ISAB Comments on Draft
NOAA Technical Recovery Team Documents
Identifying Independent Salmonid Populations
Within Evolutionarily Significant Units

(Review of Interior Columbia TRT Draft Document)

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In a September 10, 2003 letter from NOAA Fisheries, Dr. Usha Varanasi requested the ISAB to review the Interior Columbia River Technical Recovery Team (TRT) July 2003 draft document "Independent Populations of Chinook, Steelhead, and Sockeye for Listed Evolutionarily Significant Units within the Interior Columbia River Domain."

The review request included two specific questions:

1. Are the approaches for identifying independent populations reasonable, given the data available?

2. Do the conclusions flow logically from the data and analyses presented?

The ISAB concludes that the answer to both questions is no. Below, we provide detailed responses to each question as they pertain specifically to this document, as well as a comment on the need for consistency and rigor within the analytical procedures used in general. In our general comment on analytical procedures we did not restrict ourselves to a narrow consideration of whether the TRT used the data available in a scientifically rigorous manner in this specific instance. We also describe our concerns with the relationship among the ESA designations of "ESU, independent population, and subpopulation," under conditions of uncertainty. We offer the recommendation that a more precise and quantitative set of decision rules be developed to guide the TRTs. Finally, the document, as a self-described "working draft" suffers from some omissions and inconsistencies that preclude a detailed line-by-line review. We provide specific comments on some of these problems in the appendix to this report.

Response to Question 1:

The approaches used for identifying independent populations (i.e., the set of decision rules determining which groups are split or lumped) are not explicitly identified in the document we reviewed; as a result, it is not possible to determine if they are reasonable or not. There is an entire section, "Approach to Identifying Populations," that does a good job of describing the various data types used. In some cases, this section also does an adequate job of listing the analytical tools used to perform primary analyses and portray those results (e.g., the dendrograms or PCA Graphs for genetic data – see Appendix A). What is missing is an explicit explanation of how the data, once analyzed and portrayed (e.g., as a dendrogram for allele frequency data), are *interpreted* to make decisions on where to draw boundaries around independent populations.

Specifically, the first paragraph in that section (p. 5) states, "We used a variety of data types to define groups at both levels of population hierarchy (Table 2)." (The two levels were "major groups of potential populations within ESUs" and "independent populations within those major groups", and the ambiguity associated with the definitions of those levels is addressed in our general comment below.) Unfortunately, how the analysis of any given data type was actually used in a decision to establish the independence status for any two or more populations was not stated.

Furthermore, it is repeatedly stated in the document that multiple data sets were integrated into all of these decisions, but no explicit description is given of how that integration was accomplished. Two data types - genetic attributes and dispersal distances between spawning reaches (p. 6) - provide the primary sources of information to delineate population structure. We provide comments on the analyses of both these data sources.

Genetic attributes. In the Results Section I, Snake River Spring/Summer Chinook Salmon, in paragraph 2 on page 11, it is stated, "Based on genetic (Figures I-1 and I-2) and geographic considerations, we established five major groupings in this ESU." Later, it also states, "We further subdivided these groupings into a total of 31 extant demographically independent populations (Figure I-3)." Nowhere, however, does the report state the basis for making either of these delineations, much less, how the decision rules used to categorize major groupings and independent populations differ. We are not questioning the technical correctness of the dendrogram (Figure I-1) or the PCA analysis (Figure I-2) in portraying the genetic relatedness of the populations analyzed. We are questioning how those genetic results were used to identify "major groupings" and to define the boundaries of the independent populations as shown in Figure I-3. It is also unclear how those genetic data were weighted relative to other data types and then how the information from all of the different multiple data types were integrated to make the final decision portrayed in Figure I-3.

Dispersal distances between spawning reaches. The TRT used a 10% migration threshold attributed to Hastings (1993), below which the populations are not anticipated to bear on each other's demography or extinction risk. This approach merits a second look in the context of a metapopulation model that satisfies other conditions. For example, would not a 5% migration rate counter a 4% rate of local population decline (assuming effective inter-mating), so that the migration rate made the difference preventing deterministic local extinction?

At this time there are insufficient data available on reproduction of fish originating from one population and spawning in another to estimate migration. Consequently, straying data from tagged fish are used to estimate the distance from a release or tag site beyond which only 5% of a released population would be expected to stray. This approach is used as the basis for arguing that spawning locations beyond these distances are not contributing important numbers of spawning adults. The available data to establish these distances is unfortunately very sparse, particularly at intermediate distances. Appendix B of the report explains the approach used.

The ISAB had three summary comments concerning the analysis of dispersal distances and distances between spawning sites as presented in Appendix B (more extensive technical comments are provided at the end of this report).

1. While it was very worthwhile to try and use local data to define the dispersal distance, there are treatments of the data that could be more fully described and justified. In particular, it is not explained why individual tag recovery distances were not used. Further technical comments are provided for the authors in an appendix to this report.

2. The regression analyses used will result in very optimistic results (i.e., reporting unrealistically favorable precision and accuracy values). All sources of uncertainty in the data should be incorporated in this analysis and simulations used to estimate the range of variability in these results.

3. There seems to be a fundamental "disconnect" between the quality of data available for this analysis and the resulting estimate of small dispersal distances used to identify individual population units. A small dispersal distance will result in more individual units, and consequently may inform the decision over how many units need to be conserved. The basis for the small population units needs a sound scientific foundation. What is missing in this presentation is whether the number of population units would be sensitive to any other dispersal distance that could be estimated from these data? For example, if the upper 95% or lower 95% C.I. estimate was used, rather than the point estimate would that actually change any decisions on identifying independent population units?

Given the limitations and uncertainty of these data, an objective means to assess the uncertainty would be to conduct a sensitivity analysis (or just a review of the number of population units) using a range of dispersal values. For any population unit for which the dispersal distance contributed to the decision to establish an independent population, a consideration of these alternative distances should be included and explicitly justified. It is notable that in these authors' Discussion section, the examples from the Puget Sound and Lower Columbia/Willamette regions each chose larger "cut-off" values than the 30 km suggested from Appendix B.

As the report stands now, decisions on what constitutes an independent population seem to have a large subjective component that is, based on a process not described in the document. We understand that data sets are not perfect nor complete for all populations. We understand that no universal algorithm has been formalized to synthesize the input information into a single numerical outcome. We understand that various data inputs need to be weighed differently. Without a clear explanation of how the authors actually integrated the various datasets to come to their conclusions, then why show any data at all? Furthermore, if a synthesis was developed on a reasoned basis, why not lay out the procedure, so that it can be made consistent in future applications? This omission becomes increasingly important as decisions for independent population delineations are compared either across ESUs within a single TRT jurisdiction or across TRT jurisdictions. It is also quite likely that those comparisons will be made not only by scientists and managers, but also by stakeholders. If the decision rules are inconsistent, flawed, or not transparent, then the report will fail to accomplish its intended purpose.

Response to Question 2: Do the conclusions flow logically from the data and analyses presented?

The conclusions do not flow logically from the data and their analyses. There is a need for more analyses of the available data and for more transparent interpretation of those analyses. The presentation of the data and their analyses are embedded in lists of major groups and independent populations as the justification for those lists. Consequently, there is no visible logical transition from data, to analysis of the data, to interpretation of the analysis, and then finally to recommendations on how to subdivide or aggregate population groups into independent

populations. Each ESU section begins with very little data or analysis; major population groups and independent populations are listed almost immediately, with little text justification provided for the list. It would be better to present (cite) the data available, summarize the analyses of those data, and then provide an interpretation of those analyses as they pertain to the process of identifying independent populations, including evaluating population fragmentation and bottlenecks, as well as estimating population size and migration. Producing the list of populations would be the final step. This format for the flow of data and analysis was the format used in *Upper Columbia River Steelhead and Spring Chinook Salmon Population Structure and Biological Requirements* (Ford et al 2001). That organizational format provided a clearer picture of how and why the final conclusions were reached.

Logic Flow in the Bigger Picture

Consideration of the logic flow in the effort of any one TRT to delineate independent populations raises the natural question whether the process is consistent across the TRTs. This concern implies a need for coordination, guidance, and perhaps policy, above the level of the TRT. We believe this concern merits some attention.

The ESA, as originally written, applied to entire species. Later amendments provided the option for listing a "distinct population segment" of a vertebrate animal species population. If a distinct population segment (DPS) is so listed, all the crucial regulatory decisions under ESA, such as delisting, up or down listing, establishing recovery criteria, designation of critical habitat, and evaluation of jeopardy, must apply for this particular DPS in a manner independent of the rest of the species' population segments. That is, for example, the decision to delist such a population must be done for the entirety of the DPS; it is not legally possible to declare only part of the DPS recovered. Furthermore, because the decision to delist a DPS must be based entirely on evaluation of status and trends of that population segment, considerations of the status and trends of other population segments of that species cannot legally bear on the evaluation. As a result, in a decision to list a DPS, the delimiting of this population unit has far-reaching regulatory consequences.

The language of the ESA itself does not define a DPS very carefully. Subsequent rule making by NMFS and USFWS has developed some policy toward defining what may constitute a DPS. In particular, NMFS has defined what it calls an "evolutionarily significant unit" (ESU) as its working definition of what will constitute a DPS for purposes of ESA decision making with respect to salmon. In considering the general question of "viability" indicators for Pacific Salmon -- for the purpose of establishing recovery criteria and providing a standard against which jeopardy might be assessed -- NMFS issued a document (McElhany et al, 2000) "Viable Salmonid Populations and the Recovery of Evolutionarily Significant Units" that defined a hierarchical classification of the population components of a species. In that definition an ESU might consist of more than one "independent population", and an "independent population" might itself consist of more than one "subpopulation." This discussion drew on an existing scientific literature concerning the dynamics and genetics of spatially structured populations, called "metapopulations."

There is widespread scientific agreement about the existence and importance of spatial structure in natural populations. The available scientific evidence, however, often points more toward a continuum of degrees of local demographic and genetic independence of spatially defined units

below the level of species. That is to say, a particular hierarchy constructed of ESUs, "independent populations" and "subpopulations" as proposed in McElhany et al. (2000) may, from a scientific standpoint, be a system of definitions designed more to help organize management decisions than to delineate unambiguously recognizable building blocks. For example, although the working definition in McElhany et al. (2000) states that an "independent population" does not interbreed with other components of the species "to a substantial degree," on the same page it is acknowledged that "reproductive isolation forms a continuum." It seems, therefore, that the designation of "independent populations," may result in the imposition of an artificial black and white classification on a reality that is actually some shade of gray.

Resource management copes with such uncertainty by defining "decision rules" with margins of safety that reflect the relative severity of the consequences of decision error. The burden of proof is allocated in such a way as to make less probable the errors with the more severe consequences. (The "precautionary principle" embodies one set of priorities identifying those errors that are more rigorously to be avoided.) When decision rules are stated statistically, using statistical confidence limits on an estimated quantity, the weight given to the uncertainty is in proportion to the statistically measured amount of uncertainty in each instance.

The definitions for ESUs and "independent populations" are not formally embedded in such a set of quantitative decision rules that state how the viability of the independent populations will be quantified or how the resulting component viability estimates will be combined to make a decision about the status of the ESU. We are, therefore, in the dark as to what margins of safety are appropriate for various stages of the decision process, or how these margins of safety are to be instituted. For that reason, we have no basis for judging whether a particular attempt to identify "independent populations" from inadequate data is leaning too far in the direction of lumping or of splitting.

The ISAB believes that the lack of clear decision rules are issues that should not be the responsibility of each TRT to remedy independently. For consistency, these issues should be resolved at a higher organizational level. There is a literature that discusses the interplay between science and policy in defining management units (Taylor, 1997; Taylor and Dizon, 1999). There is a literature within applied fisheries science on the use of statistical procedures to optimize fisheries management decisions under conditions of uncertainty (Punt and Hilborn, 1997; Harwood and Stokes, 2003). There is a parallel technical literature on the use of statistical procedures for conservation decisions (Taylor and Dizon, 1996; Taylor and Wade, 2000; Martien and Taylor, 2003) and most specifically for ESA decisions (Goodman, 2003). Review of case studies in applications to fisheries management indicates that straightforward decision rules that use data inputs in a direct way have achieved the greatest level of institutional success (Harwood and Stokes, 2003).

We are aware that there are tradeoffs between a centralized and a decentralized approach. The possible liability in developing a "one size fits all" formula is that it might not really fit all. Although a less formal decision system allows more scope for local adjustment, at the same time, local adjustments in a set of similar decisions can manifest themselves as inconsistency across the set. NOAA Fisheries is facing a large number of nominally "similar" decisions in managing the many salmon ESUs listed under the ESA. Differences in how decisions are made for these ESUs

will be quite visible. If those differences can be interpreted as differences in how protective, how precautionary, or how conservative the decisions are, these differences are likely to become a cause for controversy. The challenge is to develop a formal decision rule that really is consistent, that uses all available relevant information, and that functions adequately when confronted by information gaps. Because the various TRTs are at different stages of their efforts, we would encourage NOAA Fisheries to review the entire set for consistency, and to abstract from the examples that seem more advanced and more convincing, a set of rules to guide the others.

To minimize ambiguities we offer several recommendations. First, we recommend that NOAA Fisheries develop a set of more precise quantitative definitions that link ESU, "independent population", and "subpopulation". The definitions provided in McElhaney et al. (2000) represent an obvious starting point to facilitate both internal scientific consistency and eventual integration into policy. We note that the definitions in that document constitute a vision for what each population unit *is*. The next step in making these definitions operational for decision-making purposes is to define how to *recognize* these units on the basis of available data.

Second, we recommend that these definitions be combined with a set of decision rules indicating how viability will be assessed for "independent populations," how the viability of component "independent populations" within an ESU will determine ESA status for that ESU, and what burden of proof will apply to setting boundaries of "independent populations" when the data are incomplete and the conclusions are uncertain. We are aware that some TRTs, such as Puget Sound and Lower Columbia Willamette, have produced documents describing viability criteria for independent populations in those domains, but we have not reviewed those documents. We also understand that McElhany et al. (2000) and the recovery planning documents available on the NWFSC web site discuss these issues in general, but we are unaware of any formal set of statistical decision rules adopted by NOAA to encompass the entire recovery planning process from identifying populations to formulating ESU-level recovery criteria. We encourage NOAA Fisheries to develop such a set of rules.

Technical Appendix concerning Appendix B of the TRT draft report:

Although the data used in the three examples are pooled within a stream with known recoveries of strays the distribution of the tags in a stream does not seem to be used. A "weighted distance" is estimated to represent the distance between source and strays, but it is not apparent why a weighted average is used versus the location distances of actual recoveries. The answer to this may be that the redd counts are used as a better representation of the distance that fish stray, since recoveries of strays would be affected by their downstream drift or movement after spawning. A significant source of uncertainty is how many strays were actually detected in a reach. In any carcass sampling program, there is a sample size and an estimate of the total population involved. The number of tags recovered is, therefore, an estimate of the true number of tags, plus an estimate of the uncertainty in that number. This issue becomes increasingly important when different sampling programs are being compared in one analysis. For example, if fish (total and marked) are counted past a fence at one site, but estimated in a stream in another site, what is the appropriate tag estimate to use in this comparison? The upper bound of a confidence limit on the number of tags would be most appropriate, as compared to the estimated average used in this analysis. The regression analyses are also likely to underestimate the uncertainty in their results. While the text refers to using the 95% C.I. values, the dispersal rates used are actually the regression value at the 5% stray level. Furthermore, based on the methods described, the 95% C.I. values stated from the regression analyses are estimated with an assumed normal error structure (although methods are not explicit on this point). Since these data are very sparse, however, a normal error estimate would be very conservative. A more appropriate estimate of the regression uncertainty would likely be a non-parametric simulation to derive an empirical range for any level of C.I. that many be desired. Why would only the 95% CI value be of interest? Finally, the authors actually do acknowledge the problem of finding strays as the distances from source increases. The sensitivity of results to this issue could also be investigated through simulation.

Results (p. 136) A few points would help to clarify the results. The first issue is to more clearly describe the statistics being used (e.g., page 137, 95% CI Mean versus 95% CI Estimate). Formulas may not be meaningful to some readers, but this makes the need for a clear description more important. Second, it was not apparent why Table 8 was included after Data Set 1 on page 137, and how were the John Day and Upper Columbia results combined? It also seems that the graphic display of data from Data Set 1 were not included.

A significant issue to address is the limited data in Data Set 3 between zero and about 50 km. The authors note this problem but then proceed to conclude that this data "supports the assumption that stray rates would be less than 5% for distances less than 40-50 km." This statement again does not account for uncertainty in the estimates but is also more a function of the curve fitted than the data. Confidence in this example is overstated in the Discussion also.

Discussion (p. 140) The discussion begins by introducing that most recoveries occur within 10 km from release and that "there are few to none farther than thirty km away." If the objective of this analysis was to determine the dispersal distance for 95% of the fish, what is the basis for subdividing the areas within the 30 km distance? It is certainly possible to have two populations within this distance, such as different run-timing groups, but this seems to be a separate question than the one addressed in this Appendix. The second paragraph on page 141 refers to the Data Set

3 results. The authors should consider whether the data presented in that example adequately support this statement. And in the forth paragraph of page 141, the authors compare their results with other regions and analyses. Given the concerns presented for the uncertainty in these data and the use of mean values, the authors should ensure that the distances being compared between reports are actually comparable distance metrics.

Appendix: Additional specific comments

We recognize that the document is a working draft. There are errors of fact, description, and omission to such an extent that they limit effective scientific assessment of data presentation and analysis. We trust that the TRTs and NOAA Fisheries will achieve a higher standard in the final document. This general assessment is based on the lack of a convincing framework for analyzing available data, the organization of information in the document, and style changes and editing needed to improve the readability of the document. We list some examples below.

For example, consider Figure I-1. The sample numbers in the dendrogram fall into one of six different symbols (black, white, and gray circles, black and white diamonds, and gray squares), yet only four of the symbols are identified in the legend. Sample numbers are reported to "correspond to locations described in Table CHN1", yet there is no such table in the report. Figure I-2 is supposed to be a PCA analysis of the same data for the same populations, as stated in its legend, "Sample numbers correspond to locations described in Figure I-1 and Appendix A. First, Appendix A is a summary of methodology and a glossary of terms; there is no information regarding population identification. Second, there is little correspondence between symbols in the two figures. For example, there are four gray squares in each, but in Figure I-1 they are numbered 1,2,10,11, and in Figure I-2 they are numbered 4,5,10,11. Similarly, in Figure I-1, there are white diamonds numbered 1,2,3,6, yet in Figure I-2, those numbers are presented as black diamonds, along with 7, which was a black circle in Figure I-1. It gets more confusing. Following Table I-1 (p 15), there is a listing of presumably at least some of the populations included in Figures I-1 and I-2, yet the sample numbers only range from 25 (for the Tucannon River) to 47 for MFUMA (p.23), with duplicate numbers from 24 for SRNFS to 31 for SRUMA being used. That confusion makes it impossible for the reader to identify particular populations or their location (no map is provided) throughout this section. As a result, assessing the analytical validity is impossible.

Page 6 of the introduction refers to Appendix A for detailed explanation on the genetic analysis used, but Appendix A does not provide adequate detail. Appendix A states that various parameters were estimated from genetic data, and that the Cavalli-Sforza and Edwards' chord distance was calculated and populations clustered into a dendrogram using the UPGMA algorithm. Further, allelic data was analyzed using principal components analysis.

First, there is no explanation how the UPGMA dendrogram and PCA analysis will be used to arrive at conclusions on whether samples represent major population groups or independent populations. Second, most of the analyses presented in the document do not appear to be performed by (or for) the TRT, but are simply adopted by the TRT from other cited work. For each case, it needs to be made clear which analyses are new (using existing data sets) and which analyses are cited from other sources. Finally, analyses other than UPGMA dendrograms of CSE distance and PCA are present in the document. For example a neighbor-joining tree of pairwise Fst on page 60 for Snake

River steelhead and a dendrogram (unspecified method) of pairwise Nei genetic distance for John Day steelhead on page 95. How are these different kinds of analysis synthesized? Are some given more weight? If so, why?

The discussion of population size on page 8 notes that different methods of estimating the size of a breeding population necessary to reduce genetic risks of small population sizes vary by an order of magnitude. Some discussion of the reasons and implications for such a large variation between methods would be helpful.

More discussion regarding the pros and cons of using environmental characteristics as weak proxies for population structure (p.8) would be helpful.

How is influence of hatchery fish defined (p.10)?

Results of cluster analysis and principal component analysis are presented (e.g. Figures I-1 and I-2 and others in following ESU discussions) without explanation. Some text should be included to describe each of these methods and their properties. What can be safely concluded? What are the limits of interpretation? Also, some text should define terms such as Cavalli Sforza and Edwards' chord distance and Nei genetic distance, as well as explain how dendrograms and PC graphs are interpreted. Statistical results of analyses should be presented, not just graphics. (Maybe these are in appendices). A Figure titled UPGMA dendogram of Lower Columbia and Deschutes River steelhead based on CSE chord distances (p.94), for example, should not be presented with only a publication citation. The need to communicate with diverse audiences should be kept in mind.

A noticeable example of failure to provide enough detail is Figure IV-2 (p.60). A figure this complicated cannot be presented without explanation and discussion.

The document should be more specific in descriptions of populations. E.g. #27, Wenaha River (GRWEN) (p.16), instead of saying this group meets the criteria of an independent population, specify which criteria it meets.

The comment about needing more text explanation of tables and figures applies throughout. For example, Table I-2 may be comprehensible to those who put it together or to those specialists who look at these all the time, but it is not generally communicative, and needs more documentation of statistical methods and additional explanatory text on how to interpret results Tables II-2 and II-3 (p.43), and other similar tables throughout, need explanation and interpretation. The expanded documentation and explanation is necessary for the wider audience, and will even be useful to the authors after some time has passed and memories have faded. This is needed for figures and tables in each ESU discussion.

Appendix A has more detail about methods, but these are still quite condensed and under-defined.

The relevance of pre-European spawning areas as a benchmark should be explained (e.g., p.27, discussion of Hells Canyon Dam). Could spawning areas existing immediately pre-Hells Canyon Dam construction be just as valid as pre-European conditions? The pre-European impact standard is used throughout, so some explanation should be given up front as to why. (Is it required, a

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convenience, or what? What is its relevance to recovery efforts given present land and river uses?)

The sections Monitoring and Evaluation Needs (pp.27, 47, 52, 69, etc.) are helpful inclusions, especially since some thought has gone into prioritizing needed data. Some effort should be put into making these lists as specific as possible, since they may guide the preparation of proposals submitted to the NPCC Fish and Wildlife Program and other funding sources. For example, when the document states that finer scale data collection is needed, it should be specific as to scale. Having the lists will help those preparing proposals and also encourage some consistency throughout the Interior Columbia River Domain. A minor editorial and semantic point: instead of interchangeably using the terms "data" and "information" in these lists, the report should be consistent in using data when that is the need described.

A need for data on hatchery outplantings throughout the basin is identified: are these data available through the Council's APRE effort?

When findings of other research are summarized in tables (e.g. Table II-1), more detail and discussion of these findings should be provided. For example, on p.42 there is a statement Ford et al. (2001) also present analyses of demographic correlation and describe several habitat features. The reader is referred to Table II-1, which is a summary of data analyzed. What are the results of this analysis? What are its implications? What is its relevance? All these should be included in the text.

Maps throughout need to be clearer.

On p.45 the sentence "Mullan (1992) did not believe that..." needs a little more context.

P.48, Table II-6: how should the column "habitat" under within-population diversity be interpreted?

Figure VI-6 (p.100) was blank.

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