988, 1989; Ginzburg et al. 1990; Dennis et al. 1991; Lee and Hyman 1992; Lacy 1993; Lindley 2003). We note, however, that there is considerable discussion in the literature about the value and limitations of PVA models, particularly as it relates to predicting extinction risk in small populations (see review by Beissinger and Westphal 1998; Mann and Plummer 1999; Coulson et al. 2001; Reed et al. 2002). Some specific concerns are discussed under *Metrics and Estimation* below. We also note that if data sufficient to construct a credible PVA model are available, then it is likely that the population can be assessed in relation to most or all of the alternative metrics within Table 1 as well. We therefore recommend using both approaches and comparing the outcomes, as these comparisons may illuminate potential limitations of either approach.

**Criteria:** Consistent with Allendorf et al. (1997), we define high-risk populations as those with greater than a 20% probability of extinction within 20 years; moderate-risk populations as those with at least a 5% probability of extinction within 100 years but less than 20% probability of extinction within 20 years; and low-risk populations as those with less than a 5% extinction probability within 100 years (Table 1).

**Metrics and Estimation:** Population viability models produce estimates of extinction probability over a specified time frame and are thus directly comparable to the criteria. The OCTRT (Wainwright et al., in prep) recommends applying a variety of models and averaging the results of those models due to the fact that outcomes may differ substantially depending on underlying assumptions of the model and the suite of factors considered. Data needs for PVAs vary with the specific model or models used, but in general, most PVAs estimate extinction risk based on at least four factors: current population abundance, intrinsic population growth rate, habitat capacity, and variability in growth rate arising from variation in fecundity,

growth, or survival (Lande and Orzack 1988, Lande 1993; Wainwright et al., in prep.). Thus, at a minimum, data for estimating these population attributes are required.

Although PVAs allow incorporation of population-specific information that can help refine assessment of viability, the use of PVAs must be done cautiously, as there are many limitations to these models. The OCTRT (Wainwright et al., in prep.) identifies several issues to consider when using PVAs to evaluate the status of Pacific salmon. First, PVAs for salmonids are typically based on stock-recruitment models, of which there are several commonly used forms (e.g., Ricker, Beverton-Holt, and hockey-stick). PVA outcomes may differ depending on the underlying stock-recruit model, and there is no general consensus among scientists about which of these models are most appropriate for salmonids. Second, PVAs are subject to statistical error and bias in parameter estimates that may arise from high measurement error in spawner abundance estimates or high environmental variation. Coulson et al. (2001) note that for PVAs to be meaningful, data must be of sufficiently high quality that estimates of the shape, mean, temporal variance, and autocorrelation (which could be caused by density-dependent processes) of the distribution of vital rates or population growth rate are accurate. Third, most models incorporate only a small subset of factors that may influence extinction risk. More complicated PVA models require more data, though it is not always clear that increasing complexity of models leads to superior performance, particularly when dispersal plays a role in population dynamics. Fourth, models are highly sensitive to assumptions about dispersal from other populations (Hill et al. 2002). Fifth, because PVA models represent projection into the future, the results depend critically on assumptions about future conditions, which cannot possibly be known (Coulson et al. 2001). Models that assume that the future will be similar to the recent past (i.e., the period during which data used to parameterize PVA models are collected) may be inaccurate or misleading if, as climate models suggest, the future climate is likely to differ substantially from that of the present. And sixth, obtaining reliable absolute predictions of extinction probability is difficult, as is verifying model predictions. These limits have caused some authors to suggest that PVAs should not be used to determine minimum viable population size or the specific probability of reaching extinction (Reed et al. 2002). Nevertheless, despite these limitations and concerns, PVAs represent an important tool for incorporating population-specific differences in vital rates, habitat quantity and quality, and other factors influencing persistence into assessments of extinction risk.

***Effective Population Size/Total Population Size Criteria***

**Rationale:** The first two surrogate extinction risk criteria—the effective population size criterion and the total population size criterion—are intended to address risks associated with inbreeding and the loss of genetic diversity within a population. Genetic variability is the source of adaptive potential of a population; thus, losses of genetic variability decrease the ability of a population to respond to changing environmental conditions (Allendorf et al. 1997). Furthermore, as populations decrease in size, demographic stochasticity becomes more important (Lande 1998) and inbreeding depression and genetic drift may reduce the average fitness of the population (Meffe and Carroll 1997), resulting in a greater extinction risk over short time scales. These deleterious genetic effects are a function of $N_e$, the effective population size (i.e., the size of an idealized population, where every individual has an equal probability of contributing genes to the next generation, having the same rate of genetic change as the population under study; Wright 1931), rather than the total number of spawners per generation, $N_g$. For most organisms, effective population sizes are substantially smaller than total population size because of variance in family size, unequal sex ratios, and temporal variation in population size (Lande 1995; Hartl and Clark 1997; Meffe and Carroll 1997).

The total population size criteria serve as alternative criteria when reliable direct estimates of effective population size are not available, which is likely to be the case for most populations. The criteria are based on an assumption that the ratio of effective spawners to total spawners ($N_e/N_g$) in most salmonid populations is on the order of 0.2 (Allendorf et al. 1997); thus, they are directly related to the proposed effective population size criteria.

**Criteria:**

*Effective population size per generation ($N_e$)* — We adopt three criteria related to effective population size to reflect these genetic risks. Populations are rated at high risk of extinction when $N_e \leq 50$. Below $N_e$ of 50, populations are believed to be at high risk from genetic effects, such as inbreeding depression, genetic drift, and fixation of deleterious alleles (Franklin 1980; Soule 1980; Nelson and Soule 1987). Populations are considered at moderate risk of extinction when $50 < N_e < 500$, and populations are at low risk of extinction when $N_e \geq 500$ (Table 1).

Selection of $N_e = 500$ as a threshold between low and moderate risk has been the subject of considerable discussion in the literature. Allendorf et al. (1997) proposed that long-term adaptive potential begins to be compromised due to random genetic drift at $N_e < 500$, though they note that if populations are reproductively isolated from other populations then the $N_e$ required to prevent loss of genetic variation

might be as much as an order of magnitude greater (i.e., $N_e$ = 5,000; Nelson and Soule 1987). Lande (1995) has argued that the models used to derive the $N_e$ > 500 rule assume that all mutations are mildly deleterious, whereas subsequent work suggests that most mutations with large effects are strongly detrimental, with perhaps only 10% being mildly deleterious. Thus, Lande (1995) proposed that $N_e$ of 5,000, rather than 500, may be necessary to maintain normal levels of adaptive genetic variance in quantitative characters under a balance between mutation and genetic drift. On the other hand, the models of Franklin (1980) and Soule (1980) also assume that populations are closed to immigration (Lindley et al. 2007). Low levels of immigration—as few as one or two individuals per generation—can be sufficient to prevent the loss of genetic diversity through drift (Lacy 1987). For most salmon and steelhead populations within the NCCC recovery domain, such rates of immigration among populations are reasonable, or at least were so under historical conditions. Because violations of the assumptions discussed act in opposition to one another, we accept the $N_e$ = 500 recommendation of Allendorf et al. (1997) as a reasonable criterion for defining the threshold between populations at low and moderate risk.

*Total population size per generation ($N_g$)* — The total population size criteria assume that the $N_e/N_g$ ratio for salmonids is approximately 0.2; thus, the criteria are directly proportional (five-fold higher) than those for effective population size based on the rationale given above. Populations are considered at high risk of extinction at $N_g \leq 250$, moderate risk of extinction where $250 < N_g < 2500$, and low risk of extinction where $N_g \geq 2500$. We re-emphasize that the total population size criteria are directed at genetic concerns and that reliance on $N_g$ as a metric incurs greater uncertainty as a consequence of uncertainty in the $N_e/N_g$ ratio.

**Metrics and Estimation:**

*Effective population size per generation ($N_e$)* — The specific metric to be evaluated will depend on which approach to $N_e$ estimation is used (see below). For genetic methods, the precision of the $N_e$ estimate is dependent on numerous factors, including sample sizes, number of alleles surveyed, and number of generations between samples (Waples 1989); thus, it is difficult to generalize about an appropriate formulation or temporal scale of sampling

Although direct estimates of $N_e$ based on genetic or demographic methods are theoretically the most accurate for evaluating genetic risks to populations, $N_e$ is extremely difficult to estimate in natural populations (Waples 1989, 2002b; Heath et al. 2002). Estimation of $N_e$ from demographic data requires detailed information on the mean and variance among individuals of relative reproductive success (Nunney and Elam 1994; Waples 2002b). Such information is difficult to obtain even in cultured

populations, and impossible to gather in wild populations without complete, genetically determined pedigrees. To overcome these difficulties, several authors have developed methods for indirectly estimating $N_e$ using molecular genetic data. One such approach, the temporal method, involves estimating changes in allelic frequencies through time, with the change expected proportional to $N_e$ (Waples 1989, 1990; Williamson and Slatkin 1999). Such methods require collection of genetic data from two points in time that are separated by at least a full generation (preferably longer), may produce estimates that are either biased or have large variance, can be computationally complex, and are typically based on a set of assumptions (e.g., populations are isolated and genetic markers are selectively neutral) that may not be true (Williamson and Slatkin 1999). Thus, while estimates of $N_e$ derived from genetic data can be valuable, care must be taken in their interpretation.

*Total population size per generation ($N_g$)* — We recommend that $N_g$ be approximated as the harmonic mean of the running sum of adult spawner abundance over the mean generation time for the species and population (Li 1997). Mathematically, this can be expressed as follows:

(1) $$\overline{N}_{g(harm)} = \frac{1}{\frac{1}{n}\sum_{t=1}^{n}\frac{1}{N_{g(t)}}}$$

where $N_{g(t)}$ is the running sum of adult abundance at time $t$ for a period equal to the mean generation time $k$ of the population (rounded to the nearest whole year)

(2) $$N_{g(t)} = \sum_{i=t-k}^{t} N_{a(i)}$$

and $n$ is the number of years for which the running sum can be calculated. The estimate should be based on counts of naturally spawning fish (exclusive of hatchery-origin fish, but inclusive of jacks[7]) over a period representing at least four generations. Use of the harmonic mean, which gives greater weight to low values of $N_g$, reflects concern over the potential long-term consequences of a genetic bottleneck on population persistence; populations that have experienced a recent bottleneck may require extended periods of relatively high abundance to be considered no longer at risk (see discussion on page 25).

[7] Allendorf et al. (1997) note that spawner survey data frequently exclude jacks in counts of adult fish. However, jacks may contribute genetically to subsequent generations and thus need to be accounted for. For example, Van Doornik et al. (2002) estimated that the effective proportion of two-year-old males was 35% in two wild coho populations. Some adjustment for the relative reproductive success of jacks versus older adults may be warranted.

Satisfying the low-risk criterion also requires demonstration that $N_g$ remains above critical thresholds during periods of low marine survival due to unfavorable ocean conditions.

As noted above, the total population size criteria are based on an assumption that the $N_e/N_g$ for Pacific salmonids is generally about 0.2. This ratio is based on the recommendation of Allendorf et al. (1997), who cite personal communication with R. Waples (NMFS, Northwest Fisheries Science Center). Subsequent work with Chinook salmon (Waples 2004a), steelhead (Heath et al. 2002), and coho salmon (Wainwright et al., in review) has suggested that for many populations, the $N_e/N_g$ ratio likely falls within a range of approximately 0.05 to 0.30, though Ardren and Kapucinski (2003) reported a substantially higher ratio (0.5–0.7) for a steelhead population in Washington. Based on these studies, we conclude that the value of 0.2 suggested by Allendorf et al. (1997) remains a reasonably precautionary default value for relating total population size per generation to effective population size in the absence of other information, but should be adjusted as information on the $N_e/N_g$ ratios for specific populations becomes available

In applying the total population size criteria, we note that conditions that may lead to violations in the 0.2 $N_e/N_g$ assumption should be evaluated. Factors that likely contribute to an $N_e/N$ ratio of less than 0.2 include highly skewed sex ratios, sex-biased differences in dispersal, and substantial among-family variation in survival rates (Gall 1987). The ratio of census size and effective population size may also be affected (both increasing and decreasing it) by the spatial structure of a population (Whitlock and Barton 1997), as well as by the degree of isolation of the population and hence the level of exchange of individuals among populations. And finally, total population size may be a poor predictor of long-term mean effective population size in populations that have undergone a recent population bottleneck. Where severe population bottlenecks have occurred, recovery in total population size may occur rapidly, whereas recovery of genetically effective population size may take a much longer time. The rate of recovery from genetic bottlenecks depends on the natural mutation rate and, perhaps more importantly for many salmonid populations, infusion of new variation from immigrants into the population. However, there is little information with which to speculate about how long it may take these processes to replace genetic variation in salmon and steelhead populations. Nevertheless, we advise that when there are clear indications that populations have recently declined below the proposed viability thresholds, additional genetic evidence should be gathered to demonstrate that populations are no longer at appreciable risk. We discuss this issue further in the section title *Critical Considerations for Implementation* on page 59.

***Population Decline Criteria***

**Rationale:** The population decline criteria address increased demographic risks associated with rapid or prolonged declines in abundance to small population size. Populations that experience unchecked declines may reach levels at which the probability of extinction from random demographic or environmental events increases substantially (Soule and Simberloff 1986), and if declines continue unabated, deterministic extinction results. As defined by Allendorf et al. (1997), the criteria have two components: a downward trend in population size (an indication that the population is not replacing itself) and a minimum annual adult run size. Each of these components is evaluated in the context of the other.

**Criteria:** We adopt criteria consistent with Allendorf et al. (1997), with minor modifications. A population is considered at high risk if it meets any of the following three conditions: (1) the population has undergone a recent decline in abundance (within the last two generations) to an annual run size, $N_a$, of fewer than 500 fish; (2) the population currently has an average annual run size of $N_a > 500$ but is declining at a rate of $\geq$10% per year over the last two–four generations[8], or (3) the population currently has an annual average run size of $N_a > 500$ but has been declining at a rate that, if it continued, would cause $N_a$ to fall below 500 within two generations. In this high-risk category, the progeny/parent ratio is less than one, indicating that populations are failing to replace themselves. Populations that have declined to annual run sizes at or below 500 spawners but that are currently stable (i.e., progeny/parent ratio is $\geq 1$) *or* populations that are above 500 spawners but continue on a downward trajectory (i.e., progeny/parent ratio is $< 1$) are considered at moderate risk of extinction. By extension, populations at low risk of extinction are those with annual run sizes of greater than 500 and mean progeny/parent ratios of $\geq 1$ (Table 1). Although Allendorf et al. (1997) do not specifically discuss their rationale for choosing 500 fish as the threshold between risk categories, we adopt their criteria to foster consistency between the two approaches.

**Metrics and Estimation:** The population decline criteria require estimation of two parameters: mean annual population abundance, $\overline{N}_a$, and population trend, $T$. We recommend using the geometric mean of spawner abundance for the most recent 3–4 generations as an estimator for $\overline{N}_a$:

[8] We note that it might be reasonable to argue that populations at high abundance (e.g., $N_a > 10{,}000$ individuals) might experience declines on the order of 10% or more per year for two generations without appreciably increasing the risk of extinction. However, currently within the NCCC Recovery Domain, there is little evidence to suggest that any salmon or steelhead populations approach such abundances. Should such circumstances arise in the future, it would be appropriate to re-evaluate this element of the population decline criteria, particularly if information on potential sources of variation in population size is available.

(3) $$\overline{N}_{a(geom)} = \sqrt[n]{N_{a(1)} N_{a(2)} N_{a(3)} \ldots N_{a(n)}}$$

where $N_{a(t)}$ is the total number of adult spawners in year $t$, and $n$ is the total number of years of available data. The geometric mean is slightly more conservative than the arithmetic mean, in that low values have greater influence on the mean. Mean spawner abundance should be based on counts of naturally spawning fish, exclusive of hatchery-origin fish. Our recommendation to use this estimator is consistent with analyses developed for previously published status reviews (e.g., Good et al. 2005).

We note that the abundance threshold suggested by Allendorf et al. (1997) as indicative of high risk ($N_a$ < 500 spawners per year) is adopted as appropriate in the absence of information on intrinsic growth rate (i.e., growth rate at low population density, when populations are released from intraspecific competition). Population models that predict extinction probability can be highly sensitive to assumptions about intrinsic growth rate and environmental stochasticity (which leads year-to-year variation in population growth rate)(see e.g. Lande 1993; Foley 1994; Boughton et al. in prep.). A population with $N_a$ < 500 might have a relatively low probability of extinction if the intrinsic growth rate were high and variation in growth rate low, but a high probability of extinction if the reverse conditions were true. Consequently, relaxing this criterion would require demonstration that a population of fewer than 500 spawners would not be at heightened risk of extinction[9].

Population trend, $T$, is estimated as the slope of the natural logarithm of the generational running sum of abundance, $N_{g(t)}$, regressed against time. Estimation of trend requires a time series of adult abundance for at least two generations and up to four generations[10]. It may be possible to estimate population trends using indices of abundance, so long as the indices truly reflect overall population trends. However, as estimates of total abundance are needed to evaluate other criteria in Table 1, use of total population estimates will generally be preferable to indices.

Interpretation of population trends is confounded by the fact that salmonid populations may undergo natural fluctuations at time scales ranging from annual to decadal or longer, leading to highly variable estimates of trend. As most estimates of $T$ for populations of salmonids within the NCCC Recovery

[9] Model results from Lindley (2003) suggest that a minimum of 30 years of data is likely needed to obtain unbiased estimates of variance in population growth rate within reasonable confidence limits. Such lengthy time series may be needed to accurately estimate variance when there are longer-term trends in abundance and productivity.

[10] The population decline criteria are intended to capture recent, relatively rapid declines in abundance. Over longer periods of time, populations declining at less than 10% per year may still be at high risk of extinction. In the NCCC Recovery Domain, there are few existing time series of population abundance spanning longer than 10 years. In these cases, long-term trends should be evaluated independently of the proposed population decline thresholds.

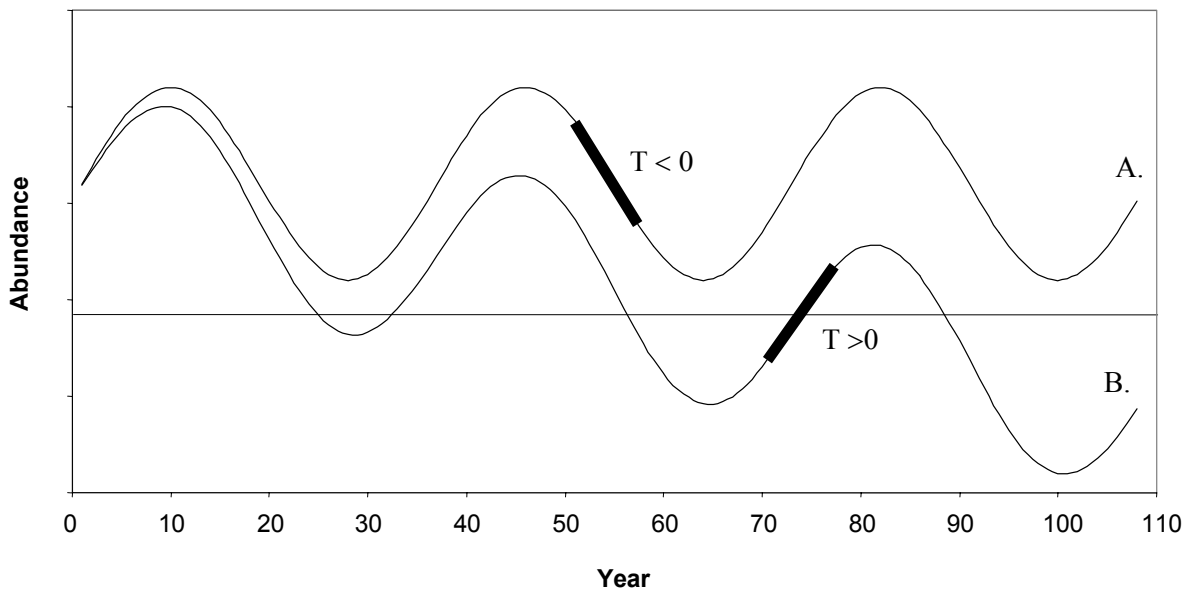


**Figure 2.** Hypothetical fluctuations in the abundance for a healthy population showing no long-term trend in abundance (A) versus a population undergoing a long-term decline (B). Thick lines depict periods where short-term population growth rates are in opposition to the long-term patterns. Figure based on a conceptual model by Lawson (1993).

Domain are likely to be based on relatively short time series of abundance, interpretation of *T* needs to be made in the context of marine and freshwater survival during the period of record and other population metrics of viability. For instance, healthy populations at little risk of extinction almost certainly experience periods of negative population growth without being at heightened risk of extinction (Figure 2, Line A). Conversely, populations experiencing a long-term downward trend in abundance may exhibit a short-term positive trend response to periods of favorable ocean conditions (Figure 2, line B). This raises questions regarding the reliability of short-term population trend as a metric in assessing viability. Our decision to include this metric is based on the fact that the criteria proposed herein are being developed for ESUs that have already been listed under ESA. In the vast majority of cases, most populations within these ESUs are considered depressed, often severely so. In this context, it would seem unreasonable to conclude that a population has recovered if it continues to decline in abundance. In future scenarios, demonstration that populations can remain above viability thresholds for other population metrics (e.g., population size, effective population size, and population density) during periods of both favorable and unfavorable conditions and that the population responds positively and rapidly to improvement in marine conditions might justify relaxation of the population trend requirement. In contrast, for populations that

otherwise satisfy viability criteria, short-term declines that lack an obvious mechanism (e.g., change in ocean conditions) would be cause for renewed concern.

### *Catastrophe, Rate and Effect Criteria*

**Rationale:** Catastrophes are large environmental perturbations that produce rapid and dramatic declines in population abundance (Shaffer 1987; Lande 1993). Such events are distinct from environmental stochasticity that arises from the continuous series of small or moderate perturbations that affect population growth rate (e.g., interannual variation in climate, ocean conditions, food resources, populations of competitors, etc.). Some population modelers have suggested that catastrophes may be more important than either environmental or demographic stochasticity in determining average persistence times of populations (Shaffer 1987; Pimm and Gilpin 1989; Soule and Kohm 1989), though Lande (1993) argues that the relative risks of environmental stochasticity and catastrophes cannot be generalized, being dependent on the mean and variance of population growth rate and the magnitude and frequency of catastrophes. Regardless, there is agreement that populations are at increased risk of extinction following a major reduction in abundance.

**Criteria:** Within the Allendorf et al. (1997) framework, the goal of the catastrophe criteria is to capture situations where a population has experienced a sudden shift from a no-risk or low-risk status to a higher risk level. Allendorf et al. (1997) defined the very high-risk criterion for catastrophic declines as a 90% decline in population abundance within one generation, and the high-risk criterion as "any lesser but significant reduction in abundance due to a single event or disturbance." These criteria depart to some degree from the IUCN criteria (Mace and Lande 1991), which proposed average population reductions over 2–4 generations of 50%, 20%, and 10% to correspond to critical, endangered, and vulnerable status, respectively. Allendorf et al. (1997) offer limited discussion of the reasoning behind these differences, noting only that Pacific salmonid stocks often exhibit substantial natural variation in abundance. We surmise that Allendorf et al. felt that declines of the magnitude specified in the IUCN criteria may be well within the range of natural variation for salmonid populations and thus adopted more stringent criteria. Further, we note that the rates of decline listed in the IUCN criteria for catastrophic risk are generally subsumed by the Allendorf et al. (1997) population decline criteria, which are adopted in this report.

We adopt the criteria of Allendorf et al. (1997) as they stand, considering populations that have experienced a 90% decline in abundance within one generation to be at "high risk" of extinction, and those experiencing a lesser but significant decline to be at "moderate risk" (Table 1). Although Allendorf

et al. (1997) do not explicitly define what constitutes a "lesser but significant decline" in abundance, we consider events such as the failure of a year class due to a catastrophic disturbance to be an example of such an event.

**Metric and Estimation:** We define the estimator of catastrophic decline, *C*, as the maximum proportional change in abundance from one generation to the next. Formally, this can be expressed as follows:

$$\hat{C} = \text{maximum}\left(1 - \frac{N_{g(t)}}{N_{g(t-2h)}}\right) \quad (4)$$

where $N_{g(t)}$ is the running generational sum of adult spawners in year *t,* and $N_{g(t-2h)}$ is the running generational sum at time *t-2h,* where *h* is mean generation time (rounded to the nearest whole year)[11]. By this formulation, estimation of $\hat{C}$ requires a time series of adult spawner abundance of at least 3 generations (but see exception below), and should be based on naturally spawning fish, exclusive of hatchery origin fish. As with the population decline criteria, it may be possible to evaluate catastrophic declines using an index of abundance (rather than a total population estimate), provided that the index faithfully reflects the characteristics of an entire population.

Although it may seem more intuitive to use the running sum in the most recent generation, $N_{(t-h)}$, in the denominator of equation (3), the value of $\hat{C}$ is highly influenced by the pattern of abundance during the transition from a period of high abundance to a period of low abundance since it is based on a running sum of abundance. For example, consider the two time series of abundance depicted in Figure 3. Line A illustrates a situation where population hovering around an average of about 50,000 spawners in years 1 through 13, drops in a single year to an average of about 5,000 spawners from year 14 to 30. Line B illustrates the same scenario, but where the decline occurs over a generation (3 years), rather than in a single year. Were $N_{(t-h)}$ used in the denominator, value of $\hat{C}$ would exceed the threshold (90%) only for the scenario shown in line A, where the decline occurs over a single year. In scenario B, the intermediate population abundances in years 14 and 15 effectively moderate the value of $\hat{C}$, such that the 90% criterion is never exceeded, despite the order of magnitude drop in abundance that occurred within 3 years. Use of $N_{(t-2h)}$ in the denominator assures that both scenarios are captured by the criteria.

[11] For example, for a coho salmon population with a mean generation time of three years, C at $t = 9$ would be 1 minus the sum of adult abundance for years 7, 8, and 9 divided by the sum of abundance for years 1, 2, and 3.

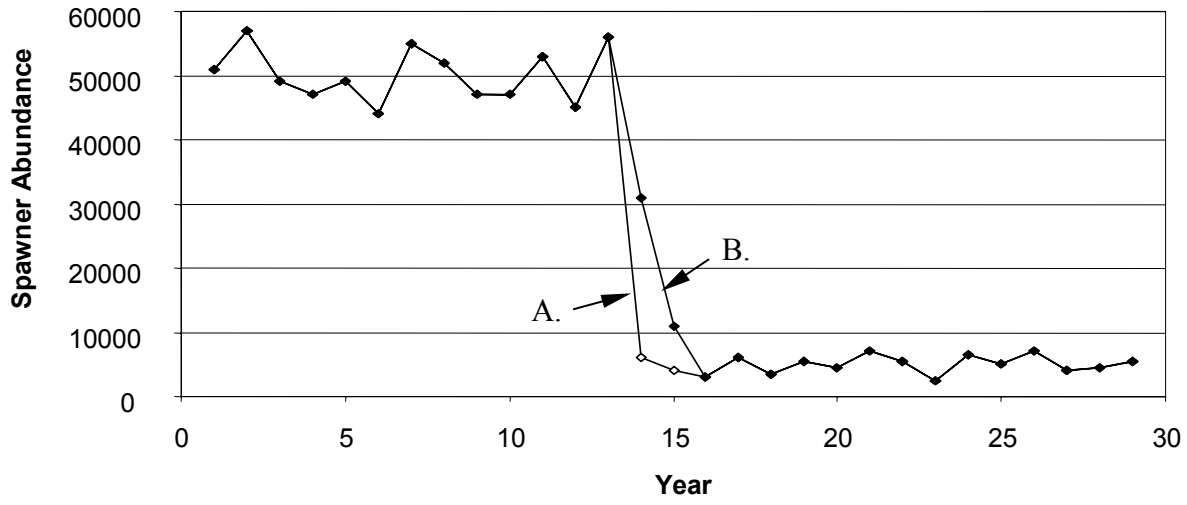


**Figure 3.** Hypothetical example where an order of magnitude decline in abundance occurs over a single year (A) versus three years (B). See text for elaboration.

We note that there may be instances where a population either exhibits a clear and precipitous decline in abundance or suffers a major loss or alteration of habitat (e.g., landslide causing a passage blockage, chemical spill affecting an entire year class, or some other catastrophic event). Clearly, in such cases, an immediate elevated risk designation could be warranted, even in the absence of a longer time series of data.

For longer time series where a population experienced a catastrophic decline in abundance at some time during the past, consideration needs to be given to the response of the population following the catastrophic decline. For example, in Figure 4, we depict three distinct trajectories in population abundance following a catastrophe, including an increasing trend in abundance (Line A), a relatively stable abundance (Line B), and a decreasing trend in abundance (Line C). Because the catastrophic decline criteria are intended to capture heightened demographic risks associated with a rapid decline in abundance, scenarios A and B are suggestive that, while the population did experience a rapid declines exceeding the low-risk threshold, the population has since exhibited signs of stabilizing or increasing. In such instances, the castastrophic decline criteria needs to be evaluated in the context of information on patterns of marine survival or more-or-less permanent, naturally caused changes in system capacity (for example, blockage of habitat due to a natural landslide or other disturbance where the blockage is expected to persist for hundred or thousands of years).

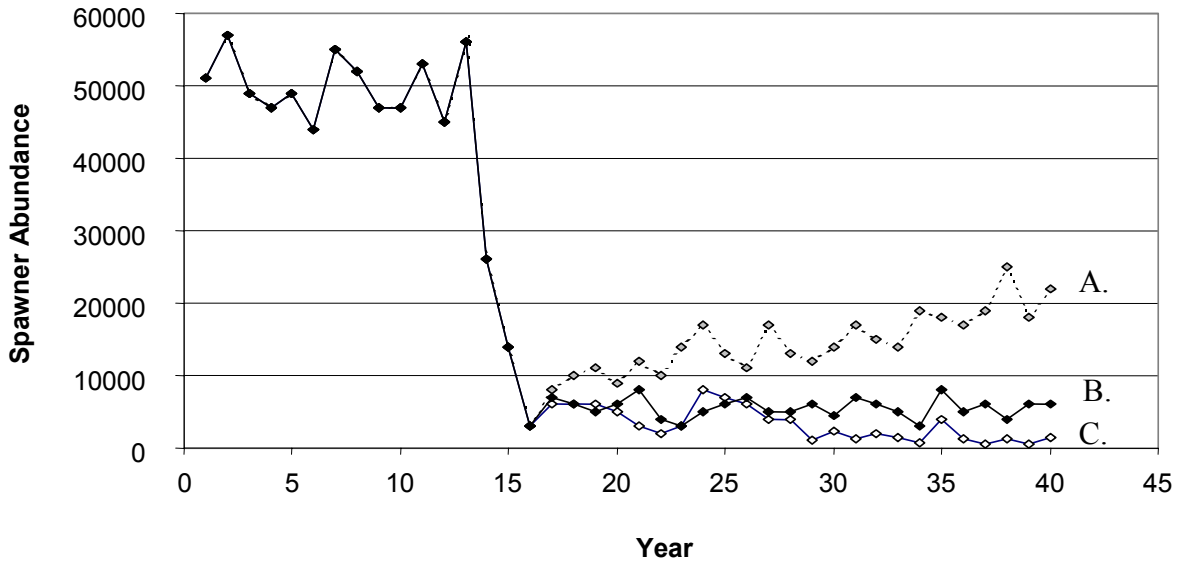


**Figure 4.** Hypothetical example catastrophic decline in abundance, showing three possible trajectories: A) apparent trend toward recovery from the decline, B) relatively stable abundance following the decline, and C) continued downward trend in abundance.

Allendorf et al. (1997) provide no details about what might be considered a "lesser but significant decline in abundance." We conclude that the most likely occurrence that would qualify as a moderate risk of extinction would be the loss or severe reduction in an individual year class due to a catastrophic disturbance (e.g., fire, landslide, severe flood or drought, chemical spill, or some other similar catastrophe). Because the risk associated with such an event is likely to vary substantially depending on specific circumstances such as the size of the population in other year classes and the degree of life-history variation (which influences how rapidly a population might recover from such a loss), we do not propose numeric thresholds for moderate risk and instead suggest that such risk will need to be evaluated on a case-by-case basis.

### *Spawner Density Criteria*

**Rationale:** The spawner density element of the viability criteria is intended primarily to fill a perceived gap in the Allendorf et al. (1997) framework with respect to population attributes identified as important to persistence in the VSP framework: spatial structure and diversity. These characteristics of populations influence viability by spreading risk through time and space and by contributing to the resiliency of populations to natural and human-caused disturbances. Historically, populations making up an ESU undoubtedly differed in average abundance as a function of differences in both the total habitat available

for spawning and rearing and the relative capacities of those habitats. Additionally, the distribution of individuals across large and potentially diverse watersheds likely further enhanced the probability of populations persisting over the long term. For example, populations where spawning occurs in multiple, relatively discrete areas are less vulnerable to localized (reach or subwatershed) disturbances such as fires or landslides, and have greater potential to recovery from such disturbances, since unaffected portions of the population can both sustain the population following the disturbance and provide colonizers to repopulate the affected habitats. Further, populations distributed over a large watershed have the potential to experience a broader range of environmental conditions, leading to greater phenotypic and genotypic diversity. Life-history variation (e.g., variation in the age and size of individuals at smoltification and maturity) potentially buffers populations from natural fluctuations in both freshwater and marine conditions, spreading risk through both space and time (den Boer 1968; Hankin and Healey 1986; Hankin et al. 1993; Mobrand et al. 1997; Hill et al. 2003). Greater genetic diversity increases the ability of a population to adapt to changes in environmental conditions over the long term. As a population departs from its historical pattern of distribution and abundance, through loss or degradation of habitat, the probability of the population persisting likely decreases as well, though numerous factors will determine how far a population can depart from historical conditions and still remain viable.

At the opposite end of the spectrum, populations that have been reduced in number due to severe and widespread degradation of habitat may be subject to directional demographic processes that result in heightened extinction risk. Specifically, at very low densities, populations may experience a reduction in per capita growth rate with declining abundance, a phenomenon referred to as *depensation*. Most population growth models typically assume that per-capita growth rate generally increases as population density decreases, a result of reduced intraspecific competition. However, if populations are reduced to extremely low densities, a variety of mechanisms can lead to reduced per-capita growth rate including reduced probability of fertilization (e.g., failure of spawners to find mates), inability to saturate predator populations, impaired group dynamics, or loss of environmental conditioning (Liermann and Hilborn 2001; Montgomery et al. 1996). Depensation can result in a negative feedback that, if unchecked, accelerates a decline toward extinction.

High densities of spawning salmonids serve the additional role of providing marine-derived nutrients from salmon carcasses, which help maintain the productivity of aquatic ecosystems. A growing body of literature has documented the substantial contribution that salmon carcasses play in the nutrient budgets of streams in the Pacific Northwest (Bilby et al. 1996, 1998, and 2001; Cederholm et al. 1999; Gresh et al. 2000; Gende et al. 2002; Naiman et al. 2002; Schindler et al. 2003). Carcasses constitute important

sources of nitrogen and phosphorous, which fuel primary production in stream ecosystems, and provide a direct source of food to juvenile salmon (Bilby et al. 1998). Reductions in abundance and spatial distribution of salmonid populations may thus fundamentally reduce the capacity of the streams to support salmonids, creating a negative feedback that could affect long-term population persistence or slow recovery. For example, Scheuerell et al. (2005) suggest that the reductions in the abundance of spring/summer Chinook salmon in the Snake River basin may have resulted in a shift to a less productive state, as evidenced by compensatory mortality in Chinook juveniles even though populations were far below their historical abundance (Achord et al. 2003), as well as failure of smolt recruits per spawner to rebound in years of higher adult abundance. Recognition of this important role has led to a growing call for the link between salmon-derived nutrients and system productivity to be considered when setting salmon recovery goals (Gende et al. 2002; Peery et al. 2003; Scheuerell et al. 2005). And though additional research will be needed before escapement goals for ensuring maintenance of ecosystem (and salmon) productivity based on nutrient subsidies can be established (Bilby et al. 1998; Gende et al. 2002), requiring minimum spawner densities increases the likelihood that such benefits will be maintained or at least not further eroded.

As fixed values, other metrics in the viability table (the effective population size criteria and population size element of the population decline criteria) do not account for these historical among-population differences in total habitat available for spawning and rearing, the relative productive capacity of those habitats, the potential role of spatial structure and diversity in population persistence, the role of nutrient subsidies in maintaining ecosystem productivity, or the possibility of depensation if individuals are sparsely distributed across the landscape. It seems particularly problematic, for example, to conclude that a population is viable at an $N_e$ of about 500 (or $N_g$ of 2,500) when historically that population was much, much larger. An effective population size of 500 fish per generation in a small watershed might seem reasonable, but a population with the same number of fish spread at low densities throughout a much larger watershed could be at moderate or high risk of extinction. Even if the 500 fish per generation were consistently concentrated in a core habitat within a watershed, reducing the risk of depensation, the risk of extinction from a single catastrophe (e.g., flood, landslide, fire) would be higher. Equally important, in either scenario the smaller population's functional contribution to ESU viability would be substantially diminished, even if the population remained strictly viable.

We propose using criteria related to spawner density to address these issues of spatial structure and depensation risk. In developing these criteria, we operate from the following set of assumptions:

- **For independent populations, the historical distribution and abundance of adult spawners represents reference conditions for which extinction risk was likely low and the population made its greatest contribution to ESU viability.** Under these conditions, populations likely tended toward their carrying capacity, and the resilience imparted by spatial structure, diversity, and ecosystem productivity (i.e., contribution of marine-derived nutrients) made it unlikely that the population would go extinct in the absence of a large-scale catastrophe.

- **The farther a population departs from its historical condition, the greater its extinction risk and the higher the uncertainty associated with its viability**. Although some departure from historical conditions due to diminished habitat quality or reduced spatial distribution (with incumbent effects on diversity) may have minimal influence on population persistence, the more restricted and/or fragmented the distribution of the population becomes, the higher its extinction risk.

- **How far a population can deviate from its historical condition and remain viable depends, in part, on how large the population was and how it was distributed historically.** Thresholds defined for the minimum amount of potential habitat (*IP-km*) required for viability in isolation are based on an assumption that, under historical conditions, populations were at or near a carrying capacity. For historically small populations (i.e., those near the IP threshold for independence), reductions in abundance or distribution would likely move this populations below levels required for viability. For populations in larger watersheds, a comparable percentage reduction in habitat is less likely to result in a substantial increase in extinction risk.

- **At extremely low densities, populations may be at heightened risk of extinction due to depensation.** Although demographic and environmental variability can make it very difficult to detect depensation in fish populations, the consequences of depensation are sufficiently severe to warrant consideration of depensatory processes when populations are at very low densities.

The first three assumptions relate directly to the establishment of low-risk thresholds, where the key question is "how far can a population depart from historical conditions and still remain viable?" This is a difficult question to answer, given that the quantitative basis for relating spatial structure, diversity, and ecosystem productivity is presently limited. The last assumption deals directly with establishment of a high-risk threshold, where the key question is "at what densities is depensation likely to occur in salmonid populations?" This too is a challenging question, as detecting depensatory processes in natural

populations has proven difficult. Despite these acknowledged uncertainties, the NCCCTRT believes that reasonable criteria can be developed from these general principles.

**Criteria:** The spawner density criteria define two thresholds. The first, which distinguishes between populations at high versus moderate risk, is based on potential depensation effects. The second defines the threshold between moderate and low risk based on spatial structure, diversity, and productivity concerns. Populations potentially at high risk of depensation are defined as those with average spawner densities of fewer than 1 adult spawner per *IP-km*. For the low-risk threshold, we propose density criteria that vary as a function of both species and population-specific estimates of potential habitat capacity (Figure 5).

For the smallest watersheds capable of supporting viable populations (as estimated based on *IP-km*), low-risk populations are defined as those exceeding 40 spawners per *IP-km*, a value assumed to approximate a natural carrying capacity for salmonids systems (see discussion below). For larger watersheds, required densities decrease to a minimum of 20 spawners/*IP-km* (Figure 5) based on the assumption that larger populations can depart farther from historical conditions before extinction risk is substantially increased.

Defining the density at which depensation is likely to occur is difficult due to high variability and few observations at low abundances in most spawner-recruit datasets (Liermann and Hilborn 1997, 2001). Nevertheless, several authors have attempted to define thresholds at which depensation appears to occur in salmonids. Based on spawner-recruit data for coho populations, Barrowman (2000; cited in Chilcote et al. 2005 and Wainwright et al., in prep), suggested that depensation may become a factor at spawner densities of 1 female per km. Likewise, Barrowman et al. (2003) found little evidence of depensation in coho salmon unless densities were less than 1 female/km. Assuming a 50:50 sex ratio, these values equate to 2 adults per km. Based on analysis of coho populations that went extinct in the lower Columbia River during the 1990s, Chilcote (1999) suggested that populations were unlikely to recover if their densities fell below about 2.4 adults/km. Similarly, Sharr et al. (2000), suggested that coho populations at densities of fewer than 2.4 adults per km should be considered “critical” based on potential risks of depensation. Based on these data, the OCTRT (Wainwright et al., in prep.) concluded that depensation risks were very likely at spawner densities of 0.61 spawners per km (1 spawner per mile). For our purposes, we chose to use *IP-km* in the denominator in order to account for potential differences in habitat

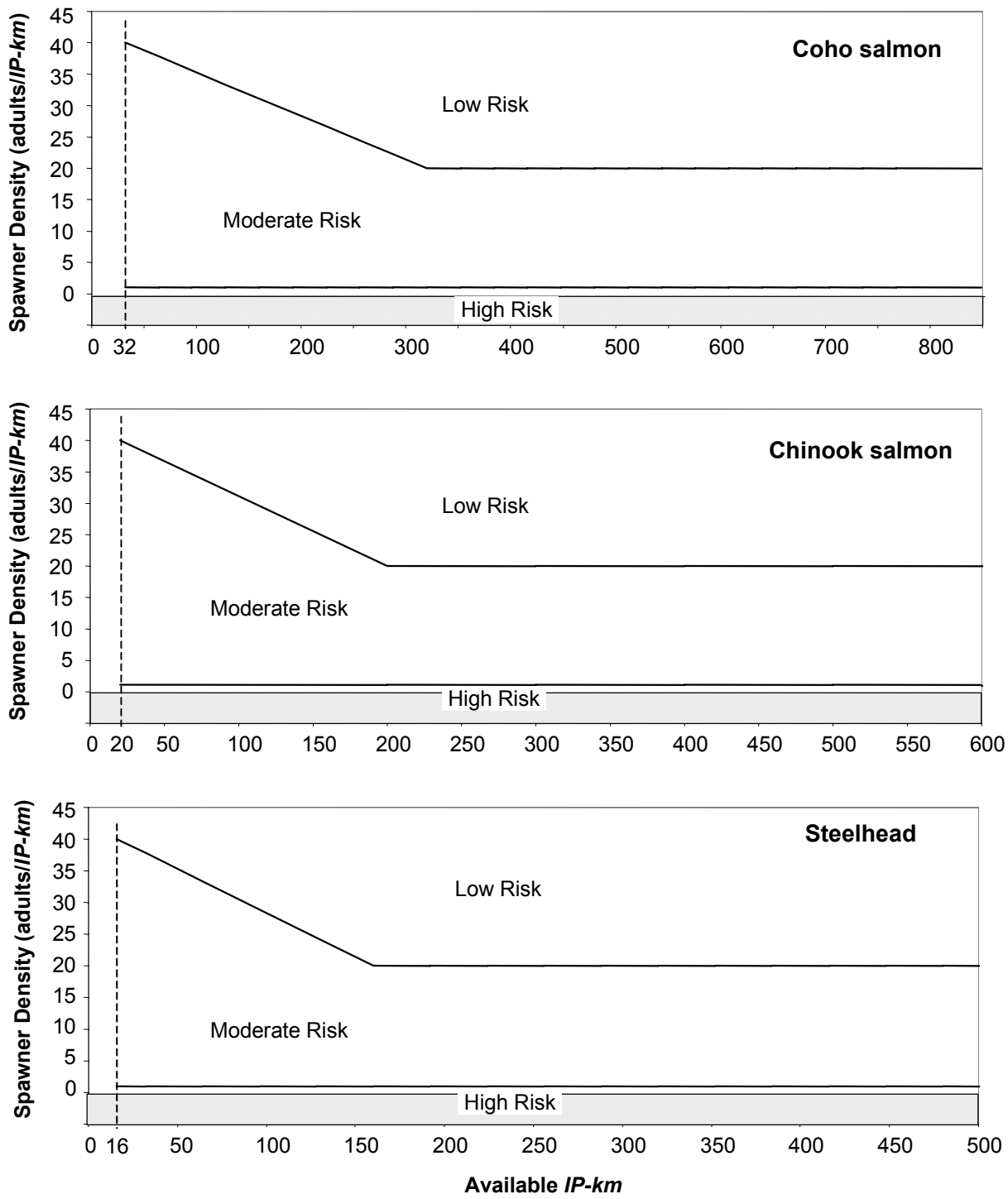


**Figure 5.** Relationship between risk and spawner density as a function of total intrinsic habitat potential for coho salmon, Chinook salmon, and steelhead. Note that scale of *x* axis varies among species. Values above upper lines indicate populations at low risk; values below this line are at moderate risk. Values below 1 spawner/*IP-km* are at high risk for all species. Dashed vertical lines indicate minimum *IP-km* for independent populations.

quality among watersheds.[12] Since the ratio of *IP-km* to total km is about 0.6 for coho salmon, the OCTRT rule of 0.6 fish per km equates to approximately 1 fish per *IP-km*, the criterion we propose. In adopting this criterion, we recognize that the empirical evidence supporting depensation in salmonid populations remains somewhat limited. However, we heed the recommendation of Liermann and Hilborn (2001) who noted that the paucity of evidence "should not be interpreted as evidence that depensatory dynamics are rare or unimportant." In practical application of our population viability criteria, the depensation criterion is likely to play a significant role in population risk classification only for the largest populations within the domain, as other criteria (e.g., effective population size, and population decline criteria) are likely to be more conservative in watersheds where potential habitat is estimated to be less than 500 *IP-km*.

The low-risk density criteria were defined based on the following rationale. First, recall that for each species, Bjorkstedt et al. (2005) defined a minimum threshold of potential habitat (expressed as *IP-km*) that was required for the population to be considered viable-in-isolation (32 *IP-km* for coho salmon, 20 *IP-km* for Chinook salmon, and 16 *IP-km* for steelhead), with the among-species differences in *IP-km* thresholds reflecting differences in life-history variation. These thresholds assume that populations historically operated at something close to the natural carrying capacity of the system. By extension, for populations in the smallest watersheds (in *IP-km* terms) capable of supporting a viable population to remain viable, they must function at something close to this historical carrying capacity, as any reduction in abundance would drop them below thresholds for viability. Consequently, the average spawner density at natural carrying capacity serves as a reasonable basis for establishing the threshold for low-risk in the smallest watersheds.

The difficulty lies in estimating this value. For coho salmon, we relied on the work of Bradford et al. (2000), who examined stock-recruit relationships for 14 historical data sets of coho salmon in the Pacific Northwest. Fitting a hockey stick model to these data, they found that, on average, the plateau in the stock-recruit relationship, which identifies number of spawners at which full smolt recruitment occurs (an estimate of carrying capacity), occurred on average at 19 females per kilometer. Assuming a sex ratio that is slightly biased in favor of males, we round this number to approximately 40 adult spawners per kilometer. For Chinook salmon and steelhead, we lack the same kind of empirical basis for setting the

[12] The decision to use *IP-km* was based on an assumption that *IP-km* provides a reasonable measure of the relative productive potential of a watershed. For watersheds that have comparable *IP-km* but somewhat different total km, the average density, expressed as fish/km might be expected to be lower in the less productive watershed, potentially leading to greater depensation risk. However, we assume that in most cases, fish distribute themselves somewhat according to habitat quality; thus, we consider these two scenarios as having comparable risk.

spawner density for watersheds with the minimum IP required for viability, and so default to the 40 spawners/km value recommended for coho salmon.

For coho salmon, we find some support in population viability models developed for coho salmon on the Oregon Coast. Recall that the NCCCTRT estimated that at least 32 *IP-km* was required for a population of coho salmon to be considered viable-in-isolation (Bjorkstedt et al. 2005). This threshold value was based on the simulation analyses of Nickelson and Lawson (1998), who used a life-cycle model to predict extinction risk for a population of coho salmon as a function of the amount of "high quality" habitat available (Bjorkstedt et al. 2005). The Nickelson-Lawson model produces quantitative extinction probabilities. These probabilities are sensitive to many of the model parameters; thus, determining an absolute extinction probability for any population is difficult. Nevertheless, the model consistently shows that extinction probabilities begin to rise rapidly when the available high-quality habitat falls below 24 kilometers. The NCCCTRT set the viability-in-isolation threshold based on an assumption that watersheds with at least 32 *IP-km* would have sufficient high-quality habitat to support a viable population (Bjorkstedt et al. 2005). These estimates assume that this quantity of habitat would be expected to produce sufficient numbers of smolts to yield 1,500 spawners during a period of 1% marine survival (Wainwright et al., in prep.). For the smallest population (i.e., in a watershed with 32 *IP-km*), 1,500 spawners would result in a density of about 47 spawners per *IP-km*, a value in reasonable agreement with the 40 spawners/*IP-km* chosen for our criteria.

For Chinook salmon the default value of 40 spawners/km value is consistent with the rationale of Bjorkstedt et al. (2005) who, based on reported values for average Chinook salmon redd densities, argued that a redd density of 20 per km (and thus a spawner density of 40 fish/km assuming a 50:50 sex ratio) over 20 *IP-km* would be required for a population to be viable. We also note that, although the density required for viability in the smallest watersheds is the same for coho salmon, Chinook salmon, and steelhead, the absolute abundance requirements would differ since the *IP-km* threshold for viability differs (i.e., the smallest watershed for viable coho salmon, Chinook salmon, and steelhead populations would require annual run sizes of 1,280, 800, and 640 spawners, respectively). This result is consistent with the hypothesis that the greater life-history diversity exhibited by steelhead and Chinook salmon enables them to persist at somewhat lower absolute abundances than coho salmon, which have a more rigid life history.

With the spawner density criteria of 40 fish/*IP-km* for the smallest populations serving as an anchoring point, the next step was to generate a function representing our general conclusion that the larger the population historically was, the more it can depart from historical conditions and still remain viable.

Here, we assume that a population with ten-fold more habitat potential than the smallest population requires an average spawner density half that of the smallest population, and that the required density declines linearly between these two reference point (Figure 5). For watersheds with greater than ten-fold the habitat potential of the minimum watershed, we assume that spawner density must be at least 20 fish/*IP-km* for the population to be at low risk.

We acknowledge that selection of the latter reference point is based largely on expert opinion, and that there is room for debate about both the shape of the density function and the floor density that is used for large watersheds. However, we believe that application of the density criteria yields results that are qualitatively consistent with general hypotheses relating watershed size and density to spatial structure, diversity, and other factors that influence population persistence. First, a result of application of the density criteria is that it establishes a watershed-specific abundance target that is scaled to the amount of potential habitat. This overcomes the unsatisfying conclusion of "fixed" abundance criteria that a population that was historically very large could be equally viable and fulfill the same role in ESU viability even if it only occupies a very small fraction of its historical habitat. A second desirable outcome is that the density criteria substantially increase the likelihood that elements of spatial structure and diversity that contribute to viability will be maintained, without rigidly asserting what that spatial structure must look like. For example, in a large watershed, the density criteria could be attained in a variety of ways, ranging from having roughly half the available habitat occupied at something near carrying capacity, with little use of remaining habitats, to having fish distributed at moderate densities throughout the watershed. Each of these scenarios offers some potential advantages and disadvantages from a population persistence standpoint. For example, populations anchored in a subset of watersheds that are functioning at or near carrying capacity may provide for greater resilience during periods of low ocean productivity (Nickelson and Lawson 1998), but be at somewhat more risk of localized disturbances than populations distributed more broadly but at lower average densities. Because these tradeoffs do not seem to be quantifiable given our current state of knowledge, the density criteria seem preferable to more stringent requirements related to spatial structure.

**Metrics and Estimation:** For the high risk of depensation threshold, we propose estimating average spawner density (expressed as spawners/*IP-km*) in the *h* consecutive years of lowest abundance within the last four generations, where *h* is mean generation time for the species. Mathematically, we express this as follows:

(5) $$\hat{D}_{dep} = \left( \min\left[ \frac{N_{g(t)}}{h} \right] \right) \Big/ IP - km$$

where $N_{g(t)}$ is running generational sum of spawner abundance at time $t$, and *IP-km* is the estimate of potential habitat capacity for the watershed in which the population resides (see Section 4 for *IP-km* estimates for each independent population). The decision to evaluate average spawner density in the $h$ consecutive years of lowest abundance (as opposed a single year or over all years) balances several considerations. Foremost, we seek an indicator that is sensitive to the possibility that a population is at risk of depensatory mortality, without being overly sensitive to natural fluctuations in abundance. For example, a population that experiences a single year of low abundance may be at minimal risk of slipping into an accelerating pattern of depensation, especially for species with overlapping generations, which may be able to rebound more rapidly after a poor year. On the other hand, a metric that uses average abundance over a longer period could be insensitive to depensation risks if a few relatively good years elevate the average to levels above the depensation threshold and thereby mask these risks. Selecting the lowest $h$ consecutive years looks for recurring evidence of population numbers sufficiently low that there is heightened potenential for depensatory dynamics that could rapidly deteriorate into a negative feedback situation. We note also that the proposed metric assumes that fish are distributed relatively uniformly across the available spawning habitats. Were spawner densities consistently higher in certain locations within a watershed, it would suggest that risks associated with depensation due to the difficulty of spawners finding mates might be low and that the criterion could therefore be relaxed, though other possible depensation mechanism (e.g., lack of predator saturation) must also be considered.

For the low-risk density threshold, we propose as a metric the arithmetic mean of adult spawner density, expressed as adult spawners per *IP-km*, for all years over the last four generations:

(6) $$\hat{D}_{ssd} = \frac{1}{4h} \sum_{t=1}^{4h} \frac{N_a}{IP\text{ - }km}$$

where $N_a$ and *IP-km* are as defined above, and $h$ is the mean generation time for the population (rounded to the nearest whole year). The estimated density is then evaluated against thresholds that are a function of both species and populations-specific estimates of potential habitat capacity or *IP-km*, as outlined in Figure 5.

Density estimates are likely to be derived in two different ways. First, where weirs or other fish passage structures exist, average density can be estimated by dividing either total fish count (if all upstream migrating fish are captured) or a total population estimate (if only a portion of adults are captured, but where the proportion can be accurately estimated)—both of which estimate annual run size, $N_a$—by the number of stream *IP-km* accessible in the watershed. Second, where randomized spawner surveys allow for population estimation, again the total population estimate, $N_a$, can be divided by total accessible *IP-km* in the basin to an average density over the entire watershed.

Of the criteria proposed in this document, the density criteria perhaps generated the most discussion among TRT members about both the selection of the specific criteria and how to most appropriately apply them. Among the specific issues debated were (1) the relationship between density and viability in populations where a significant amount of historical habitat is now inaccessible behind dams or severely degraded (which becomes a question of selecting an appropriate habitat-based denominator when estimating density); (2) whether the proposed criteria were sufficiently precautionary or overly so; (3) whether it was more appropriate to express density criteria in terms of fish per *IP-km* or fish per total accessible kilometers; and (4) whether adjustments to the criteria should be made to account for potential bias in estimates of IP. We discuss the first of these issues in the paragraphs that follows, since resolution of this issue is integral to subsequent discussion of ESU-level viability criteria that comes in Section 3. The remaining topics we treat in Appendix B.

An important issue in estimating density is how to handle situations where substantial historical habitat now lies behind impassible dams or other human-caused barriers to fish migration. This raises the question as to whether, in estimating density using the two methods above, it is more appropriate to use historical versus currently available *IP-km* in the denominator. In some instances, where significant historical habitat has been lost, use of historical *IP-km* would, in all likelihood, preclude such populations from ever attaining viable status in relation to historical standards. This seems problematic, in that there may be sufficient habitat downstream of impassible barriers (i.e., more than the minimum threshold for the population to be considered viable in isolation) to support a viable population. (Put another way, it seems illogical to conclude that a population below human-created barriers that still has access to substantial habitat cannot be viable, if a population in a watershed with comparable habitat but no such barriers can be considered viable.). On the other hand, excluding areas upstream of barriers from consideration violates one of our fundamental assumptions: that the spatial structure and diversity resulting from the distribution of individuals broadly and over diverse habitats contributes significantly to population persistence. We therefore recommend that populations be evaluated based on both historical

(pre-barrier) and current (post-barrier) conditions. Populations that fail to satisfy density criteria based on historical habitat availability, but that do satisfy the density criteria as applied to current conditions could potentially be considered viable in the sense of having a relatively high probability of persistence. But these "partial populations" represent something other than the historically defined population. Such populations could be at greater risk than if criteria for the historical habitat were met (due to loss of diversity or spatial structure), and their contribution to ESU persistence might be substantially diminished, requiring reassessment of their role in ESU viability.

A related issue is how to deal with situations where fish still have access to portions of a watershed, but where habitat alterations are both severe and permanent (e.g., intensive urbanization), and effectively preclude use by salmonids. In principle, arguments similar to those discussed above could be used to make the case that density should only be estimated in those habitats that still are capable of supporting salmonids. However, whereas in the case of dams, habitat losses are relatively easy to quantify, habitat degradation is a matter of degree, and thus defining boundaries around areas that are no longer suitable becomes problematic. We conclude that, assuming such areas could be clearly defined[13], one could evaluate density criteria using only "accessible and suitable" habitats; however, again such "partial populations" represent something other than the historical population, having substantially departed from their historical spatial structure and diversity. In no case should a population be considered viable, by any standard, when the remaining habitat that is deemed suitable does not meet the minimum viability thresholds set for each species (i.e., 32 *IP-km* for coho salmon, 20 *IP-km* for Chinook salmon, and 16 *IP-km* for steelhead). How "partial populations" may relate to viability at the levels of diversity strata and ESUs is discussed further in Section 3.

### *Hatchery Criteria*

**Rationale:** The hatchery criteria are intended to address potential impacts of hatchery operations on the viability of wild populations of salmon and steelhead. Hatchery operations can affect wild populations through a variety of ecological, demographic, and genetic mechanisms, thereby influencing their probability of persistence.

The potential ecological effects of hatchery operations and hatchery fish on wild fish are many and varied. When released into the wild, hatchery fish may compete for food, space, or mates with hatchery fish in both the freshwater (Nickelson et al. 1986) and marine (Levin et al. 2001; Ruggerone et al. 2003;

[13] Defining such areas may be complicated if fish from relatively good habitats periodically "leak" into poor habitats.

Ruggerone and Nielsen 2004) environments. Hatchery fish can alter predator-prey dynamics by preying directly on wild salmonids (Sholes and Hallock 1979) or by attracting or supporting increased numbers of avian, mammalian, or piscine predators, resulting in increased predation rates on wild fish (Collis et al. 2001; Ryan et al. 2003; Major et al. 2005). Conditions within hatcheries can increase the vulnerability of fish to infection by pathogens, cause pathogen amplification, and increase opportunities for disease transmission (Moffitt et al. 2004). These diseases can then be transferred to wild populations (Kurath et al. 2004). Marine or estuarine netpen rearing of such hatchery fish can also result in transfer of pathogens and parasites to nearby wild fish (Naylor et al. 2005; Krkosek et al. 2006). Stocking of large numbers of hatchery smolts in streams containing wild fish can also alter the behavior of wild fish, resulting in premature emigration of wild fish (Hillman and Mullan 1989). Additionally, hatchery facilities themselves may pose risks to wild populations by diverting water from natural streams in order to supply hatcheries, releasing polluted effluent (e.g., fish wastes, antibiotics) waters from hatcheries back into streams and rivers, and creating barriers to migration through installation of weirs of other fish collection structures (White et al. 1995; Pearsons and Hopley 1999; Reisenbichler 2004).

Hatchery programs also potentially pose direct demographic risks to wild populations. Production of large numbers of hatchery fish can result in increased human harvest of wild fish in mixed-stock fisheries, resulting in reduced spawning escapement (McIntyre and Reisenbichler 1986; Hilborn 1992; NRC 1996; Reisenbichler 2004). Additionally, hatchery programs that draw broodstock from wild populations, so-called broodstock mining, also pose direct demographic risks to the wild population if the survival and subsequent reproductive success of hatchery-origin fish that spawn in the wild does not at least replace production lost due to the removal of natural-origin fish for broodstock (ISAB 2003). Broodstock mining may also compromise the ability of a wild population to maintain its genetic character if too few adults are allowed to spawn naturally, increasing the risk for adverse effects associated with small population size (effects that may be exacerbated if broodstock suffer a catastrophic loss in the hatchery). In very small populations, removal of wild fish for hatchery broodstock may result in depensation, through Allee effects and other mechanisms, in the remaining wild population if too few individuals are left to spawn.

Genetic risks of hatcheries arise when wild fish interbreed with genetically dissimilar hatchery fish, which can result in changes in genetic composition of wild populations, as well as genetic structure across larger spatial scales. Under natural conditions, accurate homing to natal streams tends to result in the formation of distinct breeding groups or populations that, over time, become locally adapted to the environmental conditions they experience during their life cycle. This local adaptation and the diversity it creates over larger spatial scales are important for the long-term persistence of populations and ESUs (NRC 1996;

Hendry 2001; McElhany et al. 2000; Reisenbichler et al. 2003). Within populations, interbreeding of wild fish with hatchery-origin fish can alter the genetic characteristics of the wild population, reducing the (average) individual fitness and hence overall population productivity (ISAB 2003). When hatchery fish stray into other watersheds and interbreed with wild fish, patterns of genetic variation can likewise be altered.

Genetic differences between hatchery and wild populations can arise in several non-mutually exclusive ways. First, they may result when nonnative (i.e., out-of-basin or out-of-ESU) broodstock are used in the hatchery. Second, genetic differences can arise when hatchery broodstock are subject to various artificial selection processes, sometimes referred to as domestication selection, that result either through hatchery practices or from exposure to unnatural hatchery environments. Artificial selection processes may be intentional, such as when hatchery managers select for certain desirable traits (e.g., size of broodstock or progeny, timing of return, etc.) or inadvertent, such as when selected broodstock randomly differ in some trait from wild populations or when the hatchery environment favors (and therefore selects for) traits that improve survival in the hatchery but that may lead to reduced fitness in the wild. And third, genetic modification may occur through hybridization of distinct subspecies, races, runs or phenotypes that co-occur in the same stream or basin. For example, hybridization of spring- and fall-run Chinook in the Feather and Trinity rivers appears to have occurred in response to broodstock collection during periods of overlap in run timing (Blankenship et al., in prep; Kinziger et al., in review). Regardless of the specific mechanism, the result is hatchery populations that differ in their genetic composition from wild populations.

Another genetic risk of hatcheries is the "Ryman-Laikre effect", whereby the admixture of hatchery fish into a natural population causes a reduction in the effective population size of the combined population (Ryman and Laikre 1991). This occurs because a group of hatchery fish generally have a smaller number of parents than a similar-sized group of natural fish, due to higher juvenile survival within the hatchery. When these hatchery fish reach reproductive age and interbreed with wild fish, the average number of genetic lineages in their offspring will be lower than if they were all wild fish. The magnitude of the reduction in effective size is proportional to the percentage of spawners that are hatchery fish and the difference in the average number of parents for the hatchery and wild fish.

Of particular concern within hatchery broodstock is inbreeding depression, which is when interbreeding between closely related individuals causes a decrease in average fitness of offspring, usually resulting from increased frequency of homozygotes for deleterious recessive alleles, fixation of deleterious alleles

within a population, or loss of overdominance. Outbreeding depression is a reduction in fitness of hybrid progeny when genetically dissimilar fish interbreed. It can result when wild fish interbreed with nonnative (e.g., out-of-basin or out-of-ESU) fish or when wild fish interbreed with hatchery fish that have undergone domestication selection. Processes that contribute to outbreeding depression include the introduction of alleles from the hatchery stock that are maladaptive in the local environment or the breakdown in co-adapted gene complexes (Fleming and Petersson 2001; ISAB 2003). Evolutionary models suggest that genetic exchange between hatchery fish and wild fish has the potential to erode the fitness of wild populations, with effects depending on the strength of selection and the magnitude of the hatchery contribution to total production (Ford 2002; Goodman 2004, 2005). Such changes may occur even if a large proportion of the hatchery broodstock consists of natural-origin fish (Ford 2002). Collectively, these processes can result in a variety of population-level and ESU-level changes in genetic diversity, including decreased within-population diversity resulting from insufficient numbers of broodstock and inappropriate mating protocols; loss or dilution of distinct, locally adapted populations; and increased homogenization of populations within an ESU (through increased straying). Such changes may affect the long-term persistence of both populations and the ESUs comprising those populations.

Although the ecological, demographic, and genetic effects of hatcheries on wild populations are well documented (see NRC 1996 for a review), quantitatively relating these effects to the probability of extinction of populations is difficult. Many of the ecological impacts of hatcheries are highly context-dependent. For example, competitive interactions between hatchery and wild fish are likely to vary with the carrying capacities of different ecosystems, the size of the wild population at the time of introduction, the number of hatchery fish released, the average size of stocked fish relative to wild fish, whether fish are planted in a few locations or distributed broadly across a watershed, or any number of other confounding factors. Likewise, genetic impacts on wild populations will depend on many factors including the origin of broodstock, how the hatchery is operated (e.g., mating protocols, rearing practices), and the number and effectiveness of hatchery fish that spawn in the wild, among other things. Further complicating matters in the NCCC Recovery Domain is the fact that hatchery programs at many facilities have changed substantially in the past decade or so, from predominately large-scale production-oriented programs to smaller-scale supplementation or captive broodstock programs. For example, out-of-basin coho salmon were planted for a number of years in the Russian River basin; however, the program was terminated in the mid 1990s, and there is now a captive broodstock program in operation intended to conserve what appears to be a remnant native population. Consequently, assessing potential hatchery risks involves evaluating not only current practices, but potential lingering genetic effects resulting from historical operations as well.

**Criteria:** Because of the numerous and complex ways in which artificial propagation activities may affect wild populations of salmonids, and because of the unique histories of ongoing and recently terminated hatchery programs within the recovery domain, the NCCCTRT concluded that simple numeric criteria for assessing hatchery risk would be difficult to justify. Acknowledging both the potentially significant risks that hatcheries pose to wild populations and the uncertainty in quantitatively relating these risks to extinction risk, the NCCCTRT adopts the following narrative criteria for hatcheries: populations are considered at low risk if there is demonstrably no or negligible evidence for ecological, demographic, or genetic effects resulting from current or past hatchery operations; populations are at elevated risk (moderate-high) if there is evidence of significant ecological, demographic, or genetic effects or high uncertainty surrounding these potential effects (Table 1).

The NCCCTRT notes that other Technical Recovery Teams have developed quantitative criteria specifically addressing *genetic* risks of hatcheries. For example, the OCTRT (Wainwright et al., in prep) and SONCCTRT (Williams et al., in prep.) propose assessing genetic risk based on the fraction of natural spawners that are of hatchery origin. The ICTRT (2005) and CVTRT (Lindley et al. 2007) propose a somewhat more complicated approach in which risk is assessed based on the fraction of natural spawners of hatchery origin in relation to the degree of genetic divergence between hatchery and wild stocks, the management practices used at the hatchery, and the duration of interaction between hatchery and wild populations.

We considered using such approaches but concluded, for the reasons noted above, that few hatchery programs (current or recent) could be effectively evaluated by those criteria, and that case-by-case assessment of hatchery impacts is more appropriate for the NCCC Recovery Domain. Nevertheless, from these documents and other, we have drawn a number of important principles that can assist in guiding such assessments of risk. These principles are discussed in *Metrics and Estimation* below. Our decision not to adopt numeric criteria, as done by other TRTs, should not be construed as contradictory, but instead reflects substantial differences in the number and types of hatchery programs found in the different recovery domains. Within other recovery domains, existing programs are predominately large-scale production hatcheries that have been operated for many decades. In contrast, only two large-capacity production hatchery programs (Mad River and Warm Springs/Coyote Valley steelhead) are currently operating within the NCCC domain, the remainder being conservation hatcheries (e.g., captive broodstock programs) or small-scale cooperative supplementation hatcheries (Table 3).

**Table 3.** Current salmon and steelhead hatchery programs operating within the NCCC Recovery Domain, their purpose, mode of operation, and status.

| Species, facility, and agency | River basin | Program type | Years of operation | Description and status |
|---|---|---|---|---|
| ***Chinook salmon*** | | | | |
| Hollow Tree Creek (Eel River Restoration Project) | South Fork Eel River | Supplementation | 1983 to present | Supplementation program that uses local broodstock to boost populations in Hollow Tree Creek, tributary to the South Fork Eel River. Development of hatchery genetic management plan ongoing. |
| ***Coho salmon*** | | | | |
| Don Clausen Warm Springs (CDFG) | Russian River | Rescue/captive broodstock and restoration | 1979 to present; captive broodstock since 2001 | Historically a production program that used out-of-basin and out-of -ESU (primarily Noyo River) fish for broodstock. Captive broodstock program was initiated in 2001; juveniles are collected from tributaries (Green Valley Creek) are reared to the adult stage at the hatchery and then spawned. Juveniles are subsequently released into Russian River tributaries to re-establish depleted or extirpated subpopulations. |
| Big Creek (Monterey Bay Salmon and Trout Project) | Scott Creek | Rescue/captive broodstock, restoration, and supplementation | 1982 to present; captive broodstock since 2001 | Historically a supplementation program. Currently, a combined supplementation/captive broodstock/ restoration program. Broodstock are collected from Scott Creek; broodstock collection is prioritized so that only wild fish are taken in strong year classes, returning hatchery fish are used if wild fish are unavailable, and captive broodstock are used as last resort. Progeny are released into Scott Creek for supplementation, as well as in other watersheds to re-establish depleted or extirpated populations. |
| ***Steelhead*** | | | | |
| Mad River winter steelhead (Friends of Mad River/CDFG) | Mad River | Production | 1971 to present | Historically operated as a production program to support fisheries that was established with out-of-basin (Eel River) broodstock. Currently operating as a cooperative hatchery with a goal of releasing 150,000 yearlings annually. Development of hatchery genetic management plan ongoing. |
| Warm Springs/ Coyote Valley winter steelhead (CDFG) | Russian River | Production | 1982 to present | Large-scale production program with goal of releasing 300,000 yearlings annually from Warm Springs and 200,000 yearlings from Coyote Valley. Some history of out-of-basin transfers (Eel and Mad River fish) pre-dating hatchery construction and continuing to the early 1990s (Busby et al. 1996). Development of a hatchery genetic management plan ongoing. |
| Big Creek winter steelhead (Monterey Bay Salmon and Trout Project) | Scott Creek/ San Lorenzo River | Supplementation | 1982 to present | Supplementation program that uses local broodstock to boost populations in Scott Creek and the San Lorenzo River. Historically involved outbasin planting, but in recent years Scott Creek and San Lorenzo River fish have been planted only in their stream of origin. |

**Metrics and Estimation:** Because analysis of risks associated with hatcheries should be done on a case-by-case basis, we do not propose specific metrics for assessing risk. We do, however, offer general guidance on issues that should be considered when evaluating risks associated with hatcheries, the types of information that are needed to evaluate these risks, and some basic principles that can inform risk assessment. We draw on several recent and thoughtful treatments of hatchery programs and reform in the scientific literature. The Hatchery Scientific Review Group (HSRG 2004; Mobrand et al. 2005) provided a range of principles and recommendations for the management of both integrated and segregated hatchery programs. Several recent publications discuss specific "best management practices" for integrated supplementation programs (see e.g., IMST 2001; ISAB 2003; Flagg et al. 2004; Olson et al. 2004; Reisenbichler 2004; Mobrand et al. 2005; Williams et al. 2003). Other published studies present a variety of methods for examining ecological and genetic risks associated with hatcheries (Currens and Busack 1995, 2004; Pearsons and Hopley 1999; Ford 2002; Goodman 2004, 2005). The reader is referred to these publications for more detailed discussion of hatchery risks and management practices.

To a substantial degree, the types of risks and hence the associated risk indicators, depend on the type of hatchery program being considered. Fundamentally, there are two primary purposes of hatchery programs: 1) to help conserve naturally spawning populations and their inherent genetic composition, and 2) to provide fish for harvest[14]. The HSRG (2004) suggests that, for the purpose of assessing risks and benefits, hatchery programs can be further categorized into two types based on the management goals and protocols for propagating the hatchery broodstock. *Integrated* programs are those in which a primary goal is to minimize genetic divergence between the hatchery broodstock and a naturally spawning wild population by systematically incorporating wild fish into the hatchery broodstock. Integrated programs potentially include several distinct types of hatchery programs including "augmentation" programs intended to increase the number of fish available for harvest; "supplementation" programs, which are hatcheries designed to *"maintain or increase natural production, while maintaining the long-term fitness of the target population and keeping the ecological and genetic impacts on non-target populations within specified biological limits*" (ISAB 2003); and conservation programs, such as captive broodstock programs, which are intended to prevent extinction of specific populations while other recovery efforts are conducted[15].

[14] Other general purposes of hatcheries may include research, education, and providing cultural benefits, but there are no such hatcheries currently operating within the NCCC Recovery Domain. Mitigation for habitat loss is often mentioned as a "purpose" of hatchery programs; however, under the framework presented here, mitigation programs could fall into the category of either segregated or integrated programs.

[15] Captive broodstock programs are, in principle, a form of supplementation program. The distinction is that in supplementation programs, broodstock are generally collected to proportionally represent the genetic composition of the wild population, whereas

*Segregated* programs, in contrast, strive to maintain hatchery broodstock that are distinct from their wild counterparts by using predominately or exclusively hatchery-origin adults returning to the hatchery in subsequent broodstock. Ideally, segregated programs seek to minimize (to the extent possible) gene flow between hatchery and wild populations, both to minimize adverse effects on wild populations and to maintain variation in characteristics such as adult run timing, which may allow directed harvest on the hatchery stock. Segregated programs are generally production or augmentation programs intended to increase opportunities for harvest of stocks that are not at risk. Restoration hatcheries, defined as those intended to re-introduce fish into watersheds where they have been extirpated, might initially be considered segregated programs, though they can evolve into integrated programs if reintroduction is successful and broodstock eventually come from the naturalized population.

Approaches for meeting genetic, demographic, and ecological goals—including minimizing potential adverse effects on wild populations—will often be substantially different for integrated and segregated hatchery programs. In the discussion below, we highlight key issues related to potential effects of integrated and segregated programs, as well as information needs for evaluating whether or not goals are being met. Without thorough evaluation of these issues, populations affected by hatcheries should generally be considered at risk because of the high uncertainty surrounding these potential effects.

Genetic Risks

Before discussing specific issues associated with the evaluation of genetic risks of integrated and segregated hatchery programs, there are several general principles germane to both types of programs. These principles form the conceptual basis for quantitative criteria put forth by the Interior Columbia and Central Valley TRTs (ICTRT 2005; Lindley et al. 2007):

- **Genetic risks associated with hatcheries generally increase with increasing genetic dissimilarity between hatchery and natural populations.** Genetic dissimilarity may be a function of hatchery stock origin or artificial selection. Assuming that hatchery and wild fish freely interbreed, relative risks will follow the following order with respect to the source of hatchery populations: out of ESU > out of basin > within basin > within basin with best management practices[16]. This general ranking of relative risks can be confounded if there are differences in the

in a conservation hatchery program, populations are typically so depressed that strict mating protocols are needed to avoid adverse genetic effects that are likely to occur when closely related individuals interbreed.

[16] Best management practices for integrated supplementation programs remain an area of active research and scientific discussion. For further elaboration, see HSRG 2004; Mobrand et al. 2005; ISAB 2003; Flagg et al. 2004; IMST 2004; Olson et al. 2004; Reisenbichler 2004; Mobrand et al. 2005; Williams et al. 2003.

relative reproductive success of hatchery-origin fish versus wild fish, or if there is divergence in traits such as run timing or maturation schedule.

- **Genetic risks associated with hatcheries increase with the percentage of successful natural spawners (i.e., those spawning naturally, outside of the hatchery) that are of hatchery origin.** The higher the percentage of effective spawners that are of hatchery origin, the greater the risk to wild populations.

- **Genetic risks associated with hatcheries increase with time for a wild population exposed to a given level of interaction with hatchery fish.** Genetic effects on wild populations are cumulative; thus, long-term programs pose greater risks than short-term programs.

- **Genetic risks associated with hatcheries can be reduced if "best management practices" (BMPs) are followed.** Best management practices depend on the specific goals of the program; thus, generalizing about genetic BMPs is difficult, as discussed below.

**Integrated hatcheries —** Fundamental goals of most integrated hatcheries are 1) to minimize genetic differences between hatchery broodstock and the wild population that the program seeks to conserve or augment, and 2) to minimize change in genetic composition of the composite hatchery-wild population resulting from hatchery practices (HSRG 2004). Achieving these goals requires incorporating local-origin wild fish into the hatchery broodstock in sufficient numbers such that the genetic composition of the hatchery broodstock represents that of the wild population and avoids inadvertent effects of genetic drift, domestication, and selection in natural and hatchery environments. Typically, it is assumed that genetic representation can be achieved by proportionally representing various phenotypes found in the wild population in the hatchery broodstock, an assumption that can be evaluated using modern molecular genetic techniques. For an integrated program, the proportion of natural-origin broodstock that are needed to avoid genetic divergence remains a subject of substantial scientific uncertainty and debate, and will depend on the specific goals of the hatchery program and the status of the wild stock. For example, the HSRG (2004) recommended that 10%–20% of hatchery broodstock be composed of natural-origin adults each year to avoid genetic divergence between the hatchery and wild populations. In contrast, the ISAB (2003) suggests that for supplemental programs (i.e., programs intended to provide a "demographic boost" to rebuild a depressed natural population[17]), 100% of hatchery broodstock should be drawn from

[17] An objective of supplementation programs is to, at least temporarily, increase the number of spawners on the spawning grounds by having hatchery-origin adults spawn in the wild (ISAB 2003). However, this is not necessarily a goal of all

the products of natural spawning. However, for conservation hatcheries where the natural populations are very small, it may be more appropriate to cross wild fish with hatchery or captive fish.

Hatchery practices should also seek to minimize intentional or unintentional domestication selection by employing appropriate mating protocols, rearing environments (i.e., environmental conditions that follow natural pattern of temperature, photoperiod, etc.), and release strategies. Additionally, collection of wild broodstock should be done in a manner that leaves sufficient numbers of individuals on natural spawning grounds to avoid unintended alteration of the genetic composition of the wild component. The HSRG (2004) concludes that associated natural populations must be "viable and largely self-sustaining if they are to support successful integrated programs…." Implicit in this statement is recognition that hatcheries are subject to catastrophic losses due to mechanical failures, human error, disease outbreaks, and malicious acts. When such events happen, sufficient numbers of individuals must remain in the wild population to maintain the genetic integrity of the population[18]. And finally, integrated programs should strive to ensure that the rate of gene flow from the natural component into the hatchery broodstock should exceed gene flow in the reverse direction. The long-term goal of an integrated program is to ensure that selection in the natural environment (rather than the hatchery environment) drives the evolution of the integrated population (HSRG 2004).

Evaluating the likelihood of genetic risks of integrated programs requires a substantial amount of information, including the following:

- Estimation of the number and proportion of wild fish that are incorporated into the hatchery broodstock
- Estimation of the number of hatchery-origin fish that spawn on natural spawning grounds, their proportional contribution to the spawning population, and their effective contribution to reproductive output[19]
- Quantification of changes in the genetic composition of the integrated population through time

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integrated programs. As the HSRG (2004) notes, the goal of an integrated broodstock program is to maintain the genetic characteristics of the natural population in the hatchery-origin fish, not the reverse.

[18] These statements do not imply that integrated "supplementation programs" are not appropriate conservation tools, only that long-term viability of the population should not be dependent on the hatchery component.

[19] Estimating the contribution of hatchery-origin fish to reproductive output is complicated by the fact that, although it is now common to mark hatchery fish upon release, the progeny of hatchery fish are not easily identified. Thus, the potential influence of hatchery fish on the genetic composition of the wild population is not strictly a function of the fraction of identifiable hatchery-origin spawners.

- Quantification of phenotypic characteristics (e.g., age and size at maturity, age and size at smoltification, timing of spawning run and smolt outmigration, egg size, fecundity, etc.) of the integrated population through time
- Estimation of effective population size of the integrated population.

For captive broodstock programs, which are a highly specialized form of integrated hatchery program, substantial genetic information at the level of individual fish is required so that spawning matrices that avoid crossing of siblings and other close relatives can be implemented. By their very definition, captive broodstock programs exist because wild populations are perceived to be at high risk of extinction. When captive broodstock programs succeed and population abundance increases to levels that might suggest viability, additional evaluation of potential long-term genetic risks associated with a recent population bottleneck would be required.

**Segregated hatcheries** — A primary genetic goal of segregated hatcheries is to minimize or eliminate gene flow between the hatchery and wild populations, which entails minimizing the occurrence of hatchery fish spawning in the wild (to avoid outbreeding depression) and excluding or minimizing the contribution of wild fish to the hatchery gene pool (to avoid convergence of genotypic and phenotypic characteristics). Strategies recommended by the HSRG (2004) for achieving this goal include 1) releasing fish in areas where opportunities to capture non-harvested adults are high; 2) rearing and releasing fish in a manner or at a location that minimizes straying and opportunities for natural spawning; 3) ensuring that harvest opportunities are commensurate with adult production from segregated programs; and 4) ensuring that hatchery-origin adults make up no more than 1%–5% of natural spawners (see footnote). Several authors (ISAB 2003; Goodman 2004; Ford 2002) have argued that, even where the percentage of hatchery-origin fish on natural spawning grounds is low, the effects on fitness may still be significant over time, especially since many "wild" fish may be progeny of hatchery-origin fish. As with integrated programs, evaluation of genetic risks associated with segregated programs requires estimating the number and fraction of natural spawners that are of hatchery origin and their contribution to the next generation, as well as the proportion of wild fish incorporated into hatchery broodstock. Additionally, genetic monitoring is needed to determine whether genetic composition of the wild population is being affected by introgression by genetically divergent hatchery fish.

For both integrated and segregated programs, evaluation of genetic risks may also need to include assessment of potential residual genetic effects associated with historical hatchery practices. Within the NCCC Recovery Domain, there is a substantial history of plantings of out-of-basin and out-of-ESU fish

into many river basins (reviewed in Bjorkstedt et al., 2005). Other programs may have used local broodstock, but used mating or rearing protocols that, by today's standards, would be considered likely to result in domestication. Furthermore, many long-running programs have only recently been terminated. In most cases within the recovery domain, there is little or no information on parameters important for understanding potential genetic effects (e.g., percentage of wild fish used for broodstock, percentage of hatchery fish on natural spawning grounds, or information on historical genetic composition of wild populations that could be compared with current genetic data). Genetic evidence suggests that, among anadromous salmonids, indigenous populations may resist introgression when the introduced stock is genetically strongly divergent (Utter 2001, 2004). However, when introduced hatchery fish are from geographically proximate watersheds, the probability of introgression likely increases. Though the consequences of such releases for fitness of the wild population are unknown, they are likely generally less severe. Recent genetic data from populations of steelhead, coho salmon, and Chinook salmon from the NCCC Recovery Domain are generally consistent with these patterns (see Bjorkstedt et al. 2005 for summary of available genetic information). There is little evidence to suggest that strongly divergent stocks (primarily from Oregon and Washington) of salmon and steelhead that were introduced into various watersheds in the region have left a lasting genetic signature. However, in some instances, transfer of fish among basins that are relatively close to one another appears to have resulted in some homogenization of genetic composition (e.g., Eel River and Mad River steelhead). Little is known about whether longer-term hatchery programs that used locally-derived broodstock have resulted in loss of diversity through inbreeding or reduced fitness through domestication processes. Unfortunately, there often may be no easy way to evaluate any potential impacts of past hatchery practices. Genetic methods may provide some insight into whether past introductions have affected population genetic composition or structure. For example, occurrence of unique alleles present in the donor stock but previously absent from the recipient population would indicate introgression. Additionally, low genetic diversity in local populations with a long history of artificial propagation could be indicative of hatchery effects, though it could also arise from other processes. In general, we would expect genetic risk to be greatest in populations affected by recent out-of-basin transfers or long-running production programs that released large numbers of fish. Fish of intermediate divergence are potentially the most problematic, since they are generally expected to be more successful at reproduction and introgression in the recipient basin than highly divergent populations, but less successful at maintaining population fitness than closely related populations.

Demographic Risks

**Integrated hatcheries —** Goals for minimizing demographic risks of integrated hatcheries should consider several distinct types of risk. Of primary concern is that hatchery-reared progeny of wild adults will fail to replace those progeny that would have been produced in the wild had adults been left to spawn naturally (ISAB 2003). In this regard, assessment of whether an integrated program represents a net benefit to the target stock requires analysis not only of how many juveniles or smolts are produced in the hatchery, but how well they survive and reproduce in the wild compared to their wild counterparts (ISAB 2003). Such analyses are critical because hatchery programs can increase the number of fish on natural spawning grounds, even if there is a decrease in the productivity of the wild component of the integrated population. In such cases, any potential benefits of an integrated program to population abundance will cease when the program is ended. Where adult broodstock are being taken from small wild populations, an additional concern is that removal of adults for use in hatchery broodstock could potentially lead to depensation in the wild population (e.g., remaining adults may have difficulty locating mates or produce too few juveniles to swamp local predator populations). A third demographic concern is the potential for adverse effects on wild stocks in mixed-stock fisheries. In an integrated program, an abundance of hatchery fish may result in increased harvest pressure, while simultaneously masking decreasing productivity of the natural component. These circumstances can lead to incorrect assessment of stock status and drive wild populations toward extinction if escapement drops below replacement levels (NRC 1996).

Evaluation of these potential demographic risks involves the following information:

- Estimates of the adult spawner population size and spawner density on natural spawning grounds
- Estimates of the number and proportion of wild adults captured for broodstock
- Estimates of population growth rate (productivity over the entire life cycle) for both wild and hatchery-origin fish
- Estimates of harvest rates on the integrated stock.

**Segregated hatcheries —** For segregated hatchery programs, the intent of which is to increase the number of fish available for harvest, goals for minimizing demographic risks focus primarily on minimizing mixed-stock fishery effects on at-risk wild stocks. Evaluation of whether such goals are being met requires estimates of harvest rates on both wild and hatchery stocks in mixed-stock fisheries, which in turn requires estimates of total adult abundance (harvest+escapement), and the proportion of both harvest and escapement that are of hatchery and wild origin.

Ecological Risks

As noted earlier, releases of hatchery fish can influence the success of wild populations through a variety of ecological processes including increased competition, increased predation (direct predation of hatchery fish on wild fish or attraction of predators), transmission of diseases, and through direct effects of hatchery or rearing facilities (e.g., migration barriers, water diversions, and pollutants/pathogens in hatchery effluent). Consequently, conservation goals associated with hatchery programs should seek to minimize these negative interactions; however, the specific goals will differ for integrated and segregated programs.

**Integrated hatcheries —** For integrated hatcheries, an overarching objective is to produce hatchery fish that mirror their wild counterparts as closely as possible. Achieving this goal requires creating a hatchery rearing environment that yields fish that are similar to wild fish in terms of their physiological disposition, behavior, health status, and nutrition (HSRG 2004). This may entail regulating temperature and photoperiod regimes to match ambient conditions within the river, rearing fish at lower densities than is typical of most hatcheries, feeding fish underwater to reduce surface feeding behaviors, and providing cover and physical structure so that released fish exhibit natural responses to predators and conspecific competitors. Additionally, integrated hatchery programs need to consider the ecological context of receiving waters, such that released fish do not adversely affect the target population through competition, predation, or introduction of diseases, or other at-risk populations that may be affected when hatchery fish enter the ocean. Hatchery fish should be released in numbers consistent with productive capacities of the natural systems (both freshwater and marine) into which they enter. Because carrying capacities of both the freshwater and marine environments may vary from year-to-year, constant release targets—a standard performance measure for many existing hatcheries—will likely be inappropriate. Hatchery fish should also be released at sizes and times that minimize potential for competitive interactions with wild fish and predation on wild fish. The HSRG (2004) suggests that, in the context of an integrated program, this means mimicking to the degree possible the distribution of sizes and physiological states of wild fish[20]. However, there may be circumstances where release of large numbers of hatchery-reared coho salmon smolts may be an important temporary management tool, because such releases may increase returns of two-year-old females and thereby help re-establish depressed or extirpated year classes (Smith 2006). Hatchery fish should also be released in numbers that do not cause unnatural aggregation of predators. Only hatchery fish free of disease should be released into the wild. And finally, program operations

[20] There may be instances where the goal of minimizing competitive interactions and that of rearing fish that are similar in their developmental state to wild fish are in conflict with one another, if the carrying capacity of the receiving water is approached. In such cases, some temporal separation between wild fish and hatchery fish may be preferable.

should seek to minimize effects of hatchery and rearing facilities on the wild population (i.e., release of pollutants/pathogens, water diversions for hatchery water supplies, and barriers to migration).

Evaluating whether an integrated hatchery program is achieving ecological goals with respect to conserving the composite hatchery-wild population requires a substantial amount of information not traditionally collected for most hatchery programs, which historically have focused on producing large smolts to be released during a relatively narrow window during the migration period. Among the information needs for evaluating integrated programs are

- Assessment of carrying capacities (including their interannual variation) of the freshwater and marine systems into which fish are being released in order to prevent overstocking
- Estimation of wild fish density in relation to carrying capacity and numbers of hatchery fish released
- Monitoring the size and condition of hatchery and wild populations before release and upon return as adults to ensure that hatchery fish match the wild template
- Monitoring the effect of hatchery releases on predation rates in wild populations
- Monitoring for occurrence of disease in the hatchery population
- Monitoring for facility effects (e.g., water quality downstream of hatcheries; evaluation of fish collection structures/practices on passage by upstream- or downstream-migrating wild fish; potential effects of water withdrawals on stream discharge).

**Segregated hatcheries —** For segregated hatchery programs, the primary goal should be minimizing interactions with wild fish, but the approaches for achieving these goals will most likely involve creating either temporal or spatial separation between hatchery and wild populations, rather than trying to match the natural template. Practices designed to help achieve these goals include 1) releasing fish at sizes, times, or locations that minimize potential for competitive interactions with wild fish during the juvenile and smolt stages; 2) releasing fish in locations where opportunities for adults to stray into streams inhabited by wild fish, where they may compete for mates or spawning habitats, are low; 3) releasing fish at sizes, times, or locations that minimize potential for direct predation on wild fish by hatchery fish or attraction of large numbers of predators during the juvenile or adult phases; and 4) releasing only fish that are free of disease.

In general, information needs for evaluating segregated hatchery programs are similar to those needed for integrated programs, and include

- Assessment of carrying capacities (including their interannual variation) of the freshwater and marine systems into which fish are being released in order to prevent overstocking
- Estimates of density of wild fish in relation to carrying capacity and numbers of wild fish released
- Monitoring the effect of hatchery releases on predation rates in wild populations
- Monitoring for occurrence of disease in the hatchery population
- Assessment of facility effects (e.g., water quality downstream of hatcheries; evaluation of fish collection structures/practices on passage by upstream- or downstream-migrating wild fish; potential effects of water withdrawals on stream discharge).

In evaluating potential risks of hatcheries and developing recovery strategies, recovery planners should recognize that there is a distinction between evaluation of whether a hatchery poses a particular type of risk relative to our viability criteria versus evaluation of whether or not the hatchery program overall provides a *net benefit or risk* with respect to conservation of the population. The former analysis simply seeks to determine whether a given wild population may be at genetic, demographic, or ecological risk due to ongoing or past hatchery operations. The latter analysis, which has substantial bearing on whether a hatchery program should be continued, involves consideration of the various types of risk in the context of one another. For example, within the NCCC Recovery Domain, as well as elsewhere in the Pacific Northwest, there are several captive broodstock programs intended to conserve severely depleted populations of salmon. Without these programs, there may be little chance of recovering these populations and, under such circumstances, concerns about inbreeding depression and loss of fitness are secondary to the immediate demographic risks of small population size. Likewise, restoration programs intended to reintroduce fish into watersheds from which they have been extirpated will, by virtue of the need to use out-of-basin fish, constitute a plausible risk as assessed through our viability criteria, but may be entirely appropriate actions for recovering fish within a diversity stratum, particularly if the available hatchery broodstock are genetically similar to the extirpated population and there is reasonable certainty that the receiving habitat has recovered sufficiently to support fish through their full life cycle. Both captive broodstock and restoration programs exist because populations are perceived to be either extinct or at high risk of extinction, thus, the question of whether the associated wild population is viable or not has already been resolved.

### *Summary of Metrics and Estimators*

Most of the metrics for evaluating populations against the proposed population viability criteria require time series of adult spawner abundance spanning from three to four generations (though see preceeding discussion for possible use of abundance indices for estimation of population trends and catastrophic declines). Table 4 presents a summary of the metrics proposed in this paper and the data needs for estimating each.

### *Critical Considerations for Implementation*

The NCCCTRT cautions that the generalized criteria proposed here are subject to a substantial uncertainty arising from many different sources. For example, there is debate in the scientific literature regarding the appropriateness of the effective population size criteria of $N_e > 500$ for low risk, with various authors suggesting values as much as an order of magnitude higher. Likewise, authors have suggested depensation thresholds ranging anywhere from 1 to 5 adults per kilometer. Perhaps even greater uncertainty surrounds the low-risk density criteria established for the purpose of maintaining spatial structure and diversity. In this case, although we believe that the density criterion serves as a useful proxy for addressing spatial structure and diversity, quantifying relationships between these parameters and extinction risk remains a challenge. Adding to this uncertainty is the fact that populations may fundamentally differ in their productive potential, and hence populations of comparable size may have different extinction risks. It is entirely conceivable that some of the criteria may ultimately turn out to be overly conservative in some cases, and not precautionary enough in others.

As a consequence of these uncertainties, we strongly caution against treating the recommended thresholds as “absolutes” or “knife-edge” decision points. A preferred interpretation of these criteria is that they represent a set of indicators of viability, which, if all low-risk thresholds were met, would suggest that a population has a relatively high likelihood of persisting into the future. Obviously, the further a population deviates from any of the identified thresholds, the greater our certainty about its status in relation to that metric. And likewise, we have greater certainty about the status of populations that lie close to identified thresholds for a single metric, than we do for populations that are marginal for multiple metrics. Ultimately, however, decreasing uncertainty about the viability of populations will require gaining a better understanding of the dynamics of individual populations, which in turn can only come about with increased attention to research and monitoring of populations within the NCCC Recovery Domain. In the interim, we believe that, collectively, the criteria provide a reasonably precautionary approach to assessing viability.

**Table 4.** Estimation methods and data requirements for population viability metrics. Note that all references to population abundance refer to naturally produced adults (i.e., exclusive of hatchery returns).

| Population Characteristic | Metric | Estimator | Data Needs |
|---|---|---|---|
| Effective population size per generation<br><br>*-or-*<br><br>Total population size per generation | $\overline{N}_e$<br><br><br><br>$\overline{N}_{g(harm)}$ | Variable: several direct and indirect methods for estimating $N_e$ (see text).<br><br>Harmonic mean of spawner abundance per generation:<br>$\overline{N}_{g(harm)} = \dfrac{1}{\frac{1}{n} * \sum_{t=1}^{n} \frac{1}{N_{g(t)}}}$<br>where $n$ is the number of years, where $N_{g(t)}$ is the running sum of adult abundance over period equal to the population's mean generation time (rounded to the nearest whole year) at time $t$* | Variable<br><br><br><br>Time series of adult spawner abundance, $N_a$, for a minimum of 4 generations; demonstration that $N_g$ remains above threshold during periods of low marine survival |
| Population decline Critical run size | $\overline{N}_{a(geom)}$ | Geometric mean annual adult run size:<br>$\overline{N}_{a(geom)} = \sqrt[n]{N_{a(1)} N_{a(2)} N_{a(3)} \ldots N_{a(n)}}$ | Time series of adult spawner abundance, $N_a$, for a minimum of 4 generations; demonstration that $N_a$ remains above threshold during periods of low marine survival |
| Population trend | $T$ | Slope of natural log of the $g$-year running sum of abundance v. time:<br>$\hat{T}$ = slope ln($N_{g(t)}$) v. time<br>where $N_{g(t)}$ is as defined above | Time series of adult spawner abundance, $N_a$, for 2-4 generations; demonstration that increasing trend is not result of short-term increases in marine survival |
| Catastrophe | $C$ | Maximum 1-generation decline (proportion) in abundance:<br>$\hat{C} = \text{maximum}\left(1 - \dfrac{N_{g(t)}}{N_{g(t-2h)}}\right)$<br>where $N_{g(t)}$ is as defined above, and $h$ is the mean generation time (rounded to the nearest whole year) | Time series of adult spawner abundance, $N_a$; minimum of 3 generations to estimate short term catastrophic risk; for longer time series, need analysis of trends following risk and information on marine survival |
| Population density<br><br>Depensation | <br><br>$\overline{D}_{dep}$ | Mean spawner density expressed as spawners per IP kilometer (see text).<br><br>Arithmetic mean of spawner density for lowest 3 years in last 12 years.<br>$\overline{D}_{dep} = \dfrac{1}{3} \sum_{lowest3} \dfrac{N_a}{IP - km}$ | Time series of either adult spawner abundance, $N_a$, or mean spawner density from randomized survey locations; minimum of 4 generations. |

**Table 4.** (continued)

| | | | |
|---|---|---|---|
| Population density<br>Spatial structure and diversity | $\overline{D}_{ssd}$ | Arithmetic mean of spawner density for past 4 generations<br>$\hat{D}_{ssd} = \frac{1}{4h}\sum_{t=1}^{4h}\frac{N_a}{IP\text{-}km}$<br>where *IP-km* is the sum of available stream kilometers of habitat multiplied by their *IP* value, and *h* is mean generation time. | Time series of either adult spawner abundance, $N_a$, or mean spawner density from randomized survey locations; minimum of 4 generations. *IP-km* estimates for each population. |
| Hatchery influence | No specific metrics of estimators proposed. See text for guidance on potentially appropriate analyses. | | |

* In the absence of population-specific information, mean generation time is assumed to be 3 yrs for coho salmon, and 4 yrs for steelhead and Chinook salmon, which constitute the most common ages at spawning for these species within the recovery domain. For more southerly winter steelhead populations, 3 yr-olds may constitute the majority of adult spawners (Busby et al. 1996).

We also note that there are likely to be a number of situations where implementation of the criteria is likely to be confounded by special circumstances. The general framework we have adopted has as an underlying assumption the idea that the historical (pre-EuroAmerican settlement) abundance, distribution, and diversity of salmonids represent a set of reference conditions under which we are confident that populations had a high probability of persisting over long periods of time. With respect to diversity, we foresee several situations where assessing genetic risk will require considerations outside the scope of the relatively simple viability criteria proposed. One such case is where a population has undergone a severe population bottleneck, but has since recovered to levels that, from a demographic standpoint, appear to suggest low risk. Low genetic diversity resulting from the bottleneck would suggest that the population remains at elevated risk of extinction. However, at some point managers will need to assess whether that risk no longer appears significant. An example of such a case is the northern elephant seal, which was hunted to near extinction in the 19th century, but has since rebounded to population sizes of about 175,000 individuals (Weber et al. 2000). The population displays extremely low genetic variation, but apparently with minimal consequences for fitness. It remains unclear whether such a population may be prone to disease outbreaks, or substantial changes in environmental conditions. Similar questions will need to be addressed in cases where populations that have been reduced to low levels or have gone extinct and subsequently been restored through hatchery activities. Clearly, such cases will need a more rigorous assessment process than that proposed in our relatively simple viability approach.

# 3 ESU Viability Criteria[21]

## 3.1 Characteristics of Viable ESUs

At the ESU level, viability criteria focus primarily on maintaining the ESU as an integrated, functioning biological unit by seeking to buffer the ESU against catastrophic loss of populations by ensuring redundancy, provide sufficient connectivity among populations to maintain long-term demographic and evolutionary processes, and ensure sufficient genetic and phenotypic diversity to maintain the ESU's evolutionary potential in the face of changing environmental conditions. Because we are most certain that an ESU would have persisted more or less indefinitely under conditions that existed prior to the impacts stemming from European-American settlement of the West Coast, the historical population structure of an ESU provides a template against which proposed ESU viability criteria can be evaluated. Although ESU viability almost certainly declines with increasing departure from historical ESU structure, the precise nature of this relation is unknown. To accommodate this uncertainty in a precautionary manner, we therefore suggest that the degree of proof required to demonstrate that a proposed ESU configuration is consistent with ESU viability should increase with increasing departure from historical ESU structure. Bjorkstedt et al. (2005) identified historical population structure that explicitly recognizes variation in the functional roles that populations filled within the historical ESU (i.e., functionally independent, potentially independent, and dependent populations), and in anticipation of the present report, proposed a general structure for ESU viability criteria that accommodates this variation. We expand upon their proposal below.

The arrangement and status of populations within an ESU must balance a trade off between populations sharing common catastrophic risks and maintaining sufficient connectivity via dispersal among populations. Thus, viable populations need to be distributed across the landscape, yet not to be so distant from one another that dispersal is ineffective in maintaining connectivity across an ESU. Moreover, in order to maintain or restore connectivity patterns similar to those that historically underlay ESU structure, some populations must be sufficiently large to produce dispersers (strays) in sufficient numbers (1) to support adequate exchange among populations and subsidies to dependent populations that serve to increase connectivity within the ESU; (2) to increase overall abundance in the ESU; and (3) to provide additional capacity to buffer the ESU against catastrophic disturbance. Based on their historical roles in the ESU, functionally independent populations (FIPs) and potentially independent populations (PIPs) are essential to ensuring connectivity. However, dependent populations (DPs) and the smaller watersheds they occupy also contribute substantially to ESU connectivity and must therefore be considered to provide

[21] Again, we remind the reader that we use the term ESU to mean both salmon ESUs and steelhead DPSs.

an essential contribution to ESU viability. Likewise, dependent populations may provide important temporary refugia and potential sources of colonizers or broodstock for restoration of nearby FIPs and PIPs that have been extirpated (e.g., Scott and Waddell creeks are extant dependent populations in the Santa Cruz Mountains diversity stratum of the Central California Coast Coho Salmon ESU).

ESU structure should maintain representative diversity within the ESU and thus maintain the evolutionary potential of the ESU. To satisfy this requirement, we propose that a viable ESU include representation across diversity strata, as defined in Bjorkstedt et al. (2005) and revised in this report (see Appendix A). These diversity strata are intended primarily to reflect diversity arising from variation in environmental conditions in freshwater habitats, a major component of the selective regime affecting salmon and steelhead. Because genetic and geographic distances appear to be strongly correlated for anadromous salmonids within coastal regions of California (Bjorkstedt et al. 2005; Bucklin et al. 2007; Garza et al., in review), we expect that the consequent spatial arrangement of populations across the landscape will also contribute to maintenance of genetic diversity at the ESU scale.

## 3.2 ESU-level Criteria

In the following sections, we propose ESU viability criteria intended to ensure representation of the diversity within an ESU across much of its historical range, to buffer an ESU against potential catastrophic risks, and to provide sufficient connectivity among populations to maintain long-term demographic and genetic processes. We specify these criteria not in terms of specific sets of populations but rather as a set of conditions to be satisfied by a configuration of populations. In some cases, attainment of these conditions will require that certain populations be included in any specific scenario of ESU viability. More often, however, there will exist several plausible scenarios of population viability that could satisfy ESU-level criteria.

As with the population-level criteria, the proposed set of ESU-level criteria represent conditions for which we believe an ESU would have a high likelihood of persisting over long time frames (hundreds of years). The criteria are based on general principles of conservation biology and are intended to serve as precautionary guidelines that incorporate uncertainty about the rates at which populations historically interacted, both within and among diversity strata, as well as across ESU boundaries. Consequently, we note that there may be specific population and diversity strata configurations that could lead to ESU viability without strictly meeting all of the proposed criteria for every diversity stratum. For example, the geography of the California coastline makes certain diversity strata more important than others for

fostering within-ESU connectivity or providing representation of a significant portion of the ESUs historical range or evolutionary potential. We emphasize, however, that in evaluating such alternatives, demonstration that the primary goals of representation, redundancy, and connectivity are not compromised would be essential, and that adopting such configurations without further information on larger-scale processes necessarily entails accepting greater risk of extinction for the ESU.

### *Representation Criteria*

**1. a. All identified diversity strata that include historical FIPs or PIPs within an ESU or DPS should be represented by viable populations for the ESU or DPS to be considered viable**.

**-AND-**

**b. Within each diversity stratum, all extant phenotypic diversity (i.e., major life-history types) should be represented by viable populations.**

Representation of all diversity strata achieves the primary goal of maintaining a substantial degree of the ESU's historical diversity (i.e., genetic diversity, exposure and responses, including presumed adaptation, to diverse environmental conditions). Representation of all diversity strata, by virtue of the geographical structure of diversity strata, also contributes to ensuring that the ESU persists throughout a significant portion of its historical range and that connectivity is maintained across this distribution. The second element of the representation criteria (1.b) specifically addresses the persistence of major life-history types, specifically summer steelhead, as an important component of ESU viability.

In the NCCC Recovery Domain, evaluation of ESU viability must consider an additional complexity. Coho salmon and Chinook salmon reach their southernmost (coastal) limits within the NCCC Domain. Likewise, in two species the expression of major life-history types, spring-run Chinook and summer steelhead, also reach their southernmost extent within coastal basins[22]. Species ranges and life-history distribution patterns represent ESU edges in a geographic and evolutionary sense, respectively, which raises the issue of how much an ESU can contract and remain viable.

[22] Interior populations of spring Chinook salmon occur to the south in the Sacramento River basin. Likewise, summer steelhead may also have inhabited Central Valley streams draining the west slope of the Sierra Nevada at one time (McEwan 2001).

In two cases, the TRT expressed high uncertainty regarding whether populations were ever historically persistent in areas that lie near the edge of the species range: coho salmon in watersheds tributary to the San Francisco Bay Estuary[23] (with the possible exception of a few watersheds that enter the Bay relatively close to the Golden Gate and that drain the eastern slopes of the coastal mountains), and Chinook salmon in coastal basins from the Navarro River to the Gualala River[24] (Bjorkstedt et al. 2005). In both cases, analysis of long-term average environmental characteristics of these areas suggests that environmental conditions were substantially less favorable for these species, and were possibly favorable only on an inconsistent basis. Requiring viable populations where none may have existed historically as a prerequisite for ESU viability is obviously problematic, and it is therefore possible that a viable ESU might not include full representation of populations in these 'edge' regions. Nevertheless, persistent occurrence or frequent observation of the species in these areas would be strong evidence that nearby strata were producing dispersers and that habitat quality was improving, which would also bode well for other species (e.g., steelhead).

In the case of life-history types that have experienced tremendous reduction in abundance (e.g., summer steelhead in the NC-steelhead ESU) or extirpation (e.g., spring Chinook in the CC-Chinook ESU), it is also possible to argue that such losses do not necessarily indicate substantial risk to ESU viability in demographic terms, and that a viable ESU lacking this diversity might be possible. However, these populations represent unique components of ESU diversity and the evolutionary legacy of the ESU, and it is difficult to justify ignoring this diversity in ESU viability criteria focused on diversity, particularly if recovery planning follows the precautionary approach of requiring increasingly stronger proof of viability to counter increasing departure from the template of historical ESU structure. It appears that, in coastal ESUs, spring-run Chinook salmon arose from fall-run Chinook salmon in the same basin (Waples 2004b). Loss of these populations therefore may not be irrevocable if the genetic variability that underlies their origin has not been lost in extant fall-run populations. Likewise, coastal summer steelhead appear to be derived from local winter steelhead populations, which might retain a genetic legacy that will support re-expression of summer-run populations. In both cases, however, demonstration that this potential has not been lost would require restoration of environmental conditions (i.e., coldwater refugia that allow adults to oversummer) that allow expression of these life-history types and an unknown period of time for populations to express these phenotypes. It is worth noting that Chinook salmon from a common source

[23] Note that the uncertainty is not about whether coho salmon occurred in the San Francisco Bay Area, which is well documented (see Leidy et al. 2005a), but rather whether any populations were sufficiently large to function independently.

[24] In contrast to the coastal basins of moderate size, the Russian River is likely to have provided adequate access and spawning habitat for fall-run Chinook salmon on a consistent basis. Thus, the TRT concluded, with little uncertainty, that the population of fall-run Chinook salmon in the Russian River was a functionally independent population under historical conditions (Bjorkstedt, et al. 2005).

(Battle Creek, CA) introduced into rivers of New Zealand during the early 1900s currently exhibit a broad range of phenotypes, including differences in the period of freshwater residency and timing of adult migration (Quinn and Unwin 1993; Quinn et al. 2001), suggesting that re-expression of life-history types over periods of a few tens of generations may be possible. However, whether re-expression of clearly defined spring Chinook runs in the NCCC Recovery Domain is possible remains highly uncertain.

Efforts to set the stage for such recovery are independently justified by a slight extension of the 'historical template' argument to consider the role of these life- history types as sensitive indicators of habitat conditions. Because of their need for low summer water temperatures (for adult holding), spring-run Chinook salmon and summer steelhead are likely to be substantially more sensitive to factors that affect freshwater habitat quality than are fall-run and winter populations. Fall Chinook salmon and winter steelhead spend less time as adults in freshwater, do so under relatively benign seasonal conditions, and, in the case of fall-run Chinook salmon, usually (though not always) leave freshwater as juveniles before more stressful conditions develop during the summer. Restoration of habitat conditions that will presumably allow re-emergence of the more sensitive life-history types (even in the absence of such re-emergence) or recovery of those populations that remain extant is almost certain to benefit populations of fall-run Chinook or winter steelhead in the same watershed, and thus to provide additional assurances that these populations are, in fact, viable and contributing as expected to ESU viability. Such habitat restoration will increase the potential range of life-history variation (e.g., age at ocean-entry) that can complete the life cycle in such populations and thus increase the ability of such populations to persist in the face of a broader range of environmental perturbations. Thus, although the representation criteria do not require re-expression of diversity that has been lost due to extirpation, we encourage recovery planners to pursue actions that would benefit these more sensitive life-history types.

### *Redundancy and Connectivity Criteria*

Three additional and interrelated criteria for ESU viability are proposed for guarding against catastrophic risk (redundancy) and ensuring sufficient connectivity across and ESU. For each diversity stratum:

**2. a. At least two (2) or fifty percent (whichever number is greater) of historical FIPs and PIPs in the stratum must be demonstrated to be at low risk for extinction according to the population viability criteria developed in this report.**

**-AND-**

**b. Total abundance within the populations selected to satisfy this criterion must meet or exceed 50% of the aggregate viable population abundance for FIPs and PIPs historically predicted for the stratum based on the density criteria.**

In developing strategies to satisfy this requirement, recovery planners should seek ESU configurations that emphasize historical populations that, by virtue of their size and location, formed the foundation of the ESU. Ideally, this will mean that the first criterion will be satisfied directly, and thereby satisfy the second criterion. In some cases, however, it may prove distinctly infeasible to implement a strategy that will include restoration of the larger FIPs or PIPs in an ESU to a state relative to their historical status that will consequently lead to sufficient abundance within the stratum. Examples might be if a substantial proportion of historical habitat was either no longer accessible due to a dam or so degraded as to have a very low likelihood of being restored. In such cases, recovery planners may need to identify stratum-scale recovery strategies that include (1) restoring some (presumably historically large) FIPs so that they are demonstrably viable but occupy only a remnant of the historical population's range, and so cannot be considered as being entirely representative of the historical population, and (2) restoring additional (presumably smaller) FIPs, or PIPs, to a sufficient degree for stratum abundance to satisfy the second part of this criterion.

Note that any FIP or PIP contributing to the aggregate stratum abundance must be a viable population, and must (1) have abundance above the minimum viable level for a small basin (e.g., $N_a > 40$ fish x minimum IP requirement = 1,280 for coho, 800 for Chinook, 640 for steelhead) with the distribution of fish such that the density criterion is satisfied, and (2) meet minimum thresholds for low genetic risk ($N_g > 2500$).

**3. Remaining populations, including historical DPs and any historical FIPs and PIPs that are not expected to achieve recovery to a viable status, must exhibit occupancy patterns consistent with those expected under sufficient immigration subsidy arising from the 'core' independent populations selected to satisfy the preceding criterion.**

Within this set of populations, we recommend that recovery planners place a high priority on populations that are remnants of historical FIPs and PIPs, and, that, at a minimum, most historically independent populations should be at no greater than moderate risk of extinction when evaluated as independent populations. Although such populations no longer fully serve their historical role within the ESU, remaining elements of these populations can contribute substantially to connectivity and potentially

represent major parts of the ESUs evolutionary legacy. Additionally, planners should place high priority on maintaining dependent populations in situations where associated historical FIPs and PIPs are at high risk of extinction or have been extirpated. In these situations, dependent populations may be vital as sources of colonizers and genetic diversity to support restoration of adjacent FIPs and PIPs, and afterwards to buffer these larger populations against future disturbances. Indeed, during the recovery process, dependent populations may act (temporarily) as source populations for nearby FIPs and PIPs that have been reduced to sink status. Likewise, dependent populations can be expected to contribute to maintaining genetic diversity within a stratum and providing a source of colonizers that can reduce both genetic and demographic risks to adjacent FIPs and PIPs.

**4. The distribution of extant populations, regardless of historical status, must maintain connectivity within the diversity stratum, as well as connectivity to neighboring diversity strata.**

To ensure this, it might prove necessary to identify key watersheds that fill what would otherwise be substantial spatial gaps in the diversity stratum. Such watersheds might harbor populations considered to have been historically dependent on immigration from other populations. Ensuring that such populations persist requires ensuring that their source populations are also at a sufficient status to maintain connectivity. Currently, data on both the distances that Pacific salmonids within California's coastal region stray from their natal streams and that rates at which they do so is insufficient to provide concrete guidance on how close adjacent populations should be to maintain connectivity. However, a limited number of studies of straying by Chinook salmon (Hard and Heard 1999), pink salmon (Wertheimer et al. 2000), chum salmon (Tallman and Healey 1994), and Atlantic salmon (Jonsson et al. 2003) in other regions suggest that the majority of salmon that stray enter streams within a few tens of kilometers from their natal stream (or stream of release). Assuming that salmon and steelhead populations in coastal California exhibit similar tendencies, unoccupied gaps along the coastline of more than 20–30 km may be sufficient to disrupt normal patterns of dispersal and connectivity.

## 3.3 Example Scenarios of Application of ESU-Viability Criteria

In this section, we present a series of hypothetical scenarios to illustrate how ESU viability criteria for individual diversity strata (DS) might be applied to evaluate DS configurations proposed as the goal for recovery efforts. We propose a hypothetical diversity stratum that historically comprised three FIPs, three PIPS, and nine dependent populations (Figure 6), and then identify various scenarios of distribution and

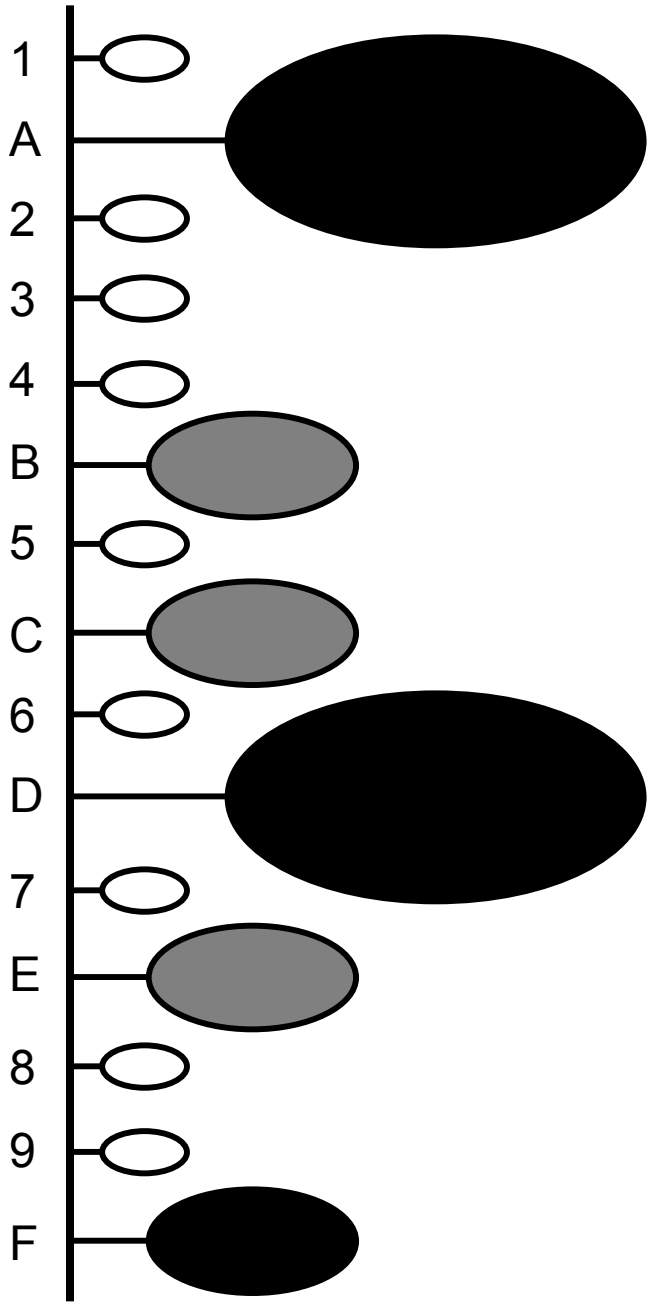


**Figure 6.** Historical population structure of a hypothetical diversity stratum within an ESU. Oval size is crudely proportional to historical population size. Black ovals are historical functionally independent populations. Grey ovals are historical potentially independent populations. White ovals are dependent populations. Population IDs correspond to those in Table 5.

abundance to evaluate whether each would be considered viable according to the criteria proposed in this document (Table 5). The set of scenarios identified below is hardly exhaustive, and serves simply to highlight a range of possible proposals and where such proposals might be expected to succeed or fail in establishing a DS that contributes to a viable ESU. Specifics regarding the cause of populations' status are left intentionally vague. Proposed reduction in habitat capacity from current measurements may arise from planned loss of habitat, or perhaps more likely, will stem from redefinition of the extent of occupied or habitable habitat to allow population viability criteria to be based on densities in occupied areas.

*Current Conditions*

In its current state (column 4 in Table 5), the DS does not contribute to ESU viability. All historically independent populations fail to satisfy requirements for population viability, some dependent populations are no longer extant, and those dependent populations that remain occupied are at low density. Connectivity is not necessarily eroded as a consequence of disruption to the spatial arrangement of populations in the DS. However, substantial declines in abundance are likely to underlie reductions in the number of dispersers, especially emigrants from historically independent populations, and therefore to compromise connectivity among populations. The spatial arrangement of populations continues to maintain a degree of independence among populations with respect to catastrophic disturbance, and is likely to maintain a substantial portion of historical diversity associated with environmental variation.

*Scenario I*

In this scenario, recovery actions are directed at increasing the quality of available habitat in historically independent populations and thus boosting abundance, but there is no effort to restore access to areas that have been effectively lost to the DS, or to improve conditions in watersheds occupied by historically dependent populations. Three historically independent populations are recovered to viability (two historically FIP and one historically PIP), but these populations do not include sufficient abundance to satisfy overall DS abundance requirements. Connectivity is likely to improve, as most populations are included in the configuration, and abundance in the larger source populations is increased.

*Scenario II*

In this scenario, recovery actions are directed at restoring all historically independent populations to viable status, but increasing access to habitat only as necessary to meet the minimum abundance requirement for viability. Watersheds that harbor dependent populations are not restored, and some (DPs 2 and 3) decline further. The three viable historically independent populations recovered in Scenario I are now joined by three additional viable populations that satisfy the minimum requirements for viability, yet

**Table 5.** Historical structure, current conditions, and potential recovery planning scenarios for a hypothetical diversity stratum in a listed ESU (illustrated in Figure 6). $N_a$ = average annual number of spawners. Under Scenarios, 'Pot' refers to target potential $N_a$ based on accessible habitat, 'Real' refers to realized $N_a$. Scenarios are described in greater detail and evaluated in text. Minimum $N_a$, which corresponds to a minimum extent of habitat and associated density criterion, is set at 1,200.

| Population | | Potential $N_a$ | | Actual | Scenario I | | Scenario II | | Scenario III | | Scenario IV | | Scenario V | | Scenario VI | | Scenario VII | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Historic | Curr | $N_a$ | Pot. | Real. | Pot. | Real. | Pot. | Real. | Pot. | Real. | Pot. | Real. | Pot. | Real. | Pot. | Real. |
| FIPs | A | 8,500 | 2,500 | 500 | 2,500 | 2,500 | 2,500 | 2,500 | 4,000 | 4,000 | 6,000 | 6,000 | 5,000 | 5,000 | 1,000 | 1,000 | 1,500 | 1,500 |
| | D | 6,000 | 3,000 | 1,000 | 3,000 | 3,000 | 3,000 | 3,000 | 4,000 | 4,000 | 5,000 | 5,000 | 4,000 | 4,000 | 1,000 | 1,000 | 3,000 | 3,000 |
| | F | 2,000 | 2,000 | 200 | 500 | 500 | 1,200 | 1,200 | 1,100 | 1,100 | 2,000 | 2,000 | 2,000 | 2,000 | 500 | 500 | 1,500 | 1,500 |
| PIPs | B | 2,200 | 1,500 | 300 | 1,500 | 1,500 | 1,500 | 1,500 | 1,500 | 1,500 | 0 | 0 | 1,000 | 1,000 | 2,200 | 2,200 | 2,200 | 2,200 |
| | C | 1,800 | 1,000 | 700 | 1,000 | 1,000 | 1,200 | 1,200 | 1,200 | 1,200 | 0 | 0 | 500 | 500 | 1,800 | 1,800 | 1,800 | 1,800 |
| | E | 1,500 | 500 | 500 | 500 | 500 | 1,200 | 1,200 | 1,200 | 1,200 | 0 | 0 | 500 | 500 | 1,500 | 1,500 | 1,500 | 1,500 |
| DPs | 1 | 200 | 50 | 50 | 50 | 50 | 50 | 50 | 50 | 50 | 0 | 0 | 0 | 0 | 50 | 50 | 50 | 50 |
| | 2 | 150 | 100 | 0 | 100 | 0 | 100 | 0 | 100 | 0 | 0 | 0 | 0 | 0 | 100 | 100 | 100 | 0 |
| | 3 | 300 | 100 | 100 | 100 | 100 | 100 | 0 | 100 | 100 | 0 | 0 | 100 | 100 | 100 | 100 | 100 | 100 |
| | 4 | 100 | 50 | 50 | 50 | 50 | 50 | 0 | 50 | 50 | 0 | 0 | 0 | 0 | 50 | 50 | 50 | 50 |
| | 5 | 200 | 100 | 0 | 100 | 0 | 100 | 0 | 100 | 0 | 0 | 0 | 0 | 0 | 100 | 100 | 100 | 0 |
| | 6 | 300 | 50 | 50 | 50 | 50 | 50 | 50 | 50 | 50 | 0 | 0 | 0 | 0 | 50 | 50 | 50 | 50 |
| | 7 | 200 | 100 | 0 | 100 | 0 | 100 | 0 | 100 | 0 | 0 | 0 | 0 | 0 | 100 | 100 | 100 | 0 |
| | 8 | 400 | 150 | 0 | 150 | 0 | 150 | 0 | 150 | 0 | 0 | 0 | 150 | 150 | 150 | 150 | 150 | 0 |
| | 9 | 150 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 0 | 0 | 0 | 0 | 100 | 100 | 100 | 100 |
| **Total DS $N_a$** | | 24,000 | 11,300 | 3,550 | | 9,350 | | 10,800 | | 13,350 | | 13,000 | | 13,250 | | 8,800 | | 11,850 |
| **% Hist. $N_a$** | | | 47 | 15 | | 39 | | 45 | | 56 | | 54 | | 55 | | 37 | | 49 |
| **$N_a$ in IPs** | | 22,000 | | 0 | | 7,000 | | 10,600 | | 11,900 | | 13,000 | | 11,000 | | 5,500 | | 11,500 |
| **% Hist. $N_a$ in IPs** | | | | 0 | | 32 | | 48 | | 54 | | 59 | | 50 | | 25 | | 52 |
| **Viable FIPs & PIPs** | | | | 0 | | 3 | | 6 | | 5 | | 3 | | 3 | | 3 | | 6 |
| **% Hist. FIPs & PIPs** | | | | 0 | | 50 | | 100 | | 83 | | 50 | | 50 | | 50 | | 100 |

this configuration still does not satisfy the overall DS abundance criterion, since it historically large populations are only partially recovered. Connectivity is likely to be locally enhanced by increased abundance in source populations, but the lack of dependent populations 2, 3, and 4 leaves a substantial spatial gap between populations A and B (Figure 6).

*Scenario III*

In this scenario, recovery actions are directed at restoring all but one of the historically independent populations to viable status, with additional effort to increase habitat access, and therefore abundance, in historical FIPs. Watersheds that harbor dependent populations are not restored, nor are they allowed to degrade further. This configuration satisfies redundancy and the viable populations include a satisfactory proportion of the historical potential $N_a$ of the DS. Connectivity is good due to the occupancy of all populations. Connectivity with the rest of the ESU to the south of this DS must be evaluated in light of the projected non-viable status of the southernmost historically independent population (population F).

*Scenario IV*

In this scenario, recovery actions are directed solely at restoring the historically large populations in the DS, and as a tradeoff, populations elsewhere are effectively allowed to go extinct (or to decline to negligible abundance). Although the number of viable populations and the abundance of fish in these populations satisfy the relevant criteria for the DS to contribute to ESU viability, the loss of connectivity (i.e., substantial gaps between the three viable populations; Figure 6) and diversity within the DS precludes concluding that this configuration allows the DS to contribute to ESU viability.

*Scenario V*

In this scenario, recovery actions are directed primarily at restoring historical FIPs, but some effort is also directed at maintaining a select set of populations as non-viable dependent populations, including populations in watersheds historically occupied by PIPs. This configuration satisfies the criteria for number of viable populations and proportion of fish in historically independent populations. The configuration also reduces risk to the DS by distributing populations across the landscape, and presumably increasing connectivity within the ESU. Diversity may also be increased, in terms of the habitats occupied, but the degree to which diversity is preserved in the dependent populations (including the non-viable PIPs) may be limited.

*Scenario VI*

In this scenario, recovery actions are focused on maintaining the status quo in historical FIPs, while restoring historical PIPs to something approaching their original status. In addition, recovery focuses on maintaining occupancy of dependent populations throughout the DS. This scenario satisfies criteria for number of viable populations and connectivity, but fails to include a sufficient abundance of fish in viable populations. Diversity might also be compromised, depending on the character of the remnants of the historical FIPs.

*Scenario VII*

In this scenario, viable populations are restored in all historically independent populations, although the viable populations in watersheds historically occupied by FIPs are now spatially restricted viable remnants of the historical populations. This scenario satisfies criteria for number of populations, abundance within viable populations, and connectivity. Again, diversity issues need to be considered in light of the fact that historical FIPs are now represented as viable remnant populations, and diversity associated with lost portions of their watersheds might not be represented elsewhere in the DS.

## 3.4 Other Considerations

The proposed criteria for DS to contribute ESU viability represent an approach that, while precautionary, is intended to correspond to a maximum acceptable level of risk for the ESU to be susceptible to future decline, disintegration, and extinction, and as such represent the minimum conditions that must be achieved in each DS for an ESU to be considered viable. Achieving these minimum conditions is not sufficient for long-term viability—these conditions must be maintained. As a consequence, recovery actions that lead to ESU configurations that exceed ESU viability criteria, even slightly, are likely to decrease the risk facing the ESU and thus the risk that future recovery crises will arise.

Although the scenarios discussed above are measured against these minimal benchmarks, comparisons among some of the scenarios illustrate how going beyond minimal viability requirements can provide additional buffering against future events. For example, the differences between Scenario IV and Scenario V involves a trade-off between concentrating efforts (and fish) in the three largest populations (Scenario IV) and distributing fish among dependent populations while retaining a focus on historical FIPs (Scenario V). The latter scenario is likely to reduce risk by increasing the resiliency of the DS as a whole through increased connectivity, and thus the potential for the other populations to buffer individual populations that experience disturbance or a temporary decline. In general, increasing the number of

extant populations will contribute to viability, even when those populations would not be considered viable independently.

One caution that must also be kept in mind is that viable ESUs and their component DSs cannot be considered as static entities. Relative abundance in populations within an ESU or DS can fluctuate substantially in response to natural environmental variation, and populations that were once numerically dominant can decline and be replaced as the most productive populations by others (see e.g., Hilborn et al. 2003). A prudent recovery strategy will accommodate this potential by creating conditions that allow populations not included in configurations designed to meet the minimum ESU/DS criteria to recover as a buffer against loss or decline of populations that are the focus of intense recovery efforts. For this reason, a recovery plan that begins with Scenario II, III or V as an initial goal, and thus avoids a trade-off such as illustrated in Scenario IV is preferable, as it allows for the development of an ESU with greater flexibility to respond to disturbance of an extant population and does not shut down options for future restoration to further increase ESU resiliency.

Finally, we note that the proposed ESU-level criteria are based on certain assumptions about historical population structure, which in turn were based on assumptions about both the minimum habitat needed to support a viable population in isolation, and the level of interaction among populations. The TRT acknowledges the possibility of more complex population structures. For example, although we defined populations occupying smaller watersheds (i.e., below minimum IP thresholds) to be "dependent", it is possible that geographically proximate dependent populations may interact to a degree sufficient to collectively form a larger unit with a likelihood of persistence comparable to a viable independent population. Should such population structures be demonstrated to exist, it is conceivable that rules regarding stratum viability could be modified accordingly (e.g., a viable group of "mutually dependent" populations might be considered comparable to a viable independent population). We draw attention to this scenario to alert recovery planners to the need to consider such possibilities when developing recovery strategies. Our concern is that, while historically independent populations should almost certainly form the core of any recovery strategy, there are specific instances where it may be more prudent to focus initial restoration and recovery efforts on extant dependent populations than on independent populations that have been extirpated or that inhabit watersheds that are so degraded as to have a low probability of supporting persistent populations for the foreseeable future.

At the present time, data are not available to identify specific instances of where sets of mutually dependent populations might function as plausible recovery units. Support of such a delineation would

require substantial information on all populations involved. First, there would need to be direct estimates of straying among putative constituent dependent populations to demonstrate that exchange of individuals among these populations is sufficiently high to warrant consideration of the group as a single unit. Second, a determination would have to be made about the amount of total habitat that would be needed to support an aggregate group of dependent populations. The minimum IP thresholds to support a viable coho salmon, Chinook salmon, and steelhead populations are estimated to be approximately 32 *IP-km*, 20 *IP-km*, and 16 *IP-km*, respectively. However, the amount of habitat needed to support a network of dependent populations depends on a number of factors including the rate of exchange of individuals among populations, the variability in population abundance, and the degree of correlation in the dynamics of contributing populations, which is a function of heterogeneity of habitats and temporal synchrony in environmental conditions. Consequently, the total aggregate habitat needed to support a viable unit might be substantially different (either higher or lower) than the identified *IP-km* thresholds and would not likely simply be an additive effect. Consequently, demonstrating that a group of populations functions as an independent unit with a specific extinction risk is not a simple undertaking.

# 4 Assessment of Current Viability of Salmon and Steelhead Populations within the NCCC Recovery Domain

The criteria presented in the preceding two chapters are intended to provide a framework for planners both to set general biologically based targets for recovery and to guide future evaluations of the status of ESA-listed salmonids within the NCCC Recovery domain. In this chapter, we apply the population-level and ESU-level viability criteria developed in Chapter 2 to salmon and steelhead within ESUs of the North-Central California Coast Recovery Domain to assess current viability. Theoretically, application of the criteria should occur in two steps. First, because the spawner density criteria for each population depend on specific watershed attributes (i.e., historical intrinsic habitat potential, expressed as *IP-km*), specific criterion values are estimated for each population. Determination of appropriate density criteria is confounded by the fact that, in some instances, habitat that was historically accessible to anadromous salmonids now lies behind impassible dams or other barriers. In some instances, remaining habitat, even if functioning properly, may be insufficient to support a viable population (i.e., available *IP-km* is less than the thresholds for viability-in-isolation established by Bjorkstedt et al. 2005). In others, it may be possible for a population to be viable without access to this historical habitat, though its functional role in relation to other populations in the ESU may have been substantially altered. For this reason, we estimate density criteria and associated population abundances (estimated as density multiplied by *IP-km*) for both historical (pre-barrier) and current (post-barrier) conditions[25]. In addition to allowing evaluation of whether or not a below-barrier population could be considered viable in its current habitat, it also highlights situations where access to blocked habitat may be either a necessary step to restore a population's viability, or a desirable step for enhancing the populations role in maintaining ESU-viability. Appendix B provides further discussion of the relationship between population viability and the current accessibility and condition of habitats.

The second step involves evaluating risk according to the criteria. In reality, we have virtually no instances where currently available data are of sufficient quality and duration to rigorously assess population viability according to our criteria. Most of the population viability metrics require adult time series of abundance sufficient for estimating total population size of wild populations for a period of at least three-to-four generations. The few available time series of adult abundance for populations within the NCCC Recovery Domain generally are either too short in duration to apply the criteria, inadequate for estimating total population abundance, influenced to an unknown degree by hatchery fish, or otherwise

[25] Our estimates of habitat lost behind barriers include only major obstructions to fish passage and do not factor in the hundreds, if not thousands, of culverts and other smaller barriers that may partially or completely prevent fish passage.

deficient. As a result, strict application of the criteria results in most, if not all, populations being classified as "data deficient". However, in some circumstances, we have ancillary data (often highly qualitative) that strongly suggest that populations would currently fail to meet one or more of the identified low-risk or moderate-risk thresholds. It seems unsatisfying to simply describe these populations as data deficient when the collective body of data strongly suggests that populations are currently at elevated risk of extinction. In these instances, we assign a population-level risk designation, identifying the specific criteria that we believe the population is unlikely to satisfy and the data we believe justifies the particular risk rating. We caution, however, that while we occasionally used this ancillary data to assign a probable moderate or high risk, in no instances did we feel that such data were sufficient to assign a low-risk designation.

## 4.1 Central California Coast Coho Salmon

### *Population Viability*

Summary of density-based criteria.

Within the Central California Coast Coho Salmon ESU, Bjorkstedt et al. (2005) identified eleven functionally independent populations and one potentially independent population. Table 6 summarizes proposed density-based criteria for these populations and the estimated population abundances (rounded to the nearest 100 spawners) that would result if density criteria were met under both historical (pre-dam) and current (post-dam) conditions. For each population, the high-risk abundance values indicate population-specific abundances below which populations are likely at substantial risk due to depensation. The low-risk estimates based on historically accessible habitat can be viewed as preliminary abundance targets that, if consistently exceeded, we believe would lead to a high probability of persistence over a 100-year time frame and would likely result in a population fulfilling its historical role in ESU viability.

Comparison of historical versus current *IP-km* provides a rough estimate of the proportion of historical habitat that is no longer accessible to the population and the affect this has on density and abundance targets. For the CCC ESU, the largest percentage losses of potential habitat have occurred in the Lagunitas Creek (49%) and Walker Creek (27%) watersheds. Estimated losses of *IP-km* due to dams in the San Lorenzo and Russian River watersheds are 6% and 3%, respectively. The relatively minor influence of dams in the Russian River is due to the fact that most of the predicted habitat lies in the lower coastal portions of the watershed, below the influence of major dams such as Coyote and Warm Springs dams. Losses of potential habitat due to dams for the remaining populations are estimated to be less than

**Table 6.** Projected population abundances ($N_a$) of CCC-Coho Salmon independent populations corresponding to a high-risk (depensation) thresholds of 1 spawner/*IP-km* and low-risk (spatial structure/diversity=SSD) thresholds based on application of spawner density criteria (see Figure 5). Values listed under "historical" represent criteria applied to the historical landscape in the absence of dams that block access to anadromous fish. Values listed under "current" exclude areas upstream from impassible dams.

| | | | | | High Risk | | Low Risk | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Historical | Current | Historical SSD | | Current SSD | |
| **Population** | **Historical *IP-km*** | **Current *IP-km*** | ***IP-km* Lost** | **IP-bias index** | **Depens. $N_a$** | **Depens. $N_a$** | **Density spawner/IP-km** | **$N_a$** | **Density spawner/IP-km** | **$N_a$** |
| **Ten Mile River** | 105.1 | 105.1 | 0% | moderate | 105 | 105 | 34.9 | 3700 | 34.9 | 3700 |
| **Noyo River** | 119.3 | 118.0 | 1% | moderate | 119 | 118 | 33.9 | 4000 | 34.0 | 4000 |
| **Big River** | 193.7 | 191.8 | 1% | moderate | 194 | 192 | 28.8 | 5600 | 28.9 | 5500 |
| **Albion River** | 59.2 | 59.2 | 0% | high | 59 | 59 | 38.1 | 2300 | 38.1 | 2300 |
| **Navarro River** | 201.0 | 201.0 | 0% | high | 201 | 201 | 28.3 | 5700 | 28.3 | 5700 |
| **Garcia River** | 76.0 | 76.0 | 0% | high | 76 | 76 | 36.9 | 2800 | 36.9 | 2800 |
| **Gualala River** | 252.2 | 251.6 | 0% | high | 252 | 252 | 24.7 | 6200 | 24.8 | 6200 |
| **Russian River** | 779.4 | 757.4 | 3% | high | 779 | 757 | 20.0 | 15600 | 20.0 | 15100 |
| ***Walker Creek*** | 103.7 | 76.2 | 27% | high | 104 | 76 | 35.0 | 3600 | 36.9 | 2800 |
| **Lagunitas Creek** | 137.0 | 70.4 | 49% | high | 137 | 70 | 32.7 | 4500 | 37.3 | 2600 |
| **Pescadero Creek** | 60.6 | 60.6 | 0% | high | 61 | 61 | 38.0 | 2300 | 38.0 | 2300 |
| **San Lorenzo River** | 135.3 | 126.4 | 7% | high | 135 | 126 | 32.8 | 4400 | 33.4 | 4200 |

1%. Overall, Lagunitas and Walker creeks provide the only two instances where abundance targets change appreciably due to loss of historical habitat (Table 6).

Evaluation of current population viability

There are virtually no data of sufficient quality to rigorously assess the current viability of any of the eleven independent coho salmon populations within the CCC ESU using the proposed criteria. Consequently, many populations are identified as data deficient (Table 7). However, recent information on occupancy of historical streams within the CCC ESU indicates that wild populations of coho salmon are extinct or nearly so in a number of watersheds within the CCC ESU (Good et al. 2005). In the San Lorenzo River, annual summer surveys conducted on the San Lorenzo River and many of its tributaries failed to produce evidence of successful reproduction by coho salmon from 1994 to 2004 (D.W. Alley and Associates, 2005). After reports of approximately 50 adult spawners passing the Felton Diversion Dam (mostly marked hatchery fish) during the 2004–2005 spawning season, a few juvenile coho salmon were independently observed in a single tributary (Bean Creek) by Don Alley (personal communication) and by NMFS biologists (Brian Spence, NMFS, Fisheries Ecology Division, Santa Cruz, unpublished data). However, extensive snorkel and electrofishing surveys elsewhere in the San Lorenzo River basin produced no other evidence of successful reproduction. Based on the apparent long-term absence of coho salmon form this watershed, we classified the San Lorenzo population as extinct (Table 7).

Pescadero Creek has been surveyed only sporadically over the last 10 years. From 1995 to 2004, small numbers of juvenile coho salmon have been observed in the mainstem of Pescadero Creek, one of its tributaries (Peters Creek), and in the Pescadero estuary (J. Nelson, CDFG, personal communication; Brian Spence and Tom Laidig, NMFS, Fisheries Ecology Division, Santa Cruz, unpublished data). All but one of these observations come from the same brood cycle (1999, 2002, 2005). Planting of hatchery smolts (from Scott Creek) into Pescadero Creek in spring of 2003 apparently resulted in successful reproduction in the 2004–2005 spawning season, as approximately 1,600 juveniles were observed in snorkel surveys conducted in pools along 21 km of the mainstem of Pescadero Creek (roughly 33% of the accessible habitat in the watershed) by NMFS biologists in summer 2005. However, surveys conducted in 2006 over approximately 8 km of both mainstem and tributary habitats revealed no juvenile coho salmon (Brian Spence, NMFS, Fisheries Ecology Division, Santa Cruz, unpublished data). We categorized the extinction risk of this population as high, assuming that current abundance is sufficiently low that it would rate at high risk for effective population size, population decline (mean annual spawner abundance), and risk of depensation (Table 7). The planting of Scott Creek fish into Pescadero Creek potentially poses a genetic risk to any remnant population that may still exist in the watershed, though

**Table 7.** Current viability of CCC-Coho Salmon independent populations based on metrics outlined in Tables 1 and 4. na indicates data of sufficient quality to estimate the population metric are not available. In some cases, risk categories have been designated for populations where ancillary data strongly suggest populations are extinct or nearly so, despite the lack of quantitative estimates of any of the viability metrics. Metrics for which we believe ancillary data support the assigned risk category are denoted with bold and asterisks. See text for justification of risk rankings.

| Population | PVA result | Effect. pop. size per generation $\overline{N}_e$ | Tot. pop. size per generation $\overline{N}_{g(harm)}$ | Population decline $\overline{N}_{a(geo)}$ | $\hat{T}$ | Catastrophe $\hat{C}$ | Density $\hat{D}_{dep}$ | $\hat{D}_{ssd}$ | Hatchery | Risk Category |
|---|---|---|---|---|---|---|---|---|---|---|
| **Ten Mile River** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Noyo River** | na | na | na | na | na | na | na | na | **na*** | Moderate/High |
| **Big River** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Albion River** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Navarro River** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Garcia River** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | High |
| **Gualala River** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | High |
| **Russian River** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | **na*** | High |
| ***Walker Creek*** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | **na*** | Extinct? |
| **Lagunitas Creek** | na | na | na | na | na | na | na | na | na | Data deficient[26] |
| **Pescadero Creek** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | **na*** | High |
| **San Lorenzo River** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | Extinct? |

[26] See text for discussion of existing data for Lagunitas Creek.

given the population's apparent small size, these genetic risks may be trivial compared with the existing demographic risks.

In the Russian River basin, only one tributary (Green Valley Creek) has produced coho salmon annually in recent years, with salmon observed only sporadically in a few other tributaries (Merritt Smith Consulting 2003). Concerns over the decline of coho salmon in the Russian River basin have led to the establishment of a captive broodstock program at the Warm Springs (Don Clausen) Hatchery. Based on the sparse distribution (Good et al. 2005), the low apparent abundance, recent evidence of a genetic bottleneck (Libby Gilbert-Hovarth et al., NMFS, Fisheries Ecology Division, Santa Cruz, unpublished data, cited in Bjorkstedt et al. 2005), and the perceived need for intervention with a captive broodstock program, we categorized the Russian River population as at high risk, assuming that it would rank at high risk for at least four of five population metrics (Table 7)

Naturally occurring coho salmon have not been observed in Walker Creek in several decades, though this stream was planted with 80 adult coho salmon (Olema Creek origin) from the Russian River captive broodstock program in January of 2004, and fingerlings—confirmed through genetic analysis to be primarily progeny of the planted adults—were observed in summer of 2004 (CDFG 2004; J. Carlos Garza, NMFS, Fisheries Ecology Division, Santa Cruz , unpublished data). We categorized this population as "extinct" based on the long-term absence of naturally spawning coho salmon from this basin (Table 7).

Limited surveys in the Garcia and Gualala rivers have documented occasional occurrence of coho salmon in the last 15 years, but the distribution of fish has been sparse in both river systems (Good et al. 2005). Observations in the Gualala River may have resulted from planting of young-of-the-year coho salmon from the Noyo River into the North Fork Gualala River in years 1995-1997 (Harris 2001). We categorized both the Gualala River and Garcia River populations as at least at high risk of extinction, as it is highly unlikely that either is sufficiently abundant to satisfy even the moderate risk criteria for effective population size, population decline (i.e., annual abundance), and density (depensation) criteria (Table 7).

The most reliable set of population data for any independent population in the CCC ESU comes from Lagunitas Creek, where spawner surveys have been conducted on a regular basis (flows permitting) since 1995. These surveys involve multiple visits to reaches representing a substantial portion of the available spawning habitats (Ettlinger et al. 2005). Redd counts from these surveys appear to provide the most consistent measure of abundance, as estimates of live spawners are likely biased high due to double-

counting of individuals on successive surveys. Over the last 10 years, an average of about 250 coho redds (range 86-496) have been observed annually in the mainstem and upper tributaries of Lagunitas Creek. Additionally, National Park Service surveys of Olema Creek (a tributary to Lagunitas Creek), where maximum live/dead fish counts are recorded, indicate that a minimum of 86 fish have, on average, spawned in Olema Creek over the last eight years. These data did not meet our minimum requirements for application of viability metrics for several reasons. First, redd counts may lead to biased (both high and low) estimates of spawner abundance for a number of reasons, such as failure of observers to detect redds do to poor viewing conditions, redd superimposition, loss of redds due to scouring, individual females constructing multiple redds, or unequal sex ratios. Consequently, they may provide only an indicator of abundance[27]. Second, there is no information about spawner abundance in unsurveyed areas; thus, obtaining a total population estimate from these data is not currently possible. And finally, the 10-year time series does not yet meet the minimum data requirement of 4 generations for estimating effective population size, population decline, or density criteria. Consequently, we categorized the population as data deficient (Table 7). However, we note that with two additional years of data collection, additional analysis of the relationship between redd counts and total spawner abundance, and analysis of the relative densities in surveyed versus unsurveyed reaches, these data could provide a reasonable basis for assessing population viability. We also note that the existing data suggest that, if current patterns continue, and assuming that one redd translates to approximately two spawning adults on average, the Lagunitas Creek population might satisfy low-risk criteria for the effective population size criteria and perhaps the population decline criteria as well. On the other hand, the population would likely be considered at moderate risk based on the density criteria. Lagunitas Creek and its tributaries received plantings of hatchery fish, primarily from the Noyo River but also from some out-of-ESU stocks, on numerous occasions between 1960 and 1987 (Bjorkstedt et al. 2005). Analysis of DNA microsatellite data from coho populations in California indicate some affinity between Lagunitas Creek and Noyo River coho salmon (J. C. Garza, NMFS Santa Cruz, unpublished data); however, it is unclear whether this is the consequence of past hatchery plants or natural straying. Thus, it is difficult to assess potential residual hatchery-related risk for Lagunitas Creek. To our knowledge, there have been no recent plantings of hatchery fish into the Lagunitas watershed, suggesting that ongoing risks due to hatchery operations is minimal.

[27] Note that under the most favorable conditions (i.e., clear observation conditions throughout the spawning season, densities sufficiently low that superimposition is unlikely, and absence of scouring events), redd counts may prove to be an appropriate means for estimating adult spawner abundance; however, additional data are needed to establish a relationship between redd counts and total spawner abundance.

Status of populations along the Mendocino Coast is less certain. Occupancy data suggest that populations in the Navarro, Albion, Big, Noyo, and Ten Mile rivers continue to persist but that their distributions have been substantially reduced (Good et al. 2005). In none of these cases are there sufficient population-level data to determine viability with any certainty; thus, we classified four of these populations (Navarro, Albion, Big, and Ten Mile) populations as data deficient (Table 7), though available occupancy data suggest that it is unlikely any are achieving the low-risk density criteria threshold and therefore may be at least at moderate risk. In the case of the Noyo River, counts of adult spawners are available from the Noyo Egg Collecting Station on the South Fork Noyo River since 1962. These counts do not represent full counts (the station was operated irregularly in most years), and all counts are strongly influenced by hatchery activities that occurred from the early 1960s to 2003, when the last releases of hatchery coho salmon were made. During the last seven years of operation, all released hatchery yearlings were marked, providing an estimate of hatchery fraction for this subbasin. In the last two generations, the hatchery fraction has averaged 59% and 45%, respectively. Based on these data, and the fact the roughly one-third of the habitat in the Noyo River lies in the South Fork subbasin, we suspect that, even if straying of South Fork Noyo hatchery fish into other subbasins is low, the total percentage of hatchery fish in the entire basin likely exceeded 15%. This conclusion assumes that density of natural spawners in areas outside of the South Fork subbasin are not substantially higher than in the South Fork. Furthermore, the long history of stocking during which practices were not consistent with current best management practices (e.g., nonnative broodstock were occasionally used, and broodstock selection and mating protocols generally did not follow modern BMPs) suggests the potential for residual genetic effects of these operations. Thus, we classified Noyo River coho salmon as being at moderate/high risk due to past hatchery influence (Table 7). Although direct plantings of coho salmon into the Ten Mile, Big, Navarro, and Albion rivers do not currently occur, the potential exists for Noyo River hatchery fish to stray into these watersheds. The degree to which they do so is not known.

### *ESU Viability*

Though quantitative data on the abundance of coho salmon in the CCC ESU are scarce and many populations were described as data deficient (Table 7), ancillary data (primarily presence-absence data) clearly indicate that coho salmon in this ESU fail to meet both the representation and redundancy/connectivity criteria. The available data indicate that no populations meet low-risk criteria in three of the identified diversity strata (Santa Cruz Mountains, Coastal, and Gualala Point-Navarro Point), and that coho salmon are no longer present in an any of the San Francisco Bay dependent populations (indicating that either neighboring populations are not producing migrants in sufficient number to maintain these populations or the available habitat is incapable of supporting any migrants that do enter

these systems). Status of populations along the Mendocino Coast is highly uncertain (all populations were categorized as data deficient), though we believe it is unlikely that any of these populations approach viable levels.

Connectivity among populations within and among diversity strata is a significant concern. Within the Santa Cruz Mountains stratum, the two identified functionally independent populations appear extinct (San Lorenzo River) or are nearly so (Pescadero Creek). Dependent coho salmon populations still persist in three watersheds near the geographic center of the stratum, but only the Scott Creek population, which is supported by ongoing hatchery activities, regularly produces spawners in all three brood lineages; both the Waddell Creek and Gazos Creek populations have lost year classes (Smith 2006). Coho salmon are occasionally observed in other watersheds (e.g., San Vicente, San Gregorio, and Laguna creeks), but these fish are likely the product of strays from either Scott Creek or hatchery fish that have been planted in area streams. Consequently, there are substantial portions of the stratum that have few or no coho salmon, and the nearest extant population to the north is Redwood Creek in Marin County, a dependent population some 100 km to the north. Likewise, in the Coastal stratum, coho salmon persist in significant numbers only in Lagunitas Creek, with a few coho found in the Russian River, as well as Redwood Creek to the south. To the north, in the Navarro Point-Gualala Point stratum, coho salmon appear scarce or extinct in all watersheds with the exception of the Navarro River. As the Lagunitas Creek and Navarro River populations are separated by an expanse for almost 160 km of coastline with almost no coho salmon, interactions among these populations may be minimal. Connectivity is currently less of a concern in the Lost Coast-Navarro Point stratum, as both independent and dependent populations of coho salmon still persist from Big Salmon Creek to the Ten Mile River (Good et al. 2005). It is unclear, however, how much recent distribution patterns have been influenced by hatchery operations within the Noyo River basin. The status of dependent populations to north of the Ten Mile River is poorly known, but it is possible that the Mattole River, in the SONCC ESU is the nearest extant population that supports coho salmon on an annual basis. Coho salmon were observed in two consecutive years in the South Fork of Usal Creek (W. Jones, CDFG retired, personal observations), but it is uncertain whether coho salmon occur in all three brood years.

In summary, the lack of demonstrably viable populations (or the lack of data from which to assess viability) in any of the strata, the lack of redundancy in viable populations in any of the strata, and the substantial gaps in the distribution of coho salmon throughout the CCC ESU strongly indicate that this ESU is currently in danger of extinction. Our conclusion is consistent with recently published status

reviews prepared by the National Marine Fisheries Service (Good et al. 2005) and the California Department of Fish and Game (CDFG 2002).

## 4.2 California Coastal Chinook Salmon

### *Population Viability*

Summary of density-based criteria

The NCCC TRT (Bjorkstedt et al. 2005) proposed that the CC-Chinook ESU historically comprised fifteen independent populations of fall-run Chinook salmon (10 functionally independent and 5 potentially independent) and six independent populations of spring-run Chinook salmon (all functionally independent[28]). However, the TRT also noted that, due to the lack of historical data on Chinook salmon abundance within the ESU, the hypothesized population structure is subject to substantial uncertainty. Contributing to this uncertainty are 1) an incomplete understanding of historical habitat connectivity and resulting spatial structure of various breeding groups, particularly in the larger watersheds such as the Eel and Russian River, where plausible structures range from one or two large populations to multiple smaller populations occupying different subwatersheds; and 2) the scarcity of historical evidence of Chinook salmon in watersheds in Mendocino and Sonoma counties, which leads to some uncertainty about whether these populations functioned as independent units. In the absence of definitive information, population designations were based primarily on predictions from our IP model and connectivity-viability analysis (Bjorkstedt et al. 2005). Table 8 presents proposed density-based criteria for these populations and the estimated population abundances (rounded to the nearest 100 spawners) that would result if density criteria were met under both historical (pre-dam) and current (post-dam) conditions. As before, high-risk abundance values indicate thresholds below which depensation is likely under both historical and current conditions. Low-risk estimates based on historically accessible habitat provide preliminary abundance targets that, if consistently exceeded, we believe would lead to a high probability of persistence over a 100-year time frame and the population fulfilling its historical role in ESU viability.

Comparison of historical versus current *IP-km* indicates that Chinook salmon in two populations, the Upper Eel River and Russian River populations, have lost access to appreciable amounts of habitat due to impassible dams. Scott Dam in the upper Eel River results in an estimated 11% loss of potential habitat.

[28] Evidence of historical occurrence is lacking for three of the six proposed spring-run populations (Redwood Creek, Van Duzen River, and the Upper Eel River). These populations were assumed to have existed based on environmental similarities between the upper portions of these watersheds and those believed to have supported spring Chinook, as well as by the historical occurrence of summer steelhead, which share similar oversummering habitat requirements (Bjorkstedt et al. 2005).

In the Russian River, a 15% reduction in habitat is attributed to dams, with Warm Springs and Coyote dams accounting for most of those losses.

Evaluation of current population viability

*Fall-run populations*

Currently available data are insufficient to rigorously evaluate the current viability of any of the fifteen putative independent populations of fall-run Chinook salmon in the CC-ESU using the proposed criteria. There are no population-level abundance estimates for any populations within the ESU that meet the minimum requirements for application of viability criteria outlined in Table 4. For certain populations, ancillary data are available, but in few cases do they allow for risk categorization. These data are reviewed below.

In the Redwood Creek watershed, spawner surveys have been conducted over approximately 17 km of Prairie Creek and its tributaries since the 1998-1999 spawning season. Population estimates for the surveyed reaches have averaged 342 (range 106-531) over six years (Walt Duffy and Steve Gough,Humboldt State University, unpublished data). However, there is no information on Chinook abundance in the mainstem of Redwood Creek or its other tributaries, which have been substantially more influenced by land-use practices. Spawner surveys have been conducted annually since the early 1980s on a 2 mi reach of Canon Creek, tributary to the Mad River (PFMC 2007). Maximum live-dead counts (including jacks) have ranged from 0 to 514 (mean = 107); however, because these surveys cover only a small portion of the available habitat and are variable from year to year in frequency, they cannot be used to derive population-level estimates of abundance or trends. Data from spawner surveys in index reaches of Tomki and Sprowl creeks in the upper Eel River are also available since the late 1970s (PFMC 2007). At Tomki Creek, maximum live-dead counts have ranged from 0 to 2,187 (mean = 244), though the average over the last twelve years has declined to 144 spawners. For Sprowl Creek, maximum live-dead counts over 4.5 mi of stream have ranged from 3 to 3,666 (mean = 741) since the late 1970s; however, over the last twelve years, counts have averaged only 68 spawners. In both these case, the estimates are most appropriately viewed as “floors” of abundance, and inconsistencies among years preclude their use as a reliable indicator of trend. Chinook salmon counts are also made at the Van Arsdale Fish Station in the upper mainstem Eel River, but these are similarly inappropriate for estimating population-level abundance (Good et al. 2005). A weir on Freshwater Creek has provided a reasonable census of adult Chinook counts for the period 1994-2004 (Good et al. 2005), with abundance averaging about 54 fish from 1994 to 2003. However, because Freshwater Creek represents only one of four Chinook-bearing streams within the putative Humboldt Bay independent population, we deem the data insufficient for

**Table 8.** Projected population abundances ($N_a$) of CC-Chinook Salmon independent populations corresponding to a high-risk (depensation) threshold of 1 spawner/*IP-km* and low-risk (spatial structure/diversity=SSD) thresholds based on application of spawner density criteria (see Figure 5). Values listed under "historical" represent criteria applied to the historical landscape in the absence of dams that block access to anadromous fish. Values listed under "current" exclude areas upstream from impassible dams.

| | | | | High Risk | | Low Risk | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | Historical | Current | Historical SSD | | Current SSD | |
| **Population** | **Historical *IP-km*** | **Current *IP-km*** | ***IP-km* Lost** | **Depens. $N_a$** | **Depens. $N_a$** | **Density Spawner/IP-km** | **$N_a$** | **Density Spawner/IP-km** | **$N_a$** |
| *Fall-run populations* | | | | | | | | | |
| **Redwood Creek (H)** | 116.1 | 116.1 | 0% | 116 | 116 | 29.3 | 3400 | 29.3 | 3400 |
| ***Little River (H)*** | 18.6 | 18.6 | 0% | 19 | 19 | 40.0 | 700 | 40.0 | 700 |
| **Mad River** | 94.0 | 94.0 | 0% | 94 | 94 | 31.8 | 3000 | 31.8 | 3000 |
| ***Humboldt Bay*** | 76.7 | 76.7 | 0% | 77 | 77 | 33.7 | 2600 | 33.7 | 2600 |
| **Lower Eel River** | 594.4 | 594.4 | 0% | 594 | 594 | 20.0 | 11900 | 20.0 | 11900 |
| **Upper Eel River** | 554.2 | 495.3 | 11% | 554 | 495 | 20.0 | 11100 | 20.0 | 9900 |
| ***Bear River*** | 39.4 | 39.4 | 0% | 39 | 39 | 37.8 | 1500 | 37.8 | 1500 |
| **Mattole River** | 177.5 | 177.5 | 0% | 178 | 178 | 22.5 | 4000 | 22.5 | 4000 |
| **Ten Mile River** | 67.2 | 67.2 | 0% | 67 | 67 | 34.8 | 2300 | 34.8 | 2300 |
| **Noyo River** | 62.2 | 62.2 | 0% | 62 | 62 | 35.3 | 2200 | 35.3 | 2200 |
| **Big River** | 104.3 | 104.3 | 0% | 104 | 104 | 30.6 | 3200 | 30.6 | 3200 |
| **Navarro River** | 131.5 | 131.5 | 0% | 131 | 131 | 27.6 | 3600 | 27.6 | 3600 |
| ***Garcia River*** | 56.2 | 56.2 | 0% | 56 | 56 | 36.0 | 2000 | 36.0 | 2000 |
| ***Gualala River*** | 175.6 | 175.6 | 0% | 176 | 176 | 22.7 | 4000 | 22.7 | 4000 |
| **Russian River** | 584.2 | 496.4 | 15% | 584 | 496 | 20.0 | 11700 | 20.0 | 9900 |
| *Spring-run populations* | | | | | | | | | |
| **(Redwood Creek (H))** | 116.1 | 116.1 | 0% | * | * | * | * | * | * |
| **Mad River** | ? | ? | ? | * | * | * | * | * | * |
| **(Van Duzen River)** | 88.3 | 88.3 | 0% | * | * | * | * | * | * |
| **North Fk Eel River** | 76.8 | 76.8 | 0% | * | * | * | * | * | * |
| **Middle Fk Eel River** | 188.3 | 188.3 | 0% | * | * | * | * | * | * |
| **Upper Eel River** | 88.3 | ? | ? | * | * | * | * | * | * |

* Density criteria are not applied to spring-run Chinook salmon; availability of deep "resting" pools used by oversummering adults are more likely to limit abundance than IP-based predictions of available spawning habitat.

assessing status at the population level. For both Bear River and Little River populations, we know of no current datasets of adult abundance. For these reasons, we categorized the Redwood Creek, Mad River, Humboldt Bay, Eel River, Little River, and Bear River populations as data deficient (Table 9).

The Mattole Salmon Group has conducted spawner and redd surveys on the Mattole River and its tributaries since 1994. Local experts have used these surveys and ancillary data to develop a rough "index" estimates of spawner escapement to the Mattole River; however, sampling intensity and spatial extent of surveys have varied from year to year, which makes them unsuitable for rigorous estimates of abundance or trend (MSG 2005; Good et al. 2005). The redd counts, which provide the best indicator of escapement, have ranged from 27 to 88 during the ten years of surveys. Based on the these data, we conclude that the population is likely at elevated risk of extinction, but are unable to assess whether the population is at moderate or high risk of extinction (Table 9).

The status of Chinook salmon in coastal watersheds of the Mendocino and northern Sonoma counties, from the Ten Mile River to the Gualala River, is highly uncertain. To our knowledge, recent documented occurrences are limited to observations of a few adult spawners in the Ten Mile River during the mid-1990s (Maahs 1996)[29], and collection of juvenile Chinook salmon in downstream migrant traps located on the Noyo River (Gallagher et al. 2001). Additionally, adult Chinook salmon are occasionally observed in the Noyo River during spawner surveys or at the Noyo Egg Collecting Station, and a single adult was observed in the Navarro River in the 2006–2007 spawning season (Scott Harris, California Department of Fish and Game, Willits, pers. comm.). Bell (2003) reports that Chinook salmon in the Garcia River are extinct. We know of no recent document reports of Chinook salmon in the Big River or Gualala rivers, though anecdotal reports from fisherman suggest that Chinook salmon occasionally visit these watersheds. Based on this limited information, the TRT suspects that these six independent populations of Chinook salmon from Ten Mile River to the Gualala River are at least at high risk of extinction, and in some cases may be extinct (Table 9). We chose to categorize them as high-risk (rather than extinct) because of the lack of spawner surveys conducted on mainstem portions of these rivers, where spawning by Chinook is most likely to occur.

Spawner surveys were initiated in the Russian River in 2000 and video monitoring at two fish ladders located at the Mirabel Inflatable Dam has provide counts of Chinook adults since 2002. Although the time series does not meet our minimum criteria for duration (four generations), and does not represent full

[29] Maahs (1996) estimated the total number of adult spawners in the Ten Mile River to be fewer than 10 in the 1995-1996 spawning season.

**Table 9.** Current viability of CC-Chinook salmon independent populations based on metrics outlined in Tables 1 and 4. na indicates data of sufficient quality to estimate the population metric are not available. In some cases, risk categories have been designated for populations where ancillary data strongly suggest populations are extinct or nearly so, despite the lack of quantitative estimates of any of the viability metrics. Metrics for which we believe ancillary data support the assigned risk category are denoted with bold and asterisks. See text for justification of risk rankings.

| Population Name | PVA result | Effect. pop. size per generation | Tot. pop. size per generation | Population decline | | Catastrophe | Density | | Hatchery | Risk Category |
|---|---|---|---|---|---|---|---|---|---|---|
| | | $\overline{N}_e$ | $\overline{N}_{g(harm)}$ | $\overline{N}_{a(geo)}$ | $\hat{T}$ | $\hat{C}$ | $\hat{D}_{dep}$ | $\hat{D}_{ssd}$ | | |
| *Fall-run populations* | | | | | | | | | | |
| **Redwood Creek (H)** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Little River (H)*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Mad River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Humboldt Bay*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Lower Eel River** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Upper Eel River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Bear River*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Mattole River** | na | **na*** | **na*** | **na*** | na | na | na | **na*** | na | Moderate/High |
| **Ten Mile River** | na | **na*** | **na*** | **na*** | na | na | na | **na*** | na | High |
| **Noyo River** | na | **na*** | **na*** | **na*** | na | na | na | **na*** | na | High |
| **Big River** | na | **na*** | **na*** | **na*** | na | na | na | **na*** | na | High |
| **Navarro River** | na | **na*** | **na*** | **na*** | na | na | na | **na*** | na | High |
| ***Garcia River*** | na | **na*** | **na*** | **na*** | na | na | na | **na*** | na | High |
| ***Gualala River*** | na | **na*** | **na*** | **na*** | na | na | na | **na*** | na | High |
| **Russian River** | na | na | na | na | na | na | na | na | na | Data deficient |
| *Spring-run populations* | | | | | | | | | | |
| **(Redwood Creek (H))** | - | - | - | - | - | - | - | - | - | Extinct |
| **Mad River [5]** | - | - | - | - | - | - | - | - | - | Extinct |
| **(Van Duzen River)** | - | - | - | - | - | - | - | - | - | Extinct |
| **North Fk Eel River** | - | - | - | - | - | - | - | - | - | Extinct |
| **Middle Fk Eel River** | - | - | - | - | - | - | - | - | - | Extinct |
| **Upper Eel River** | - | - | - | - | - | - | - | - | - | Extinct |

count (some adults spawn lower in the basin, and the dam is typically deflated in December when flows get too high), the data do suggest the Chinook run has been substantial in recent years. Chinook counts have averaged more than 3,600 fish (range 1383 to 6103) over the last six years (Cook 2005, 2006). Were such patterns to continue, the population would likely meet most low-risk viability thresholds for all criteria except perhaps the density criterion.

*Spring-run populations*

All six spring-run independent populations of Chinook salmon in the CC-Chinook ESU are believed extinct.

### *ESU Viability*

The complete lack of population-level information on the distribution and abundance of Chinook salmon throughout the CC-Chinook salmon ESU precludes application of the ESU-level viability criteria (Table 9). Most available information consists of spawning surveys in index reaches, for which the limited and non-random spatial extent, coupled with variation in survey frequency, render the data inappropriate for assessing population abundance or trend. Though more rigorous sampling has been conducted on Prairie Creek (tributary to Redwood Creek) and Freshwater Creek, in both cases, estimates represent only a portion the total population. Monitoring of spawning Chinook salmon in the Russian River has improved considerably in the last 5–6 years; however, this time series is not sufficiently long to assess trends.

With data limitations in mind, we identify several areas of significant concern as they relate to viability of the CC-Chinook salmon ESU. The current distribution of extant populations includes several watersheds in Humboldt County including Redwood Creek, Little River, Mad River, Humboldt Bay, Eel River (with two populations), Bear River, and Mattole River, as well as some smaller watersheds such as Maple Creek, Jacoby Creek, and Salmon Creek. However, the lack of population data precludes us from determining whether there are viable independent populations of fall run Chinook in the North Coastal or North Mountain Interior strata. Additionally, spring Chinook salmon within the ESU are thought to be extinct, indicating loss of diversity within the ESU. Currently, there are no known extant and persistent populations between the Mattole River in Humoldt County and the Russian River in Sonoma County, a distance of approximately 200 km. Consequently, there appears to be no representation of the North-Central Coastal stratum, and connectivity between the Mattole River population and the Russian River population is likely substantially reduced from historical patterns. Because of the lack of population data, viability of the Russian River population is uncertain. However, even if the Russian River population is

eventually deemed viable, the lack of other viable populations within the Central Coastal stratum places this stratum at greater risk due to catastrophic risks, such as disturbances to the mainstem Russian River where most spawning is believed to occur.

In summary, the lack of data from which to assess viability of extant populations in the northern part of the ESU, the apparent lack of extant populations, with the exception of the Russian River, in the southern half of the ESU, the loss of important life-history diversity (i.e. spring-run populations), and the substantial gaps in the distribution of Chinook salmon throughout the CC ESU strongly indicate that this ESU fails to meet low-risk criteria and is therefore at elevated risk of extinction. The data are not sufficient for assessing whether this risk is moderate or high. Our conclusion is qualitatively consistent with a recently published NMFS status reviews (NMFS 1999; Good et al. 2005).

## 4.3 Northern California Steelhead

### *Population Viability*

Summary of density-based criteria

Bjorkstedt et al. (2005) proposed that the NC-Steelhead ESU historically consisted of forty-three independent populations of winter-run steelhead (16 functionally independent and 27 potentially independent), and 10 populations of summer steelhead (all functionally independent). Table 10 summarizes proposed density-based criteria for these populations and the projected population abundances (rounded to the nearest 100 spawners) that would result if density criteria were met under both historical (pre-dam) and current (post-dam) conditions. High-risk abundance values indicate thresholds below which depensation is likely, and low-risk abundance values for historical conditions represent preliminary abundance targets that, if consistently exceeded, would likely lead to a high probability of persistence over a 100-year time frame and result in a population likely fulfilling its role in ESU viability.

Comparison of historical versus currently available *IP-km* indicates that two steelhead populations, the Mad River population and the Upper Mainstem Eel River population, have lost substantial habitat due to dams. In the Mad River, an estimated 36% of potential steelhead habitat lies above Ruth Dam, though a partial barrier well downstream of Ruth Dam may control use of the upper watershed by steelhead. For the upper mainstem Eel River, the Scott Dam blocks access to more than 90% of available habitat. Although the remaining 37 *IP-km* of habitat is theoretically sufficient to support a viable population, it is clear that such a population would have a substantially different functional role within the Eel River

**Table 10.** Projected population abundances ($N_a$) of NC-Steelhead independent populations corresponding to a high-risk (depensation) threshold of 1 spawner/IP-km and low-risk (spatial structure/diversity=SSD) thresholds based on application of spawner density criteria (see Figure 5). Values listed under "historical" represent criteria applied to the historical landscape in the absence of dams that block access to anadromous fish. Values listed under "current" exclude areas upstream from impassible dams.

| | | | | | High Risk | | Low Risk | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Historical | Current | Historical SSD | | Current SSD | |
| **Population** | **Historical IP-km** | **Current IP-km** | **IP-lost** | **IP bias index** | **Depens. $N_a$** | **Depens. $N_a$** | **Density Spawner/IP-km** | **$N_a$** | **Density Spawner/IP-km** | **$N_a$** |
| **Redwood Creek (H)** | 301.1 | 301.1 | 0% | low | 301 | 301 | 20.0 | 6000 | 20.0 | 6000 |
| ***Maple Creek/Big Lagoon*** | 94.7 | 94.7 | 0% | low | 95 | 95 | 29.1 | 2800 | 29.1 | 2800 |
| ***Little River (H)*** | 76.2 | 76.2 | 0% | low | 76 | 76 | 31.6 | 2400 | 31.6 | 2400 |
| **Mad River** | 553.2 | 351.8 | 36% | low | 553 | 352 | 20.0 | 11200 | 20.0 | 7000 |
| **Humboldt Bay** | 283.0 | 283.0 | 0% | low | 283 | 283 | 20.0 | 5700 | 20.0 | 5700 |
| Eel River - Full | | | | | | | | | | |
| ***Price Creek*** | 20.6 | 20.6 | 0% | low | 21 | 21 | 39.4 | 800 | 39.4 | 800 |
| **Larabee Creek** | 101.0 | 101.0 | 0% | low | 101 | 101 | 28.2 | 2800 | 28.2 | 2800 |
| **Van Duzen River** | 362.6 | 362.6 | 0% | low | 362 | 362 | 20.0 | 7300 | 20.0 | 7300 |
| **South Fork Eel River** | 1182.1 | 1182.1 | 0% | low | 1182 | 1182 | 20.0 | 23600 | 20.0 | 23600 |
| ***Dobbyn Creek*** | 52.5 | 52.5 | 0% | low | 52 | 52 | 34.9 | 1800 | 34.9 | 1800 |
| ***Jewett Creek*** | 18.2 | 18.2 | 0% | low | 18 | 18 | 39.7 | 700 | 39.7 | 700 |
| ***Pipe Creek*** | 18.2 | 18.2 | 0% | low | 18 | 18 | 39.7 | 700 | 39.7 | 700 |
| ***Kekawaka Creek*** | 35.3 | 35.3 | 0% | low | 35 | 35 | 37.3 | 1300 | 37.3 | 1300 |
| ***Chamise Creek*** | 38.0 | 38.0 | 0% | low | 38 | 38 | 37.0 | 1400 | 37.0 | 1400 |
| **North Fork Eel River** | 372.8 | 372.8 | 0% | low | 373 | 373 | 20.0 | 7500 | 20.0 | 7500 |
| ***Bell Springs Creek*** | 18.5 | 18.5 | 0% | moderate | 19 | 19 | 39.6 | 700 | 39.6 | 700 |
| ***Woodman Creek*** | 39.4 | 39.4 | 0% | moderate | 39 | 39 | 36.7 | 1400 | 36.7 | 1400 |
| **Outlet Creek** | 313.8 | 292.9 | 7% | moderate | 314 | 293 | 20.0 | 6300 | 20.0 | 5900 |
| **Tomki Creek** | 131.7 | 131.7 | 0% | moderate | 132 | 132 | 23.9 | 3200 | 23.9 | 3200 |
| **Middle Fork Eel River** | 584.3 | 581.4 | 0% | low | 584 | 581 | 20.0 | 11700 | 20.0 | 11600 |
| ***Bucknell Creek*** | 21.1 | 21.1 | 0% | moderate | 21 | 21 | 39.3 | 800 | 39.3 | 800 |
| **Upper Mainstem Eel River** | 422.1 | 37.7 | 91% | moderate | 422 | 38 | 20.0 | 8400 | 37.0 | 1400 |
| ***Bear River*** | 116.0 | 116.0 | 0% | low | 116 | 116 | 26.1 | 3000 | 26.1 | 3000 |
| **Mattole River** | 613.9 | 613.9 | 0% | low | 614 | 614 | 20.0 | 12300 | 20.0 | 12300 |
| ***Usal Creek*** | 18.8 | 18.8 | 0% | low | 19 | 19 | 39.6 | 700 | 39.6 | 700 |
| ***Cottaneva Creek*** | 26.1 | 26.1 | 0% | low | 26 | 26 | 38.6 | 1000 | 38.6 | 1000 |

**Table 10.** (continued)

| | | | | | High Risk | | Low Risk | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Historical | Current | Historical SSD | | Current SSD | |
| Population | Historical IP-km | Current IP-km | IP-lost | IP bias index | Depens. $N_a$ | Depens. $N_a$ | Density Spawner/km | $N_a$ | Density Spawner/km | $N_a$ |
| ***Wages Creek*** | 19.9 | 19.9 | 0% | low | 20 | 20 | 39.5 | 800 | 39.5 | 800 |
| **Ten Mile River** | 204.7 | 204.7 | 0% | moderate | 205 | 205 | 20.0 | 4100 | 20.0 | 4100 |
| ***Pudding Creek*** | 32.0 | 32.0 | 0% | moderate | 32 | 32 | 37.8 | 1200 | 37.8 | 1200 |
| **Noyo River** | 199.1 | 196.7 | 1% | moderate | 199 | 197 | 20.0 | 4000 | 20.0 | 3900 |
| ***Hare Creek*** | 18.1 | 18.1 | 0% | moderate | 18 | 18 | 39.7 | 700 | 39.7 | 700 |
| ***Caspar Creek*** | 16.0 | 16.0 | 0% | moderate | 16 | 16 | 40.0 | 600 | 40.0 | 600 |
| ***Russian Gulch (Me)*** | 19.2 | 19.2 | 0% | moderate | 19 | 19 | 39.6 | 800 | 39.6 | 800 |
| **Big River** | 316.6 | 312.9 | 1% | high | 317 | 313 | 20.0 | 6300 | 20.0 | 6300 |
| **Albion River** | 77.1 | 77.1 | 0% | high | 77 | 77 | 31.5 | 2400 | 31.5 | 2400 |
| ***Big Salmon Creek*** | 24.8 | 24.8 | 0% | high | 25 | 25 | 38.8 | 1000 | 38.8 | 1000 |
| **Navarro River** | 458.2 | 457.9 | 0% | high | 458 | 458 | 20.0 | 9200 | 20.0 | 9200 |
| ***Elk Creek*** | 24.1 | 24.1 | 0% | high | 24 | 24 | 38.9 | 900 | 38.9 | 900 |
| ***Brush Creek*** | 28.3 | 28.3 | 0% | high | 28 | 28 | 38.3 | 1100 | 38.3 | 1100 |
| **Garcia River** | 169.0 | 169.0 | 0% | high | 169 | 169 | 20.0 | 3400 | 20.0 | 3400 |
| **Gualala River** | 478.0 | 476.3 | 0% | high | 478 | 476 | 20.0 | 9600 | 20.0 | 9500 |

basin, as the IP model predicts that this population may have joined the South Fork Eel, North Fork Eel, Middle Fork Eel, and Van Duzen populations as the largest populations in the watershed. Outlet Creek has dams that block access to about 7% of historical habitat. Habitat loss attributable to dams is 1% or less for all other populations (Table 10).

Evaluation of current viability

*Winter-run populations*

Currently available data are insufficient to rigorously evaluate the current viability of any of the 41 independent populations of winter steelhead in the NC-steelhead DPS using our viability criteria. Perhaps the best available time series of adult spawner abundance comes from Freshwater Creek, one of several streams that collectively make up the Humboldt Bay independent population. The Humboldt Fish Action Council has operated a weir on Freshwater Creek since 1994–1995 season, and annual adult steelhead counts during this period have averaged about 73 adults (Seth Ricker, CDFG, unpublished data). Within the last four years, mark-recapture studies have been conducted to derive escapements estimates for Freshwater Creek, and these have suggested that the weir has sampled from 38 to 74 percent of the upstream migrants. However, because the time series of escapement estimates of insufficient length to meet our criteria, and because the data represent only a portion of the Humboldt Bay population, which also includes Jacoby Creek, Elk River, and Salmon Creek (among others) we categorize the Humboldt population as data deficient (Table 11).

The Mattole Salmon Group conducts spawner surveys on the Mattole River; however, these surveys target Chinook and coho salmon, collecting only incidental data on winter steelhead (MSG 2005). Steelhead spawner surveys on the Gualala River were initiated in 2001 (DeHaven 2005). These surveys are conducted on approximately 29 km of habitat in the Wheatfield Fork of the Gualala, and thus do not allow for estimation of total population abundance in the Gualala River basin. Consequently, we categorize these populations as data deficient as well (Table 11).

The only other time series of abundance for winter-run steelhead populations within this ESU is the counts of both hatchery and wild steelhead at Van Arsdale Fish Station on the upper Eel River. The counts of wild fish represent a composite of several delineated populations: the Upper Middle Mainstem Eel River (the portion of the population from Van Arsdale to Bucknell Creek), Bucknell Creek, and the Upper Mainstem Eel River (the mainstem and tributaries upstream of Bucknell Creek). As such, the data cannot be used to evaluate any of these populations directly. However, annual counts of wild fish have averaged about just under 200 fish over the last 11 years (Grass 2007). Thus, even if all fish were

**Table 11.** Current viability of NC-steelhead populations based on metrics outlined in Tables 1 and 4. na indicates data of sufficient quality to estimate the population metric are not available. In some cases, risk categories have been designated for populations where ancillary data strongly suggest populations are extinct or nearly so, despite the lack of quantitative estimates of any of the viability metrics. Metrics for which we believe ancillary data support the assigned risk category are denoted with bold and asterisks. See text for justification of risk rankings.

| Population | PVA result | Effect. pop. size per generation $\overline{N}_e$ | Tot. pop. size per generation $\overline{N}_{g(harm)}$ | Population decline $\overline{N}_{a(geo)}$ | $\hat{T}$ | Catastrophe $\hat{C}$ | Density $\hat{D}_{dep}$ | $\hat{D}_{ssd}$ | Hatchery | Risk category |
|---|---|---|---|---|---|---|---|---|---|---|
| *Winter-run populations* | | | | | | | | | | |
| **Redwood Creek (H)** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Maple Creek/Big Lagoon*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Little River (H)*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Mad River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Humboldt Bay*** | na | na | na | na | na | na | na | na | na | Data deficient |
| Eel River - Full | | | | | | | | | | |
| ***Price Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Larabee Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Van Duzen River** | na | na | na | na | na | na | na | na | na | Data deficient |
| **South Fork Eel River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Dobbyn Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Jewett Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Pipe Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Kekawaka Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Chamise Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **North Fork Eel River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Bell Springs Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Woodman Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Burger Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Outlet Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Tomki Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Middle Fork Eel River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Bucknell Creek*** | na | na | **na*** | na | na | na | **na*** | na | **na*** | Moderate/High |
| **Upper Mainstem Eel River** | na | na | **na*** | na | na | na | **na*** | na | **na*** | Moderate/High |
| ***Bear River*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Mattole River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Usal Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |

**Table 11.** (continued)

| Population | PVA result | Effect. pop. size per generation $\overline{N}_e$ | Tot. pop. size per generation $\overline{N}_{g(harm)}$ | Population decline $\overline{N}_{a(geo)}$ | $\hat{T}$ | Catastrophe $\hat{C}$ | Density $\hat{D}_{dep}$ | $\hat{D}_{ssd}$ | Hatchery | Risk Category |
|---|---|---|---|---|---|---|---|---|---|---|
| ***Cottaneva Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Wages Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Ten Mile River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Pudding Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Noyo River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Hare Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Caspar Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Russian Gulch (Me)*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Big River** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Albion River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Big Salmon Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Navarro River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Elk Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Brush Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Garcia River** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Gualala River** | na | na | na | na | na | na | na | na | na | Data deficient |
| *Summer-run populations* | | | | | | | | | | |
| **Redwood Creek (H)** | na | na | 18 (high) | 4.6 (high) | -0.10 (high) | **na*** | - | - | low | High |
| **Mad River** | na | **na*** | **na*** | **na*** | **na*** | na | - | - | na | Moderate |
| **Van Duzen River** | na | na | na | na | na | na | - | - | na | Data deficient |
| **South Fork Eel River** | na | na | na | na | na | na | - | - | na | Data deficient |
| **Larabee Creek** | na | na | na | na | na | na | - | - | na | Data deficient |
| **North Fork Eel River** | na | na | na | na | na | na | - | - | na | Data deficient |
| **(Up. Mid. Mainstem Eel R)** | na | na | na | na | na | na | - | - | na | Data deficient |
| **Middle Fk Eel River** | na | na | 2335 (mod) | 569 (low) | -0.04 (mod) | 0.52 (low) | - | - | low | Moderate |
| **(Upper Mainstem Eel R)** | na | na | na | na | na | na | - | - | na | Data deficient |
| **Mattole River** | na | **na*** | **na*** | **na*** | na | na | - | - | na | High |

concentrated in either Bucknell Creek or the Upper Mainstem Eel River, which does not appear to be the case (Scott Harris, CDFG, Willits, CA , personal communication), the abundances still would not be sufficient to meet low risk criteria for effective population size or spawner density. Additionally, in eight of the last 11 years, there has been a substantial hatchery influence, with hatchery fish outnumbering wild fish by almost 10 to 1 during those years (Grass 1997-2007). For these reasons, we conclude that the Bucknell and Upper Mainstem Eel River populations of winter steelhead are at least at moderate risk and possibly at high risk.

*Summer-run populations*

Data on the abundance of summer-run steelhead are more readily available due to the fact that adults congregate in "resting pools" during the summer, and can be observed when water is relatively clear. Currently, there are four ongoing efforts to estimate populations of summer steelhead in rivers within the NC-steelhead DPS: Redwood Creek, Mad River, Middle Fork Eel River, and Mattole River.

Summer dive surveys covering almost the entire mainstem of Redwood Creek have been conducted annually since 1981. There is some question about the reliability of some of the early counts, and it is unclear about how much summer steelhead may use tributaries to Redwood Creek for holding. However, recent abundance estimates in the mainstem clearly indicate a population that is at very high risk of extinction. Mean adult abundance has averaged only 6 fish over the past four generations, and the population has declined at an average rate of 10% per year during this period (Dave Anderson, Redwood State and National Park, unpublished data). Effective population size is estimated to be at just 3.6 fish. Consequently, we conclude this population is at high risk of extinction (Table 11).

Diver counts of summer steelhead have been conducted on portions of the Mad River since 1982. From 1982 to 2002, the Forest Service conducted surveys on the reach from Ruth Dam to Deer Creek; however, that effort was terminated due to budget constraints. Since 1994, Green Diamond Resource Company (formerly Simpson Timber Company) and the California Department of fish and Game have surveyed the reaches from Deer Creek to Mad River Hatchery, and from the hatchery to Cadle Hole, respectively. Although the data do not meet the minimum requirements to formally assess viability using our criteria, they do provide some indications of population status. For the period form 1994 to 2002, the period where all three reaches were surveyed, mean abundance averaged just under 300 fish and the population declined at a rate of about 23% per year. Hatchery fish constituted about 2% for the two generations covered during this period (Matt House, Green Diamond Resource Company, Korbel, unpublished data;

Andrew Bundschuh, US. Forest Service, Six Rivers National Forest, Eureka, unpublished data). Based on these data, we conclude that the population is at least at moderate risk of extinction (Table 11).

The Middle Fork Eel River constitutes perhaps the only population within the entire recovery domain where the existing time series of adult abundance estimates meet requirements outlined in Table 4. Summer surveys of adults in summer resting pools have provided a reasonable census of the adult population size dating back to the 1960s. Counts have ranged from 198 to 1601 during that period (Jones 1980, 1992; Jones et al. 1980; and Scott Harris, California Department of Fish and Game, Willits, unpublished data). Calculation of extinction risk metrics, shown in Table 11, indicates that the population currently ranks at low risk of extinction according to the population decline criteria (but only marginally so) and for the catastrophe criteria. For the last four generations, the geometric mean abundance has been over the 500 fish threshold, but only by a small amount, and the trend suggests a decline in abundance of about 4% per year; continued decline at this rate would have it approaching an $N_a$ of less than 500 within two generations. The population ranks at moderate risk according to the effective population size criteria. Hatcheries do not appear to play a significant role in the current viability of this population (summer steelhead are not released into the Middle Fork Eel, and we assume that straying of summer steelhead from the Mad River is negligible). Based on the moderate risk rankings for population decline and effective population size, we conclude that the population is at moderate risk of extinction (Table 11).

Finally, the Mattole Salmon Group has conducted summer diver surveys in the mainstem Mattole and two tributaries annually since 1996 (MSG 2005). Although the data set does not meet our minimum standards for evaluation using our criteria, they do suggest that the Mattole River population is at high risk of extinction, with an average adult count of just 16 individuals (range 9-30) during the period (Table 11).

Little is known about the status of the remaining six putative summer steelhead populations in the DPS (Van Duzen River, South Fork Eel River, Larabee Creek, North Fork Eel River, Upper Middle Mainstem Eel River, and Upper Mainstem Eel. We categorize all of these populations as data deficient (Table 11), though note that the lack of even anecdotal reports in recent years suggest that many if not all of these populations are either extirpated or extremely depressed.

***ESU Viability***

The complete lack of data with which to assess the status of any of the 41 independent populations of winter steelhead within the NC-Steelhead DPS (all deemed data deficient) precludes evaluation of ESU viability using the quantitative criteria developed in this paper. For summer steelhead, the limited

available data provide no evidence of viable summer steelhead populations within the ESU. Consequently, it is highly likely that representation and redundancy/connectivity criteria are not being met and that the DPS is at elevated risk of extinction. Good et al. (2005) reaffirmed the conclusion of Busby et al. (1996) that the ESU was likely to become endangered in the foreseeable future, the lack of population information being cited as a contributing risk factor. Our conclusion is consistent with their assessments.

## 4.4 Central California Coast Steelhead

### *Population Viability*

Summary of density-based criteria

Bjorkstedt et al. (2005) proposed that the CCC-Steelhead ESU historically contained 11 functionally independent populations and 26 potentially independent populations. Table 12 presents proposed density-based criteria for these populations and the estimated population abundances (rounded to the nearest 100 spawners) that would result if density criteria were met under both historical (pre-dam) and current (post-dam) conditions. High-risk abundance values indicate thresholds below which depensation is likely, and low-risk estimates represent preliminary abundance targets that, if consistently exceeded, would likely lead to a high probability of persistence over a 100-year time frame and result in a population likely fulfilling its historical role with respect to ESU viability.

More so than any other ESU within the NCCC Recovery Domain, impassible dams have had a substantial effect on the available habitat of steelhead population in the CCC ESU. These effects are most pronounced for San Francisco Bay populations, Russian River populations, and coastal Marin County populations. Within San Francisco Bay, populations experiencing substantial reductions in accessible habitat include Novato Creek (22%), Napa River (17%), Walnut Creek (96%), San Pablo Creek (72%), San Leandro Creek (80%), San Lorenzo Creek (48%), Alameda Creek (95%), Coyote Creek (49%), Guadalupe River (21%), Stevens Creek (54%), San Francisquito Creek (33%), and San Mateo Creek (83%). In the Russian River basin, populations that have experienced significant reductions in habitat include the Upper Russian River (21%), Dry Creek (56%), and Mark West Creek (7%). In Lagunitas Creek, an estimated 49% of steelhead habitat lies upstream of Kent and Nicasio dams. In the Walker Creek drainage, 26% of the predicted habitat lies upstream of dams (Table 12).

**Table 12.** Projected population abundances ($N_a$) of CCC-Steelhead independent populations corresponding to a high-risk (depensation) threshold of 1 spawner/*IP-km* and low-risk (spatial structure/diversity=SSD) thresholds based on application of spawner density criteria (see Figure 5). Values listed under "historical" represent criteria applied to the historical landscape in the absence of dams that block access to anadromous fish. Values listed under "current" exclude areas upstream from impassible dams.

| | | | | | High Risk | | Low Risk | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Historical | Current | Historical SSD | | Current SSD | |
| **Population** | **Historical *IP-km*** | **Current *IP-km*** | ***IP-km* lost** | **IP bias index** | **Depens. $N_a$** | **Depens. $N_a$** | **Density Spawner/*IP-km*** | **$N_a$** | **Density Spawner/*IP-km*** | **Div/SS $N_a$** |
| **Russian River** | 2348.8 | | | | | | | | | |
| ***Austin Creek*** | 111.9 | 111.9 | 0% | high | 112 | 112 | 26.7 | 3000 | 26.7 | 3000 |
| ***Green Valley Creek*** | 61.7 | 61.3 | 1% | high | 62 | 61 | 33.7 | 2100 | 33.7 | 2100 |
| ***Mark West Creek*** | 366.5 | 340.8 | 7% | high | 367 | 341 | 20.0 | 7300 | 20.0 | 6800 |
| ***Dry Creek*** | 384.9 | 167.7 | 56% | high | 385 | 168 | 20.0 | 7700 | 20.0 | 3400 |
| ***Maacama Creek*** | 106.9 | 105.2 | 2% | high | 107 | 105 | 27.4 | 2900 | 27.6 | 2900 |
| **Upper Russian River** | 892.3 | 703.5 | 21% | high | 892 | 704 | 20.0 | 17800 | 20.0 | 14100 |
| **Salmon Creek (S)** | 63.5 | 63.5 | 0% | high | 63 | 63 | 33.4 | 2100 | 33.4 | 2100 |
| **Americano Creek** | 64.2 | 64.2 | 0% | high | 64 | 64 | 33.3 | 2100 | 33.3 | 2100 |
| **Stemple Creek** | 73.1 | 73.1 | 0% | high | 73 | 73 | 32.1 | 2300 | 32.1 | 2300 |
| **Tomales Bay** | | | | | | | | | | |
| **Walker Creek** | 134.1 | 98.9 | 26% | high | 134 | 99 | 23.6 | 3200 | 28.5 | 2800 |
| **Lagunitas Creek** | 170.7 | 87.2 | 49% | high | 171 | 87 | 20.0 | 3400 | 30.1 | 2600 |
| **San Francisco Bay** | | | | | | | | | | |
| *Northwest SF Bay* | | | | | | | | | | |
| ***Corte Madera Creek*** | 41.3 | 41.3 | 0% | high | 41 | 41 | 36.5 | 1500 | 36.5 | 1500 |
| ***Miller Creek*** | 44.4 | 44.4 | 0% | high | 44 | 44 | 36.1 | 1600 | 36.1 | 1600 |
| ***Novato Creek*** | 79.8 | 61.5 | 22% | severe | 79 | 62 | 31.3 | 2500 | 33.7 | 2100 |
| *North SF Bay* | | | | | | | | | | |
| ***Petaluma River*** | 225.4 | 223.0 | 1% | severe | 225 | 223 | 20.0 | 4500 | 20.0 | 4500 |
| **Sonoma Creek** | 268.7 | 268.7 | 0% | high | 269 | 269 | 20.0 | 5400 | 20.0 | 5400 |
| **Napa River** | 593.9 | 491.0 | 17% | severe | 594 | 491 | 20.0 | 11900 | 20.0 | 9800 |
| *Suisun Bay* | | | | | | | | | | |
| ***Green Val./Suisun Creek*** | 164.0 | 162.2 | 1% | severe | 164 | 162 | 20.0 | 3300 | 20.0 | 3200 |
| ***Walnut Creek*** | 202.2 | 7.5 | 96% | severe | 202 | 8 | 20.0 | 4000 | - | - |
| *East SF Bay* | | | | | | | | | | |
| ***San Pablo Creek*** | 67.9 | 18.8 | 72% | severe | 68 | 19 | 32.8 | 2200 | 39.6 | 700 |
| **San Leandro Creek** | 80.5 | 16.0 | 80% | severe | 81 | 16 | 31.0 | 2500 | 40.0 | 600 |
| **San Lorenzo Creek** | 79.8 | 41.5 | 48% | severe | 80 | 42 | 31.1 | 2500 | 36.5 | 1500 |

**Table 12.** (continued)

| Population | Historical *IP-km* | Current *IP-km* | % Lost | IP bias index | High Risk Historical Depens. Na | Current Depens. $N_a$ | Low Risk Historical SSD Density Spawner/IP-km | $N_a$ | Current SSD Density Spawner/IP-km | Div/SS $N_a$ |
|---|---|---|---|---|---|---|---|---|---|---|
| *Southeast SF Bay* | | | | | | | | | | |
| **Alameda Creek** | 816.6 | 39.5 | 95% | severe | 817 | 39 | 20.0 | 16300 | 36.7 | 1500 |
| **Coyote Creek** | 498.3 | 252.7 | 49% | severe | 498 | 253 | 20.0 | 10000 | 20.0 | 5100 |
| *Southwest SF Bay* | | | | | | | | | | |
| **Guadalupe River** | 157.3 | 124.5 | 21% | severe | 157 | 125 | 20.4 | 3200 | 24.9 | 3100 |
| ***Stevens Creek*** | 39.6 | 18.4 | 54% | severe | 40 | 18 | 36.7 | 1500 | 39.7 | 700 |
| ***San Francisquito Creek*** | 59.2 | 39.8 | 33% | severe | 59 | 40 | 34.0 | 2000 | 36.7 | 1500 |
| ***San Mateo Creek*** | 57.4 | 9.9 | 83% | severe | 57 | 10 | 34.2 | 2000 | - | 400 |
| ***Pilarcitos Creek*** | 41.9 | 30.6 | 27% | high | 42 | 31 | 36.4 | 1500 | 38.0 | 1200 |
| **San Gregorio Creek** | 77.6 | 77.6 | 0% | high | 78 | 78 | 31.4 | 2400 | 31.4 | 2400 |
| **Pescadero Creek** | 93.5 | 93.5 | 0% | high | 94 | 94 | 29.2 | 2700 | 29.2 | 2700 |
| ***Waddell Creek*** | 16.2 | 16.2 | 0% | high | 16 | 16 | 40.0 | 600 | 40.0 | 600 |
| ***Scott Creek*** | 23.5 | 23.5 | 0% | high | 24 | 24 | 39.0 | 900 | 39.0 | 900 |
| ***Laguna Creek*** | 17.4 | 17.4 | 0% | high | 17 | 17 | 39.8 | 700 | 39.8 | 700 |
| **San Lorenzo River** | 225.6 | 215.3 | 5% | high | 225 | 215 | 20.0 | 4500 | 20.0 | 4300 |
| ***Soquel Creek*** | 66.4 | 66.4 | 0% | high | 66 | 66 | 33.0 | 2200 | 33.0 | 2200 |
| ***Aptos Creek*** | 41.0 | 41.0 | 0% | high | 41 | 41 | 36.5 | 1500 | 36.5 | 1500 |

Evaluation of current viability

The lack of data on spawner abundance data for steelhead populations in the CCC-Steelhead ESU precludes a rigorous assessment of current viability for any of the 37 independent populations, and in only a few cases do ancillary data provide sufficient information to allow reasonable inference about population risk at the present time.

Spawner surveys have been conducted annually on Lagunitas Creek since 1994–1995 (Ettlinger et al. 2005). However, the primary purpose is to enumerate coho salmon, and surveys typically end before the steelhead spawning season is complete. Steelhead counts are made at the Noyo Egg Collecting station on the South Fork Noyo River; however, steelhead have little trouble passing over the weir, so the number passing through the counting facility is considered an unreliable indicator of total abundance (Scott Harris, CDFG, Willits, pers. comm.). Partial counts of steelhead are made at the Felton Diversion Dam on the San Lorenzo River; however, operation is inconsistent and no population estimates are made. To our knowledge, these efforts represent the only potential source of information on adult abundance within the ESU, and there is little ancillary data from which to speculate about current status. Thus we classify the majority of coastal populations as data deficient (Table 13).

Likewise, within the San Francisco Bay region, there are no population-level estimates of adult abundance for any tributaries entering the Bay. However, Leidy et al. (2005b) recently completed a comprehensive review of available survey information on streams entering San Francisco Bay. For many streams, recent observations of *O. mykiss*, indicate that they still persist in these watersheds. However, as noted above, several populations have been affected by dams that block access to the majority of their historical habitat, and areas below these dams are often severely impacted by urban development. In many cases, it is unclear whether the anadromous life-history continues to be expressed downstream of these barriers, though resident *O. mykiss* remain present upstream (and sometimes downstream) of the dams. Based on information provided in Leidy et al. (2005b), we conclude that in six watersheds—Walnut Creek, San Pablo Creek, San Leandro Creek, San Lorenzo Creek, Alameda Creek, and San Mateo Creek—it is highly likely that, if steelhead still persist in these watersheds, they are at high risk of extinction. Steelhead appear to persist in most other functionally and potentially independent populations in the San Francisco Bay area, including Arroyo Corte Madera de Presidio, Novato Creek, Sonoma Creek, Napa River, Green Valley Creek, Coyote Creek, Guadalupe River, San Francisquito Creek, and possible Corte Madera Creek, Miller Creek, and Petaluma River (Leidy et al. 2005b); however, data are limited to observations of occurrence. All of these populations are classified as data deficient, though some are likely at high risk or possibly even extinct (Table 13).

**Table 13.** Current viability of CCC-steelhead populations based on metrics outlined in Tables 1 and 4. na indicates data of sufficient quality to estimate the population metric are not available. In some cases, risk categories have been designated for populations where ancillary data strongly suggest populations are extinct or nearly so, despite the lack of quantitative estimates of any of the viability metrics. Metrics for which we believe ancillary data support the assigned risk category are denoted with bold and asterisks. See text for justification of risk rankings.

| Population | PVA Result | Effect. pop. size per generation $\overline{N}_e$ | Tot. pop. size per generation $\overline{N}_{g(harm)}$ | Population decline $\overline{N}_{a(geo)}$ | $\hat{T}$ | Catastrophe $\hat{C}$ | Spawner density $\hat{D}_{dep}$ | $\hat{D}_{ssd}$ | Hatchery | Risk Category |
|---|---|---|---|---|---|---|---|---|---|---|
| **Russian River** | | | | | | | | | | |
| ***Austin Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Green Valley Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Mark West Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Dry Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Maacama Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Upper Russian River [H]** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Salmon Creek (S)** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Americano Creek** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Stemple Creek** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Tomales Bay** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Walker Creek** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Lagunitas Creek** | na | na | na | na | na | na | na | na | na | Data deficient |
| **San Francisco Bay** | | | | | | | | | | |
| *Northwest SF Bay* | | | | | | | | | | |
| ***Corte Madera Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Miller Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Novato Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| *North SF Bay* | | | | | | | | | | |
| ***Petaluma River*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Sonoma Creek** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Napa River** | na | na | na | na | na | na | na | na | na | Data deficient |
| *Suisun Bay* | | | | | | | | | | |
| ***Green Val./Suisun Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Walnut Creek*** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | High |
| *East SF Bay* | | | | | | | | | | |
| ***San Pablo Creek*** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | High |
| **San Leandro Creek** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | High |
| **San Lorenzo Creek** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | High |

**Table 13.** (continued)

| Population | PVA Result | Effect. pop. size per generation $\overline{N}_e$ | Tot. pop. size per generation $\overline{N}_{g(harm)}$ | Population decline $\overline{N}_{a(geo)}$ | $\hat{T}$ | Catastrophe $\hat{C}$ | Spawner density $\hat{D}_{dep}$ | $\hat{D}_{ssd}$ | Hatchery | Risk Category |
|---|---|---|---|---|---|---|---|---|---|---|
| *Southeast SF Bay* | | | | | | | | | | |
| **Alameda Creek** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | High |
| **Coyote Creek** | na | na | na | na | na | na | na | na | na | Data deficient |
| *Southwest SF Bay* | | | | | | | | | | |
| **Guadalupe River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Stevens Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***San Francisquito Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***San Mateo Creek*** | na | **na*** | **na*** | **na*** | na | na | **na*** | **na*** | na | High |
| ***Pilarcitos Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **San Gregorio Creek** | na | na | na | na | na | na | na | na | na | Data deficient |
| **Pescadero Creek** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Waddell Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Scott Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Laguna Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| **San Lorenzo River** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Soquel Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |
| ***Aptos Creek*** | na | na | na | na | na | na | na | na | na | Data deficient |

***ESU Viability***

Because of the extreme data limitations, we are unable to assess the status of the CCC-Steelhead DPS using the quantitative criteria outlined in this paper. All populations within North Coastal, Interior, and Santa Cruz Mountains strata were categorized as data deficient, as were many of the populations in the Coastal and Interior San Francisco Bay strata (Table 13). The presence of dams that block access to substantial amounts of historical habitat (particularly in the East and Southeast portions of San Francisco Bay), coupled with ancillary data (see Leidy et al. 2005b) that suggest that it is highly unlikely that the Interior San Francisco Bay strata has any viable populations, or that redundancy criteria would be met. Elsewhere in the ESU, the lack of demonstrably viable populations remains a significant concern. Good et al. (2005) reaffirmed the conclusion of Busby et al. (1996) that the ESU was likely to become endangered in the foreseeable future, citing the lack of population information as a contributing risk factor. Our conclusion is consistent with their assessments.

## 4.5 Conclusion

In the preceding sections we have attempted to apply quantitative population and ESU-level criteria developed in the paper to ESA-listed ESUs and DPSs within the NCCC Recovery Domain: Central California Coast Coho Salmon, California Coastal Chinook, Northern California Steelhead, and Central California Coast Steelhead. The extremely high fraction of populations that are categorized as data deficient highlights the critical need for development of a comprehensive monitoring plan for salmonid populations in the NCCC Recovery Domain. At a bare minimum, application of the criteria proposed here requires estimates of population abundance for functionally and potentially independent populations within the domain, as well as information on the spatial distribution of individuals within these populations. Existing monitoring programs in California are generally limited to index reaches and, as such, do not produce estimates at the population level. Even with such abundance data, information on freshwater and marine survival rates of at least a representative set of populations for each species will be required to ascertain whether observed trends in abundance reflect improvement in freshwater conditions or merely reflect changes in marine conditions. More sophisticated viability models that would account for population-specific differences in vital rates (and therefore potentially improve on the general criteria proposed here) will have even greater data requirements. It is imperative that California, which is well behind other states in the Pacific Northwest, begin conducting monitoring at spatial scales relevant to recovery planning if we are to have any hope of accurately evaluating status and progress toward recovery.

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# Appendix A. Revisions to NCCC Population Structure Report

## Introduction

The hypothesized historical population structure for two listed Evolutionarily Significant Units (ESUs) of salmon and two listed Distinct Population Segments (DPSs) of steelhead within the NCCC Recovery domain was described in detail in (Bjorkstedt et al. 2005). Following publication of this report, the Technical Recovery Team discovered several errors and inconsistencies in the document that require some modification to our assessment of historical population structure. This appendix presents corrected summaries of population structure for each of the four ESUs and DPSs within the recovery domain. These revised summaries supercede previously published tables and figures and should be used as the basis for further recovery planning efforts.

Most of the errors in the *Population Structure Report* involved inconsistencies among the text, tables, and figures for each ESU with respect to population classifications (i.e., functionally independent, potentially independent, and dependent) or placement of populations into diversity strata. These errors have been corrected in the summary tables and figures that follow. Additionally, we found two instances where historically accessible habitat above dams was not included in our estimates of *IP-km*, and several other instances where we have discovered long-standing barriers that likely prevented access to stream reaches that were assigned positive IP values. In these cases, we have since corrected estimates of *IP-km* for these populations and re-estimated self-recruitment values for each of the populations. In most cases, these changes have had a relatively minor influence on our overall conclusions, though in a few instances, populations have been downgraded from potentially independent to dependent.

In addition to correcting these errors, the TRT has also revised the diversity strata for the four ESUs and DPS within the domain. In a few cases, these revisions involve minor adjustments of diversity strata boundaries to better reflect environmental similarities and differences, as well as to foster consistency in diversity strata boundaries among species. More significantly, we have restructured diversity strata for the CC-Chinook salmon ESU with respect to the treatment of fall versus spring runs, and the NC-steelhead DPS with respect to summer and winter runs. These modifications are intended to more accurately represent the evolutionary history of different life-history types within each watershed. Finally, the CCC-Steelhead DPS boundary was recently modified by NMFS (71 FR 834-862) to include tributaries to Suisun Bay and Carquinez Strait; we have added a small number of populations to reflect these changes.

**Central California Coast Coho Salmon Diversity Strata**

Revisions to the Central California Coast coho salmon diversity strata were minor. Upon further examination of environmental data, the TRT felt that it was more appropriate to group the Gualala River population with populations to the north, including the Navarro River and Garcia River independent populations. These three basins fall within the Coast Range ecoregion, share similar geologies, and have comparable precipitation and temperature patterns. These similarities appear stronger than those between the Gualala River basin and basins farther to the south including the Russian River and smaller basins in coastal regions of southern Sonoma and northern Marin counties. Furthermore, the TRT feels that the stretch of coastline between Gualala Point and the mouth of the Russian River, which is characterized by very small watersheds few of which contain habitat that appears suitable to coho salmon, constitutes a more meaningful geographic break (i.e., potential migration barrier) than that of Point Arena. The realignment of the Gualala River required us to change the names of diversity strata to accurately reflect natural geographic breaks that define the strata. The historical population status of coho populations within the ESU is presented in Table A.1, and the placement of populations with respect to diversity strata is shown in Figure A.1 and Plate A.1.

**Table A.1.** Historical population structure of coho salmon in the CCC-Coho ESU. Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005). This table supercedes Table 2.2 in Bjorkstedt et al. (2005).

| Population | IP km | IP Bias Index | Self-Recruitment* | Historical Population Status |
|---|---|---|---|---|
| Jackass Creek [b] | 4.33 | low | 0.851 | dependent |
| Usal Creek [17] | 10.60** | low | 0.911 | dependent |
| Cottaneva Creek [18] | 13.80 | low | 0.910 | dependent |
| Juan Creek [20] | 5.98 | low | 0.871 | dependent |
| Howard Creek [c] | 3.27 | moderate | 0.817 | dependent |
| DeHaven Creek [21] | 5.72 | moderate | 0.919 | dependent |
| Wages Creek [22] | 9.95 | low | 0.897 | dependent |
| Abalobadiah Creek [c] | 4.08 | low | 0.614 | dependent |
| Ten Mile River [23] | 105.14 | moderate | 0.990 | **Functionally Independent** |
| Mill Creek [c] | 4.70 | low | 0.618 | dependent |
| Pudding Creek [24] | 28.86 | moderate | 0.936 | dependent |
| Noyo River [25] | 119.27 | moderate | 0.990 | **Functionally Independent** |
| Hare Creek [26] | 12.44 | moderate | 0.879 | dependent |
| Jug Handle Creek [c] | 4.84 | moderate | 0.705 | dependent |
| Caspar Creek [27] | 12.84 | moderate | 0.883 | dependent |
| Russian Gulch (Me) [28] | 6.40 | moderate | 0.727 | dependent |
| Big River [30] | 193.66 (194.76) | high | 0.992 | **Functionally Independent** |
| Little River (M) [31] | 6.49 | moderate | 0.667 | dependent |
| Albion River [32] | 59.18 | high | 0.964 | **Functionally Independent** |
| Big Salmon Creek [33] | 17.04 | high | 0.926 | dependent |
| Navarro River [34] | 201.04 (232.51) | high | 0.988 | **Functionally Independent** |
| Greenwood Creek [35] | 5.10** | high | 0.633 | dependent |
| Elk Creek [36] | 9.90** | high | 0.769 | dependent |
| Mallo Pass Creek [c] | 3.64 | high | 0.573 | dependent |
| Alder Creek [37] | 5.99** | high | 0.796 | dependent |
| Brush Creek [38] | 18.00 | high | 0.921 | dependent |
| Garcia River [39] | 76.04 (105.25) | high | 0.979 | **Functionally Independent** |
| Point Arena Creek [d] | 3.91 | high | 0.586 | dependent |
| Schooner Gulch [40] | 4.80 | high | 0.485 | dependent |
| Gualala River [41] | 252.18 (277.90) | high | 0.976 | **Functionally Independent** |
| Russian Gulch (S) [d] | 6.02 | moderate | 0.219 | dependent |
| Russian River [42] | 779.41 (1661.99) | high | 0.997 | **Functionally Independent** |
| Scotty Creek [d] | 3.78 | high | 0.333 | dependent |
| Salmon Creek (S) [43] | 47.60 | high | 0.893 | dependent |
| Bodega Harbor [44] | 11.72 | high | 0.672 | dependent |
| Americano Creek [45] | 60.63 | high | 0.938 | dependent |
| Stemple Creek [46] | 77.36 | high | 0.960 | dependent |
| Tomales Bay [47] | 234.52 | | 0.969 | |
| Walker Creek [TB1] | 103.68 | high | | ***Potentially Independent****** |
| Lagunitas Creek [TB2] | 136.96† | high | | **Functionally Independent** |
| Drakes Bay [48] | 8.00 | high | 0.468 | dependent |
| Pine Gulch [49] | 7.41 | high | 0.636 | dependent |
| Redwood Creek (M) [50] | 7.99 | high | 0.623 | dependent |

**Table A.1.** (continued)

| Population | IPkm | IP Bias Index | Self-recruitment | Historical Population Status |
|---|---|---|---|---|
| San Francisco Bay [51] | 339.18†† (669.26) | | 0.996 | |
| Arroyo Corte Madera del Presidio[S1] | 10.55 | high | | dependent |
| Corte Madera Creek [S2] | 35.18 | high | | dependent |
| Miller Creek [S3] | 31.02 | high | | dependent |
| Novato Creek [S4] | 73.98 | severe | | dependent |
| Petaluma River [S5] | 233.01 | severe | | dependent |
| Sonoma Creek [S6] | 227.10 | high | | dependent |
| Napa River [S7] | 491.76 (500.04) | severe | | dependent |
| San Pablo Creek [S8] | 18.40 | severe | | dependent |
| Strawberry Creek [e] | 4.90 | severe | | dependent |
| San Leandro Creek [S9] | 21.56 | severe | | dependent |
| San Lorenzo Creek [S10] | 58.94 | severe | | dependent |
| Alameda Creek [S11] | 105.52 (435.60) | severe | | dependent |
| Coyote Creek [S12] | 182.84 (338.98) | severe | | dependent |
| Guadalupe River [S13] | 153.64 | severe | | dependent |
| Stevens Creek [S14] | 23.28 | severe | | dependent |
| San Francisquito Creek [S15] | 46.94 | severe | | dependent |
| San Mateo Creek [S16] | 42.09 | severe | | dependent |
| Pilarcitos Creek [52] | 31.79 | high | 0.818 | dependent |
| Tunitas Creek [53] | 8.33 | high | 0.762 | dependent |
| San Gregorio Creek [54] | 40.12 | high | 0.978 | dependent |
| Pomponio Creek [55] | 8.52 | high | 0.892 | dependent |
| Pescadero Creek [56] | 60.62 | high | 0.985 | **Functionally Independent** |
| Arroyo de los Frijoles [e] | 6.67 | high | 0.806 | dependent |
| Gazos Creek [57] | 8.16 | high | 0.887 | dependent |
| Whitehouse Creek [e] | 4.19 | high | 0.914 | dependent |
| Cascade Creek [e] | 4.15 | high | 0.820 | dependent |
| Waddell Creek [58] | 9.23 | high | 0.884 | dependent |
| Scott Creek [59] | 15.00 | high | 0.892 | dependent |
| San Vicente Creek [60] | 3.12 | high | | dependent |
| Wilder Creek [62] | 4.90 | high | 0.647 | dependent |
| San Lorenzo River [63] | 135.31† | high | 0.995 | **Functionally Independent** |
| Soquel Creek [64] | 33.03 | high | 0.962 | dependent |
| Aptos Creek [65] | 27.35 | high | 0.928 | dependent |

* Self-recruitment values may differ from those presented in Bjorkstedt et al. (2005) due to minor corrections in estimates of *IP-km* in several watersheds.

** The *IP-km* values for Usal Creek, Greenwood Creek, Elk Creek, and Alder Creek differ from those presented in Bjorkstedt et al. (2005) due to the subsequent identification of long-standing natural barriers on each of these streams.

*** Status of historical population in Walker Creek is especially uncertain due to environmental and ecological conditions; this population might have been dependent (mostly on the population of coho salmon in Lagunitas Creek) under historical conditions.

† The *IP-km* values for Lagunitas Creek and the San Lorenzo River differ from those presented in Bjorkstedt et al. (2005) due to corrections in IP calculations, which account for historically available habitat that currently lies behind dams.

†† IP km for San Francisco Bay is conservative, and includes only those watersheds for which there is reasonable support for presence of coho salmon.

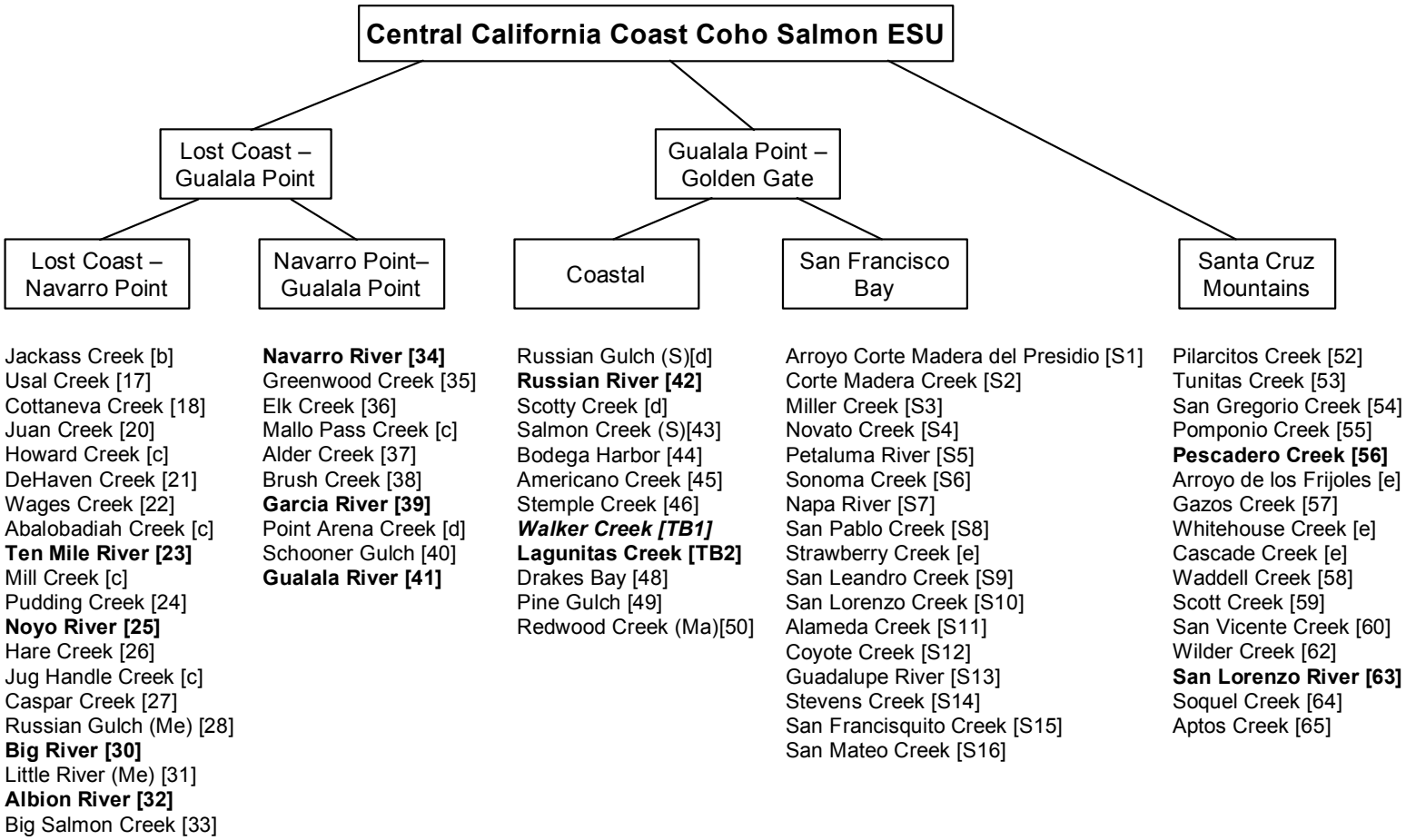


Figure A.1. Historical population structure of the CCC-Coho Salmon ESU, arranged by diversity strata. Functionally independent populations are listed in **bold font**. Potentially independent populations are listed in ***bold-italic*** font. Dependent populations are listed in regular font.

## California Coastal Chinook Salmon Diversity Strata

Bjorkstedt et al. (2005) proposed a population structure that included major strata representing the two life-history types found in CC-Chinook salmon (i.e., fall-run and spring run), with fall-run Chinook being further subdivided into four diversity strata: North Coastal, Northern Mountain Interior, North-Central Coastal, and Central Coast. Subsequent deliberations by the TRT have led us to conclude that this proposed structure does not accurately reflect the likely evolutionary relationship between spring-run and fall-run populations. At issue is whether spring Chinook salmon populations in the ESU historically constituted a single monophyletic group, or alternatively, reflected independent parallel evolution of the spring-run life-history type from fall-run populations within each individual watershed. Because spring Chinook populations have been extirpated from the ESU, there is no way to definitively answer this question. However, analysis of genetic data from Chinook salmon in western North America indicates that, while both structures are possible, parallel evolution appears more common in coastal populations (Waples 2004)[30]. The nearest extant spring Chinook populations north of the CC-Chinook ESU are found in the Klamath River basin and show stronger genetic affinity for fall-run Chinook populations in the same basin than for other spring Chinook populations to the immediate north. These data argue for independent evolution of the spring-run life history within each watershed, and we thus conclude that it is more appropriate to consider the two life-history types as substrata under the major environmentally based strata previously defined (Figure A.2). From the standpoint of implementing diversity criteria, the consequences of violating this assumption would be relatively minor. If in fact spring Chinook salmon are monophyletic, attainment of diversity strata goals would result in the monophyletic group being represented in the multiple diversity.

Finally, the TRT moved the Big Salmon Creek population from the Central Coastal stratum to the North-Central Coastal stratum. This change reflects the greater environmental similarity between Big Salmon Creek and watersheds to the immediate north (e.g., Albion River), and fosters consistency with diversity strata breaks defined for coho salmon and steelhead. The revised population structures of fall-run and spring-run Chinook salmon in the ESU are shown in Table A.2 and A.3, respectively. The arrangement of all populations with respect to diversity strata is shown in Figure A.2 and Plates A.2 and A.3.

[30] This contrasts with interior Columbia River basin spring-run populations, which form a coherent genetic group that is strongly divergent from summer- and fall-run populations in the same geographic region.

**Table A.2.** Historical population structure of fall-run Chinook salmon in the CC-Chinook ESU. This table supercedes Table 3.2 in Bjorkstedt et al. (2005). Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005).

| Population | *IP-km* | Self-recruitment | Historical Population Status |
|---|---|---|---|
| Redwood Creek (H) [1] | 116.05 | 0.987 | **Functionally Independent** |
| Little River (H) [3] | 18.55 | 0.761 | ***Potentially Independent*** |
| Mad River [5] | 93.95 | 0.948 | **Functionally Independent** |
| Humboldt Bay [6] | 76.66 | 0.866 | ***Potentially Independent*** |
| Lower Eel River* | 549.37 | 0.993 | **Functionally Independent** |
| Upper Eel River** | 498.49 | | **Functionally Independent** |
| Bear River [10] | 39.44 | 0.745 | ***Potentially Independent*** |
| Mattole River [14] | 177.50 | 0.968 | **Functionally Independent** |
| Usal Creek [17] | 6.04 | 0.530 | Dependent† |
| Cottaneva Creek [18] | 5.17 | 0.780 | Dependent† |
| DeHaven Creek [19] | 2.41 | 0.685 | Dependent† |
| Wages Creek [22] | 5.17 | 0.843 | Dependent† |
| Ten Mile River [23] | 67.18 | 0.975 | **Functionally Independent** |
| Pudding Creek [24] | 8.34 | 0.788 | Dependent† |
| Noyo River [25] | 62.18 | 0.989 | **Functionally Independent** |
| Hare Creek [26] | 2.83 | 0.695 | Dependent† |
| Caspar Creek [27] | 2.30 | 0.500 | Dependent† |
| Big River [30] | 104.31 | 0.982 | **Functionally Independent** |
| Albion River [32] | 17.57 | 0.895 | Dependent† |
| Big Salmon Creek [33] | 2.86 | 0.771 | Dependent† |
| Navarro River [34] | 131.46 | 0.989 | **Functionally Independent** |
| Greenwood Creek [35] | 4.74 | 0.694 | Dependent† |
| Elk Creek [36] | 7.70 | 0.747 | Dependent† |
| Alder Creek [37] | 4.71*** | 0.647 | Dependent† |
| Brush Creek [38] | 6.14 | 0.825 | Dependent† |
| Garcia River [39] | 56.22 | 0.926 | ***Potentially Independent*** |
| Gualala River [41] | 175.63 | 0.923 | ***Potentially Independent*** |
| Russian River [42] | 584.16 | 0.992 | **Functionally Independent** |
| Salmon Creek (S)[43] †† | 13.80 | 0.639 | Dependent† |
| Americano Creek [45] †† | 13.29 | 0.727 | dependent† |
| Stemple Creek [46] †† | 18.38 | 0.840 | dependent† |
| Tomales Bay [47] †† | 67.35 | 0.806 | dependent† |

* The Lower Eel River population occupied tributaries of the Eel River downstream from the confluence of the South Fork Eel River (inclusive) and is concentrated in the South Fork Eel River.
** The Upper Eel River population occupied tributaries upstream of the confluence of the South Fork Eel River (exclusive) and is concentrated in the Middle Fork Eel River.
*** The *IP-km* value for Alder Creek differs from that presented in Bjorkstedt et al. (2005) due to the subsequent identification of a long-standing natural barrier on Alder Creek.
† On the basis of environmental considerations and potential IP bias in the relation between IP km and population carrying capacity, it is unlikely that fall-run Chinook salmon consistently occupied these basins. Historical records of Chinook salmon are not available for any of these basins, save Wages Creek, from which a recent sample was collected. See Bjorkstedt et al. 2005 for further details.
†† These streams are south of the currently accepted range of the CC-Chinook ESU (Myers et al. 1998); we concur that persistent populations of Chinook salmon are not likely to have occupied these watersheds under historical conditions, although Chinook have been observed in Lagunitas Creek in recent years.

**Table A.3.** Historical population structure of spring-run Chinook salmon in the CC-Chinook ESU. This table supercedes Table 3.3 in Bjorkstedt et al. (2005). Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005).

| Population | Historical Population Status |
|---|---|
| (Redwood Creek (H)[1]) | **(Functionally Independent)** |
| Mad River [5] | **Functionally Independent** |
| (Van Duzen River [E2]) | **(Functionally Independent)** |
| North Fork Eel River [E5] | **Functionally Independent** |
| Middle Fork Eel River [E7] | **Functionally Independent** |
| Upper Eel River [8] | **Functionally Independent** |

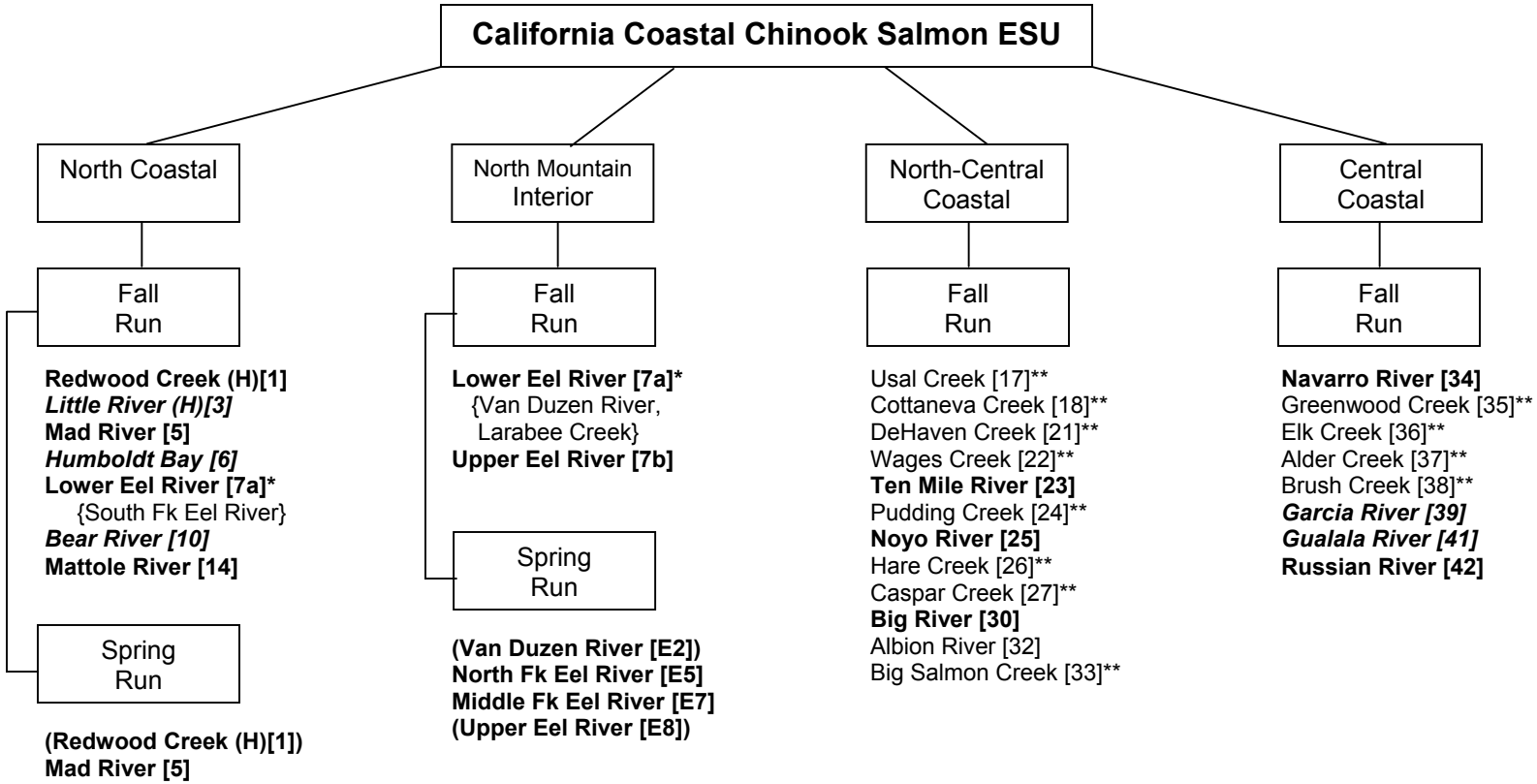


**Figure A.2**. Historical population structure of the CC-Chinook Salmon ESU, arranged by diversity strata. Functionally independent populations are listed in **bold font**. Potentially independent populations are listed in ***bold-italic*** font. Dependent populations are listed in regular font. Populations indicated by single asterisk are listed under multiple diversity strata and occupy environmentally diverse basins; subpopulations that occur within these different strata are shown in squiggly brackets. Populations indicated by a double asterisk are dependent populations in small watersheds, and are expected to be critically dependent on dispersal for occupancy. Spring-run Chinook salmon populations listed parenthetically are those for which potential historical existence is tentatively inferred from environmental correlates.

## Northern California Steelhead Diversity Strata

As with Chinook salmon, the TRT's original proposal for diversity strata for steelhead posited two major groupings based on life-history type: winter versus summer run (Bjorkstedt et al. 2005). Winter-run fish were further divided into five diversity strata (Northern Klamath Mountains, Southern Klamath Mountains, Northern Coastal, Central Coastal, and Southern Coastal) based on environmental characteristics. Summer-run fish were placed into two diversity strata (Interior and Coastal), also based on environmental characteristics (Figure 4.18 in Bjorkstedt et al. 2005). Upon further consideration, we have revised this structure to more accurately reflect what we believe to be the likely evolutionary relationship between winter-run and summer-run steelhead occupying the same watershed—specifically, that summer-run steelhead populations in the DPS likely represent independently evolved life-history types within each watershed rather than a single monophyletic group. Our reasoning parallels that for modifications to the Chinook salmon diversity strata. Although there are no data from which to compare summer steelhead populations within the domain (or within the Eel River basin), microsatellite data indicate that summer steelhead from the Middle Fork Eel River group more closely with winter steelhead from the Middle Fork Eel than to other winter steelhead in the either the South Fork or upper mainstem Eel River (A. Clemento and J. C. Garza, NMFS, Fisheries Ecology Division, Santa Cruz, unpublished data, cited in Bjorkstedt et al. 2005). The strong genetic affinity between summer and winter steelhead in the Middle Fork Eel River suggest a recent divergence, and we hypothesize that this pattern is likely to hold for other summer steelhead populations as well.

To reduce confusion, we have also renamed the steelhead diversity strata so they correspond more closely with those defined for Chinook salmon. The "Southern Klamath Mountains" stratum of Bjorkstedt et al. (2005) is now called the Lower Interior stratum; the "Northern Klamath Mountains" is now the North-Mountain Interior stratum; the "Central Coastal" stratum is renamed the North-Central Coastal stratum; and the "Southern Coastal" stratum is now the "Central Coastal" stratum. The Northern Coastal stratum remains as such.

Several other changes were made in the placement of populations into these diversity strata. First, we consider the Mattole River and South Fork Eel River populations to fall entirely within the Northern Coastal stratum. These two populations were originally considered to span two diversity strata (Northern Coastal and Lower Interior) based on east-west gradients in environmental conditions across these two basins (Bjorkstedt et al. 2005). However, the entire Mattole River basin and the vast majority of the South Fork Eel River fall within the Coast Range ecoregion (see Plate 2 of Bjorkstedt et al. 2005). Further, examination of environmental data indicates that precipitation and temperature regimes in these

basins are generally more similar to the more coastal region than they are to the interior portions of the Eel River basin, though they are intermediate to the coastal and interior regions for certain variables. Nevertheless, while environmental gradients do occur across these basins, we believe they are comparable to gradients observed across other coastal basins where we did not assign populations to multiple strata. We do note, however, that in assessing viability of populations, recovery planners should consider the spatial structure of populations across these basins, as environmental gradients may be a source of phenotypic diversity that could contribute to population viability.

We reaffirm our conclusion (Bjorkstedt et al. 2005) that the Mad River steelhead populations (both winter- and summer-run) each span two diversity strata: the Northern Coastal and North Mountain Interior strata. In this case, the east-west environmental gradient is sufficiently large that it represents the boundary between the Coast Range and Klamath Mountains ecoregions (EPA 2006; see Plate 2 of Bjorkstedt et al. 2005). Further consideration of the Redwood Creek populations (winter- and summer-run) suggests that it likewise is more appropriately placed in both the Northern Coastal and North Mountain Interior strata, as approximately half of this basin falls into each of the aforementioned ecoregions. This departs from Bjorkstedt et al. (2005), who placed the population exclusively into the Northern Coastal stratum. The TRT notes that spawning distribution of summer-run steelhead in both Mad River and Redwood Creek is not well known. In general, summer steelhead tend to penetrate farther into watersheds than do winter steelhead, which raises the possibility that the summer-run populations might spawn primarily in the headwater portions of Mad River and Redwood Creek. However, data from summer surveys of adult steelhead in holding pools indicates that they use both the upper and lower portions of the watershed for summer rearing. As we cannot determine whether fish holding in the lower portions of these basins ultimately spawn in the lower or upper reaches, we tentatively conclude that, like winter-run steelhead, summer steelhead span both strata.

Several other changes to population designations warrant discussion. First, within the Lower Interior stratum, the Outlet Creek and Tomki Creek winter steelhead populations have been changed from potentially independent to functionally independent populations, as has been the Larabee Creek winter steelhead population in the North Mountain Interior stratum. Each of these watersheds contain substantial steelhead habitat (*IP-km* > 100 in all cases), and for all three populations, estimates of self-recruitment are well above our threshold of 95%, even assuming a higher rate of straying (10%) for within-Eel River basin populations. In the case of Tomki Creek, some uncertainty remains at to whether this population is most appropriately characterized as functionally or potentially independent. In recent years, significant portions of Tomki Creek have gone dry during the summer (Weldon Jones, CDFG retired, personal

obsrvations). However, it is unclear whether this phenomenon is natural or is the result of water diversions, channel aggradation, modification of riparian vegetation, or other anthropogenic factors (Scott Harris, CDFG, Willits, personal communication). In the event that our estimate of intrinsic potential for steelhead in this basin is biased high, then predicted self-recruitment may also be biased high, which would suggest that it might be more appropriate to categorize the Tomki Creek population as potentially independent.

The historical population structure for winter steelhead in the NC Steelhead DPS is shown in Tables A.4 (coastal region) and A.5 (Eel River basin), and summer steelhead population structure is shown in Table A.6. The arrangement of winter and summer steelhead populations is illustrated in Figure A.3 and Plates A.4 and A.5.

**Table A.4.** Historical population structure of winter steelhead in the NC-Steelhead DPS. This table supercedes Table 4.4 in Bjorkstedt et al. (2005). Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005).

| Population | IP km | IP bias index | Self-recruitment | Historical Population Status |
|---|---|---|---|---|
| Butler Creek [a] | 1.98 | low | 0.747 | dependent |
| Boat Creek [a] | 1.62 | low | 0.536 | dependent |
| Fern Canyon [a] | 5.99 | low | 0.933 | dependent |
| Squashan Creek [a] | 4.00 | low | 0.720 | dependent |
| Gold Bluff [a] | 4.35 | low | 0.574 | dependent |
| Redwood Creek (H) [1] | 301.07 | low | 0.992 | **Functionally Independent** |
| McDonald Creek [a] | 6.38 | low | 0.528 | dependent |
| Maple Creek/Big Lagoon [2] | 94.67 | low | 0.913 | ***Potentially Independent*** |
| Little River (H) [3] | 76.16 | low | 0.864 | ***Potentially Independent*** |
| Strawberry Creek [a] | 6.08 | low | 0.498 | dependent |
| Widow White Creek [4] | 9.07 | low | 0.641 | dependent |
| Mad River [5] | 553.21 | low | 0.980 | **Functionally Independent** |
| Humboldt Bay [6] | 283.02 | low | 0.877 | **Functionally Independent** |
| Eel River - Full [7] | 4029.44 | | 0.995 | See Table 4.5 |
| Fleener Creek [a] | 4.14 | low | 0.243 | dependent |
| Guthrie Creek [8] | 10.10 | low | 0.623 | dependent |
| Oil Creek [9] | 11.17 | low | 0.551 | dependent |
| Bear River [10] | 116.03 | low | 0.928 | ***Potentially Independent*** |
| Singley Creek [11] | 11.83 | low | 0.563 | dependent |
| Davis Creek [12] | 8.14 | low | 0.591 | dependent |
| Domingo Creek [a] | 3.41 | low | 0.578 | dependent |
| McNutt Gulch [13] | 14.14 | low | 0.772 | dependent |
| Peter Gulch [a] | 2.26 | low | 0.326 | dependent |
| Mattole River [14] | 613.88 | low | 0.996 | **Functionally Independent** |
| Fourmile Creek [15] | 8.77 | low | 0.569 | dependent |
| Cooskie Creek [16] | 7.98 | low | 0.677 | dependent |
| Randall Creek [b] | 1.95 | low | 0.436 | dependent |
| Spanish Creek [b] | 1.89 | low | 0.585 | dependent |
| Oat Creek [b] | 1.84 | low | 0.477 | dependent |
| Big Creek [b] | 3.84 | low | 0.625 | dependent |
| Big Flat Creek [b] | 6.14 | low | 0.776 | dependent |
| Shipman Creek [b] | 2.28 | low | 0.565 | dependent |
| Gitchell Creek [b] | 2.52 | low | 0.641 | dependent |
| Horse Mountain Creek [b] | 3.23 | low | 0.782 | dependent |
| Telegraph Creek [b] | 5.57 | low | 0.944 | dependent |
| Humboldt Creek [b] | 1.64 | low | 0.456 | dependent |
| Whale Gulch [b] | 5.07 | low | 0.681 | dependent |
| Jackass Creek [b] | 3.57 | low | 0.801 | dependent |
| Little Jackass Creek [b] | 6.25 | low | 0.777 | dependent |
| Usal Creek [17] | 18.79 | low | 0.905 | ***Potentially Independent*** |
| Cottaneva Creek [18] | 26.09 | low | 0.912 | ***Potentially Independent*** |
| Hardy Creek [19] | 10.01 | low | 0.904 | dependent |
| Juan Creek [20] | 11.26 | low | 0.935 | dependent |
| Howard Creek [c] | 6.64 | moderate | 0.832 | dependent |

**Table A.4.** (continued)

| Population | IPkm | IP Bias Index | Self-recruitment | Historical Population Status |
|---|---|---|---|---|
| DeHaven Creek [21] | 13.01 | moderate | 0.936 | dependent |
| Wages Creek [22] | 19.93 | low | 0.947 | ***Potentially Independent*** |
| Chadbourne Gulch [c] | 3.74 | moderate | 0.562 | dependent |
| Abalobadiah Creek [c] | 6.92 | moderate | 0.714 | dependent |
| Seaside Creek [c] | 2.79 | moderate | 0.844 | dependent |
| Ten Mile River [23] | 204.7 | moderate | 0.996 | **Functionally Independent** |
| Inglenook Creek [c] | 3.19 | moderate | 0.520 | dependent |
| Mill Creek [c] | 5.58 | moderate | 0.631 | dependent |
| Virgin Creek [c] | 4.42 | moderate | 0.698 | dependent |
| Pudding Creek [24] | 32.04 | moderate | 0.939 | ***Potentially Independent*** |
| Noyo River [25] | 199.06 | moderate | 0.990 | **Functionally Independent** |
| Hare Creek [26] | 18.06 | moderate | 0.939 | ***Potentially Independent*** |
| Digger Creek [c] | 2.00 | moderate | 0.569 | dependent |
| Mitchell Creek [c] | 5.54 | moderate | 0.740 | dependent |
| Jug Handle Creek [c] | 5.35 | moderate | 0.743 | dependent |
| Caspar Creek [27] | 16.00 | moderate | 0.928 | ***Potentially Independent*** |
| Doyle Creek [c] | 2.40 | moderate | 0.547 | dependent |
| Russian Gulch (Me) [28] | 19.18 | moderate | 0.858 | ***Potentially Independent*** |
| Jack Peters Creek [29] | 7.98 | moderate | 0.799 | dependent |
| Big River [30] | 316.62 | high | 0.993 | **Functionally Independent** |
| Little River (M) [31] | 9.87 | moderate | 0.754 | dependent |
| Buckhorn Creek [c] | 1.72 | moderate | 0.397 | dependent |
| Dark Gulch [c] | 1.99 | moderate | 0.421 | dependent |
| Albion River [32] | 77.06 | high | 0.976 | **Functionally Independent** |
| Big Salmon Creek [33] | 24.83 | high | 0.910 | ***Potentially Independent*** |
| Navarro River [34] | 458.16 | high | 0.992 | **Functionally Independent** |
| Greenwood Creek [35] | 8.64 | high | 0.606 | dependent |
| Elk Creek [36] | 24.09 | high | 0.876 | ***Potentially Independent*** |
| Mallo Pass Creek [c] | 7.07 | moderate | 0.584 | dependent |
| Alder Creek [37] | 9.14* | high | 0.764 | dependent |
| Brush Creek [38] | 28.25 | high | 0.908 | ***Potentially Independent*** |
| Garcia River [39] | 169.01 | high | 0.984 | **Functionally Independent** |
| Point Arena Creek [d] | 4.43 | moderate | 0.536 | dependent |
| Moat Creek [d] | 5.11 | moderate | 0.676 | dependent |
| Ross Creek [d] | 4.04 | moderate | 0.796 | dependent |
| Galloway Creek [d] | 2.37 | moderate | 0.747 | dependent |
| Schooner Gulch [40] | 9.52 | moderate | 0.838 | dependent |
| Slick Rock Creek [d] | 2.77 | moderate | 0.509 | dependent |
| Signal Port Creek [d] | 3.18 | moderate | 0.498 | dependent |
| Saint Orres Creek [d] | 1.80 | moderate | 0.254 | dependent |
| Gualala River [41] | 478.03 | high | 0.987 | **Functionally Independent** |
| Miller Creek [d] | 3.16 | moderate | 0.137 | dependent |
| Stockhoff Creek [d] | 3.18 | moderate | 0.283 | dependent |
| Timber Cove Creek [d] | 1.66 | moderate | 0.266 | dependent |

* The *IP-km* value for Alder Creek differs from that presented in Bjorkstedt et al. (2005) due to the subsequent identification of a long-standing natural barrier on Alder Creek. Two consequences of this error are that the self-recruitment estimate is biased high and that the population is now designated as a dependent population.

**Table A.5.** Historical population structure of winter steelhead in the Eel River basin. This table supercedes Table 4.5 in Bjorkstedt et al. (2005). Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005).

| Population | IP km | IP bias index | Self-recruitment | Historical Population Status |
|---|---|---|---|---|
| Lower Mainstem Eel River* | | moderate | | dependent populations |
| Price Creek [A] | 20.56 | low | 0.987 | ***Potentially Independent*** |
| Howe Creek [B] | 15.29 | low | 0.948 | dependent |
| Larabee Creek [C] | 100.95 | low | 0.971 | **Functionally Independent** |
| Van Duzen River [E2] | 366.59† | low | 0.996 | **Functionally Independent** |
| South Fork Eel River [E3] | 1182.14 | low | 0.998 | **Functionally Independent** |
| Lower Middle Mainstem Eel River* | | low | | dependent populations |
| Dobbyn Creek [D] | 52.47 | low | 0.926 | ***Potentially Independent*** |
| Jewett Creek [F] | 18.17 | low | 0.874 | ***Potentially Independent*** |
| Pipe Creek [G] | 18.22 | low | 0.838 | ***Potentially Independent*** |
| Kekawaka Creek [H] | 35.27 | low | 0.926 | ***Potentially Independent*** |
| Chamise Creek [J] | 37.95 | low | 0.904 | ***Potentially Independent*** |
| North Fork Eel River [E5] | 372.83 | low | 0.983 | **Functionally Independent** |
| Upper Middle Mainstem Eel River* | | moderate | | dependent populations |
| Bell Springs Creek [K] | 18.54 | moderate | 0.837 | ***Potentially Independent*** |
| Woodman Creek [L] | 39.42 | moderate | 0.894 | ***Potentially Independent*** |
| Outlet Creek [N] | 313.8 | moderate | 0.975 | **Functionally Independent** |
| Tomki Creek [P] | 131.73 | moderate | 0.968 | **Functionally Independent** |
| Middle Fork Eel River [E7] | 584.26 | low | 0.989 | **Functionally Independent** |
| Bucknell Creek [R] | 21.07 | moderate | 0.812 | ***Potentially Independent*** |
| Upper Mainstem Eel River** | 422.13 | moderate | 0.997 | **Functionally Independent** |

* Indicate the set of small watersheds tributary to each section of the mainstem Eel River that are not listed by name in this table.
** The Upper Mainstem Eel River population occupies the mainstem and tributaries below the confluence of Bucknell Creek (exclusive), and thus differs slightly from the basin designated "Upper Mainstem Eel River" in the multivariate environmental analysis (See Bjorkstedt et al. 2005 for details).
† The *IP-km* value for the Van Duzen River differs from that presented in Bjorkstedt et al. (2005) due to the subsequent identification of a long-standing natural barriers on the river.

**Table A.6.** Historical population structure of summer steelhead in the NC-Steelhead DPS. This table supercedes Table 4.6 in Bjorkstedt et al. (2005). Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005).

| Population | Historical Population |
|---|---|
| Redwood Creek (H)[1]) | **Functionally Independent** |
| Mad River [5] | **Functionally Independent** |
| Van Duzen River [E2] | **Functionally Independent** |
| South Fork Eel River [E3] | **Functionally Independent** |
| Larabee Creek | **Functionally Independent** |
| North Fork Eel River [E5] | **Functionally Independent** |
| (Upper Middle Mainstem Eel River [E6])** | **(Functionally Independent)** |
| Middle Fork Eel River [E7] | **Functionally Independent** |
| (Upper Mainstem Eel River [8])*** | **(Functionally Independent)** |
| Mattole River [14] | **Functionally Independent** |

* All summer steelhead populations are considered functionally independent; see Bjorkstedt et al. 2005 for discussion.
** Summer steelhead have not been documented in this area; however , some of the watersheds that drain the north bank of the Eel River are environmentally similar to Larabee Creek and the major subbasins on the north Side of the Eel River basin and might have harbored historical populations of summer steelhead. Such populations, if shown to exist, would be considered functionally independent, pending further analysis.
*** The extent of habitat suitable for summer steelhead populations in the upper Eel River and its tributaries is unknown, and is likely to be restricted to the northeast corner of the basin (near the Middle Fork Eel River, where annual snowpack occurs.

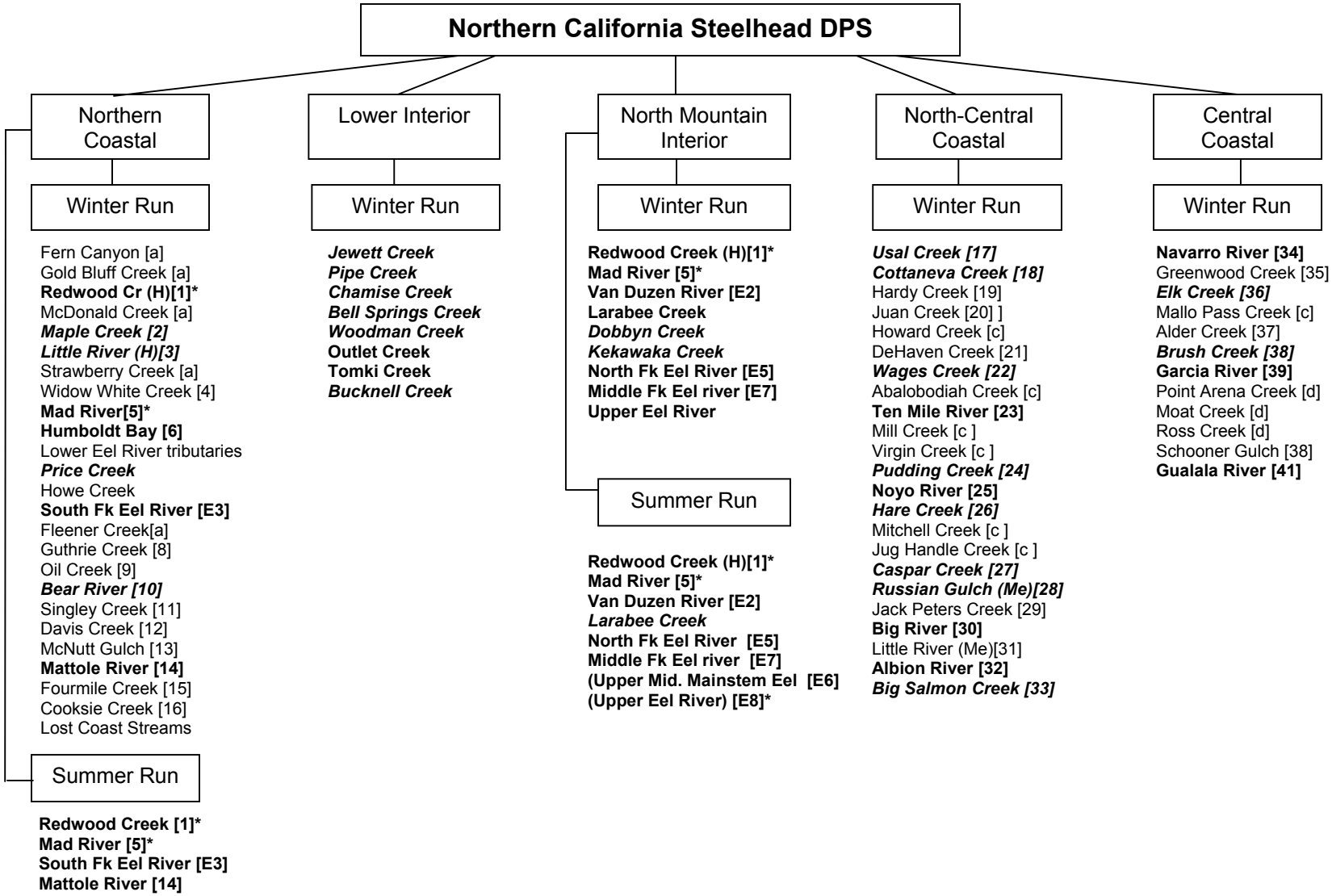


**Figure A.3.** Historical structure of the NC-steelhead DPS, arranged by diversity strata. Functionally independent populations are listed in **bold** font. Potentially independent populations are listed in ***bold-italic*** font. Dependent populations are listed in regular font (not all dependent populations are shown). Populations indicated by an asterisk are listed under multiple diversity strata and occupy environmentally diverse basins. Populations listed parenthetically are those for which potential historical existence is inferred from environmental correlates.

## Central California Coast Steelhead Diversity Strata

Minor modifications have been made to the historical population delineations proposed by Bjorkstedt et al. (2005) for the CCC-Steelhead DPS. First, since Bjorkstedt et al. (2005) was published, the National Marine Fisheries Service has clarified the eastern boundary of the Central California Coast DPS within the San Francisco Bay Region. This DPS was originally defined as including populations in San Francisco Bay east to and including the Napa River (62 FR 43937-43954); however, language defining the Central Valley DPS, which includes steelhead populations in tributaries to the Sacramento and San Joaquin River, was vague as to whether streams entering into the Suisun Bay region were considered part of the Central Valley DPS. The Central Valley Technical Recovery Team (Lindley et al. 2006) considered steelhead in creeks within this region to be part of the Central Valley DPS, proposing that collectively, fish within these tributaries (Green Valley Creek/Suisun Creek, Walnut Creek, Mt Diablo Creek, Arroyo del Hambre, and other smaller watersheds) constituted a single independent population. However, NMFS subsequently concluded that steelhead within the Susiun Bay region from Carquinez Strait to Chipps Island (the confluence of the Sacramento and San Joaquin rivers) are more appropriately considered part of the CCC-Steelhead DPS (71 FR 834-862).

We thus here consider the plausible population structure within this region, and its relation to other populations in the San Francisco Bay region. Based on our IP model, four watersheds within the region are predicted to potentially have had sufficient habitat to support independent populations of steelhead (Table A.9). The smallest of these, Arroyo del Hambre and Mt. Diablo Creek, we conclude likely supported dependent populations. Although the predicted IP exceeds our independence threshold of 16 *IP-km* in both watersheds, the predicted IP bias is "severe" and we therefore believe it doubtful that these watersheds historically supported populations of sufficient size to be viable in isolation. Green Valley and Suisun creeks both enter into a common slough before reaching Suisun Bay; thus, the exchange of individuals between these two subwatersheds was likely high enough to constitute a single demographically coupled unit. Collectively, these two watersheds contain sufficient potential habitat to for an independent population. Likewise, the Walnut Creek also likely contained sufficient habitat to support an independent population. Determining whether these two populations should be classified as functionally independent or potentially independent population is problematic, as not only would these populations have been influenced by strays from other San Francisco Bay tributaries, but they were also undoubtedly influences by strays from the Sacramento-San Joaquin basin, which historically may have produced as many as 1-2 million fish annually (McEwan 2001)[31]. Because of the potentially large influx

[31] We do not have estimates of intrinsic potential for streams within the Central Valley DPS and thus are unable to run an analysis of self-recruitment.

of stray from neighboring systems, we tentatively conclude that both the Green Valley/Suisun Creek population and Walnut Creek population were most likely potentially independent populations. We do note that it is plausible that the four identified populations (along with other smaller dependent populations in the area) formed a single interdependent unit (as proposed by the Central Valley TRT; Lindley et al. 2006). However, without any direct evidence supporting such aggregations, we opt to consider these populations separate, as we did elsewhere in the San Francisco Bay area. These populations, along with any other dependent populations that enter into Susiun Bay or Carquinez Strait, we consider to be part of the Interior San Francisco Bay diversity stratum.

Finally, we offer some clarification as to the geographic boundaries of diversity strata as they relate to populations in the Russian River basin. Populations downstream of the confluence of Mark West Creek are considered part of the North Coastal stratum, which also includes coastal watersheds in southern Sonoma and Marin counties. The Interior stratum includes Russian River populations upstream of Mark West Creek (inclusive). Tables A.7, A.8, and A.9 show population structure for the DPS, and Figure A.8 and Plate A.6 show these populations arranged into diversity strata.

**Table A.7.** Historical population structure of winter steelhead in the CCC-Steelhead DPS. This table supercedes Table 4.7 in Bjorkstedt et al. (2005). Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005).

| Population | IP km | IP bias index | Self-recruitment | Historical Population Status |
|---|---|---|---|---|
| Kolmer Creek [d] | 3.86 | moderate | 0.517 | dependent |
| Fort Ross Creek [d] | 2.07 | moderate | 0.160 | dependent |
| Russian Gulch (S) [d] | 7.05 | moderate | 0.251 | dependent |
| Russian River [42] | 2348.83 | | 0.999 | See Table A.8 |
| Scotty Creek [d] | 5.82 | high | 0.243 | dependent |
| Salmon Creek (S) [43] | 63.45 | high | 0.820 | ***Potentially Independent*** |
| Bodega Harbor [44] | 14.05 | high | 0.535 | dependent |
| Americano Creek [45] | 64.22 | high | 0.887 | ***Potentially Independent*** |
| Stemple Creek [46] | 73.11 | high | 0.921 | ***Potentially Independent*** |
| Tomales Bay [47] | 294.71 | high | 0.944 | |
| Walker Creek [TB1] | 134.08 | high | | ***Potentially Independent*** |
| Lagunitas Creek [TB2] | 170.73† | high | | ***Potentially Independent*** |
| Drakes Bay [48] | 10.12 | high | 0.303 | dependent |
| Pine Gulch [49] | 12.90 | high | 0.302 | dependent |
| Redwood Creek (M) [50] | 10.37 | high | 0.212 | dependent |
| San Francisco Bay [51] | 3054.61 | | 0.999 | See Table A.9 |
| Pilarcitos Creek [52] | 41.88 | high | 0.494 | ***Potentially Independent*** |
| Canada Verde Creek [e] | 4.27 | high | 0.232 | dependent |
| Tunitas Creek [53] | 16.40 | high | 0.668 | dependent |
| San Gregorio Creek [54] | 77.59 | high | 0.953 | **Functionally Independent** |
| Pomponio Creek [55] | 11.51 | high | 0.742 | dependent |
| Pescadero Creek [56] | 93.52 | high | 0.961 | **Functionally Independent** |
| Arroyo de los Frijoles [e] | 6.60 | high | 0.551 | dependent |
| Gazos Creek [57] | 16.10 | high | 0.842 | dependent |
| Whitehouse Creek [e] | 7.46 | high | 0.873 | dependent |
| Cascade Creek [e] | 5.88 | high | 0.898 | dependent |
| Green Oaks Creek [e] | 3.27 | high | 0.720 | dependent |
| Ano Nuevo Creek [e] | 4.22 | high | 0.692 | dependent |
| Waddell Creek [58]** | 16.24 | high | 0.869 | ***Potentially Independent*** |
| Scott Creek [59] | 23.51 | high | 0.938 | ***Potentially Independent*** |
| Molino Creek [e] | 2.90 | high | 0.659 | dependent |
| San Vicente Creek [60] | 7.99 | high | 0.859 | dependent |
| Liddell Creek [e] | 6.58 | high | 0.866 | dependent |
| Laguna Creek [61]** | 17.41 | high | 0.923 | ***Potentially Independent*** |
| Baldwin Creek [e] | 7.30 | high | 0.799 | dependent |
| Wilder Creek [62] | 14.12 | high | 0.850 | dependent |
| San Lorenzo River [63] | 225.64† | high | 0.994 | **Functionally Independent** |
| Rodeo Creek Gulch [e] | 6.10 | high | 0.726 | dependent |
| Soquel Creek [64]$*** | 66.41 | high | 0.978 | ***Potentially Independent*** |
| Aptos Creek [65] | 41.00 | high | 0.919 | ***Potentially Independent*** |

* The threshold for viability-in-isolation is set at 16 IP km (see Bjorkstedt et al. 2005 for details).
** Conclusions for these watersheds reflect the high likelihood that lagoon habitats at least partially offset potential bias in the IP model.
*** The historical status of Soquel Creek depends in part on whether substantial immigration from populations in the South-Central California Coast ESU, especially the Pajaro and Salinas rivers, was substantial under historical conditions.
† The *IP-km* values for Lagunitas Creek and San Lorenzo River differ from those presented in Bjorkstedt et al. (2005) due to a correction in IP calculations.

**Table A.8.** Historical population structure of winter steelhead in the Russian River basin. This table supercedes Table 4.8 in Bjorkstedt et al. (2005). Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005).

| Population | IP km* | IP bias index | Self-recruitment | Historical Population Status |
|---|---|---|---|---|
| Lower Russian River** | | high | | dependent populations |
| Austin Creek [A] | 111.85 | high | 0.981 | ***Potentially Independent*** |
| Dutch Bill Creek [B] | 17.38 | high | 0.973 | dependent |
| Green Valley Creek [C] | 61.67 | high | 0.988 | ***Potentially Independent*** |
| Mark West Creek [D] | 366.52 | high | 0.997 | ***Potentially Independent*** |
| Middle Russian River*** | | high | | dependent populations |
| Dry Creek [E] | 384.86 | high | 0.998 | ***Potentially Independent*** |
| Maacama Creek [F] | 106.91 | high | 0.991 | ***Potentially Independent*** |
| Sausal Creek [G] | 17.27 | high | 0.957 | dependent |
| Upper Russian River [H] † | 892.29 | high | >0.999 | **Functionally Independent** |

* The threshold for viability-in-isolation is set at 16 IP km (see Bjorkstedt et al. 2005 for details). ** Unnamed and smaller tributaries downstream of the confluence of Mark West Creek. ***Unnamed and smallert tributaries between Mark West and Big Sulphur creeks. † The Upper Russian River population occupies the mainstem and tributary habitats upstream from the confluence of Big Sulphur Creek (inclusive).

**Table A.9.** Historical population structure of winter steelhead in tributaries of San Francisco, San Pablo, and Suisun bays. This table supercedes Table 4.9 in Bjorkstedt et al. (2005). Bracketed codes correspond to watershed delineations defined in Bjorkstedt et al. (2005).

| Population | IP km | IP Bias index | Self-recruitment | Historical Population Status |
|---|---|---|---|---|
| **Northwest Bay** | | | | |
| Arroyo Corte Madera del Presidio [S1] | 12.75 | high | 0.294 | dependent |
| Corte Madera Creek [S2] | 41.33 | high | 0.527 | ***Potentially Independent*** |
| Miller Creek [S3] | 44.39 | high | 0.883 | ***Potentially Independent*** |
| Novato Creek [S4] | 78.58 | severe | 0.778 | ***Potentially Independent*** |
| **North Bay** | | | | |
| Petaluma River [S5] | 225.39 | severe | 0.939 | ***Potentially Independent*** |
| Sonoma Creek [S6] | 268.70 | high | 0.955 | **Functionally Independent** |
| Napa River [S7] | 593.93 | severe | 0.978 | **Functionally Independent** |
| **Suisun Bay** | | | | |
| Green Valley/Suisun Creeks [S17] | 164.04 | severe | na | ***Potentially Independent*** |
| Arroyo del Hambre [S18] | 25.45 | severe | na | dependent |
| Walnut Creek [S19] | 202.24 | severe | na | ***Potentially Independent*** |
| Mt. Diablo Creek [S20] | 44.85 | severe | na | dependent |
| **East Bay** | | | | |
| San Pablo Creek [S8] | 67.93 | severe | 0.754 | ***Potentially Independent*** |
| San Leandro Creek [S9] | 80.53 | severe | 0.954 | **Functionally Independent** |
| San Lorenzo Creek [S10] | 79.77 | severe | 0.985 | **Functionally Independent** |
| **Southeast Bay** | | | | |
| Alameda Creek [S11] | 816.59 | severe | 0.975 | **Functionally Independent** |
| Coyote Creek [S12] | 498.29 | severe | 0.936 | **Functionally Independent** |
| **Southwest Bay** | | | | |
| Guadalupe River [S13] | 157.25 | severe | 0.958 | **Functionally Independent** |
| Stevens Creek [S14] | 39.55 | severe | 0.775 | ***Potentially Independent*** |
| San Francisquito Creek [S15] | 59.22 | severe | 0.655 | ***Potentially Independent*** |
| San Mateo Creek [S16] | 57.41 | severe | 0.752 | ***Potentially Independent*** |
| unnamed tributaries | | | | dependent populations |

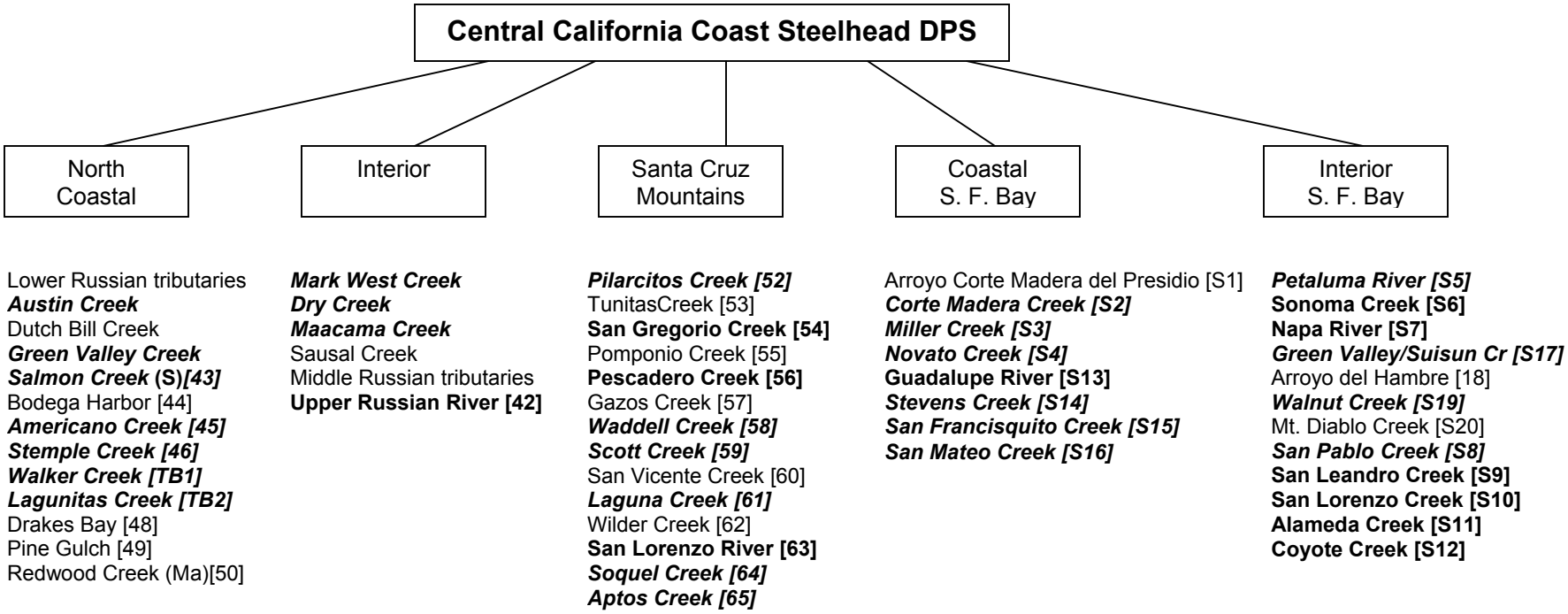


**Figure A.4.** Historical structure of the CCC-steelhead DPS, arranged by diversity strata. Functionally independent populations are listed in **bold** font. Potentially independent populations are listed in ***bold-italic*** font. Dependent populations are listed in regular font. Not all dependent populations have been included in this figure. See table A.4 for complete list.

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**Plate A1.** Diversity strata for populations of Central California Coast coho salmon. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

(see back pages for color plates)

**Plate A2.** Diversity strata for populations of fall-run California Coastal Chinook salmon. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

(see back pages for color plates)

**Plate A3.** Diversity strata for populations of spring-run California Coastal Chinook salmon. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

(see back pages for color plates)

**Plate A4.** Diversity strata for populations of winter-run Northern California steelhead. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

(see back pages for color plates)

**Plate A5.** Diversity strata for populations of summer-run Northern California steelhead. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

(see back pages for color plates)

**Plate A6.** Diversity strata for populations of Central California Coast steelhead. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

(see back pages for color plates)

# Appendix B. Discussion of density criteria and their application

As noted in the text, the NCCC TRT spent substantial time debating the appropriateness and application of density criteria. Much of the discussion revolved around four central issues: (1) how to estimate density in situations where substantial habitat is no longer accessible due to impassible or so degraded as to preclude use by salmonids; (2) whether the density criteria (or abundance targets dictated by density criteria) for populations at "low risk" were sufficiently precautionary or overly so; (3) whether it was more appropriate to express density criteria in terms of fish per *IP-km* or fish per total accessible kilometers; and (4) whether adjustments to the criteria should be made to account for potential bias in estimates of IP. The first of these issues was covered in the main body of this report. The remaining three issues are treated in the sections that follow

**Are the density criteria sufficiently precautionary or overly so?**

During the course of our discussions, some TRT members expressed concern that the implementation of low-risk density criteria might result in abundance targets that are overly optimistic for certain watersheds (i.e., they might exceed what was historically possible), particularly in watersheds where the IP bias index (see discussion below) suggests that the IP model likely overestimates historical habitat potential. Conversely, other TRT members worried that perhaps the criteria might not be precautionary enough. Ultimately, the TRT concluded that the proposed density criteria—40 spawners per IP-kilometer for watersheds with the minimum amount of potential habitat (*IP-km*) thought to be capable of sustaining an independent population, declining to 20 spawners per kilometers for watershed with 10-fold the habitat potential of the minimum watershed—represented a reasonable "floor" for interim criteria in lieu of more sophisticated population viability analyses.

This conclusion is based on several lines of reasoning. First, recall that for each species, we have defined a minimum threshold of potential habitat (32 *IP-km* for coho salmon, 20 *IP-km* for Chinook salmon, and 16 *IP-km* for steelhead) that was required for the population to be considered viable-in-isolation when populations were functioning at their historical carrying capacity. Thus, estimates of carrying capacity in relatively undisturbed systems might provide a reasonable basis for determining spawner density criteria for these smallest systems. Unfortunately, the scientific literature lacks estimates of carrying capacities for relatively pristine systems. Our estimate of 40 spawners/*IP-km*, was based on the analysis of Bradford et al. (2000), who examined inflection points in stock-recruitment curves of 14 coho salmon populations and found that on average full smolt recruitment occurred at spawner densities of 19 female per kilometer (which assuming a sex ratio slightly biased in favor of males translates to roughly 40 spawners/km). In

using this value as the basis for spawner density criteria, several things should be kept in mind. First, the watersheds used to estimate spawner densities at full smolt recruitment represented habitats with varying levels of human disturbance, with few in relatively pristine condition. Thus, historical carrying capacities were, in all probability, somewhat higher on average than those suggested by data collected post human disturbance. Additionally, to estimate spawner densities, Bradford et al. (2000) divided adult spawner abundance by an estimate of total accessible kilometers of habitat (though they acknowledge that in some cases this may underestimate total available habitat). In contrast, the NCCC TRT proposes using *IP-km* as the denominator in calculating density (see discussion below). Within the NCCC Recovery Domain, the ratio of *IP-km* to total accessible kilometers typically averages about 0.6 for coho salmon. Assuming that this ratio is similar in other streams in the Pacific Northwest, this would again suggest that densities at carrying capacity may have been higher than suggested by our density criteria.

Ideally, information on historical population abundance prior to extensive human disturbance could provide a means of validating the proposed density thresholds. Unfortunately, such data are not generally available for salmon and steelhead populations in the NCCC Recovery Domain. The only published comprehensive (in geographic scope) coastwide estimates of historical abundance are contained in a report prepared by CDFG (1965). These estimates are generally considered "ballpark" guesses at abundance based on a combination of spawner observations (limited), harvest information, a few dam counts (Benbow dam on the South Fork Eel River and Sweasy Dam on the Mad River), and the professional judgment of local biologists working in the area at the time. Though there is very high uncertainty surrounding these estimates, they nevertheless provide the only basis for assessing whether the abundance projections produced by application of the density criteria fall within or outside a plausible range. Comparison of the NCCC TRT density-based population projections and the 1965 CDFG estimates indicates that, for many systems, there is reasonably good concordance between the two (Table B1). For most populations on the Mendocino and Humboldt County coasts, the projected low-risk abundances tend to be somewhat lower than the CDFG estimates, whereas in more southern populations, the projected abundances tend to be somewhat higher than the CDFG estimates (particularly for coho and Chinooks salmon). Part of this pattern almost certainly reflects the fact that, in the 1960s, while all populations in domain had likely experience significant declines due to a variety of human impacts (CDFG 1965), the southern portion of the domain were more severely disturbed. However, it may also reflect a north-south gradient in the degree of IP-bias (see below). Overall, however, comparison with the 1965 estimates adds support to the argument that the projected abundances are within a plausible range. We do note, however, that if the 1965 abundance estimates, made at a time when habitat degradation from land and water use were already widespread, are even somewhat close to reality, then the density-based

low-risk abundances suggested by our criteria might be more appropriately viewed as minimum "floors", rather than historical carrying capacities. Achieving these criteria would substantially reduce risk in most populations and thus be a useful part of a precautionary strategy. However, a highly precautionary approach might call for even higher numbers of spawners.

## Should density criteria be expressed in terms of IP-km or total accessible km?

Another issue that faced the TRT was whether density criteria should be expressed in terms of spawners per *IP-km* or total accessible kilometers within a watershed. In the literature, spawner densities (including those in Bradford et al. 2000) are obviously most commonly expressed in terms of spawners per kilometer of stream. However, productive capacity within and among watersheds may be highly variable depending

**Table B.1**. Comparison of projected spawner abundances satisfying the NCCCTRT "low risk" density criteria with population estimates taken from CDFG (1965).

| Population | Projected Low-risk Abundance | CDFG 1965 Estimate |
|---|---|---|
| *CCC-Coho salmon* | | |
| Ten Mile River [23] | 3,700 | 6,000 |
| Noyo River [25] | 4,000 | 6,000 |
| Big River [30] | 5,600 | 6,000 |
| Navarro River [34] | 5,700 | 7,000 |
| Garcia River [39] | 2,800 | 2,000 |
| Gualala River [41] | 6,200 | 4,000 |
| Russian River [42] | 15,600 | 5,000 |
| San Lorenzo River [63] | 4,400 | 1,600 |
| *CC-Chinook salmon* | | |
| Redwood Creek (H) | 3,400 | 5,000 |
| Mad River [5] | 3,000 | 5,000 |
| Eel River | 22,100* | 55,000 |
| Mattole River [14] | 4,000 | 5,000 |
| Ten Mile River [23] | 2,300 | 0 |
| Noyo River [25] | 2,200 | <50 |
| Big River [30] | 3,200 | 0 |
| Navarro River [34] | 3,600 | 0 |
| *Garcia River [39]* | 2,000 | 0 |
| *Gualala River [41]* | 4,000 | 0 |
| Russian River [42] | 11,700 | 500 |

| Population | Projected Low-risk Abundance | CDFG 1965 Estimate |
|---|---|---|
| *NCC Steelhead* | | |
| Redwood Creek (H) [1] | 6,000 | 10,000 |
| Mad River [5] | 11,200 | 6,000 |
| Eel River - Full [7] | | |
| Van Duzen River [E2] | 10,900 | 10,000 |
| South Fork Eel River [E3] | 23,600 | 34,000 |
| North Fork Eel River [E5] | 7,500 | 5,000 |
| Middle Fork Eel River [E7] | 11,700 | 23,000 |
| Mattole River [14] | 12,300 | 12,000 |
| Ten Mile River [23] | 4,100 | 9,000 |
| Noyo River [25] | 4,000 | 8,000 |
| Big River [30] | 6,300 | 12,000 |
| Navarro River [34] | 9,200 | 16,000 |
| Garcia River [39] | 3,400 | 4,000 |
| Gualala River [41] | 9,600 | 16,000 |
| *CCC Steelhead* | | |
| Russian River | 40,800* | 50,000 |
| San Lorenzo River [63] | 4,900 | 19,000 |

* denotes aggregate abundance for Upper and Lower Eel River independent populations

** denotes aggregate abundance of independent steelhead populations in the Russian River; excludes dependent populations

on the nature and quality of habitats. For example, for coho salmon, certain habitat types such as alcoves and dam pools typically found in unconstrained, low-gradient reaches of small-to-moderate-sized streams often account for a disproportionate portion of the total smolt production in a system (Nickelson et al. 1992). Thus, streams with comparable numbers of total accessible miles may produce substantially different numbers of fish. The IP models seek to predict such differences in the potential for different stream reaches (and watersheds) to express habitat characteristics that are likely to be favorable to each species, and thus we chose to use the integrated *IP-km* in as the basis for density calculations. Doing so assumes that, in general, density increases in direct proportion to the IP value for a reach, which may not be entirely true (and is difficult to validate in the absence of reference streams that have not been altered by human activities). However, the fact that estimates of *IP-km* were strongly correlated with historical estimates of total abundance in coastal watersheds or Oregon (Lawson et al. 2004) suggests that *IP-km* provides a reasonable basis for scaling differences in density criteria (and resulting abundance projections) among watersheds.

**Should adjustments to density criteria be made to account for potential IP Bias?**

In our population structure report, the TRT acknowledged potential bias in the IP-model that may arise due to regional differences in precipitation-runoff relationships or other local factors that are not accounted in this relatively simple model (Bjorkstedt et al. 2005). Stream hydrology is strongly influenced by complex interactions among a variety of factors including the amount and timing of precipitation, seasonal temperature patterns, and topographic and geomorphic characteristics of watershed that affect water routing and groundwater storage. All of these attributes vary across the NCCC Recovery Domain, some in systematic fashion. Consequently, while we used appropriate regional precipitation and runoff data to develop estimates of mean annual discharge, how stream discharge is distributed through time is likely to vary across the region. This potentially may result in the IP model over-predicting potential habitat in areas with the strongest seasonal patterns in precipitation, the warmest summer temperatures, or the least water storage capacity. We characterized this potential bias using an index of IP bias, specifically, the ratio of mean annual precipitation to mean annual air temperature (Bjorkstedt et al. 2005, page 55). Potential IP bias was qualitatively considered when assigning populations into the categories of functionally independent, potentially independent, and dependent. Where predicted habitat potential for populations fell near the minimum thresholds we used for discriminating between independent and dependent populations, the index of potential bias was used to adjust our final independence categorizations.

In recognizing that such bias may exist, the TRT was then faced with the question of whether the density criteria should be adjusted to account for this bias. More specifically, the TRT debated three interrelated questions. First, if there are regional differences in the degree of IP bias, is it reasonable to assume that the densities required for viability should be consistent among populations across an ESU? Second, because the practical outcome of density criteria (based on a prediction of *IP-km*) is to produce a population size requirement (i.e., the density threshold multiplied by the predicted *IP-km*), is it reasonable to have two basins with similar predicted *IP-km* but different IP bias to have comparable target population size requirements? And third, if some adjustment for IP-bias is deemed necessary, can the IP bias be quantitatively incorporated into the density criteria?

After considerable discussion, the TRT concluded that the density criteria should not be adjusted to accommodate IP bias for two primary reasons. First, we could find no satisfactory way to quantitatively relate the density criteria and IP bias. The IP model is a very coarse-scale model intended to predict the potential for development of habitat suitable for a particular species. We felt it inappropriate to further adjust IP values based on a relatively simple indicator without any empirical basis for doing so. Second, while from a conceptual basis, it may seem reasonable to expect that population density would, on average, be lower per unit *IP-km* near the edge of the species' distributions, the same cannot be said for total population abundance for a viable population. Extinction risk in a population increases with decreasing intrinsic productivity and increasing variability in abundance and vital rates. Populations near the periphery of a species range, and where IP-bias may be strongest, would be expected to exhibit lower productivity and greater variability than populations more toward the center of the species distribution. In this context, it is likely that abundance in southern or more interior populations needs to be larger than more northern populations to attain comparable viability. Because these two factors oppose one another, we concluded that no adjustment should be made for IP bias.

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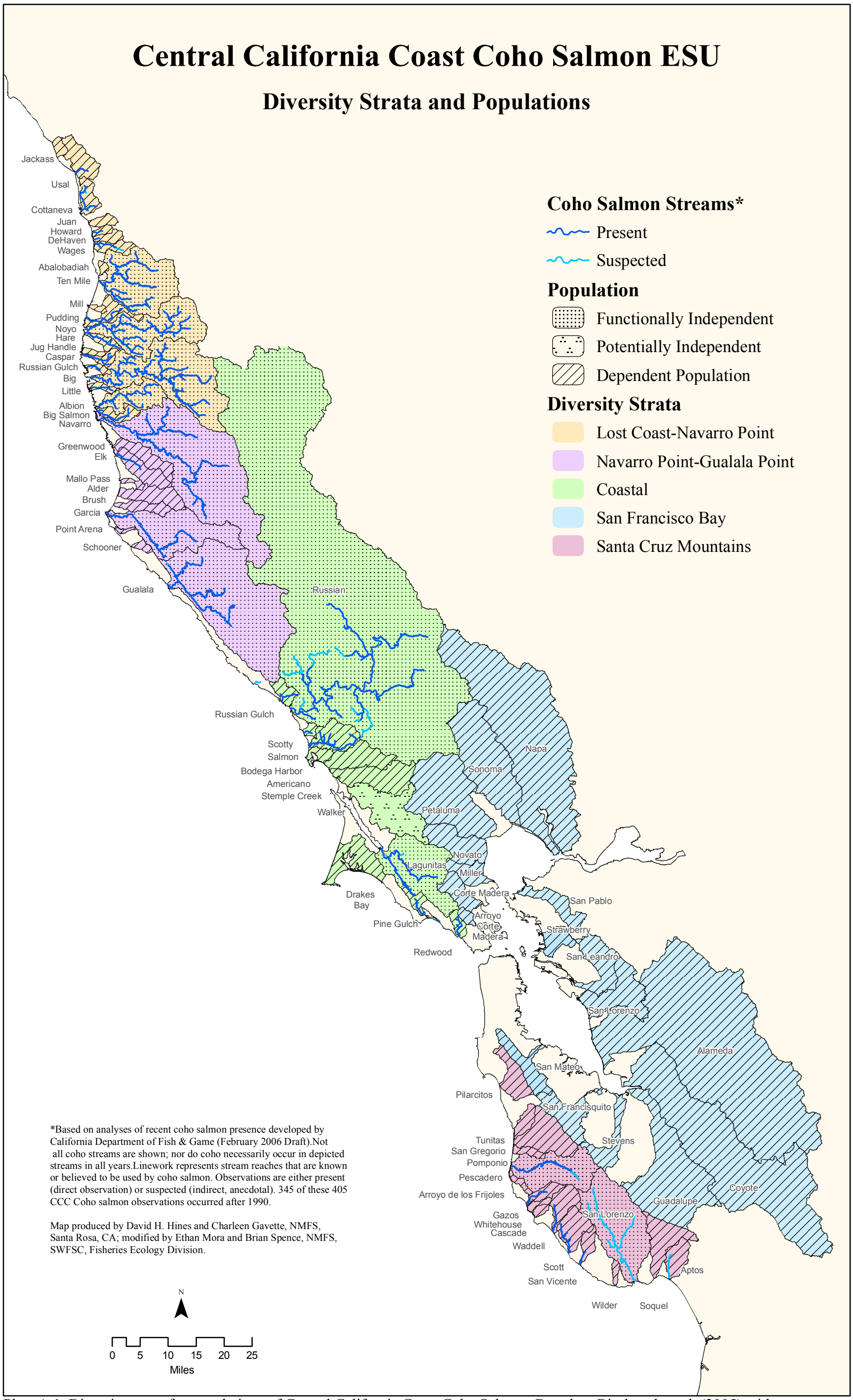



Plate A.1. Diversity strata for populations of Central California Coast Coho Salmon. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

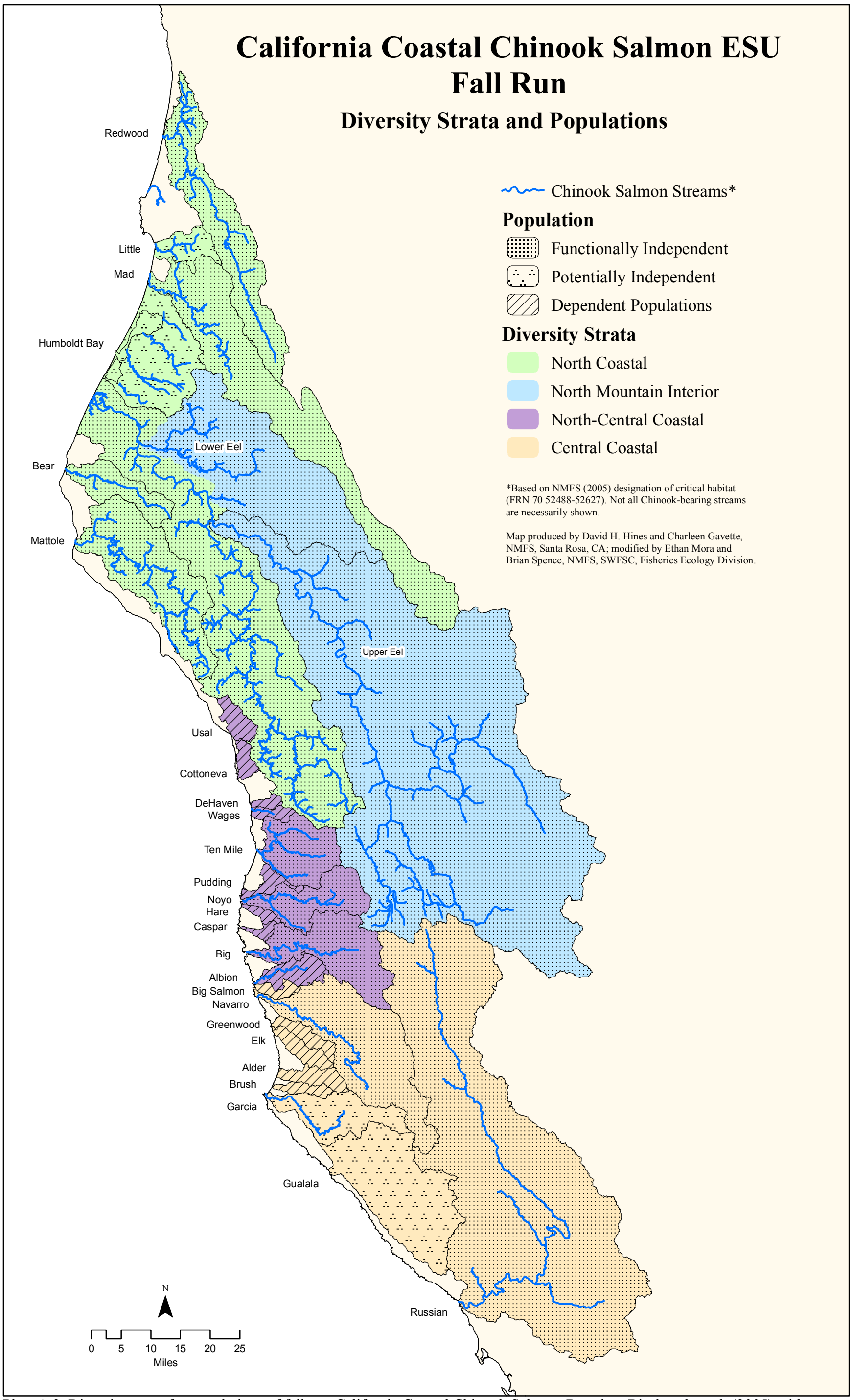



Plate A.2. Diversity strata for populations of fall-run California Coastal Chinook Salmon. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

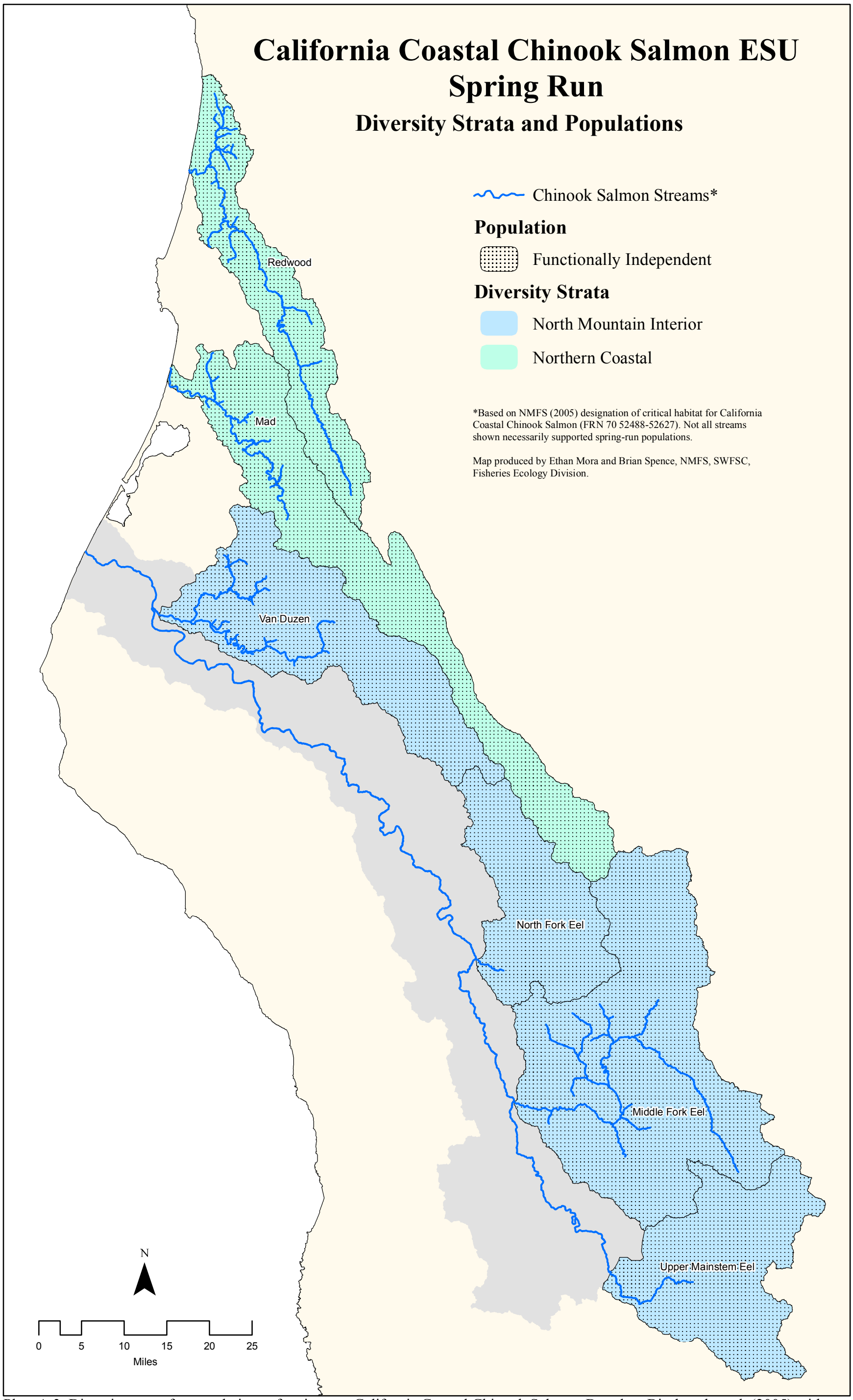



Plate A.3. Diversity strata for populations of spring-run California Coastal Chinook Salmon. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

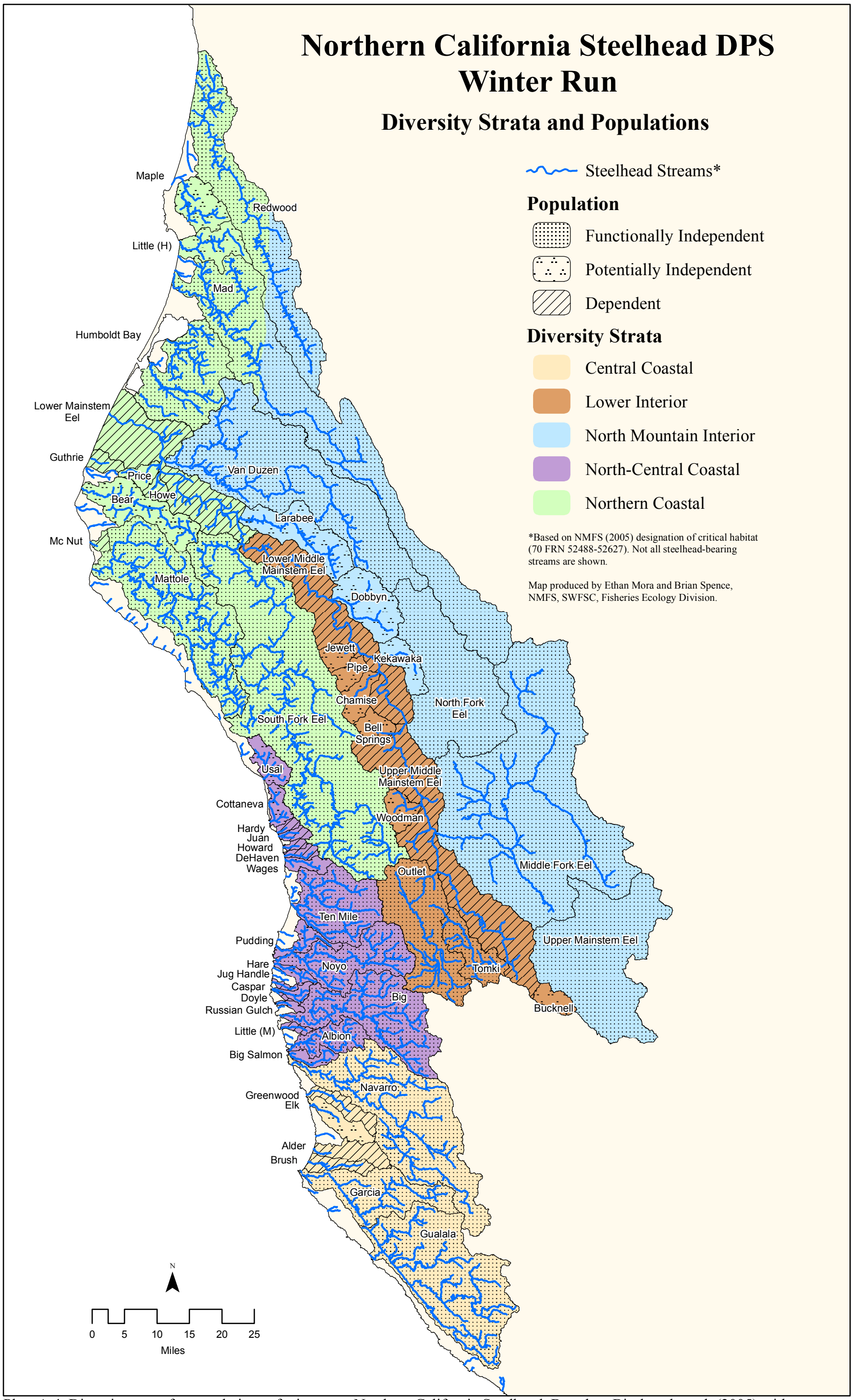



Plate A.4. Diversity strata for populations of winter-run Northern California Steelhead. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

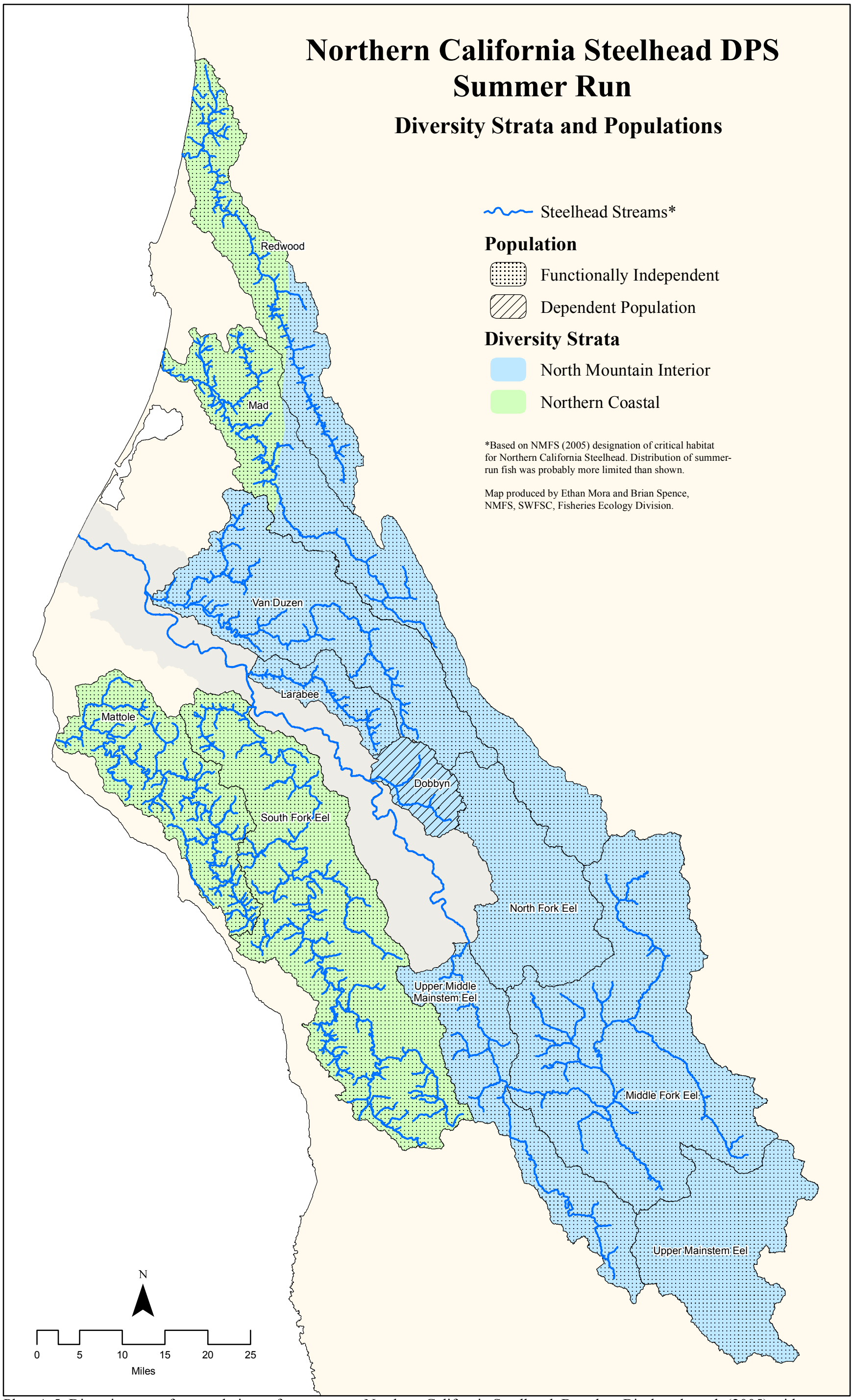
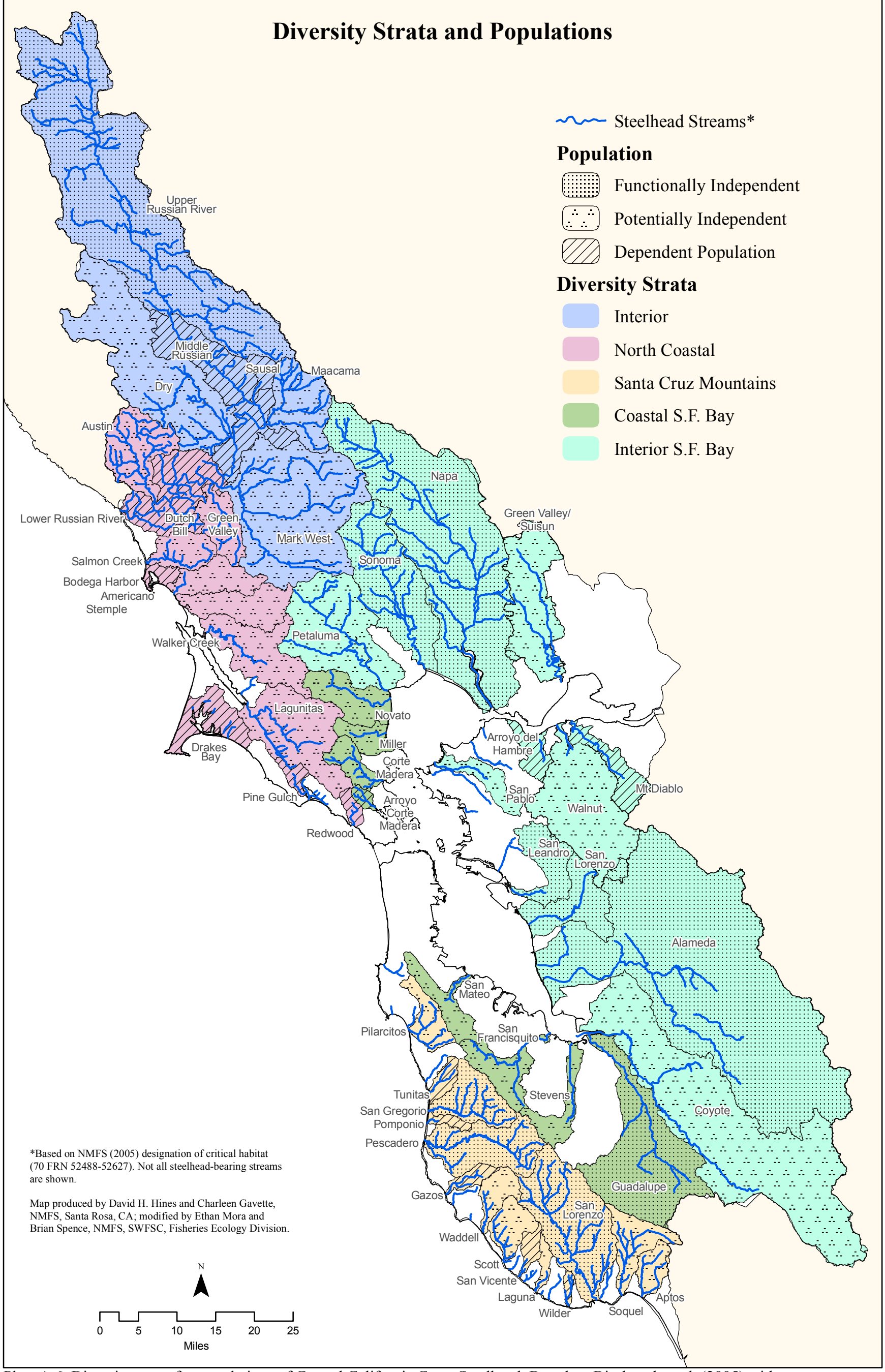



Plate A.5. Diversity strata for populations of summer-run Northern California Steelhead. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.

# Central California Coast Steelhead DPS

## Diversity Strata and Populations




*Based on NMFS (2005) designation of critical habitat (70 FRN 52488-52627). Not all steelhead-bearing streams are shown.

Map produced by David H. Hines and Charleen Gavette, NMFS, Santa Rosa, CA; modified by Ethan Mora and Brian Spence, NMFS, SWFSC, Fisheries Ecology Division.

Plate A.6. Diversity strata for populations of Central California Coast Steelhead. Based on Bjorkstedt et al. (2005) with modifications described in Appendix A.