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MEMORANDUM

TO:	Bill Templin, Chief Fisheries Scientist Salmon Division of Commercial Fisheries	DATE:	January 8, 2017
FROM:	Chris Habicht, Principal Geneticist Gene Conservation Laboratory	SUBJECT:	Guidelines for MSA reanalysis under new objectives

This memo outlines the criteria and process for providing a reanalysis of stock composition estimates for revised reporting groups after the completion of a genetic mixed stock analysis (MSA) project.

Reporting groups (aka "stocks") are groups of populations in a genetic baseline to which portions of a mixture are allocated with MSA. Reporting group definitions are determined at the beginning of the project and are based on a combination of management and stakeholder needs (project objectives), adequacy of the genetic baseline, genetic identifiability, and expectations of stock composition.

In some situations, stakeholders may request that the department provide stock composition estimates for reporting groups not originally used in the study design. These requests should be directed to the Chief Fisheries Scientist for Salmon for consideration by the department.

The Gene Conservation Laboratory developed guidelines for defining reporting groups over years of analyses and were formalized during the Western Alaska Salmon Stock Identification Project. The same criteria are applicable when determining reporting groups for new objectives. The following criteria and processes are provided for guidance when considering these requests.

Criteria

1. <u>Stakeholder need (including ADF&G)</u>: Examples of new objectives that address additional stakeholder needs are: improving run reconstructions, informing management decisions, evaluating new information.
   - Are new objectives in the best interest of the people of the State of Alaska?
   - Do redefined reporting groups inform new objectives?
2. <u>Representation in genetic baseline</u>: The accuracy and precision of a reporting group's composition estimates are affected by the population samples used to represent the group in the genetic baseline.
   - Do the populations in the baseline adequately represent all populations in the reporting group?

- Are adequate numbers of individuals (≥ 70) available for each population in the baseline to estimate allele frequencies?
- Are adequate numbers of individuals (≥ 400) available in the baseline to represent genetic diversity within a reporting group?

3. <u>Genetic identifiability for mixed stock analysis</u>: The accuracy and precision of a reporting group's composition estimates rely on the ability to distinguish the populations representing the reporting group from populations in other reporting groups in the genetic baseline.
    - Can the revised reporting groups be correctly identified with adequate accuracy ($\geq 90\%$) in baseline evaluation tests?

4. <u>Expected stock contribution to the mixture</u>: Statistical sampling theory demonstrates that contributions from rare and uncommon stocks are often poorly estimated with cost-effective sample sizes (200-400 individuals). Error in estimating these small contributions will detract from accuracy and precision of other reporting group estimates.
    - Is the expected contribution of a reporting group within the fishery harvest adequate ($\geq 5\%$)?
    - Is the coefficient of variation (CV) of the contribution estimate reasonable small ($< 50\%$)?

5. <u>Value of new information</u>: Reanalysis for revised objectives using information from a project completed using a different design is not always straightforward. While sampling and laboratory cost will already be completed, defining new reporting groups, assessing the baseline, summarizing mixture compositions into new reporting groups, and reporting will require availability of staff and time (see Process below).
    - Is the additional information to be produced sufficiently valuable to invest additional resources?

Process

Reporting groups initially used in a study may be revised after the completion of the study to meet new objectives. The method for reanalysis involves the following steps:

1. Evaluation of revised reporting groups necessary to meet new objectives for the criteria above. This step requires:
    - Reorganization of the baseline populations into revised reporting groups,
    - Examination and testing of the baseline, and
    - Evaluation of baseline testing results by fishery experts.
2. Reanalysis of the output files from the original analysis using the revised reporting groups. This involves:
    - Computer analysis to estimate contributions from revised reporting groups, and
    - Quality control of the process.
3. Reporting results of the reanalysis to achieve the new objectives. This involves:
    - Summarizing results from individual fishery strata,
    - Preparation of tables and figures presenting the new results, and
    - Production of a report addendum.