

Review of

“The analysis of population genetic structure in Alaskan harbor seals, *Phoca vitulina*, as a framework for the identification of management stocks”¹

for

**The University of Miami Independent System for Peer Reviews
Center for Independent Experts (CIE)
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By

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¹ O’Corry-Crowe, G. M., K. K. Martien, and B. L. Taylor. 2003. The analysis of population genetic structure in Alaskan harbor seals, *Phoca vitulina*, as a framework for the identification of management stocks. Administrative Report LJ-03-08. Southwest Fisheries Science Center, 8604 La Jolla Shores Drive, La Jolla, CA 92037.

Review of “The analysis of population genetic structure in Alaskan harbor seals, *Phoca vitulina*, as a framework for the identification of management stocks²”

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I. Executive Summary:

The genetic studies conducted by O’Corry-Crowe et al. (2003) represent an important population study of a widely distributed marine mammal based with a relatively large sample size. The totality of the evidence generated by several analytical methods provides persuasive evidence that the previous recognition of three stocks of harbor seals in Alaska state waters is too gross and that there are at least five population stocks in those waters. Exclusion of groups of samples from some important intermediate areas limits conclusions about further subdivision. Additional samples should be collected from those areas, additional genetic markers should be assayed (including nuclear DNA loci), and a more balanced presentation of population structuring analyses should be incorporated into further assessment of the genetic characteristics of groups of harbor seals in Alaska state waters and patterns of gene flow among them. A redrafting of the document should focus on the scientific program that the research laboratory was tasked to perform and eliminate discussions of policy and law which distract and detract from the strengths of the execution of the study and the basic molecular genetic findings. The incorporation of non-genetic data and information is important in guiding interpretations but should be conditioned on their direct relevance and substantive depth.

II. Background:

The management office authority for NOAA Fisheries (delegated authority to implement the Marine Mammal Protection Act [MMPA] 1972 16 U.S.C §1361 et seq.) has up to now considered there to be three stocks of harbor seals in Alaska state waters³. That stratification was argued from regional trends in abundance and gross, quasidisjunct distribution of seal haulout sites. However, NOAA Fisheries also recognized that those presumed “stocks” may have important internal genetic and ecological elements that could justify splitting the three units further. Under the MMPA, certain population stocks may require special management considerations, particularly when the animals in those

² O’Corry-Crowe, G. M., K. K. Martien, and B. L. Taylor. 2003. The analysis of population genetic structure in Alaskan harbor seals, *Phoca vitulina*, as a framework for the identification of management stocks. Administrative Report LJ-03-08. Southwest Fisheries Science Center, 8604 La Jolla Shores Drive, La Jolla, CA 92037.

³ Southeast Alaska stock; Gulf of Alaska stock; Bering Sea stock.

stocks are subjected to mortality incidental to human activities (principally fishing operations). In those cases, the human activities may be regulated to limit incidental mortality to less than a 'potential biological removal level' (PBR), calculated to be demographically tolerable from consideration of several factors (16 U.S.C. §1362(20)(A)-(C)). Such incidental mortality does occur in various areas of coastal Alaska, though it appears to be negligible in all areas regardless of the number of stocks defined and their population sizes. Effective identification of stocks is nonetheless important for establishing and implementing management policies regarding subsistence harvests of harbor seals in some areas. In the latter case, the application of PBR may not be straightforward, may not be appropriate, or may be overruled by other considerations of policy by the management office authority of NOAA Fisheries.

To help inform and resolve these management concerns and issues, the NOAA Fisheries scientific research laboratory in San Diego (Southwest Fisheries Science Center) was directed to conduct molecular genetic studies to evaluate the relatedness of harbor seals among haulout sites throughout the Alaska state waters. The project's strategic scientific objective was to assess gene flow within and among the three stocks of harbor seals now recognized for management purposes by documenting the magnitude and patterns of variability at particular genetic loci. The project's tactical scientific goals were to collect genetic samples from haulout sites throughout Alaska state waters, sequence the DNA from those samples, and assess the relatedness of those sampled seals using several statistical methods to provide some measure of population structuring (inter-group gene flow) among groups of seals that haulout at various sites that are geographically separated from other groups to varying extent.

III. Review

III.A. Genetic samples and data:

III.A.1. Were the methods of selecting, collecting, and handling samples adequate relative to the conclusions drawn?

I think the authors did an exceptional job in attempting to collect a quite large number of genetic samples over a very large geographic area, balanced by logistic and financial realities and constraints. Because of the geographic scope of the study, these samples were necessarily collected opportunistically (and haphazardly in the statistical sense as opposed to randomly) and also involved various methods of collection and tissues collected. These collections included: 1) skin samples collected at haulout sites during dedicated research projects; 2) samples of molted hair recovered from haulout sites; and 3) tissue samples from seals killed by Alaskan natives for subsistence purposes; 4) tissue samples from stranded sick or moribund seals; and 5) tissues from historic scientific collections. Most of the samples evidently came from direct sampling during the dedicated research projects during the past several years and are the most relevant as their collection sites and individual uniqueness can be unequivocally determined. The relevance of the other samples may arguably be weaker as there are reasonable questions

about either their uniqueness (e.g., molted hair from retrieved from haulout sites attributable to unknown seals that may have been sampled by other means), their true affiliations with the collection sites (e.g., stranded or dead seals often occur at sites different from their home sites; the true haulout sites of seals killed by subsistence hunters may not be known unequivocally for various reasons), or the temporal connection of some samples to the primary, large sample (e.g., museum and historic collections may have been from geographic sites where the genetic characteristics of the extant population may differ from the historic population). The report did not identify the contribution of these various categories of samples. If they are minor, then it would be better to not include them in the analyses. If they are more substantial, then this issue might be discussed more, with strong logical and substantive arguments presented for their inclusion. But I think it would still be best to leave them out of the analyses. The argument is already made in the discussion and the conclusions about the need for and benefit of enhanced sampling in some areas, and this issue is really just one element of that argument.

III.A.2. Were limitations of the sampling scheme and data adequately acknowledged and considered?

Notwithstanding my comments above, the authors did acknowledge the limitations of the sampling scheme and the data used in various analyses. The exclusion of data from some of the analyses owing to the authors' construction of a new index of sample size ('adjusted sample size' with 4 as a threshold, though the distinction between that threshold and the inclusion of areas with 6 or 10 is arguably subjective) is a problem. Those excluded samples generally represent groups of haulout sites that are intermediate to other sample sites and may represent part of a continuous transition of gene flow among sites or groups of sites. It is in these areas where intermediate sites were excluded (i.e., South East Alaska; Kenai-Cook Inlet-Kodiak) where the assessment of population structure is most equivocal and where it may be most likely to be contested legally. I think it would be more appropriate to objectively present the analyses of the full data set but qualify any conclusions about an inability to distinguish population structure by parenthetically noting that the large genetic variability versus small effective sample size in these areas may conceal any structuring and suggest that more sampling in these areas may help test this hypothesis.

III.B. Analytical methods.

III.B.1. "Were the laboratory analyses appropriate and applied correctly?"

The authors chose to only present the analyses of mitochondrial DNA loci. They briefly present their argument for this. Though it seems mostly reasonable, I think the more appropriate approach would be to present the results of analyses of as many genetic markers as possible, including nuclear DNA loci. Selectively presenting only the results

of a method of preference, no matter how strongly argued, will likely procedurally weaken the study when it is considered in a legal forum. Otherwise, the extraction and amplification, and sequencing of DNA were performed by traditional and well accepted methods.

III.B.2. “Were the statistical analyses appropriate and applied correctly?”

The analyses of genetic diversity by assessing the number of variable sites and the number of unique haplotypes at particular genetic loci, and the calculation of estimates of haplotype diversity (H) and nucleotide diversity (δ) as measures of genetic variation within geographically stratified populations are traditional, accepted methods, and routinely applied commercial computer analysis programs were used.

The authors highlighted two approaches to estimating genetic differentiation among harbor seals at haulout sites in Alaska state waters. The analyses under both approaches started with the same stratified groups of haulouts, which were established by reference to non-genetic information (e.g., short term foraging movements, geographic distribution). The validity of these units must be conditioned on and qualified by the quantity and quality of the data used to infer distinction. The authors argue for the relevance and strengths of those data, but I think that those arguments are mostly overstated and some are not on point (below). This factor does arguably challenge the strengths of the authors’ conclusions on the extent of subdivision and on a further view that further, substantial division is warranted.

One method used was a traditional hypothesis testing approach. The results indicated that the mixing among the 16 pre-designated units was not random, suggesting that most may be separate subpopulations. In some cases where distance between groups would suggest genetic isolation was not in line with the results based on mitochondrial DNA, the adjusted sample size for one or both sites in the pair-wise comparisons was low (i.e., 5 for Kamishak Bay, not really different from the threshold cutoff to exclude from analyses of 4). But the general pattern reflects support for division clearly into the three recognized stocks and support for redefinition into five stocks similar to the clustering method results. Yet this traditional scientific method was heavily discounted and criticized. The clustering method favored and promoted by the authors is new and its advertised strength of incorporating other information to initially stratify data into small units is materially dependent on the joint and several forces of the elements of that information. Consequently, the favored method is likely to fail at least three of the four prongs of the test for admissibility as evidence in a US Federal legal forum. In that event, the hypothesis testing results should be the evidence available as the strongest for multiple stock distinctions. But the value and indeed availability of those results appear to be substantially harmed by the criticism and apparent rejection of the method. I think it would be more appropriate to simply present and compare the results of all of the approaches and analyses and then make conclusions and interpretations based on the overall weight of the evidence rather than only pursuing, or appearing to pursue, a favored approach.

The other approach was parameter estimation using clustering analysis. Here, the authors discussed several clustering methods but clearly favored one, a recently

developed and promoted method (by two of the authors on this report) for first defining geographic units of animals as a preliminary step in testing for differences among them by cluster analysis. The favored clustering approach (Boundary Rank) is certainly one way to address the harbor seal stock definition question and its merits of using other information to inform it are theoretically important. But the focal presentation of this approach throughout the report consistently appears to advance it as the best method and perhaps the only reasonably acceptable one. This is done even when the other methods have similar results, and the argument is then that such agreements support the Boundary Rank as the most robust. I think that this is dangerous logic. I think it would be more appropriate to present the results of all of the methods and their results as similarly situated alternatives and then to base the conclusions and interpretations on the weight of the evidence emerging from all of them collectively. Those results generally agree in rather persuasively arguing for a minimum of five stocks in Alaska State waters, conditioned on the collection and analysis of additional mitochondrial DNA samples from several locations and on the presentation of data for other genetic markers, particularly for nuclear loci.

A similar issue appeared in the authors' favoring the use of $X^2/\text{degree of freedom}$ as a measure of performance, as it resulted in the best performance of the method. If other measures suggested that the method did not perform well, then there seems to be an argument for perhaps not using the method rather than searching for a measure that would support it. The authors did use the traditional estimate of genetic differentiation (F_{ST}), but they appeared to include it only as an afterthought. It would seem more appropriate to simply report the results of both index estimators and compare the results. If both support the same conclusion, then the argument for distinguishing the groups is more convincing. The report, on a number of occasions, highlights the same issue, that the authors are driving the methods that they favor rather than consulting a number of methods to investigate consensus, which would provide the most convincing arguments about the strengths of the results.

The exclusion of data for some haulout sites and groups of sites after the sample sizes of those sites were reduced to an arguably subjective and arbitrary threshold presents a few procedural and substantive issues and problems. This is a rather novel way to reclassify the acceptability of data. Though it may find some justifiable support in scientific discussions and fora, it may present admissibility barriers when put at issue in legal fora. And substantively, many of those sites that were excluded may be important links between and among other haulout sites or groups of haulout sites. The consequences of leaving them out of analyses may indeed have important influences on the residual patterns and conclusions. A more appropriate approach would be to leave them in all of the analyses. In any event, I think the strongest supportable argument that the authors have to present is that there does not appear to be population structuring in some of these areas (i.e., Southeast Alaska, Kenai-Cook Inlet-Kodiak).

The estimates of dispersal rates are highly dependent on the value used for generation time. The value used (8 yrs) was a theoretical, hypothetical average. Life history theory and empirical studies of a variety of mammals have indicated that generation time varies or co-varies with age structure, population size, and population growth rates. As the population status and growth trends and rates have varied substantially among the prior and proposed geographic groupings of harbor seals in

Alaska, actual generations likely have also differed substantially. The use of different estimates of generation time in the model used to estimate dispersal rates would result in substantially different computed dispersal rates. Indeed, they would be much higher in several of those areas where differences in population structure have been argued from the calculation of low dispersal rates. This would appear to provide less support for some of the interpretations of the output of the Boundary Rank exercises.

III.B.3. “Were the novel methods used in the study developed and tested in a scientifically sound manner?”

The two most apparent novel methods used in the study were the Boundary Rank clustering method and the re-stratification of data used in the Boundary Rank analyses by constructing a screening method for reducing (‘adjusting’) the sample size for various sites and then establishing a threshold value to justify excluding some sites from the analyses. The report indicated that “extensive simulation-based performance testing” has been done (citing an unpublished manuscript) on the Boundary Rank clustering approach and that “the method performs well in a management context under a wide range of conditions”. This is the only apparent support for testing the method. The statement alone is not convincing and the idea that a single paper may establish the method without qualification as a touchstone as suggested seems to be too hopeful.

The argument for excluding data from analyses was derived from another novel method that reduces the sample size and then considers those below a particular threshold to be unusable or believed to have the potential to introduce bias. The genetic basis for this argument is scientifically reasonable, although there will probably be differences of opinion and disagreements in scientific fora about the method itself and about the threshold value that was adopted for excluding data. Whether areas with adjusted sample sizes of 5 to 10 versus 4 or fewer should be left out or used cautiously is, I think, a standing question and does weaken the interpretations of stock definitions particularly in the two areas which are controversial (Southeast Alaska, and the Kodiak-Kenai-Cook Inlet area). The excluded groups were also mostly in areas that are intermediate between groups of seals that the authors argue should be distinguished as separate stocks. To the extent that these intermediate areas are important links for quasi-continuous gene flow in those areas, the argument for distinguishing stocks is vulnerable because of the exclusions. It seems more appropriate to depend on the persuasive argument for the five stocks and then qualify those conclusions with the recommendation for additional sampling in those couple of areas where either the sample sizes may greatly affect any interpretation of inter-group relatedness or where apparent patterns cannot be adequately probed. In any U.S. federal legal fora that address this issue, the use of the method may, arguably, not satisfy extant threshold evidentiary admissibility standards.

III.C. Discussion and interpretation of other studies.

III.C.1. “Was the interpretation of other, non-genetic evidence relevant to harbor seal population structure logical and appropriate?”

The authors thoroughly consulted the scientific literature for natural and life history and behavioral information on harbor seals that may be relevant to understanding the interactions among various aggregations of harbor seals in Alaska state waters. That information was used to guide the authors in attributing seals at various haulouts to particular geographically-based groups which were considered to be relatively independent sources to seed the clustering analyses. Consequently, the construction of those initial units is highly dependent on the quality and quantity of the background information and data and the assumptions that the authors generated from their evaluations of it. The authors do acknowledge the constraints and limitations of those data when they first consider it and construct arguments for its logical and substantive relevance. Their interpretations of the outputs of the modeling exercises and their conclusions should, I think, better reflect the limitations of the supporting data and assumptions. Some key evidence used by the authors were data and observations from various sources on short term movements, primarily seasonal foraging movements, which was advanced as proxy for patterns of dispersal (i.e., natal or breeding dispersal indicating emigration/immigration and gene flow). Though those seasonal movements may be suggestive evidence for gene flow or constraints on gene flow, they are too circumstantial and limited to provide the basis for even persuasive arguments in support of views about regional patterns of gene flow or dispersal. I think this limitation needs to be acknowledged as a strong qualifier on the authors’ argument or belief that there may be more than five stocks based on the data presented in the report.

Some new thinking about harbor seals may enlighten the incorporation and interpretation of these data. For example, harbor seal haulout sites cover a vast coastal region in the North Pacific Ocean. These are rather discrete locations separated from one another by varying distances. Thus, on regional spatial scales, the distributions of these haulout sites are more disjunctive than continuous. In this sense, harbor seals distribution may be more appropriately considered to be structured as a metapopulation or a series of metapopulations. Under a metapopulation model, the rigorous splitting of groups of haulout sites into ‘stocks’ may be far less important and relevant than considerations of the dynamics of colonization and ‘extinction’ of various haulout sites. Indeed, the population distributions of most species of pinnipeds arguably suggest that they are structured as metapopulations. And the patterns of recolonization and population increase of many species following local extermination of populations or near extinction of species indicate that they are resilient to local impact, robust in recolonization, and that traditional approaches to species conservation involving management of stocks may not be appropriate or effective. Metapopulation thinking may be an important alternative to stock splitting using genetic approaches alone. In that event, compelling arguments may need to be developed to motivate Congress to modify the extant legal regime and framework for conserving and managing marine mammals in waters under U.S. jurisdiction.

III.D. Conclusions.

III.D.1. “Were the conclusions sound and derived logically from the results? Specifically, are the twelve population units described in the report consistent with the definition of stocks, as provided in the Marine Mammal Protection Act (MMPA) and as implemented by NMFS (see reference 4, Wade and Angliss, 1997)?”

I think that the data analysis is persuasive for concluding, from the totality of the methods used, that there are five⁴ population units in Alaska state waters that could be considered stocks under the MMPA. The evidence that the authors use to argue for more than five populations is suggestive but I think it must be conditioned on the need for additional samples from directed research efforts to explore and test that hypothesis. Moreover, the authors reflect that “it is very difficult to detect population structure [in harbor seals] using genetics” (O’Corry-Crowe et al. 2003:22) which should highlight the need to qualify with caution any suggestions or conclusions that go beyond the five proposed stocks, pending additional sample collection and analysis. The correlative issue of whether any additional designation of population units would be consistent with the definition of stocks must consider the statutory definition of stock in the MMPA, the legislative history of the MMPA, and any subsequent juridical interpretations of the definition and application of the term. That issue is clearly not within the domain of the scientific offices and laboratories of NOAA Fisheries and should not, I think, be discussed in a document of the results of a tasked study on population genetics of harbor seals. Certainly, the MMPA and its implementation are relevant to the tasked study, but I think it is appropriate and necessary to only briefly introduce that relevance in the report’s preamble. Otherwise it will appear that research offices and laboratories that are not responsible for policy are both pursuing the establishment of policy in creating extra-legal definitions of stocks and determining what units are appropriate to fit within those extra-legal definitions. The text and legislative history of the MMPA provides a simple definition of stock. There is no evidence of its legal meaning distinguishing or implying “both a biological and a management meaning” nor that stock or population stock “carries the same double meaning: (1) groups that are delineated by a very low rate of genetic exchange, or (2) groups of animals that are essentially demographically separate and may experience differential risk and therefore need to be managed separately”. Although it may be logical and reasonable to discuss this issue in the scientific literature, those discussions do not make or change law, and they have no substantive weight for interpretations of the law. The MMPA also makes no mention of “demographically separate” or an “evolutionary significant unit”, “management unit”, etc. These kinds of discussions of law and policy in the O’Correy-Crowe et al. document are unnecessary, sometimes confused and inaccurate, and distract and detract from the strengths and key findings of the scientific research that the research laboratory was tasked to conduct. I strongly urge that the redrafting of the document eliminate the treatments about law and

⁴ Southeast Alaska, Copper River Delta-Prince William Sound, Kenai-Kodiak-Cook Inlet, Bristol Bay, Pribilof Islands. Whether harbor seals in the Aleutian Islands may be another population unit is equivocal because genetic data from that area were not included in any analyses owing to sample size considerations.

policy and include a simple few sentences in the preamble to the study about why it was conducted...i.e., to examine the potential relatedness and population structure of harbor seals in Alaska using molecular genetic techniques.

IV “Address the primary conclusions as stated in the ‘Executive Summary’ of O’Corry-Crowe et al. (2003) [Itemized below, IV.A. through IV.D.]. Specifically, state whether each of the following conclusions is scientifically sound, and provide justifications for each of their assessments.

IV.A. “These findings indicate that current stocks of harbor seals in Alaska are too broadly defined to meet the management objectives of the MMPA of maintaining population stocks as functioning elements of their ecosystem.”

There are two elements to this conclusion. The first is a scientific element, and I think that the statement in that element is correct and supported by the totality of the analyses. The findings of O’Corry-Crowe et al. (2003) do, in my view, indicate that the three currently recognized stocks of harbor seals in Alaska are too broadly defined. The data and analyses are persuasive that there are five stocks, notwithstanding the residual groups of harbor seals in the Aleutian Islands, which were not included in the analyses.

The second element is a policy issue and within the domain of the policy offices of NOAA Fisheries and the Department of Commerce to address. Moreover, it also does not accurately reflect the statutory language, intent, and objective of the MMPA. The preambular language in the MMPA first highlights the target of the statute which were/are “*certain species and population stocks* (my emphasis) of marine mammals [that] are or may be in danger of extinction or depletion as a result of man’s activities”. Continuing, Congress identified a “major objective” of implementation of the statute: “*such species and population stocks* (my emphasis) should⁵ not be permitted to diminish beyond the point at which they cease to be a significant functional element in the ecosystem of which they are a part “(16 USC § 1361(2)(2). Section 2(2) unambiguously refers to the “certain species and population stocks of marine mammals” contemplated in Section 2(1), rather than every species and every population stock of marine mammal regarding this objective. Further, Congress very clearly articulated that the “primary” management objective “should be to maintain the health and stability of the marine ecosystem”, that the goal of their management “should” be “to obtain an optimum sustainable population keeping in mind the carrying capacity of the habitat”, and that this goal should be conditioned on the objective of maintaining a healthy marine ecosystem (16 USC § 1361(2)(6).

I think that the first element is scientifically sound, relative to five stocks, but that the second element is not appropriate as a part of the conclusion.

⁵ Important here and throughout the preamble to the MMPA is the intentional use of aspirational language (“should”), rather than mandatory language (“shall”), the result of difficult compromises in crafting the law which are clearly articulated in the record of legislative history and contemplation for flexibility in implementation of the statute owing to various policy concerns and considerations.

IV.B. “These findings also provide a framework for the identification of more meaningful management stocks and highlight the need for a re-appraisal of other information of relevance to stock structure including the interpretation of information on distribution, movement patterns, trends in abundance and foraging ecology as well as the incorporation of traditional ecological knowledge.”

This conclusion has two elements. The first is that the authors’ findings provide a framework for the identification of “more meaningful management stocks”. I don’t think that the data and analyses support this conclusion. The objective of the tasked research was to assess relatedness of harbor seals at various haulouts or groups of haulouts using molecular genetic techniques as an aid to policy makers in distinguishing among groups of harbor seals for management purposes. The authors favored and promoted one newly developed clustering method for evaluating the relatedness of groups of seals derived from one neutral genetic marker as a proxy for assessing patterns of gene flow. That framework is certainly one of several that might be considered by policy makers and managers, but I don’t think that the findings support the implicit conclusion that it should be the framework used. The idea that such a framework would result in identifying ‘management stocks’ that would be “more meaningful” than alternative frameworks is also not supported by the data and the analyses.

The second element is that the findings highlight the need to reconsider nongenetic information and data. I think that the variability and uncertainty that the authors present and discuss regarding the genetic data do support this conclusion.

IV.C. “The genetic study is still limited by sample coverage. Substantial gaps exist in areas of high conservation concern (non-circled areas in Figure ES-3 of O’Corry-Crowe et al. (2003), including the Aleutian Islands, the Alaska Peninsula, the northeastern Gulf of Alaska and parts of Southeast Alaska and the Kodiak Archipelago. Active collaboration with Alaska Native subsistence hunters and directed sampling is necessary if these important areas are to be sampled.”

There are several elements and issues in this conclusion. The first element is that the study of the patterns of genetic variability in harbor seals in Alaska state waters was affected by sampling logistics and sample size. Though the authors did a superb job in collecting a large number of samples over a very large geographic area, there were important limitations of sample size in some areas. Those areas were in the Aleutian Islands, the Alaska Peninsula, certain areas of Southeast Alaska, and certain areas of the Kodiak Island-Kenai Peninsula-Cook Inlet region. The conclusion is an important one and presents a strong legitimate argument for additional sampling in those areas to help further test hypotheses about the population integrity of groups of harbor seals in those areas. The authors’ conclusion that these gaps in sample coverage are in areas of “high conservation concern” is puzzling, and I don’t think that it is supported by the study. It is

not clear why there is or should be a high concern for conservation of harbor seals in those areas (implying that there are substantial threats to population vitality now), but that would seem to be a matter for policy makers and managers to address. The element of needs for collaboration with Alaska subsistence hunters is a relevant recommendation. But the logistics of those collaborative collections should be conditioned on vigilance and hard scrutiny about where those samples might specifically have been collected (exact location is an important issue for the questions being addressed). The conclusion that more directed sampling is needed in certain areas is a restatement but highlights an important need and recommendation.

IV.D. “Although further sampling is needed to refine stock boundaries, the conclusion that there are multiple small units that need to be managed as separate stocks is not likely to change.”

I think this conclusion is neither well supported logically nor necessary. The point about the need for additional sampling has already been said and emphasized. The authors’ findings argue persuasively that there are more than three stocks and at least five has also been argued. This statement seems to weaken the argument for more sampling by implying that the authors’ may already know the outcome and that additional data won’t change their interpretations. This is counter to the logic that has been developed to this point. I think it should be deleted.

V. Appendices:

Appendix V.1. Bibliography of Materials

Appendix V.1.A. O’Corry-Crowe, G. M., K. K. Martien, and B. L. Taylor. 2003. The analysis of population genetic structure in Alaskan harbor seals, *Phoca vitulina*, as a framework for the identification of management stocks. Administrative Report LJ-03-08. Southwest Fisheries Science Center, 8604 La Jolla Shores Drive, La Jolla, CA, 92037.

Appendix V.1.B. The Marine Mammal Protection Act (MMPA) of 1972. 13. U.S.C. 1361 *et seq.*

Appendix V.1.C. Taylor, B.L. 1997. Defining populations to meet management objectives for marine mammals. pp. 49-65 in *Molecular Genetics of Marine Mammals* (A.E. Dizon, S.J. Chivers, and W.F. Perrin, eds.) Special Publication 3. Society of Marine Mammalogy, Lawrence, Kansas.

Appendix V.1.D. Wade, P.R. and R. A. Angliss. 1997 Guidelines for identifying population stocks: Report of the GAMMS Workshop. April 3-5, Seattle, Washington. NOAA Technical Memorandum NMFS-OPR-12. National Marine Fisheries Service, Office of Protected Resources, Silver Spring, MD. 69 pp.)

Appendix V.1.E. Anonymous. 1999. Agreement between the Alaska Native Harbor Seal Commission and the National Marine Fisheries Service, for conservation and management of harbor seals. 12 pp.

Appendix V.1.F. Westlake, R. L., and G. M. O’Corry-Crowe. 2002. Macrogeographic structure and patterns of genetic diversity in harbor seals (*Phoca vitulina*) from Alaska to Japan. *Journal of Mammalogy* 83(4): 1111-1126.

Appendix V.1.G. National Marine Fisheries Service, National Oceanic and Atmospheric Administration. Notice of Information, request for comments. 67 F.R. (165) 54792-54794.

Appendix V.1.H. Martien, K. K., and B. L. Taylor. In Press. Limitations of hypothesis testing in defining management units for continuously distributed species. *Journal of Cetacean Research and Management*.

Appendix V.1.I. Taylor, B. L. 2003. Determining Units to Conserve. Unpublished manuscript.

Appendix V.1.J. Martien, K. K., A. B. Sellas, P. E. Rosel, B. L. Taylor, and R. S. Wells. In Review. Defining management units in Gulf of Mexico bottlenose dolphins in the absence of long-term observational data. *Journal of Cetacean Research and Management*.

Appendix V.1.K. Small R. J., L. F. Lowry, J. M. Ver Hoff, K. J. Frost, R. A. DeLong, and M. J. Rehberg. In Prep. Movements of satellite tagged harbor seal pups in Prince William Sound and the Gulf of Alaska.

Appendix V.1.L. Boveng, P. L., J. L. Bengtson, D. E. Withrow, J. C Cesarone, M. A. Simpkins, K. J. Frost, and J. J. Burns. 2003. The abundance of harbor seals in the Gulf of Alaska. *Marine Mammal Science*. 19: 111-127.

Appendix V.2. Statement of Work; Consulting Agreement between the University of Miami (CIE) and Dr. Brent S. Stewart

Background

In the 1995 Alaska Marine Mammal Stock Assessment Reports, the National Marine Fisheries Service (NMFS) defined three stocks of harbor seal in Alaska, based primarily on broad-scale geographic differences in trends in abundance. NMFS, however, recognized that considerable uncertainty about Alaskan harbor seal stock structure remained and in the fall of 1994 initiated genetic studies of harbor seal stock structure in Alaska. The report resulting from these studies, “The Analysis of Population Genetic Structure in Alaskan Harbor Seals, *Phoca vitulina*, as a Framework for the Identification of Management Stocks,” is the subject of this review.

The format of this review will include an interactive panel to ensure a thorough presentation of the science as well as the management context. Further, the best way to obtain review and scientific recommendations from the panel is to establish a process that allows reviewers with different expertise both to interact with one another and to interact with the scientists responsible for the research being reviewed. These interactive presentations and discussions may require up to two full days of the panel’s time. A third day should be planned for the review panel to provide feedback to the authors and to begin to draft the review. Although this review is for scientific research, the motivation for the research was to provide guidance for resource management. The management context is summarized in the report to be reviewed.

Reviewer Responsibilities

Expertise needed to review this analysis will include the following expertise: (1) knowledge of harbor seal biology, especially expertise in behavior and movements; (2) knowledge of population genetics, including statistical analysis of genetic data to detect/delineate population structure; (3) knowledge of conservation genetics including the different uses of mitochondrial and nuclear DNA in a conservation context; and (4) general knowledge of marine-mammal biology, bearing on population structure including basic population dynamics and an understanding of metapopulation dynamics.

Documents supplied to the consultant shall consist of draft manuscripts and a number of background papers (relevant publications and reports). The consultant shall become familiar with the ten references (see Appendix I), focusing on references 1, 3, and 10. Reference 10 provides the details needed to address the novel method referred to in Task 3B, described below. The consultant’s duties shall not exceed a maximum total of three weeks, including one week to read all relevant documents, three days to attend a meeting with scientists at the NMFS La Jolla Laboratory, in San Diego, California, and several days to produce individual written reports comprised of the consultant’s comments and

recommendations. It is expected that the consultant's report shall reflect that his/her area(s) of expertise; therefore, no consensus opinion (or report) will be required.

Specific Reviewer Tasks and Schedule

1. Read and become familiar with the relevant documents provided in advance of the panel meeting.

2. Discuss relevant documents with scientists at the NMFS La Jolla Laboratory, in San Diego, CA, for three days, March 16-18, 2004.

3. Specifically address the following points (at a minimum):

A) Genetic samples and data:

Were the methods of selecting, collecting, and handling samples adequate relative to the conclusions drawn?

Were limitations of the sampling scheme and data adequately acknowledged and considered?

B) Analytical methods:

Were the laboratory analyses appropriate and applied correctly?

Were the statistical analyses appropriate and applied correctly?

Were the novel methods used in the study developed and tested in a scientifically sound manner?

C) Discussion and interpretation of other studies:

Was the interpretation of other, non-genetic evidence relevant to harbor seal population structure logical and appropriate?

D) Conclusions:

Were the conclusions sound and derived logically from the results? Specifically, are the twelve population units described in the report consistent with the definition of stocks, as provided in the Marine Mammal Protection Act (MMPA) and as implemented by NMFS (see reference 4, Wade and Angliss, 1997)?

4. Address the primary conclusions as stated in the executive summary of reference 1. Specifically, state whether each of the following conclusions is scientifically sound, and provide justifications for each of their assessments.

A) These findings indicate that current stocks of harbor seals in Alaska are too broadly defined to meet the management objectives of the MMPA of maintaining population stocks as functioning elements of their ecosystem.

B) These findings also provide a framework for the identification of more meaningful management stocks and highlight the need for a re-appraisal of other information of relevance to stock structure including the interpretation of information on distribution,

movement patterns, trends in abundance and foraging ecology as well as the incorporation of traditional ecological knowledge.

C) The genetic study is still limited by sample coverage. Substantial gaps exist in areas of high conservation concern (see the non-circled areas in Figure ES-3), including the Aleutian Islands, the Alaska Peninsula, the northeastern Gulf of Alaska and parts of Southeast Alaska and the Kodiak Archipelago. Active collaboration with Alaska Native subsistence hunters and directed sampling is necessary if these important areas are to be sampled.

D) Although further sampling is needed to refine stock boundaries, the conclusion that there are multiple small units that need to be managed as separate stocks is not likely to change.

5. No later than April 1, 2004, submit a written report of findings, analysis, and conclusions (see Annex 1). The report should be addressed to the University of Miami Independent System for Peer Reviews, and sent to David Die, UM/RSMAS, 4600 via email to ddie@rsmas.miami.edu, and to Mr. Manoj Shivilani via email to mshivilani@rsmas.miami.edu.

ANNEX I: REPORT GENERATION AND PROCEDURAL ITEMS

1. The report should be prefaced with an executive summary of comments and/or recommendations.
2. The main body of the report should consist of a background, description of review activities, summary of comments, and conclusions/recommendations.
3. The report should also include as separate appendices the bibliography of materials provided by the Center for Independent Experts and a copy of the statement of work.
4. Individuals shall be provided with an electronic version of a bibliography of background materials sent to all reviewers. Other material provided directly by the Center must be added to the bibliography in the appendix of the final report.

Please refer to the following website for additional information on report generation:

<http://www.rsmas.miami.edu/groups/cie>