Response to *The University of Miami Independent System for Peer Review
Review of Alaskan Harbor Seal Stock Assessment by* **Brent Stewart**

by Greg O'Corry Crowe, Karen Martien & Barbara L. Taylor
Southwest Fisheries Science Center

Introduction

Dr. Brent Stewart's review for the Center for Independent Expertise (CIE) contains helpful comments for SWFSC scientists to use in writing the results of our study on population structure of harbor seals in Alaska for journal publication. Here we respond not to positive points but rather to points that require clarification or, when we disagree, a rebuttal. Dr. Stewart also gives legal advice and comments to which we do not respond as scientists, but will consider as background for future analyses and publications. We separate our responses into major and minor points with numbering of issues corresponding to numbering in his review.

Major points

Four major points are made: 1) although more than three stocks are justified, the current data justify five stocks instead of the 12 suggested by the Administrative Report, 2) exclusion of intermediate sampling sites limits further conclusions on subdivision, 3) discussions of policy and law should be greatly reduced, and 4) the limitations of non-genetic data should be amplified. These themes ran throughout the review, so rather than referring to numbered sections in the review, we will treat them here by the above numbers.

1. Current data justify 5 stocks.

Dr. Stewart's position:
"I think that the data analysis is persuasive for concluding, from the totality of the methods used, that there are five population units in Alaska state waters that could be considered stocks under the MMPA." These five stocks are: Southeast Alaska, Copper River Delta-Prince William Sound, Kenai-Kodiak-Cook Inlet, Bristol Bay, and the Pribilof Islands. He points out under a paragraph on hypothesis testing (III.B.2.) that "the general pattern reflects support for division clearly into three recognized stocks and support for redefinition into five stocks similar to the clustering method results." Near the end of this section, he states "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).

Rebuttal:

Dr. Stewart provides no criterion on which to base his conclusion for these five stocks. In fact, some of the strongest evidence for stock structure is within his "Southeast Alaska" stock and his "Kenai-Cook Inlet-Kodiak" stock. The full table of pairwise

comparisons is presented in the Admin. Rpt. Table 4. Here we excerpt comparisons within Southeast Alaska (Table 1) and Kenai-Cook Inlet-Kodiak (Table 2). Note that in Table 1 only a single pairwise comparison (Ketchikan to Frederick Sound) exceeds the often used significance criterion of alpha = 0.05. This pair was also shown to be consistent with about 4 dispersers per year, which translates to an annual dispersal rate of 0.0003 seals per year. We suggested that this would meet nearly anyone's definition of a demographically trivial rate. Note that the Vixen-Sitka unit strongly differs from all other units, which is consistent with this unit having a different trend in abundance from the trend route that includes Ketchikan. Grand also differs from all other units. It is unclear what criterion Dr. Stewart would use on these data to suggest "that there does not appear to be population structuring."

Furthermore, these units do not cluster together early in any of the clustering methods. For example, Vixen-Sitka remains its own unit until very late in the clustering process. In the two geographically unconstrained clustering analyses, this Southeast stock is not nested together: Grand joins with the Prince William Sound grouping and then to Kodiak before it this larger cluster joins with Ketchikan-Frederick Sound (Figure 8, Admin. Rpt.). Similarly, the Neighbor-joining tree (Figure 9, Admin. Rpt.) has Vixen-Sitka join the Prince William Sound grouping before that larger cluster then joins Glacier Bay-Kamishak Bay and that larger cluster finally joins Grand-Ketchikan-Frederick Sound.

These unlikely pairings of strata in the unconstrained cluster analyses, like Glacier Bay and Kamishak Bay, are one reason why we found the available methods to be less than optimal for the questions we were addressing. These methods may be more reliable when sampling is high for all strata. However, by allowing all pairwise comparisons to be made, chances are enhanced of linking two biologically untenable sites simply because sample size in one was limited. This is clearly shown for the case of Kamishak Bay, which groups with Glacier Bay in both of the unconstrained analyses. Given all we know about harbor seal movements from tagging studies, it is not biologically plausible that there would be a direct link between these widely geographically separated sites and not to any intervening sites. From a biological perspective, this is a clear mistake made by these analyses that is avoided in Boundary Rank. We are disappointed that we took such care about analyzing these data that we created a new method to avoid clear biological mistakes resulting from available methods and were then castigated for promoting our method.

Table 1. P-values for permutation χ^2 tests within Southeast Alaska.

	Grand (34)	Frederick Sd (44)	Vixen-Sitka (50)
Ketchikan (42)	0.029	0.063	0.000
Grand (34)		0.003	0.001
Frederick Sd (44)			0.002

Similar arguments can be made for the units in his "Kenai-Cook Inlet-Kodiak" stock (Table 2). South Kodiak is one of the few units that differs by < 0.05 from **all** other

units (including those with quite poor sampling like Kamishak Bay). Within the Kodiak archipelago the question we struggled with was not whether there is more than one demographically independent unit but where the boundaries might lie. South Kodiak is clearly very different from west Kodiak ($p = 0.00$) but sampling constraints led to equivocal results in boundary placement. We are now processing further samples from this area that we hope will clarify the boundary issue, but we do not expect those additional samples from east and north Kodiak to erase the difference between south and west Kodiak.

This example also shows why scientists struggle using hypothesis testing to define stocks. Although the testing of hypotheses has a long statistical history, there still exists no validated process for when or how one uses p-values to cluster strata. For example, Kamishak doesn't differ from East Kenai (assuming a critical alpha = 0.05) and Kamishak doesn't differ from West Kodiak, but East Kenai does differ from West Kodiak. This type of logical inconsistency is common in pairwise p-value tables. There are no sets of decision rules to guide a geneticist through how one might cluster based on a table of pairwise comparisons of p-values. Furthermore, interpreting the results of hypothesis tests is often difficult. Again consider Kamishak Bay. Of the 20 samples, 16 have unique haplotypes and essentially contribute nothing to statistical frequency comparisons (see Appendix 3 in the Admin. Rpt. and discussion of the issue in Minor Points III.A.2.). This unit was the poorest sampled of the strata that we allowed in the analysis, so we know that any comparison will have a high chance of having low statistical power. Another way of stating this is that if there were differences between Kamishak Bay and other strata our chances of detecting such a difference given the small sample size would be very low. Thus, it is unclear whether one should make the decision that the *p*-value of 0.111 between Kamishak Bay and East Kenai should be interpreted as indicating that these two strata came from a single stock.

We put a great deal of thought into how and whether one could base stock definition of a continuously distributed species solely on hypothesis testing. We provided reviewers with a published paper on that subject (Martien & Taylor 2004) that showed that hypothesis testing usually resulted in defining too few stocks. However, in this analysis, we avoided the pitfall common to most population structure studies of starting with large initial strata. Thus, we corrected for the largest likely problem in using hypothesis testing to these ends and therefore feel that Table 1 does provide very useful insights to population structure. For certain strata, such as the Pribilof Islands and South Kodiak, both of which differed from all other initial strata, the way forward is clear: the strata should be treated as stocks. For other strata, such as east Prince William Sound, it is clear that the strata is not demographically independent of neighboring strata and that some clustering is needed. And for still other strata, such as Kamishak Bay, the p-values indicate that genetic patterns are inconsistent and that more sampling is required before structure is understood with confidence.

Table 2. P-values for permutation chi-square tests within Kenai-Cook Inlet-Kodiak.

	Kamishak (20)	West Kodiak (37)	South Kodiak (51)
East Kenai (47)	0.111	0.010	0.018
Kamishak (20)		0.085	0.030
West Kodiak (37)			0.000

In conclusion, we could find no quantitative basis for Dr. Stewart's suggested 5 stocks. Even if we limited our conclusions to the standardly used alpha = 0.05 criterion, the data suggest 9 stocks and this is almost certain to be biased too low because of known low statistical power. Indeed the additional 3 stocks that meet alpha = 0.10 all show dispersal rates of less than 0.002 individuals/year. We would have preferred, if alternate numbers of stocks were suggested by Dr. Stewart, to be given specific criterion on which those stocks were defined, such as a different threshold for percent dispersing/year.

2. Exclusion of groups of samples from some important intermediate areas limits conclusions about further subdivision.

" 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)…"

The decision to exclude some areas from the analysis of population differentiation was taken to limit the probability of conducting misleading hypothesis tests and clustering analyses due to inadequate sample size in these areas. Thus, rather than limiting our ability to make inferences about further structure, the exclusion of poorly sampled areas prevented erroneous conclusions about population structure.

As stated in Conclusion 4 of the Report, we recognize that more samples should be collected from a number of areas, and we are currently working closely with the Alaska Native community and all relevant agencies to improve sample coverage.

With regard to Dr Stewart's recommendation that 'additional genetic markers should be assayed (including nuclear DNA loci)', no rationale is given as to the necessity of such work in furthering the study's objective of providing a scientific framework for the reappraisal of management stocks of harbor seals. Although we agree that additional analysis of bi-parentally inherited, nuclear DNA markers, such as microsatellites, could strengthen our understanding of population structure in Alaskan harbor seals, we fundamentally disagree that inclusion of nuclear DNA is a necessary component to identifying stock structure and note a confusion between demographic isolation and reproductive isolation. We went to some length in the Administrative Report to pull language from agency guidelines on the definition of "stock" to avoid confusion on this issue. The salient sentences are "For the purposes of management under the MMPA, a stock is recognized as being a management unit that identifies a demographically isolated biological population." And "Demographic isolation means that the population dynamics of the affected group is more a consequence of births and deaths within the group

(internal dynamics) rather than immigration or emigration (external dynamics). Thus, the exchange of individuals between population stocks is not great enough to prevent the depletion of one of the populations as a result of increased mortality or lower birth rates." And finally, "*Interbreed when mature* is acknowledged to include cases in which either: i) mating occurs primarily among members of the same demographically isolated group; or ii) the group migrates seasonally to a breeding ground where its members interbreed with members of the same group and with members of other demographically distinct groups that have migrated to the same breeding ground from other feeding areas (e.g., North Atlantic and central North Pacific humpback whales)." These regulatory definitions allow for stocks to be demographically isolated while not necessarily being reproductively isolated, as is the case for humpback whales. In such a case, the demographically isolated units would be identifiable through their mtDNA but not through nuclear DNA (a more detailed explanation follows in the next paragraph). Using these definitions, a positive finding of structure using mtDNA can never be negated by negative findings using nuclear DNA. In the cases where populations are both demographically and reproductively isolated, nuclear DNA would strengthen results from mtDNA. Because limited tagging data indicate that adult male harbor seals appear not to disperse more frequently than females, it may be worthwhile to pursue nuclear DNA analyses, and we have begun such a study (see B below). However, we emphasize that this is not *necessary* given positive findings for population structure using mtDNA.

Many genetic markers have found application in the analysis of population structure and dispersal patterns in wildlife species, including blood proteins, enzymes, coding and non-coding segments of DNA, and nuclear and cytoplasmic genomes. The analysis of variation within mtDNA has special application to the resolution of demographic relationships among animal groupings, and has been widely used in the identification of units of conservation and management (Moritz, 1994; Avise, 1995). As the limiting sex, females define the reproductive potential of a population. Female dispersal, and not male dispersal, therefore defines the demographic relationships among groups of animals. Because of its strict maternal mode of inheritance, patterns of variation within mtDNA reflect the dispersive behavior of females over time, and thus the demographic relationships among groupings. By contrast, patterns of variation within bi-parentally inherited nuclear markers, including microsatellites, are influenced by both male and female patterns of dispersal. In many mammalian species, dispersal is biased towards males (Greenwood, 1980) such that differentiation may be minimal and often undetectable in nuclear markers even when females are highly philopatric. Considering the added effects of a much slower rate of genetic drift in nuclear markers due to a much larger effective population sizes (N_e), it is expected that differentiation will be much lower, and thus harder to detect in nuclear markers than in mtDNA in most mammal species. This has proven to be the case in a number of species where male-biased dispersal was documented independently (e.g., macaques, Melnick and Hoelzer, 1992).

The particular utility of mtDNA in the analysis of stock structure at the demographic level was the consensus opinion at an international workshop on Molecular Genetics of Marine Mammals (Dizon et al., 1997), and mtDNA has become the marker of choice in the identification of marine mammal stocks under the MMPA.

3. A revised Administrative Report should eliminate discussions of policy and law

Dr. Stewart's position:
"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 findings." He defines "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."

Clarification & Rebuttal:

The Administrative Report was written for several reasons, in order of priority: 1) the need for full transparent documentation of the study for all stakeholders, 2) to fulfill the need for a comprehensive document for the purposes of an outside independent review, and 3) to serve as a timely interim document that could be used in the management process in the anticipated several years before a scientific publication would be expected in a journal. Scientific journals are written for scientists and limit the amount of detail that can be included. The management of harbor seals in Alaska is of interest to seal hunters, the Alaska Harbor Seal Commission, various Non-Governmental Organizations and the public. Because the definition of stocks has the potential to affect these groups, we produced an Administrative Report that included as much of the background material (like the definition of stocks in the PBR Guidelines) in one document as possible. We feel that this makes our logic transparent and that the various management bodies can then decide how to use the information and interpretation provided.

We do not intend to revise this Administrative Report. We will follow some of the excellent suggestions made by reviewers by providing supplementary analyses made available on the web. Web links will be provided from the Administrative Report to these analyses. We do, however, fully intend to submit a manuscript to a scientific journal and that document will follow Dr. Stewart's suggestion of reducing the non-scientific portions to a few sentences in the introduction and discussion.

Dr. Stewart's characterization of our "strategic scientific objective" (see statement above) is incorrect. We were actually given a very broad remit to use genetic methods to better define stocks of harbor seals within Alaska. Both scientists at the agency and the Alaska Scientific Review Group recognized that the initial definition of three stocks was based on inadequate data and was likely to be revised. A great deal of research on distribution and abundance, trends in abundance and tagging has gone on in addition to the genetic research. We utilized these data together with the genetic data in the analyses provided in the Admin. Rpt.

A larger philosophical difference is that Dr. Stewart implies that we can objectively report whether the scientific data indicate the number and location of stocks without getting into the messy definitions given in the law (MMPA), the interpretation of the law (PBR Guidelines), or management agreements (the co-management agreement). In fact, nature does not break down into discreet and recognizable units that can be "tested" with some sort of purely objective genetic litmus paper. Scientists have a very hard time deciding how to define a species or sub-species, and the levels of uncertainty and disagreement increases on structure below that level. Again, in the interest of transparency, we laid out as completely as possible the standards that we were using to interpret the data. Dr. Stewart chose to take issue with the interpretation that we used. At least he knew what our definition was. It is unclear what alternate definition Dr. Stewart is using (see discussion under Major Point 1).

4. The limitations of non-genetic data should be amplified.

"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 a 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 glow 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."

In our interpretation of the genetic findings on population subdivision we compared our results to other information of relevance to population structure (Discussion 4.4) including, movements, foraging ecology and trends in abundance. We disagree with the Reviewer that these data were advanced as a proxy for patterns of dispersal. We took great care to stress that these other lines of evidence are only suggestive of subdivision on spatial scales similar to our genetic findings. Furthermore, we recognized that incomplete data in some cases limited our ability to interpret the data in terms of population structure, while in other cases alternative explanations were possible. However, we also contended that the collective interpretation of these various data types in the context of our genetic study and population subdivision in Alaskan harbor seals was instructive. It should be noted that managers will, likewise, have to assess all relevant data in much the same manner when re-defining management stocks. We take this opportunity to re-iterate and elaborate on these opinions.

Specifically, the current limitations on the duration of telemetry studies (typically less than one year) can only provide data on site fidelity and movement patterns for part of an individual's life. It is clear that in a relatively long-lived species such as the harbor seal, such limitations prevent a comprehensive assessment of dispersal. Nevertheless, even limited data can reveal much about the relationships among groups of seals. In a number of regions our failure to detect genetic differentiation among locations was supported by extensive movements of tagged seals between these sites. For example, long-term telemetry studies in Prince William Sound recorded extensive movements by tagged

animals within the Sound, suggesting a close relationship among seals within the Sound. We reached a similar conclusion with our genetic study.

With regard to our interpretation of differing trends in abundance, we recognized that differences may occur 'even with extensive dispersal among regions'. It would have been remiss of us, however, not to present the alternative argument that the different trends in abundance in different regions of the State, which 'occur on similar spatial scales to the genetic findings presented and do not correspond to currently recognized stock structure' may reflect the underlying pattern and scale of subdivision.

Minor points:

III.A.1. Source of samples

"The report did not identify the contribution of [the] various categories of samples.. If [the contributions] are...substantial, then the issue might be discussed more, with strong logical and substantive arguments presented for their inclusion".

As outlined in the report, samples were collected in a number of ways, including: samples collected during research projects, samples from subsistence harvest, molted hair recovered from haulout sites, and samples from historic scientific collections. Here we provide details on their relative contributions to the complete data set, and present arguments for their inclusion in the final analysis of population subdivision. The most common source of samples (n=378) was dedicated research projects conducted between 1985 and 2001. All had very precise data on location. A large number of samples (n=245) were from the ADF&G and UAF archives. These animals dated from the mid or late 1970s and had information on capture site that was precise enough for inclusion in our initial strata. A total of 207 samples were from subsistence harvest, the vast majority of which had accompanying details on the exact location of harvest. Only 27 samples were collected from stranded seals, all with details of locality, while 24 were from hair samples collected during the molt. The method of collection and resulting mtDNA data from these latter samples led us to conclude that they were likely to have come from 24 different seals.

The temporal spread in sampling (from the mid-1970s to 2001) raised the issue of whether the genetic differences observed among areas could be due to underlying structure or just sampling effects. None of the original 31 strata, however, had sufficient sample numbers from the full range of sampling time periods to allow a comparison. Only by combining the three initial strata from Prince William Sound were we able to assess potential changes in genetic composition of this region over time. Although a loss in haplotypic diversity was detected between the 1970s and 1990s, no differentiation was found between time periods within Prince William Sound (Westlake and O'Corry-Crowe, 2002), indicating that the differentiation observed among geographic strata in the current study were not due to sampling effects. Concerns were further minimized by the

exclusion of many of the 1970s samples (n=127) from the final analysis of population structure because they were from the poorly sampled initial strata.

III.A.2. Exclusion of samples

The reviewer argues that the exclusion from our final analyses of 228 of the sequenced samples from poorly sampled areas is a problem because the 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." We agree that these represent important areas. However, we argue that the 'problem' is the lack of adequate sample coverage from these areas, not our decision to exclude the few samples we have from them. From a scientific viewpoint, the exclusion of these samples is not only justifiable, but is required in order to avoid producing results that are biased and potentially misleading.

Although the threshold value chosen for the adjusted sample size, n_a=4, was somewhat subjective, the exclusion of poorly sampled areas from the analysis of population subdivision is well founded. The reverse, their inclusion, is not. As we explain in Appendix 3 of the reviewed document, if the sample size from an area is small relative to the haplotypic diversity of the area, as is the case for the initial units we excluded from our analyses, then any frequency-based measure of genetic differentiation between that area and another will be negatively biased. In other words, the two areas will appear to be more genetically similar to each other than they actually are. If we had included such poorly sampled areas in our analyses, they would have tended to cluster together early in each of the three clustering analyses, suggesting that they are more genetically similar to each other than to better sampled strata. This result would have been corroborated by the hypothesis-testing analysis, which would have shown these poorly-sampled units to be not significantly differentiated. However, this apparently robust result would not have been a true reflection of population structure, but rather a result of a known bias in the statistical measure used to assess differentiation. By excluding these areas, we were able to largely eliminate this source of bias and produce results that, though less comprehensive, are more accurate. A series of trials were undertaken during the review that demonstrated the effects of sample size on the clustering results and confirmed that the exclusion of poorly sampled sites was a necessary and objective decision.

By excluding poorly sampled areas we were also able to avoid creating the impression that genetic data were able to provide useful information in areas from which sampling is simply inadequate to do so. The Alaskan Peninsula and Aleutian Islands are an excellent example. Though this region accounts for a quarter of the initial units defined in our analyses, it contains only 6% of the total samples sequenced for the study. With only 54 samples distributed along more than 2,100 km of coastline, it would clearly be inappropriate to make management decisions in this area on the basis of the available genetic data. By excluding this and other poorly-sampled areas of the state from our analyses, we were able to highlight areas from which further genetic sampling and/or the analysis of other types of data will be necessary before stock boundaries can be drawn.

Improving sample coverage by the inclusion of intermediate areas in the analysis of population subdivision is a somewhat separate issue. We are currently engaged in collecting and analyzing samples from these regions. As these areas become better sampled, we will be able to further refine our analysis of population subdivision. It is important to stress, however, that the inclusion of intermediate areas is unlikely to change our reported inference on the spatial scale of population structure that we observed in Alaskan harbor seals or on the demographic relationships among those areas where we already have amassed sufficient samples.

III.B.1. Used only mtDNA

" 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."

The subject of the Report, as stated in the title and detailed in the Executive Summary and Introduction, was to provide recent information on population genetic structure in Alaska harbor seals that would form the scientific basis, to be used in conjunction with other information, for a revision of management stocks as defined under the U.S. Marine Mammal Protection Act (MMPA). The guidelines for implementation of the Act recognize that the definition of stocks should be based on demographic isolation. Thus, it was under the MMPA's goals of maintaining population stocks as functioning elements of their ecosystem, and the respective guidelines of the Act of the necessity to resolve the demographic relationships among groups of animals in order to achieve these goals that we focused on an analysis of mtDNA variation. A detailed response to our rationale behind our emphasis on mtDNA is in Major Point 4 above.

III.B.3. Statement about performance testing "unconvincing"

        The reviewer asserts that the only evidence offered for the validity of the Boundary Rank clustering method was our statement that the method had been subjected to extensive performance testing, and that he did not find that statement alone to be convincing. In fact, a manuscript describing the performance testing in great detail was provided as one of the background documents to the review. Each reviewer received a copy of this document in advance. In addition, we made this and all other background documents available on a website specifically set up for the review. We did not discuss the performance testing in detail during our presentations due to time considerations, but we informed the review panel that we were prepared to give a presentation on the performance testing and results if they were interested. The reviewers declined, stating that they found the background document on the subject sufficient.

IV.A. Discussion of legal interpretation of the MMPA

Dr. Stewart feels that the conclusion "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" contains a policy statement. This policy statement refers to our inference that all species and population stocks should be maintained as functioning elements of their ecosystem. Dr. Stewart feels this is inconsistent with the word "certain" used in the law, which he feels implies that only certain species are to be maintained as functioning elements of their ecosystem. We restate that we relied on definitions used in the PBR Guidelines and in the objectives of the co-management agreement. If and when these implementation documents are changed, we will change our interpretation accordingly. We do not, therefore, further deal with this issue in this response.

IV.C. Clarify which areas are of high conservation concern and why

"It is not clear why there is or should be concern for conservation of harbor seals in…. areas *[where substantial gaps in sample coverage exist]* (implying that there are substantial threats to population viability now)".

This statement refers to Conclusion 3 of the Report. Detailing the conservation and management issues relating to harbor seals in every region of the State is beyond the scope of the Report and of this response. Citations to the most relevant texts can, however, can be found in the former. To clarify our statement, we believe that the dramatic declines in harbor seal numbers that have been observed throughout much of the species' Alaskan range in recent decades justifies the characterization of many areas as places of high conservation concern. Furthermore, in areas like the Aleutian Islands where few data are currently available on population trend or threats, declines in other marine mammal species have naturally raised concerns as to the status and viability of harbor seals. Many of these areas remain to be sampled. We do not agree that our recognition of certain parts of the range of harbor seals as areas of high conservation concern necessarily implies that "substantial threats to population viability" have already been documented and regret that such an interpretation could have been made.

IV.D. Clarify why we felt this conclusion #4 was useful

"I think this conclusion [no.4.] *is neither well supported logically nor necessary."*

This statement refers to Conclusion 4 of the Report, which asserts that although further sampling is required, it will not likely change our conclusion that there are many small units of harbor seals that need to be managed as separate stocks. To clarify, our analysis of mtDNA variation enabled us to document the scale and configuration of population structuring in harbor seals in Alaska. By finding that female dispersal was limited over spatial scales that were much smaller than the current stocks, we were able to show that demographic independence was occurring on a smaller scale than the present stocks, and thus conclude that harbor seal stocks in Alaska were too broadly defined. This

conclusion is unlikely to change with the addition of more samples. As scientists, our goal is to strive to collect the most complete data set possible. How well we sample an area affects our ability to document scientific fact, in this case the population structure and dispersal patterns of harbor seals. It does not, however, influence the underlying truth we are interested in resolving, i.e., harbor seal population subdivision. Filling in sampling gaps and enhancing sample size will help us further refine stock structure in Alaskan harbor seals but will not change the fact that harbor seals disperse over shorter distances than the current stocks accommodate.