

Central Bering Sea Pollock Workshop on Allowable Harvest Level and Stock Identification

June 6-9, 2005 Seattle, Washington USA

Background: At the Ninth Annual Conference of the Parties to the Convention on the Conservation and Management of Pollock Resources in the Central Bering Sea held last September in Kushiro, Japan, the Parties agreed on a Scientific and Technical (S&T) Committee Work Plan for 2005. This Plan requires that two working groups be formed: 1) a genetics working group to address research on the composition of pollock stocks in the Bering Sea, and 2) a working group to identify scientific factors that should be considered in deriving an AHL (Acceptable Harvest Level) after the Allowable Biological Catch (ABC) is determined by the S&T Committee. The United States offered to host an AHL workshop in May-June 2005 at the NOAA Alaska Fisheries Science Center in Seattle, Washington, and suggested that the Parties consider holding a Genetics Workshop at the same time.



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1. Introductions and Election

- 1.1. The meeting nominated L. Low as meeting chair and J. Ianelli as head rapporteur with assistance from each delegation.
- 1.2. Individual opening statements and introductions were made. There was considerable discussion over the interpretation of the language under Agenda 5. The workshop noted that rather than spend too much time on the wording of this agenda and given that the agenda was already agreed upon by the Parties to the Convention, issues related to concern were better highlighted in this report.
- 1.3. The workshop reviewed the text of the convention specifically as relates to how the AHL is prescribed. It was agreed that the focus should be on the scientific aspects within the context of the convention. *The workshop adopted the agenda as it was drafted.*

2. Health, status, and trends of Aleutian Basin pollock stock

- 2.1. The workshop convened with a summary discussion on the status and trend of what is known about Aleutian Basin pollock. No new information was tabled specifically on survey or experimental fishing within the convention area. The subsequent agenda items present more detailed discussion on these aspects based on survey and other data from adjacent regions.

3. Present biomass level of stock

- 3.1. D. McKelvey (AFSC) presented survey results from the Bogoslof survey and this is included in WP-3.
- 3.2. The delegate from Korea asked about the presence of myctophids in the region and apparently they were not found close to pollock aggregations.
- 3.3. The Russian delegation requested information on the magnitude of observation errors in the survey estimate. The response was that the coefficient of variation was about 17%. They also suggested that a type of adaptive sampling strategy to focus on concentrations may be useful to improve estimation precision. Ms. McKelvey noted that these are areas of research that could lead to improvements. It was also noted that over time, the transect length into the basin and transect-spacing has changed.



- 3.4. The question arose about the age composition of the biomass. Based on preliminary examination of the age-data that was released early this week, the stock appears to consist mainly of the 2000 year-class, followed by the 1999 year-class (numerically).
- 3.5. An extensive discussion revolved around different characteristics between Samalga Pass fish compared to that of Umnak Island (which were much smaller). There was a suggestion that the 2000 year-class might be from Bogoslof spawning concentrations. It was pointed out that it would be important to have a survey in 2006 to see if this year-class continues to recruit.
- 3.6. In Russian waters (specifically, in the Sea of Okhotsk) survey data suggest that biomass estimates were highest during peak of spawning. Perhaps the timing issue may affect biomass estimates since the goal for the Bogoslof survey is to arrive prior to the peak of spawning. Also, it was also noted that younger pollock seem to reach peak spawning later in March with older pollock spawning first.
- 3.7. *Agenda items 3-8 were suspended temporarily so that presentations for Agenda item 9 could be heard for background purposes.*
- 3.8. The Chair resumed discussion with a review of the methods for arriving at biomass levels for the CBS region. Under the convention, the default formula for the Basin stock is to assume that the Bogoslof region (the convention's "Specific Area") stock represents 60% of the basin stock.
- 3.9. Since Bogoslof pollock spawn in deep-water, this is a characteristic that differentiates them from shelf area spawners and hence, these may truly have Aleutian Basin characteristics. It was also noted that this pattern of distribution (aggregations concentrated around Samalga pass and NE of Umnak Island) was very common in many surveys over the past several years.
- 3.10. Other issues that affected biomass level of the stock included the timing of the survey (i.e., there may be evidence that the survey occurs too early and higher concentrations are found during or slightly after spawning. Also, adaptive sampling of transect lines may provide better estimates (current CV of the 2005 biomass estimate is on the order of 17%).
- 3.11. The Russian delegation suggested that the proportion attributed to the basin as coming from the Bogoslof region has changed substantially. Russia suggested that there is evidence that the proportion of Basin pollock occurring in the Bogoslof Region is more than 60% now. They proposed that estimation of this proportion be estimated and that this be on the agenda for discussion at the next convention meeting.
- 3.12. The Russian delegation proposed that it is necessary to develop a comprehensive program for the Bering-Aleutian Pollock International Survey (BAPIS) which has as a main goal to study pollock biomass distributions between the Donut Hole and Bogoslof regions and include surveys from surrounding US and Russian zones. This should be carried out throughout the period of Bogoslof stock recovery. A plan with a budget should be formulated for presentation at the annual conference.
- 3.13. Japan noted that the current BASIS (Bering-Aleutian Salmon International Survey) program is for salmon which is a relatively large industry compared to the pollock fishery, especially in the Convention area. For that reason, presently it would be difficult to gain support for undertaking this type of research.
- 3.14. The Russian delegation commented that the cumulative total catch was 7 million tons in the Aleutian Basin. This is a large amount and survey work should be done according to this magnitude. The delegation proposed that such a survey program be carried out for one or two years by each member country and include ichthyoplankton surveys.

4. Safe exploitation rates on the stock

- 4.1. The US delegation presented WP-4 and WP-7. The use of SPR rates as done for domestic fisheries were presented along with the control rules for setting ABC. A specific application to the Bogoslof region was presented and three alternatives were given as examples. These were discussed in more detail under the next agenda item.

5. Anticipated exploitation rate of different AHLs on the stock

- 5.1. Exploitation rates under the three alternative approaches presented in WP-4 give:

Option	ABC approach	2006 ABC (Bogoslof fraction)	Exploitation rate (relative to Bogoslof survey estimate, 253,000 t)
1)	Tier 3 (with target 2 mt)	5,501 t	2.15%
2)	Simple rate of 75% of M ($M=0.2$)	37,950 t	15%
3)	Age-structured model (Tier 3 $F_{40\%}$ using NPFMC control rule)	Approximately 42,000 t	Approximately 16%

- 5.2. The meeting discussed factors that should be considered in choosing approaches for ABC and the above table is provided as background.
- 5.3. The workshop noted that the “target level” for rebuilding Bogoslof stock (and by extension, the Aleutian Basin pollock) may be affected by environmental change. The first option was considered appropriate given the current status (relatively low abundance levels). The target level of 2 million t was recognized to be very high. The target level and approach to estimating ABCs should be evaluated each year as new data become available.
- 5.4. The delegation from Japan proposed that for practical purposes of calculating Aleutian Basin ABC, the Bogoslof ABC value should be divided by 0.6 (as implied by the description in the Annex). They consider that the data are lacking to provide an alternative value other than that specified in the convention. The Russian delegation stated that they believe the pollock stock distribution between the Aleutian Basin and Bogoslof (i.e., the specific area detailed in the Convention) has changed. Therefore, the biomass of pollock in the Aleutian basin should be calculated accordingly. There was discussion about what evidence exists to estimate the current proportions. Dr. Stepanenko provided insight on direct observations from surveys in this region. Some participants noted that this highlights the need for a directed research program to evaluate pollock distribution patterns.
- 5.5. The delegate from Korea noted concerns on the assumption that fish migrate throughout the Basin. According to results from three years of hydroacoustic surveys (1996, 1997, and 1999) the echosign of pollock was present in 1996 and 1997, but not in 1999. Based on this, they thought that pollock appeared to be moving toward the east and west of Bogoslof region, not northward into the Basin. This may be due to environmental conditions. However, recent information is lacking (from their research) on the distribution and movement patterns of pollock in these regions.
- 5.6. The delegation from Japan proposed to set the AHL = ABC for the Aleutian Basin pollock.
- 5.7. The US delegation proposed that the level of AHL should be \leq ABC, but that the degree of departure should be part of the Annual conference. They felt that the workshop should focus on the biological issues related to estimating pollock ABC.

6. Biological reference biomass levels for the stock; such as minimum biomass, $B_{40\%}$, B_{msy} and optimum biomass

- 6.1. These concepts were reviewed and presented under Agenda item 4, specific from working papers WP-4 and WP-7. The approach of computing the minimum-stock size threshold (MSST) was discussed and it was noted that the value most appropriate would be on the order of 120,000 t (compared to the current estimate of 253,000 t for the Bogoslof region). This takes the assumption that the proxy for B_{msy} is equal to $B_{35\%}$ as derived from the preliminary age-structured model presented in WP-4. It was noted in the presentation that this value ($0.5B_{msy}$) of MSST was imposed for Steller sea lion considerations under the domestic US pollock fisheries management.

7. Desirable rebuilding schedule of the stock

- 7.1. This topic was discussed under agenda item 5. Since there are concerns about the changed conditions and the impact of highly variable recruitment for Aleutian Basin pollock, the workshop recommended that the rebuilding level should be reevaluated as needed (see paragraph 5.3). An exact schedule for attaining high stock sizes is difficult to detail due to the unpredictability of year-class strength.

8. Effects of different levels of AHL on the rebuilding schedule of the stock

- 8.1. The US party proposes that for the purposes of having a reasonable expectation of recovering pollock within the convention area, having a rebuilding target set high (as in option 1, with a 2 million t biomass target) would provide the most likely scenario for achieving the levels of catches observed in the convention area during the 1980s. However, they note that there is a large degree of uncertainty in this rebuilding effort since anomalous year-classes such as the 1978 event are unpredictable and likely a consequence of complex ecosystem and environment interactions.

9. Biological relationships between the Aleutian Basin pollock stock and those in the adjacent waters

- 9.1. Steve Barbeaux presented WP-5 which provided background on recent developments on stock assessment modeling for the Aleutian Islands region. In this assessment, the authors recognized that many catches were outside of the coastal areas that were covered by the main summer-time bottom trawl surveys. Dr. Choi (ROK) noted that the research done by the RV Tamgu 1 covered areas in the Convention area in the late 1990s and found no echosign of pollock. This report was presented at the 2000 CBS workshop and is available online.
- 9.2. It was noted that in the early 1990s Japan conducted EIT surveys and found little pollock in the region south of Bowers Ridge. This suggests that the pollock found around the Bowers Ridge area is unlikely to be part of the Aleutian Islands group and may belong to the Aleutian Basin pollock stock.
- 9.3. Dr. Ianelli presented an overview of EBS pollock on the shelf with particular reference to current patterns in fishing concentrations by region and within seasons (WP-6).
- 9.4. Dr. Stepanenko presented survey results of pollock from the Eastern and Western Bering Sea shelf (WP-11). The abundance of young-of-year in Anadyr Bay are comparable to Bristol Bay in 2003 and that recruitment could be derived from these regions to respective areas. However, recognition of these potential components is not possible in 2004.

- 9.5. Dr. Vasilyev presented a stock assessment model for the Navarin area (separable cohort model, WP-12). This approach includes many sources of information (two young-fish surveys, age structure, two CPUE indices (partitioned by vessel size classes), catch-at-age, and an age-zero survey. The model was introduced at ICES and should be useful for any stock in the Bering Sea and an appendix detailing the model configuration was also provided to the workshop (appendix to WP-12). They are also doing joint-research with Norway in order to create a joint model for herring stock assessment, partially based on robust properties of the above model. Confidence bounds were computed based on bootstrap methodology.
- 9.6. In summary, the biological relationships between Aleutian Basin pollock and surrounding areas are not well understood. Pollock are known to be one of the main biological components of the ecosystem for these regions and that further study on potential impacts is warranted.

10. Effects of fishing outside the central Bering Sea Convention Area on the status, biomass, and trend of the Aleutian Basin stock

- 10.1. The Russian party noted that the “shelf” and “basin” (Bogoslof) pollock is thought to inhabit the shelf area as juveniles (prior to first maturation). The fisheries in these regions attempt to avoid these small immature fish since they are not marketable. Therefore the total catch of “Basin” pollock on the shelf is relatively low.
- 10.2. They further noted that if Bogoslof pollock abundance is high, the bycatch in shelf fisheries is unlikely to have a large influence. If Bogoslof abundance is low, the bycatch is likely to be low on the shelf and hence have minimal impact on the “Basin” stock. Some participants conclude that fishing effort outside of the Convention area have little impact on Aleutian Basin pollock.
- 10.3. The Japanese party expressed the opinion that the bycatch levels from adjacent fisheries may impact Aleutian Basin pollock and also that predation on pollock by other animals and competition for food should also be considered.

11. Other scientific factors that are considered relevant

- 11.1. No papers were presented under this topic. There was some discussion that addressing ecosystem effects (in particular, trophic interactions) in the Aleutian Basin region and surrounding areas would be useful. Environmental changes were also discussed as playing an important role.

12. Recommendations to the Scientific and Technical Committee on Determination of AHL

- 12.1. All parties reviewed methodologies for calculating AHL on the basis of ABC and agreed that the present procedure for calculating ABC used in the USA is appropriate and also should be applied to the Aleutian Basin pollock stock given its current condition.
- 12.2. Some parties proposed that in order to determine the transformation from ABC to AHL new information about the distribution of pollock in the Aleutian Basin is needed. The workshop recommends that the committee consider their proposals about possible approaches for collecting such information including the proposal of the Russian party for an international survey effort (BAPIS).

Workshop for Genetic Research on Pollock Resources in the Central Bering Sea June 6-9, 2005 Seattle, Washington USA

1. Introductions and Election of Meeting Officials

- 1.1. The meeting nominated L. Low as meeting chair and I. Spies as rapporteur with assistance from each party.
- 1.2. The agenda was agreed upon by all parties.

2. Review of Current Information and Research

- 2.1. M. Canino (AFSC) put together a list of studies on Pollock genetic stock structure (WP-8). Earlier studies using allozymes and mtDNA may represent mixed stocks because they were not taken during spawning season. Studies of Atlantic cod have shown considerable genetic differentiation between spawning groups, and thus it would be worth while to re-examine stock structure of other gadids. Russian party inquired how many samples were used in they study and where the NCBS sample was collected (in September by a US catcher-processor, slightly northwest of the donut hole).
- 2.2. The Russian party presented 'Microsatellite analysis of population structure of Bering Sea Pollock' (WP-10). They found weak but significant structuring, using nine microsatellite loci. The North Kuril grouping appears genetically distinct, as do the East Bering Sea samples. There was some discussion on sampling and analysis with U.S. party and Japanese party.
- 2.3. Dr. Canino discussed his work on gene frequency stability over time using work on both microsatellite and pantophysin. More discussion centered on the question of genetic differentiation between year classes.
- 2.4. The Japanese party presented work they had done on walleye pollock (WP-13) by mtDNA sequencing of the mitochondrial control region, plus mtDNA, RFLP, and SNP analysis of the Calmodulin gene. Sampling locations ranged from Japan to Shelikov Strait. The mtDNA analyses found an east-west split, between Japan and the Bering Sea. SNP analysis of the Calmodulin gene indicated three major clusters: EBS, Japan, and WBS/Russia. Questions centered on desire for larger sample sizes in the future and historical explanations for observed broad scale genetic differentiation. The question of future work was brought up in order to ascertain with statistical confidence the population structure of walleye pollock and use the data for fisheries management.
- 2.5. Further discussion centered on the accuracy of genetic analysis and the desire to ascertain discrete population structure of walleye pollock, which to date has not been possible given various limitations (i.e., sample size, marker selection, funding, etc.).



3. Research Planning, Specimen Collection and Exchanges

- 3.1. The workshop began discussion on this agenda by first reviewing existing samples. The US scientists noted that they have genetic samples from spawning pollock aggregates from various locations including the Bering Sea dating back to 1997. These samples are available to any interested parties. The Russian scientists stated they have samples from the Western and Northern part of the Bering Sea and from the areas listed in WP-10, and that they are open to sharing samples. It was noted that 50-100 individuals should be collected from each spawning aggregation (or sampling location), in order for them to be representative. Any tissue will be sufficient (muscle/bones/fin clip), but fish should be sampled within a half an hour or so of death.
- 3.2. Sample preservation in ethanol can last typically for 3-5 years, but in some cases as long as 30 years. Preservation of DNA is best done in -80°C freezer. It was noted that samples preserved for more than 5 years, can result in “noise” in the microsatellite loci. Some genetic research has been successful on herring scale samples that were in storage for about 30 years. Many times scales are stored dry and that this can degrade the sample quality. It was noted that properly preserved otoliths could be used for genetic analysis as long as there is sufficient tissue left on the otolith and that microsatellite analysis is more robust than allozyme analysis because the sampling requirements are not as stringent. Fin clips are easy to take in the field and are good for DNA extraction. SNPs should work the same as nuclear analysis. The Poland scientist noted that they have some otoliths from the past fishery operations on pollock in the CBS, EBS, Aleutian Islands, and GOA since 1978. Similar collections are also likely available from Korean research cruises. The US party noted that they have opportunities to collect fin clips from fisherman but that such cooperative agreements usually require producing results fairly quickly (within several years).
- 3.3. Ichthyoplankton surveys should be pursued as another source of DNA (ensuring that the eggs/juveniles are pollock). The BASIS surveys may be a possible source of samples. The Japanese scientists noted that they may have juvenile pollock samples collected in recent years.
- 3.4. The need for a definitive study on pollock was highlighted. It was noted that a definitive study would entail having 20 good microsatellite markers and multi-year samples from spawning pollock collected in all the main areas.
- 3.5. The issue of using of muscle tissue and more easily collected samples (e.g., fin clips) was discussed at length. The Japanese scientists stated that they had some difficulties extracting DNA from the fin clips they received from the AFSC. They had no problems extracting DNA from muscle and thus would prefer this type of sample. The main advantage for using fin-clips is the ease of collection. While both tissue types can be used, where possible the workshop felt that innovative sampling approaches (e.g., simply taking muscle tissue with each otolith collection) should be pursued.

- 3.6. The issue on the need to focus attention on developing better markers arose. WP-8 states that small sample sizes and samples from non-spawning individuals were possible issues related to the lack of differentiation between Bogoslof pollock and that from surrounding areas. The lack of sufficient markers was listed as another possible issue. This question of criteria to use to determine if different stocks exist was raised. Evidence for genetic differentiation implies a self recruiting, genetically distinct stock. If one is able to provide evidence that genetic differentiation is constant over time, then that is evidence of genetic differentiation. Typically, however, discrete boundaries do not exist in marine fishes. Instead, there is often isolation by distance and some sort of cline in genetic characteristics. As an example, the AFSC recently completed a genetic analysis of Atka mackerel in the Aleutian Islands using nine microsatellite loci. Four locations were sample with results of a high degree of correct classification to region (76-80% certainty location of origin). This study suggests that since similar methods are being used for pollock, the genetic markers that were used should be adequate.
- 3.7. The issue on the ability of genetic research to address questions on the degree to which the Bogoslof population represents the entire Aleutian Basin pollock was discussed. It was pointed out that distinguishing Aleutian Basin pollock from EBS and other areas is largely a different issue than understanding the relative abundance between the Aleutian Basin stock and the Bogoslof portion of that stock during the winter spawning aggregations. Analysis of historical collections may provide some new insights on genetic discreteness of the Bogoslof region as compared to the pollock from the Aleutian Basin and other regions.

4. Recommendations to the Scientific and Technical Committee

- 4.1. *Historical specimen availability.* The workshop recommends that parties to the Convention develop an inventory of historical samples. It is envisioned that these data will be presented and updated eventually to be available on a website. The data should include basic information such as geographic position, the storage method, date collected, and availability of subsidiary data (e.g., age, length, sex, gonad maturity, etc.).
- 4.2. *Current and planned research.* The workshop recommends that parties present a report on the ongoing and planned activities on genetics research related to pollock. This should be broken into three main areas: current sample collection and processing efforts, historical sample analysis, and research on developing new markers or methods. This will help guide areas where research is lacking and inform on activities around the region.
- 4.3. *Development of baseline research.* The workshop encouraged member countries to pursue research on improving genetic markers for pollock. The use of alternative markers will help improve the understanding of how stocks are related.
- 4.4. *Sample exchange.* The workshop recommends that sample-exchange among member parties be facilitated.

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Agenda

Day 1 (June 6, 2005):

1. Introductions and Election of Meeting Officials
2. Health, status and trends of the Aleutian Basin pollock stock
3. Present biomass level of the stock
4. Safe exploitation rates on the stock
5. Anticipated exploitation rate of different AHLs on the stock
6. Biological reference biomass levels for the stock; such as minimum biomass, $B_{40\%}$, B_{msy} and optimum biomass

Day 2 (June 7, 2005):

7. Desirable rebuilding schedule of the stock;
8. Effects of different levels of AHL on the rebuilding schedule of the stock;
9. Biological relationships between the Aleutian Basin pollock stock and those in the adjacent waters;
10. Effects of fishing outside the central Bering Sea Convention Area on the status, biomass, and trend of the Aleutian Basin stock; and
11. Other scientific factors that are considered relevant

Day 3 (June 8, 2005, morning session)

12. Recommendations to the Scientific and Technical Committee on Determination of AHL
13. Summary Report of the Workshop

Workshop for Genetic Research on Pollock Resources in the Central Bering Sea

Day 3 (June 8, 2005, afternoon session):

1. Introductions and Election of Meeting Officials
2. Review of Current Information and Research

Day 4 (June 9, 2005):

3. Research Planning, Specimen Collection and Sample Exchanges
4. Recommendations to the Scientific and Technical Committee
5. Summary Report of the Workshop

Meeting coordinator:

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List of documents

AHL Meeting Report	AHL Meeting Report
Genetics Meeting Report	Genetics Meeting Report
Background and Draft Agenda	WP-1
List of documents	WP-2
Preliminary report on the 2005 Bogoslof EIT survey	WP-3
Approaches for setting ABC in the Bogoslof Region under US Fishery Management practices	WP-4
Recent research activities and stock assessment approaches for the Aleutian Islands region	WP-5
Update on the status of Eastern Bering Sea pollock	WP-6
Review of the NPFMC approach for setting ABC and OFL levels and levels set for 2005 and 2006	WP-7
Summary of genetic stock identification studies in the Bering Sea	WP-8
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Microsatellite analysis of the population structure of the Bering Sea pollock	WP-10
Status of stocks and reproduction of the Eastern Bering Sea pollock (<i>Theragra chalcogramma</i>) in 2003-2005	WP-11
Update of Navarin walleye pollock stock assessment (including an appendix of ISVPA model)	WP-12
Summary of DNA analyses of pollock by Japanese scientist 2005	WP-13



Preliminary results of the 2005 Bogoslof EIT pollock survey

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March 6 –13, 2005
RV Miller Freeman



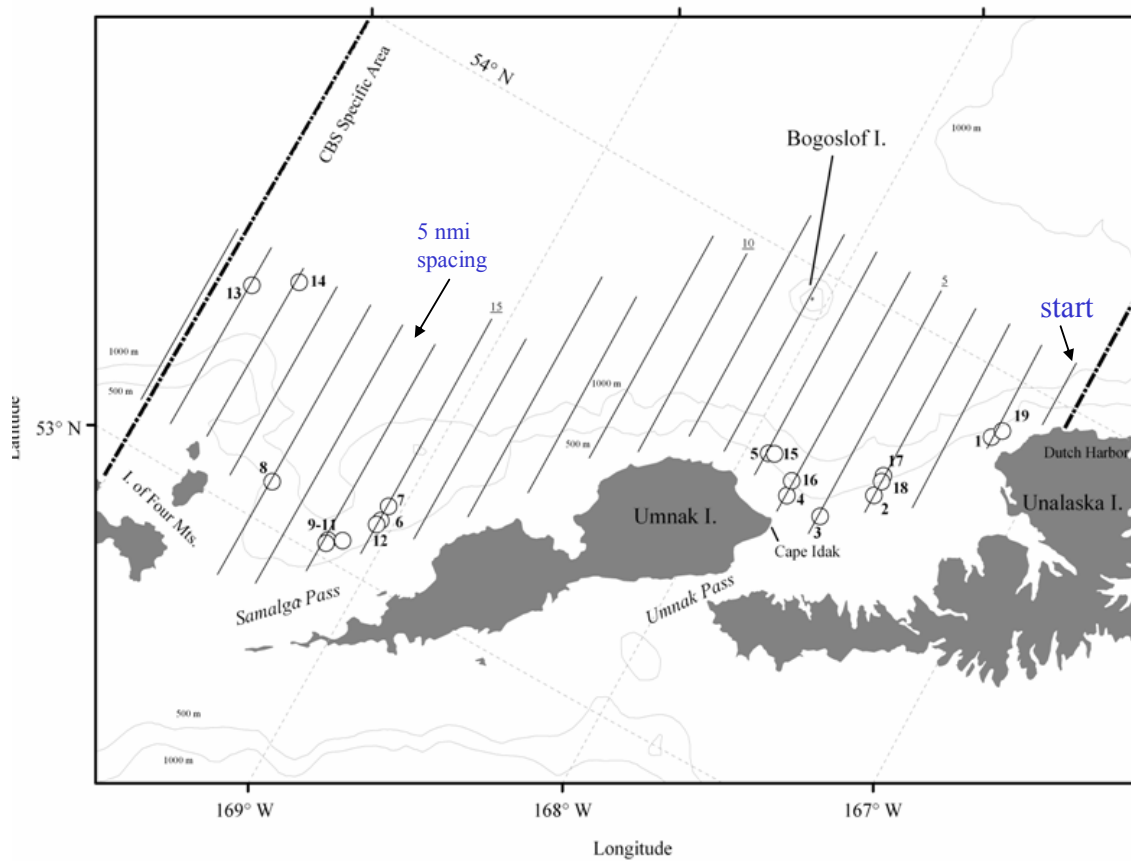


Figure 1. Trackline (22) and haul location (19 circles) from the winter 2005 echo integration-trawl survey in the Bogoslof Island area. Transect numbers are underlined. The dash-dotted line indicates the NPFMC Area 518/Central Bering Sea Specific Area.

Table 1.--Catch by primary species from 19 midwater trawl hauls during the winter 2005 echo integration-trawl survey of walleye pollock in the Bogoslof Island area.

Species Name	Scientific Name	Weight (kg)	Percent by weight	Numbers
walleye pollock	<i>Theragra chalcogramma</i>	14,489.28	94.3	12,009
Pacific ocean perch	<i>Sebastes alutus</i>	616.51	4.0	625
*other		255.45	1.7	13,137
		15361.24		25,771

* mostly lanternfish

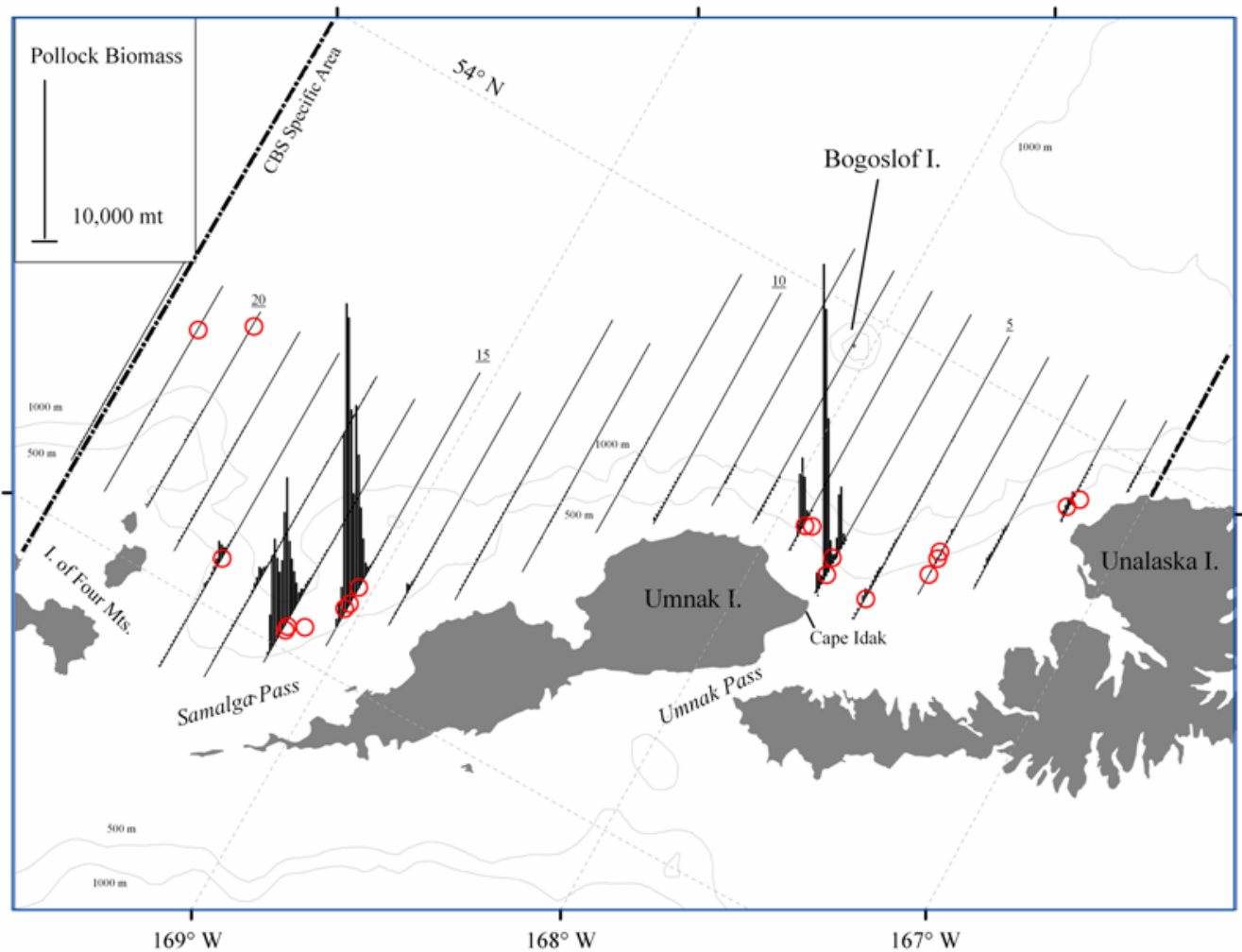


Figure 2. Trawl haul location (circles) and biomass (10,000 metric tons) attributed to pollock observed during the winter 2005 echo integration-trawl survey in the Bogoslof Island area.

Echogram of transect 15, Samalga Pass region

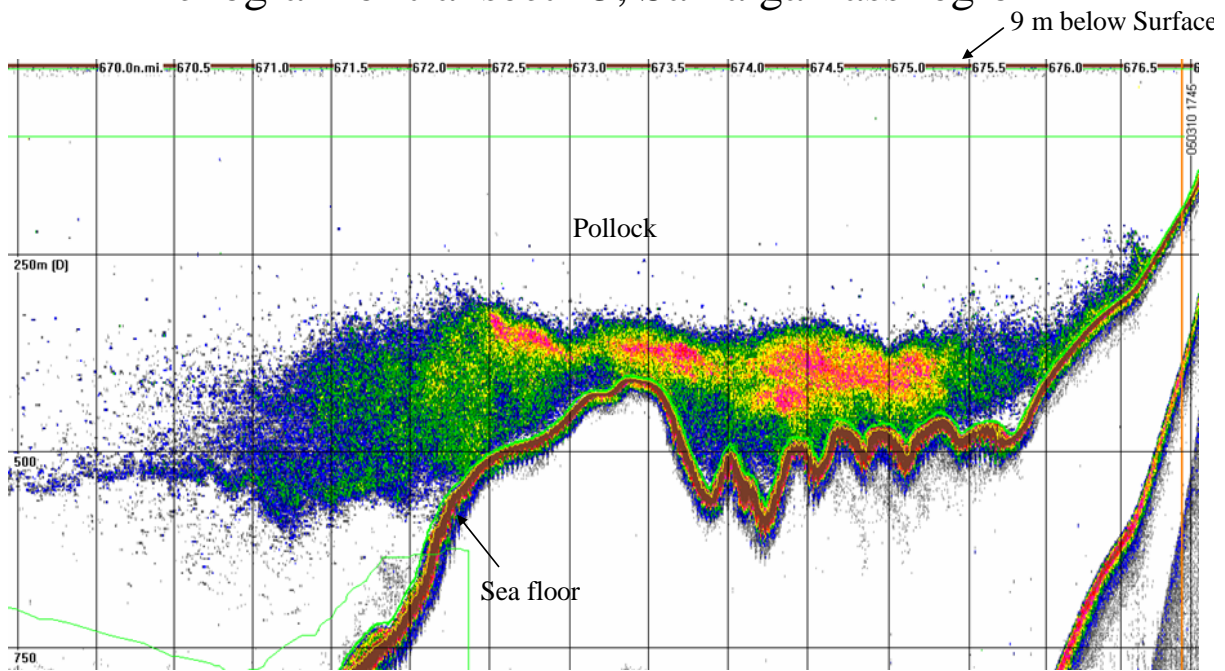


Figure 3. Pollock backscatter along transect 15, Samalga Pass region, where 3 trawl hauls were conducted.

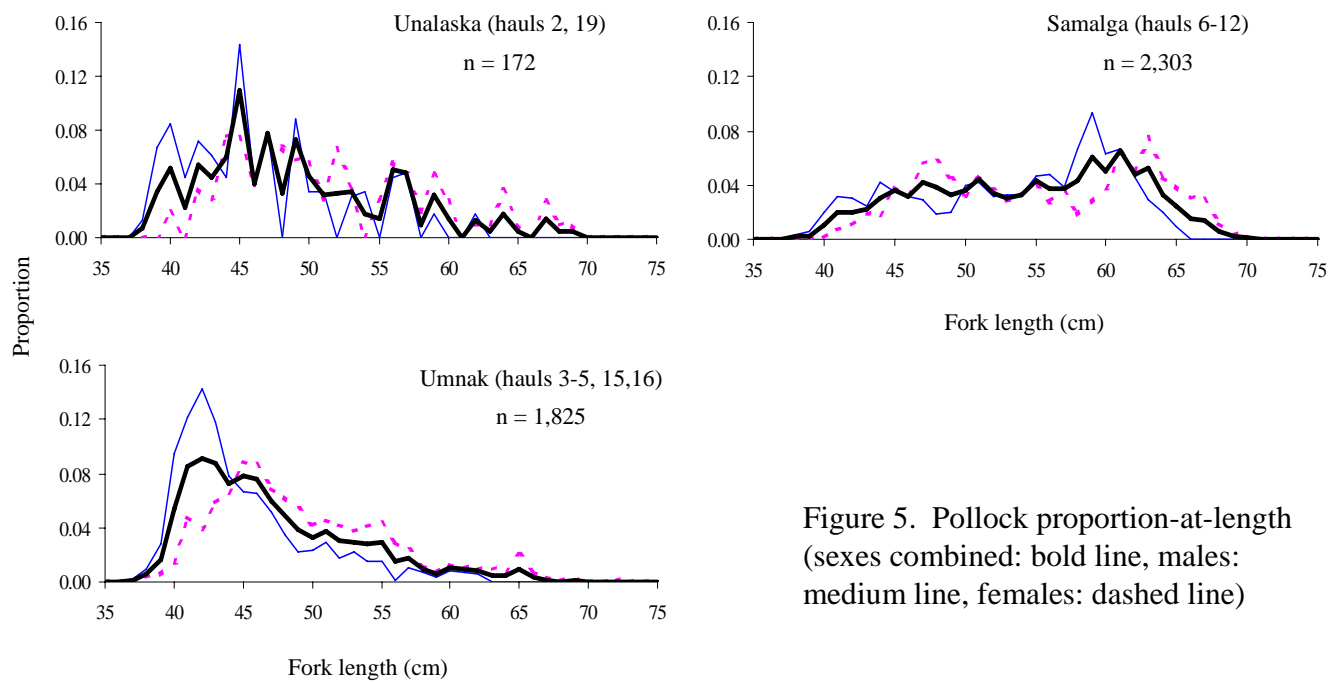


Figure 5. Pollock proportion-at-length (sexes combined: bold line, males: medium line, females: dashed line)

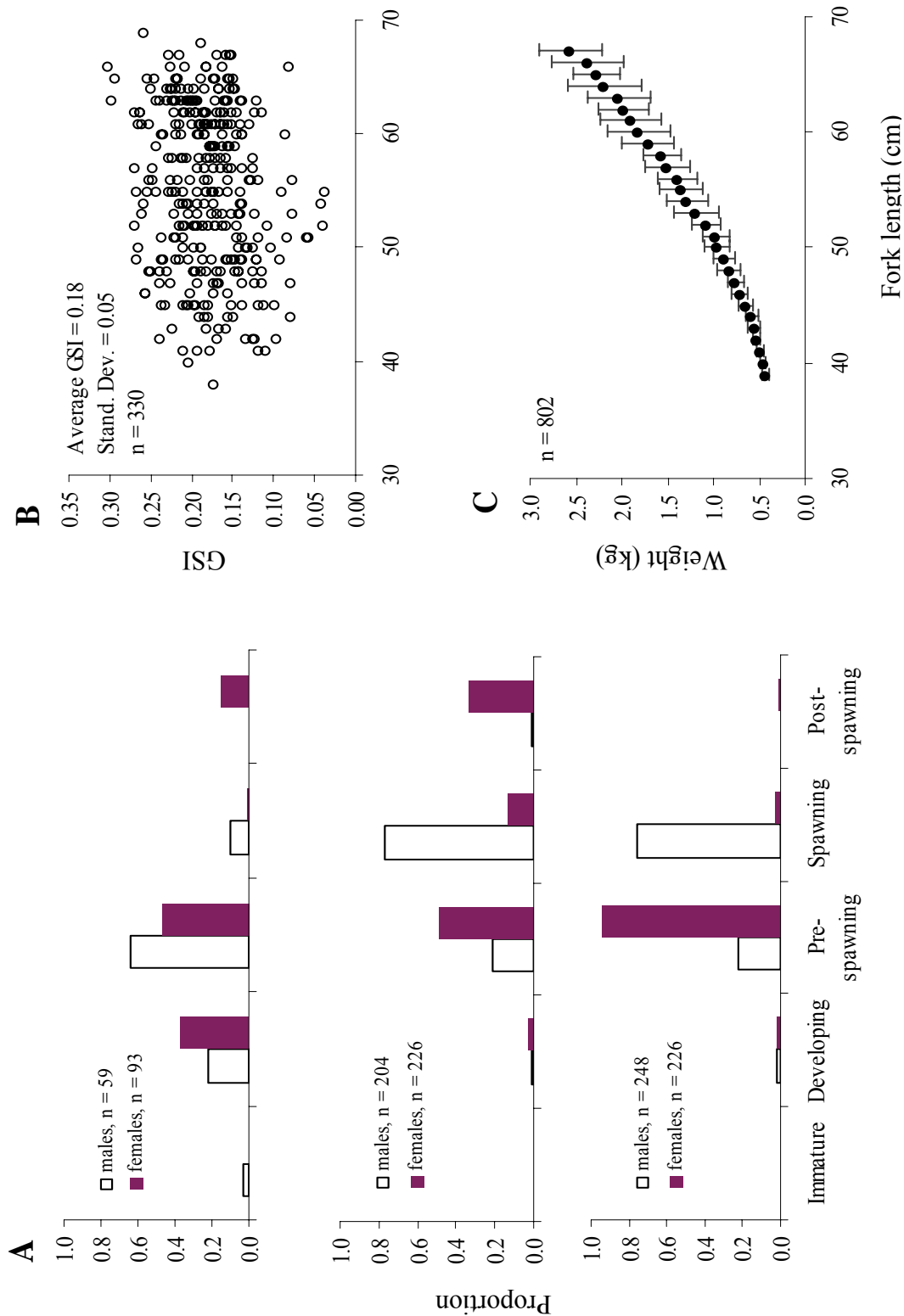


Figure 4. Pollock maturity stages for strata 1-3 (A), gonado-somatic index (GSI) for pre-spawning females as a function of fork length (cm) (B), and mean weight at length, where at least 5 fish were measured (sexes combined) (C). Vertical bars indicate one standard deviation.

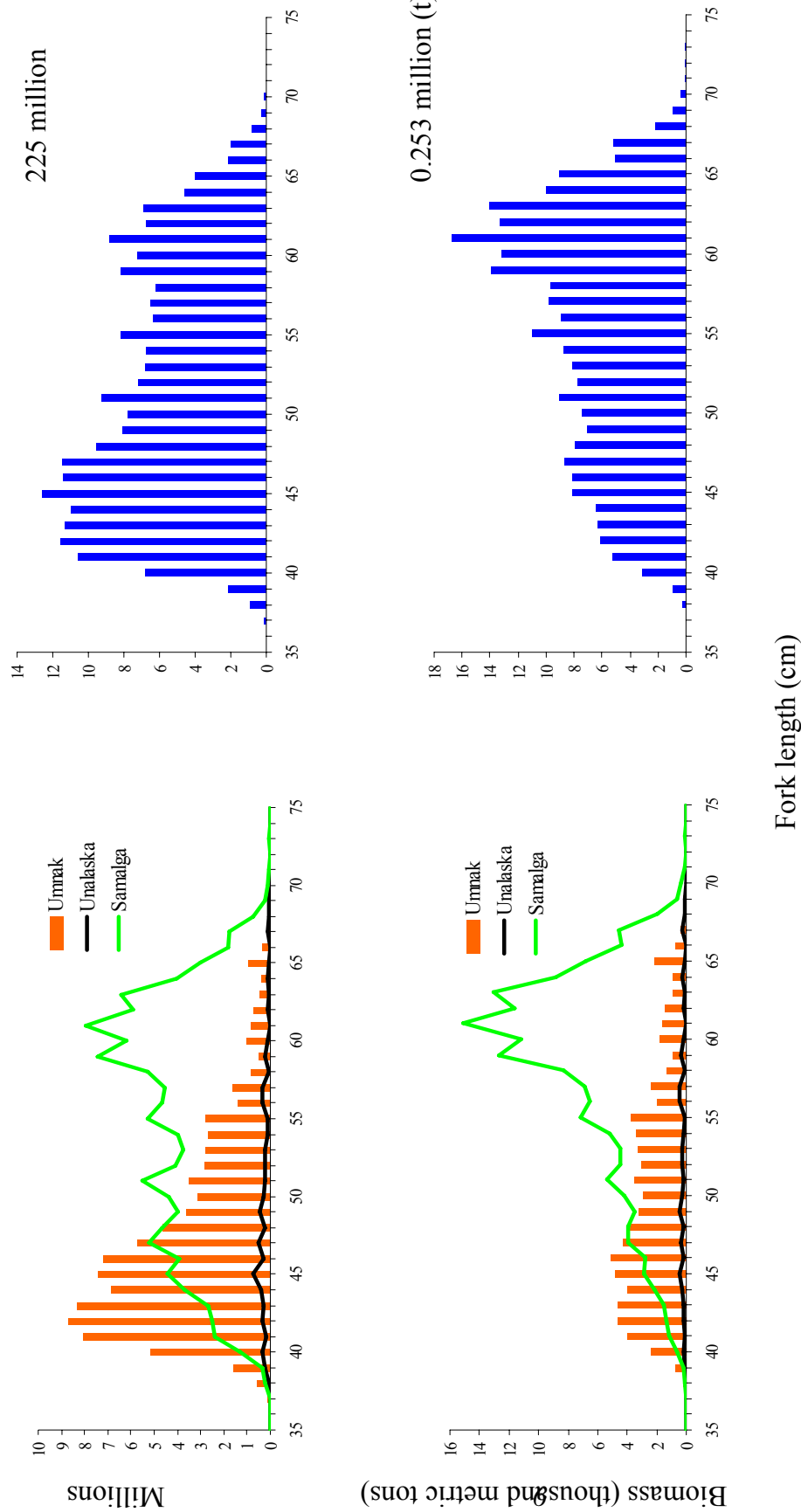


Figure 6. Population-at-length (top) and biomass-at-length (bottom) estimates from the winter 2005 echo integration-trawl survey of walleye pollock in the Bogoslof Island area.

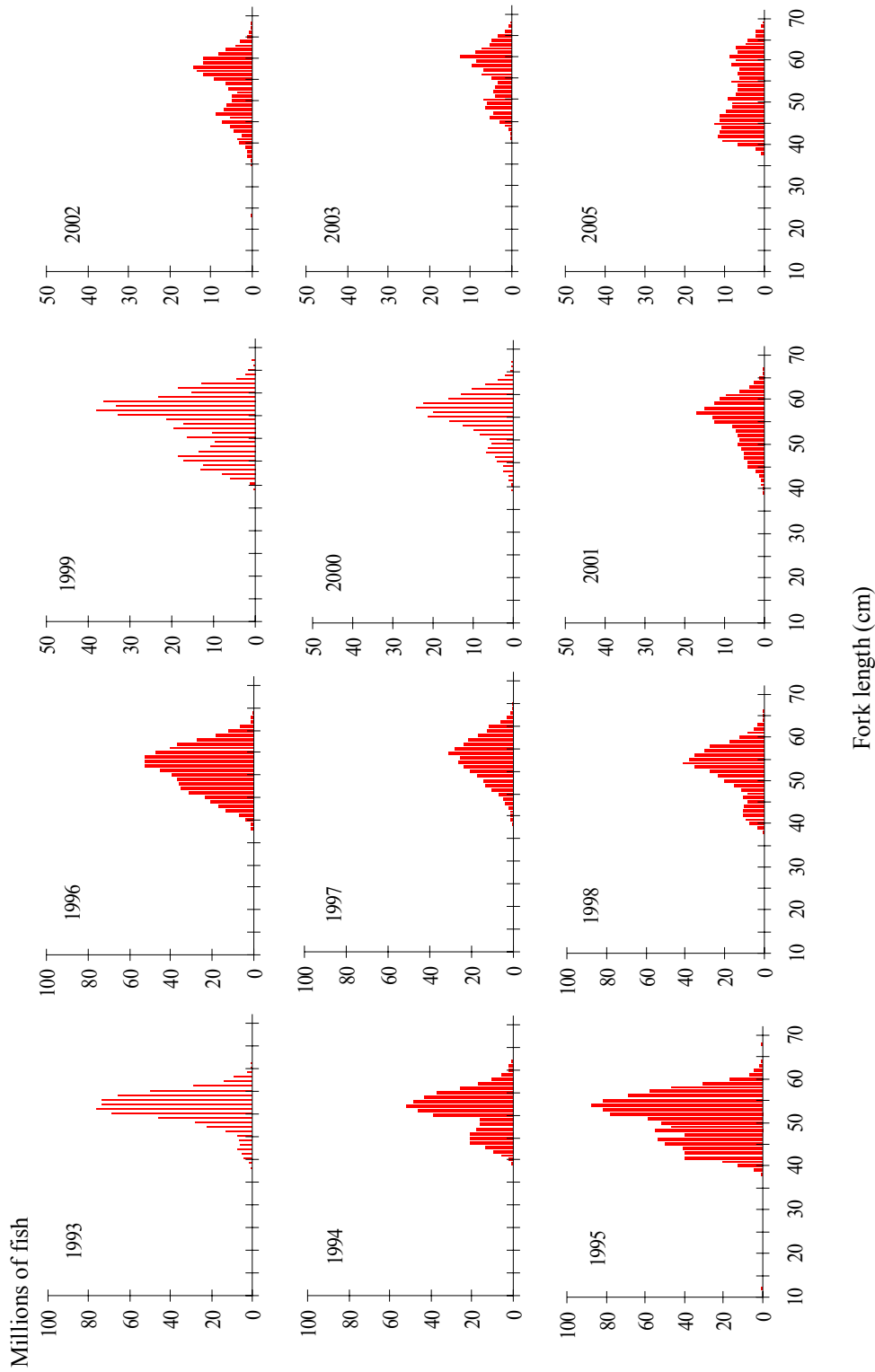


Figure 7. Numbers-at-length estimates (millions) from echo integration-trawl surveys of spawning pollock near Bogoslof Island in winter 1993-2005. The United States conducted all but the 1999 survey, which was conducted by Japan. Note y-axis scales differ.

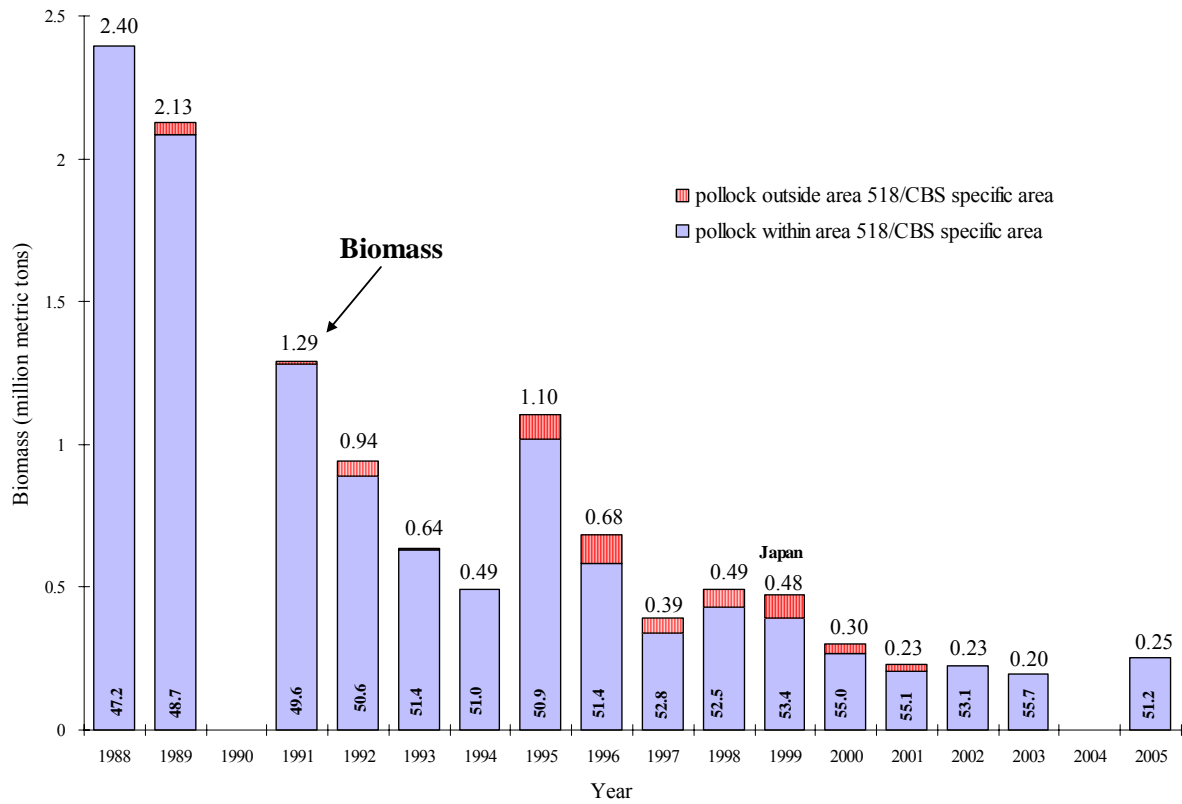


Figure 8. Biomass estimates (top of each bar) and average fork lengths (cm) (inside bar) obtained during winter echo integration-trawl surveys for walleye pollock in the Bogoslof Island area, 1988-2005. The U.S. conducted all but the 1999 survey, which was conducted by Japan.

Approaches for setting ABC in the Bogoslof Region under US Fishery Management practices

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Stock status summary

The National Marine Fisheries Service has conducted echo-integration-trawl (EIT) surveys for Aleutian Basin pollock spawning in the Bogoslof Island area annually since 1988, with three exceptions: a Bogoslof Island area EIT survey was not conducted in 1990, 2004 and in 1999 the survey was conducted by the Fisheries Agency of Japan. The annual Bogoslof Island area EIT survey results (Fig 1) show that population decline occurred between 1988 and 1994, was stable and variable then dropped again to the level it has maintained since 2000. The 2003 Bogoslof Island EIT survey results have been published as an AFSC Processed Report (McKelvey and Williamson 2003). The 1989 year class moved into the Bogoslof Island area and was partly responsible for the 1995 increase (Fig. 2), but the abundance of all ages increased between 1994 and 1995. The decrease between 1995 and 1996 was followed by a continued decline in 1997. This suggests that the 1995 estimate may have been over-estimated, or that conditions in that year affected the apparent abundance of pollock. The summary Bogoslof Island area EIT survey biomass estimates, 1988-2005, are shown in Table 1. The 1996 and 1999 year classes have thus far failed to materialized to any great extent in this region even though their abundance on the EBS shelf region is above average. The current population levels on the eastern Bering Sea shelf, and the absence of extremely large year classes, suggests that pollock distribution throughout the Bering Sea has shifted. The extent that this is due to environmental causes is unclear.

The information available for pollock in the Aleutian Basin and the Bogoslof Island area indicates that these fish belong to the same “stock”. The pollock found in winter surveys are generally older than age 5 and are considered distinct from eastern Bering Sea pollock. Data on the age structure of Bogoslof-Basin pollock show that a majority of pollock in the Basin originated from year classes that were also strong on the shelf, 1972, 1978, 1982, 1984, 1989, 1992, and 1996 (Fig. 3). There has been some indication that there are strong year classes appearing on the shelf that have not been coincidentally as strong (in a relative sense) in the Bogoslof region (Ianelli et al., 2001). The conditions leading to strong year classes of pollock in the Basin appears to be density related and may be functionally related to abundance on the shelf. Additional information relating the total mortality of the 1992 cohort shows that the estimate is much higher than expected in the Bogoslof region compared to the EBS shelf (Fig. 4).

Differences in spawning time and fecundity have been documented between eastern Bering Sea pollock and Aleutian Basin pollock. Pollock harvested in the Bogoslof Island fishery (Area 518) have noticeably different age compositions than those taken on the eastern Bering Sea shelf. For example, the average number of age 15 and older pollock observed from the Bogoslof EIT survey since 1988 is 18% while for the same period in the EBS region, age 15 and older averages only 2% (by number for all fish older than age 7). Pollock in the northern shelf have a similar size at age as Aleutian Basin pollock although a very different age composition. However, Aleutian Basin pollock may not be an independent stock. Very few pollock younger than 5 years old have ever been found in the Aleutian Basin including the Russian portion. Recruits to the basin are coming from another area, most likely the surrounding shelves either in the US or Russian EEZ.



Computation of ABC and OFLs

Since 1999 the North Pacific Fishery Management Council (NPFMC) have generally been presented with a number of alternative methods for computing ABC values for the Bogoslof region. These have included:

- 1) Using a biomass-adjusted harvest rate rule (with 2,000,000 ton estimate as a target stock size) with an estimate of a F_{ABC} based on growth, natural mortality, and maturation rate.
- 2) Using a harvest rate as a simple fraction of natural mortality rate (e.g., $F_{ABC} = 0.75M$).
- 3) An approach using a simple age-structured model.

The NPFMC Science and Statistical Committee (SSC) considered the third approach using an age-structured model to be inappropriate since it covered only part of the stock. The approach 1) and 2) above are provided below for comparison (along with alternative assumptions about F_{ABC} level for 1). The section included in this document reviews the details of the current NPFMC's Tier system for setting ABCs and OFLs.

Using method 1) above and given the survey estimate of exploitable biomass of 0.253 million t and $M = 0.2$ and considering of a target stock size of 2 million tons, the F_{ABC} level is computed as:

$$F_{abc} \leq F_{40\%} \cdot \left(\frac{B_{2005}}{B_{40\%}} - 0.05 \right) / (1 - 0.05) .$$

Assuming that $F_{40\%} = 0.27$ (as in past assessments), this gives a fishing mortality rate of 0.0217 that translates to an exploitation rate of 0.0215. This value multiplied by 253,000 t, gives a **2006 ABC of 5,501 t for the Bogoslof region**. The value assumed for $F_{40\%}$ that is critical for this calculation was based on uncertain assumptions about selectivity, natural mortality, growth, and maturation. Some of these assumptions were reevaluated here using a simple knife-edged selectivity at age 4 and age 5. Female pollock were specified to be 50% mature by age 5 and immature for younger pollock and 100% mature for older pollock with a natural mortality of 0.3. This results in an $F_{40\%}$ level of 0.22 for age-4 knife edge assumption and $F_{40\%} = 0.33$ for the age-5 knife-edge assumption. These two scenarios provide ABCs for 2006 that would be 4,482 t or 6,723 t for the age-4 and age-5 knife edge assumptions, respectively. Clearly, these rules are sensitive to assumptions about expected selectivity, assumed growth, natural mortality, and maturation rates.

The approach for computing ABC levels under 2) above (a Tier 5 computation) simply uses the most recent survey biomass estimate applied to an adjusted natural mortality. Given a value of $M=0.3$ then the ABC level would be (2005 survey biomass $\times M \times 0.75$) of **56,925 t** at a biomass of 253,000 t. With $M = 0.2$, the ABC would be 37,950 t.

Further work on developing a simple age-structured model tuned to the EIT winter survey data (Fig. 5) suggest that, by the same NPFMC rules used for setting groundfish ABCs, the current Bogoslof stock size is about 75% of the target level ($B_{40\%}$) and that the "unfished" level (given observed recruitment at age 6 to this region) is approximately 330,000 t (female spawning biomass). This is substantially lower than the 1 million t "target" currently in use. Forward simulations using this model result (and fishing using the maximum permissible ABC) shows that the 90 percentile range of female SSB is between about 50,000 t and 430,000 t while under a no-fishing scenario, this range increases to nearly 1 million t (Fig. 6). This reflects the main characteristic that seems to prevail for basin pollock: they are highly susceptible to year-class variability.

In summary, there is a range of ABC levels that have been calculated under the NPFMC guidelines. The second approach results in the highest ABC level since the levels are not adjusted by some perceived

target level. The first approach results in ABC levels that are nearly an order of magnitude lower due to the built-in adjustment to recover stock sizes to a target level. This approach was sensitive to assumptions about selectivity (and maturation rates). The age-structured model, while not accepted by the SSC due to stock structure concerns, could be argued to represent an alternative method to set ABCs and subsequent TACs. In practice, all of these approaches undergo scientific review each year in light of available data. The NPFMC has a record of being very conservative and setting a low ABC level and NMFS has responded by prohibiting any directed pollock fishery in this region.

Literature cited

- Ianelli, J.N., T. Buckley, T. Honkalehto, N. Williamson and G. Walters. 2001. Bering Sea-Aleutian Islands Walleye Pollock Assessment for 2002. *In*: Stock assessment and fishery evaluation report for the groundfish resources of the Bering Sea/Aleutian Islands regions. North Pac. Fish. Mgmt. Council, Anchorage, AK, section 1:1-105.
- Ianelli, J.N., S. Barbeaux, G. Walters, T. Honkalehto, and N. Williamson. 2004. Bering Sea-Aleutian Islands Walleye Pollock Assessment for 2004. *In*: Stock assessment and fishery evaluation report for the groundfish resources of the Bering Sea/Aleutian Islands regions. North Pac. Fish. Mgmt. Council, Anchorage, AK, section 1:37-126.
<http://www.afsc.noaa.gov/refm/docs/2004/EBSpollock.pdf>

Table 1. Biomass of pollock as surveyed in the Bogoslof region, 1988-2005. Note that in 1999 the Fishery Agency of Japan conducted the survey.

Biomass (millions of t)								
Year: 1988	1989	1990	1991	1992	1993	1994	1995	1996
2.4	2.1	-	1.3	0.9	0.6	0.49	1.1	0.68
Year: 1997	1998	1999	2000	2001	2002	2003	2004	2005
0.39	0.49	0.48	0.30	0.23	0.23	0.20	-	0.253

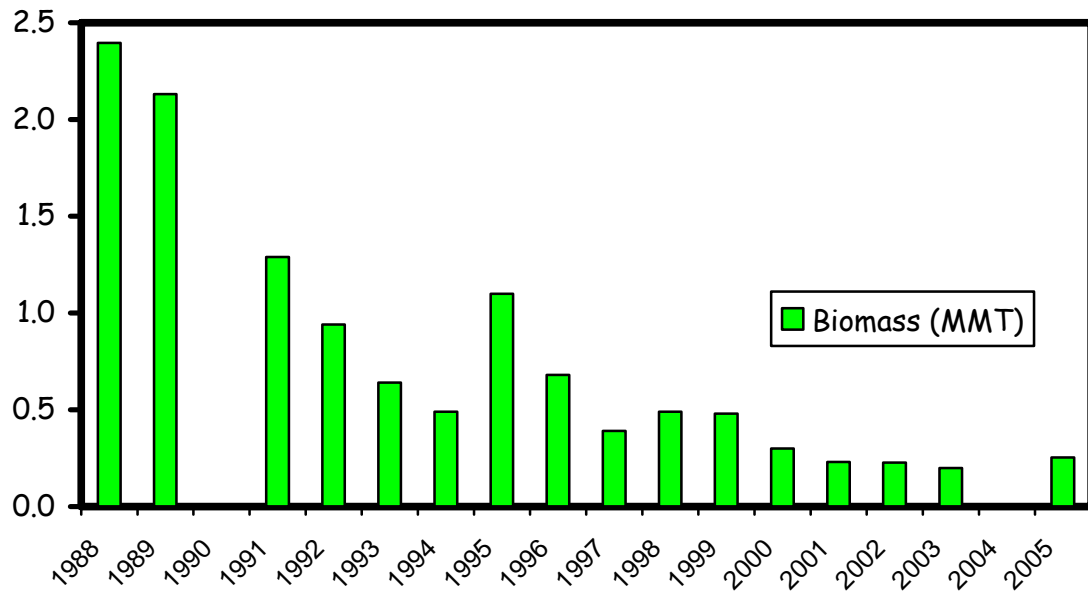


Figure 1. Pollock biomass estimates from the 1988-2005 Bogoslof Area EIT surveys in millions of tons. There were no surveys in 1990 and in 2004.

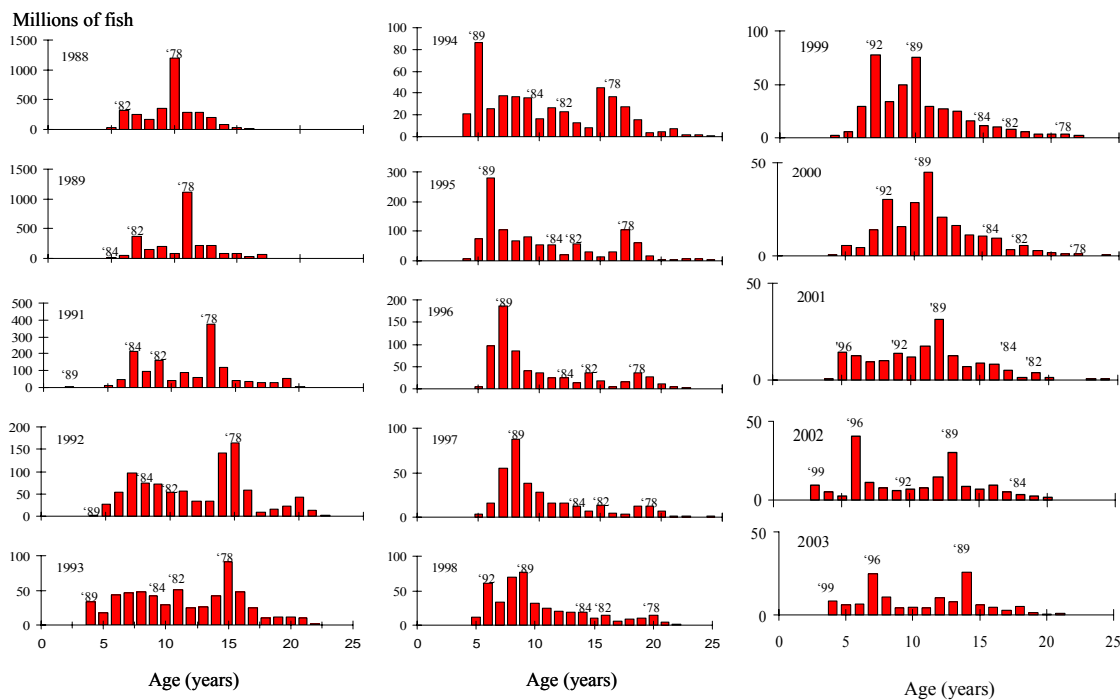


Figure 2. Numbers-at-age estimates (millions) obtained during echo integration-trawl surveys of walleye pollock near Bogoslof Island in winter 1988-2003. Major year classes are indicated. The United States conducted all but the 1999 survey (Japan). No survey was conducted in 1990. Note y-axis scales differ.

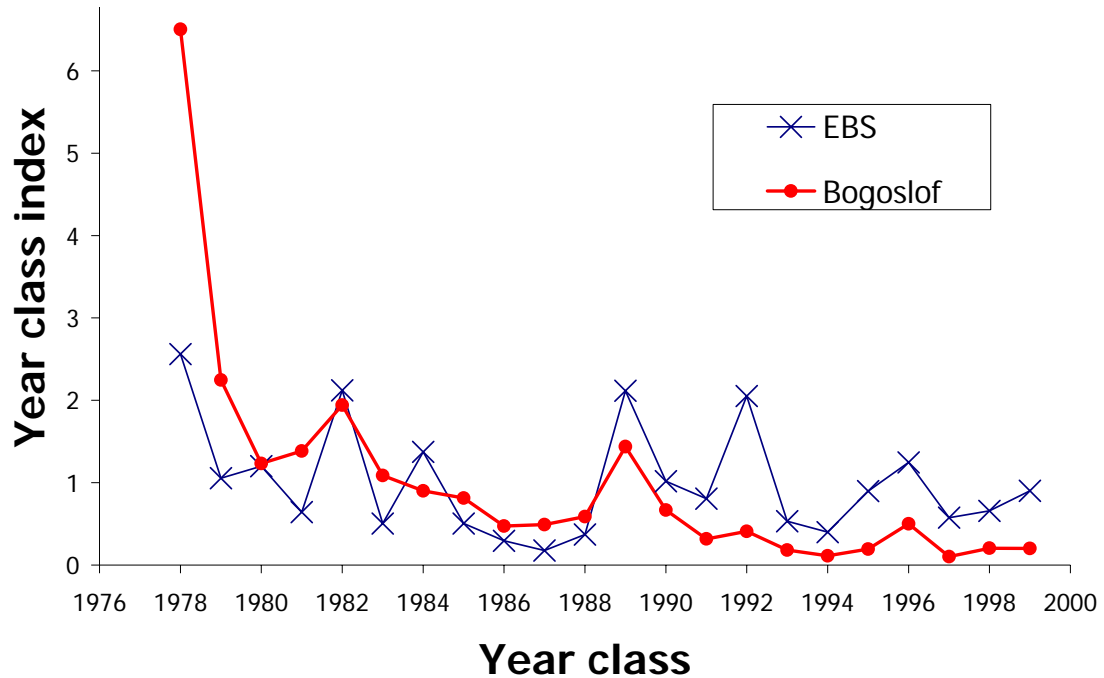


Figure 3. Relative year-class strengths (normalized to have a mean value of 1) for pollock as observed (averaged) from the Bogoslof EIT surveys and from a simple age-structured model for the Bogoslof Island stock compared with those observed from the main EBS pollock stock assessment model (Ianelli et al. 2004).

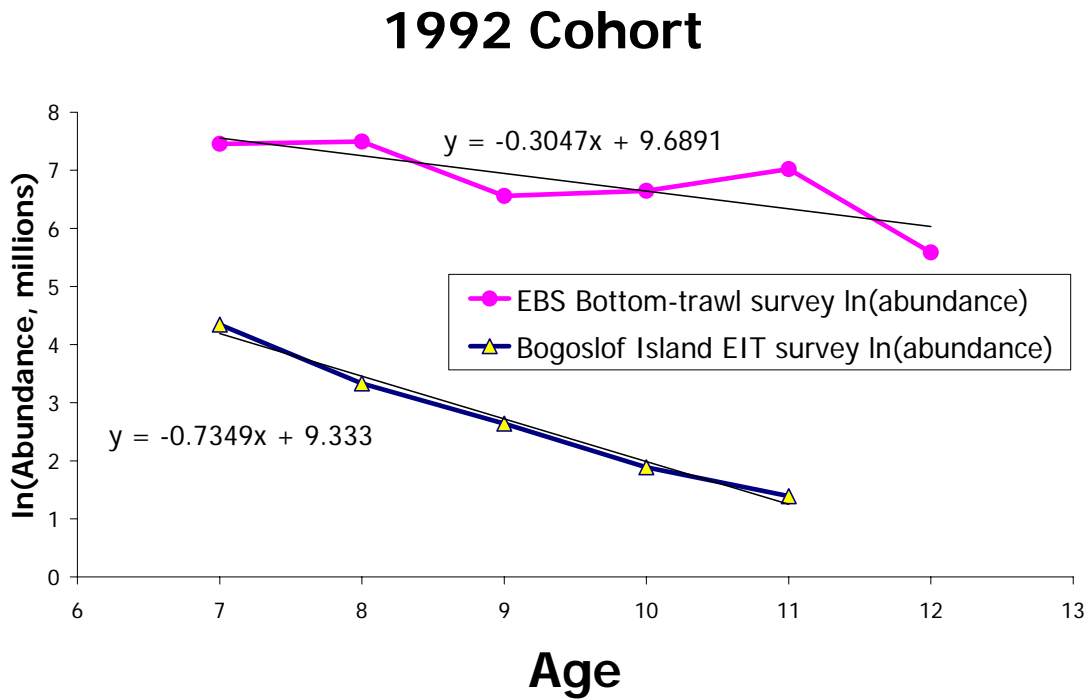


Figure 4. The 1992 pollock cohort abundances-at-age as observed from the EBS summer bottom trawl survey (top lines) and from the EIT survey in the Bogoslof region (lower lines).

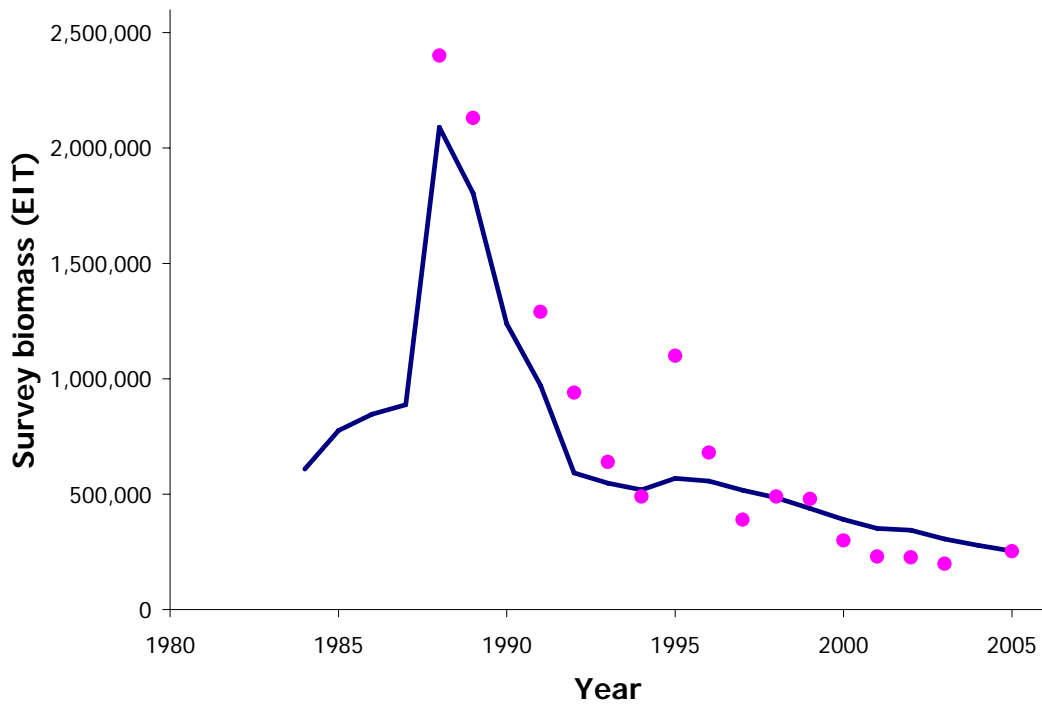


Figure 5. Simple age-structured model (line) tuned to the winter EIT Bogoslof pollock survey biomass estimates (points) 1984-2005.

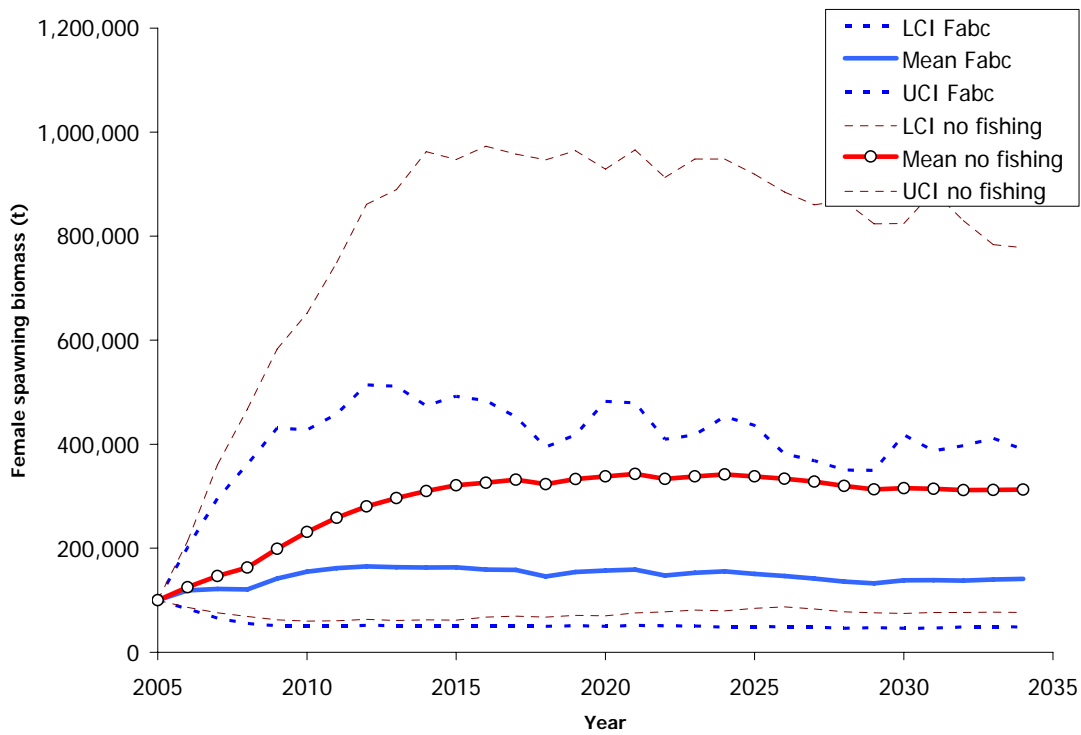


Figure 6. Projection simulations for Bogoslof region pollock based on the simple age structured model under no fishing and under fishing at the maximum permissible rate (as defined for the NPFMC for Tier 3 stocks).

Recent research activities and stock assessment approaches for the Aleutian Islands region

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Walleye pollock are distributed throughout the Aleutian Islands with concentrations in areas and depths dependent on season. Generally, larger pollock occur in spawning aggregations during February – April. Three stocks of pollock are identified in the U.S. portion of the Bering Sea for management purposes. These are: eastern Bering Sea which consists of pollock occurring on the eastern Bering Sea shelf from Unimak Pass to the U.S.-Russia Convention line; the Aleutian Islands Region encompassing the Aleutian Islands shelf region from 170°W to the U.S.-Russia Convention line; and the Central Bering Sea—Bogoslof Island pollock. These three management stocks probably have some degree of exchange. The Bogoslof stock is a group that forms a distinct spawning aggregation that has some connection with the deep water region of the Aleutian Basin. Bailey et al. (1999) present a thorough review of population structure of pollock throughout the north Pacific region. Recent genetic studies using mitochondrial DNA methods have found the largest differences to be between pollock from the eastern and western sides of the north Pacific.

The following is largely extracted from Barbeaux et al. (2004). See <http://www.afsc.noaa.gov/refm/docs/2004/AIpollock.pdf> for further details.

Previously, Ianelli et al. (1997) developed a model for Aleutian Islands pollock and concluded that the spatial overlap and the nature of the fisheries precluded a clearly defined “stock” since much of the catch was removed very close to the eastern edge of the region and appeared continuous with catch further to the east. In some years a large portion of the pollock removed in the Aleutian Islands Region was from deep-water regions and appear to be most aptly assigned as “Basin” pollock. This problem was confirmed and can be seen in the spatial distribution of historical catch patterns (Fig. 1). Hence, the data used here are organized to cover a region that is more consistent with survey observations and historical fishing patterns (Fig. 2).

The nature of the pollock fishery in the Aleutian Islands Region has varied considerably since 1977 due to changes in the fleet makeup and in regulations. During the late 1970s through the 1980s the fishing fleet was primarily foreign. In 1989, the domestic fleet began operating in earnest and has continued in the Aleutian Islands Region until 1999 when the North Pacific Fishery Management Council (NPFMC) recommended closing this region for directed pollock fishing due to concerns for Steller sea lion recovery. Length frequency data shows rather distinct characteristics when broken out by regions over this period (Fig. 3). There are notable similarities to the patterns over time for data from the eastern portion of the Aleutian Islands. This can also be seen from the mean-length of fish observed in the catch by these regions (Fig. 4). Another characteristic of the Aleutian Islands pollock is that mean length at age has changed substantially over time (Fig. 5). This pattern reflects the areas that are fished during these periods rather than actual changes in growth. I.e., during the early period, most of the pollock were caught towards the eastern edge of the Aleutian Islands region whereas the more recent period the pollock were from catch broadly distributed throughout the region.

The summer bottom trawl survey showed highly variable success in finding pollock in recent years, often with considerable concentrations toward the eastern edge (Fig. 6).

The R/V Kaiyo Maru conducted a survey between 170°W and 178°W longitude in the winter of 2002 after completing a survey of the Bogoslof region (Nishimura et al 2002; Fig. 7). Due to difficulties in operating their large mid-water trawl on the steep slope area they felt their catches in this area were insufficient for accurate



species identification and biomass estimation. They did however come up with some preliminary biomass estimations. For the entire area from 170°W and 178°W longitudes they estimated a biomass of 93,000 mt of spawning pollock biomass with between 61,000 mt estimated in the NRA east of 173°W and 32,000 mt in the remainder of the survey area to 178°W longitude. The largest aggregations in the NRA area were observed at 174°W longitude north of Atka Island. Most of the pollock echo sign was observed along the slope of the Aleutian Islands relatively near shore.

Process for setting ABC in Aleutian Islands

For many years, the Aleutian Islands pollock stock has lacked an age-structured model and the SSC has determined that the stock qualified for management under Tier 5 (see section below). In last year's assessment, preliminary explorations of several age-structured models were provided, all of which focused on the portion of the stock to the west of 174°W. For the 2004 management cycle, five alternative age-structured models were developed and evaluated. The 2004 assessment focused on two of those models, one of which (Model 1) uses data only from the portion of the stock to the west of 174°W, and the other of which (Model 1B) includes survey data from the entire Aleutian Islands management area. The Plan Team recommended the use of Model 1B, but due to the uncertainty in the survey catchability coefficient recommended setting the ABC below the maximum permissible level. The Plan Team, in their review of the assessment recommended setting the 2005 ABC at the equilibrium level associated with an $F_{40\%}$ harvest rate, which was 43,200 t.

The SSC determined that the Aleutian pollock stock did not qualify for management under Tier 3 and the stock remained at Tier 5. This was largely for concerns about conservation and acknowledged uncertainty that interacts with stock structure uncertainties and a reliable survey (summer bottom-trawl surveys done every other year are currently undertaken). The SSC therefore recommended a maximum permissible ABC for 2005 was computed as the product of the most recent survey biomass estimate (130,451 t) and 75% of the natural mortality rate (0.30), resulting in an ABC of 29,400 t, and an OFL of 39,100 t. The actual TAC was specified this year by congressional mandate at no more than 19,000 t. Under Tier 5, the stock is technically not evaluated for overfished determinations nor whether it is approaching an overfished condition. Nonetheless, based on the best available information the stock is not considered overfished nor is it approaching an overfished condition.

The 2005 Fishery

The directed Aleutian pollock fishery started in March, but little pollock was harvested. From 20 January – 15 April a total of 2,661 t of pollock were harvested in the Aleutian area out of the total 9,250 t first-season TAC. Preliminary reports from fishermen indicate that there was not adequate pollock sign outside of designated Steller sea lion critical habitat closure areas to justify continuation of the fishery in the first season. Also reported was large quantities of Pacific ocean perch in both the echosign and bycatch in the areas that vessels were allowed to fish. Since this was intended as primarily a roe-fishery, it is expected that much of the 2005 second-season TAC of 9,250 t will not be caught.

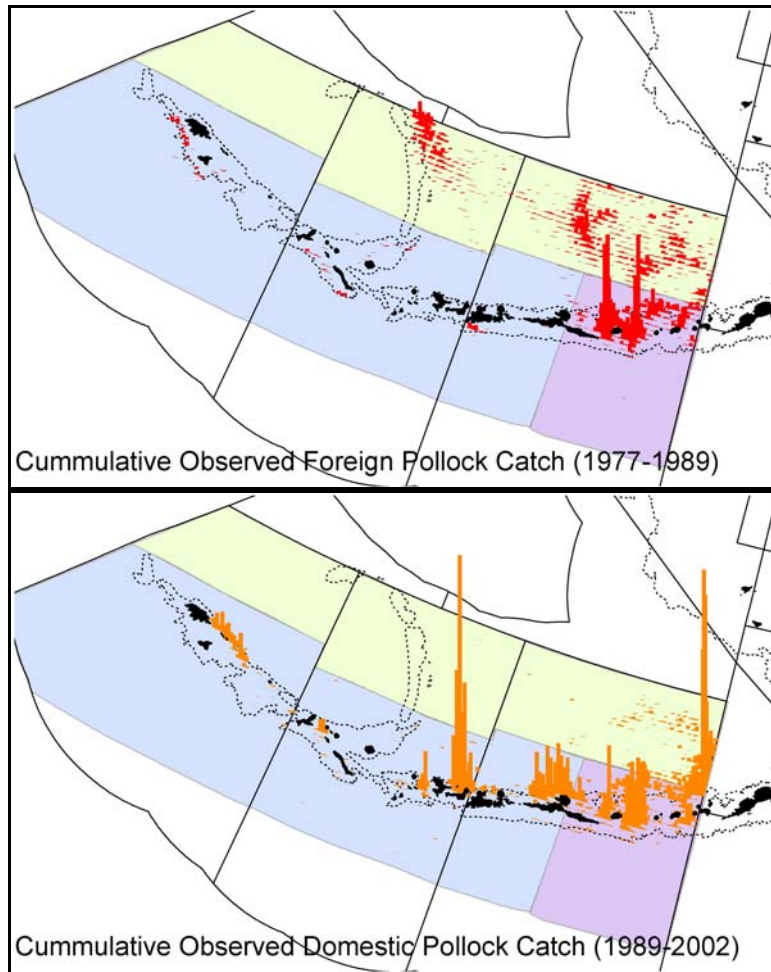


Figure 1. Observed foreign and J.V. (1978-1989), and domestic (1989-2002) pollock catch in the Aleutian Islands Area summed over all years and 10 minute latitude and longitude blocks. Both maps use the same scale (maximum observed catch per 10 minute block: foreign and J.V. 8,000 t and Domestic 19,000 t). Catches of less than 1 t were excluded from cumulative totals.

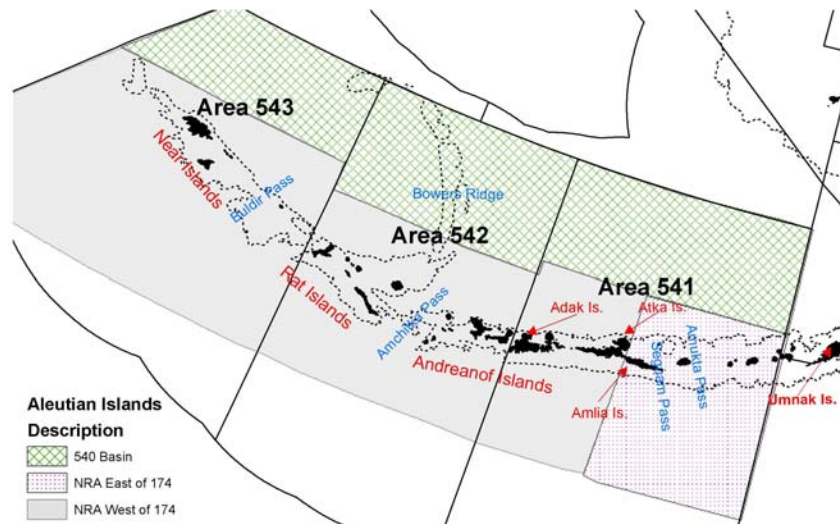


Figure 2. Regions defined for consideration of alternative data partitions for Aleutian Islands Region pollock. The abbreviation “NRA” represents the Near, Rat, and Andreanof Island groups.

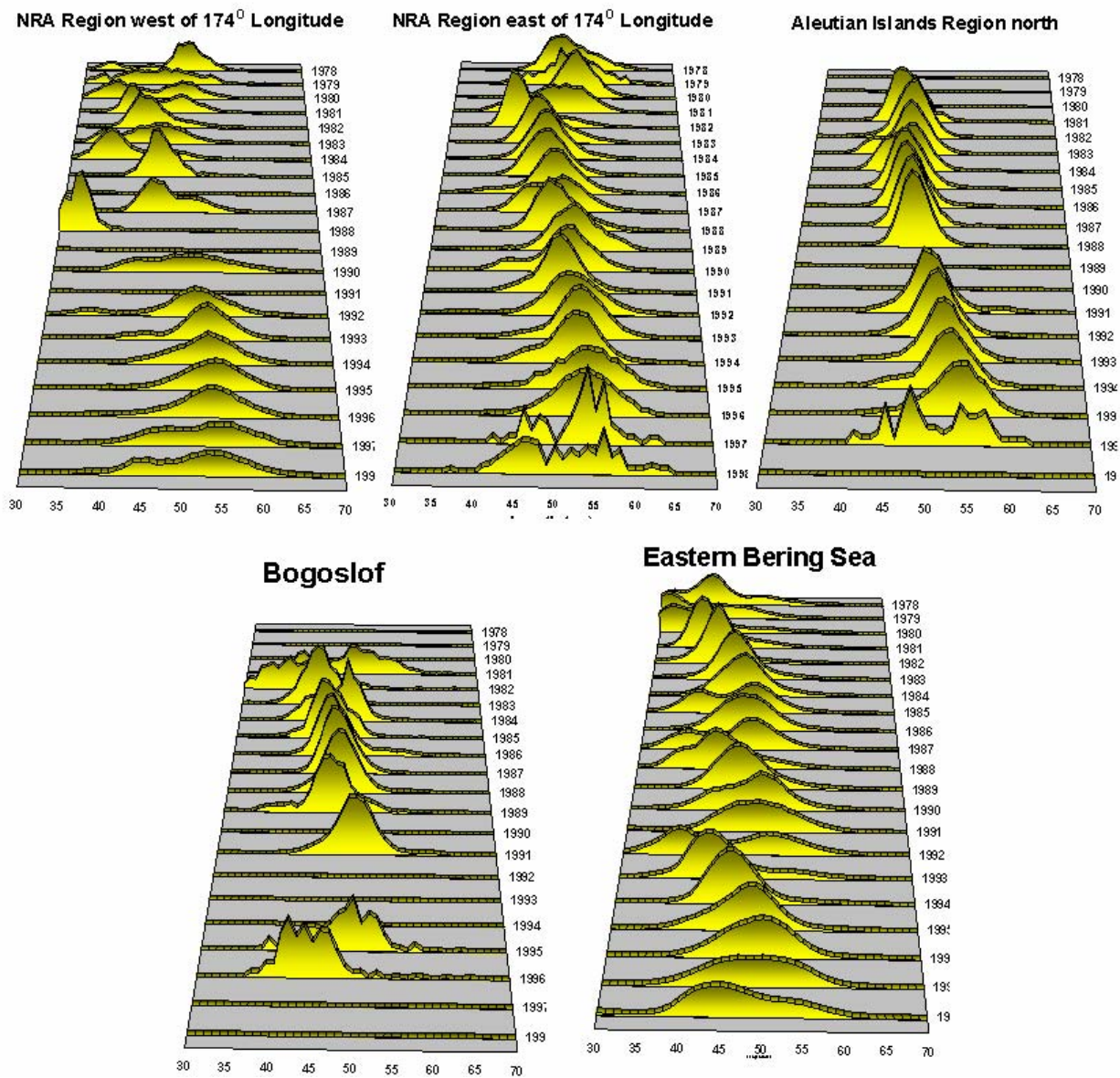


Figure 3. Pollock length frequency distributions by region.

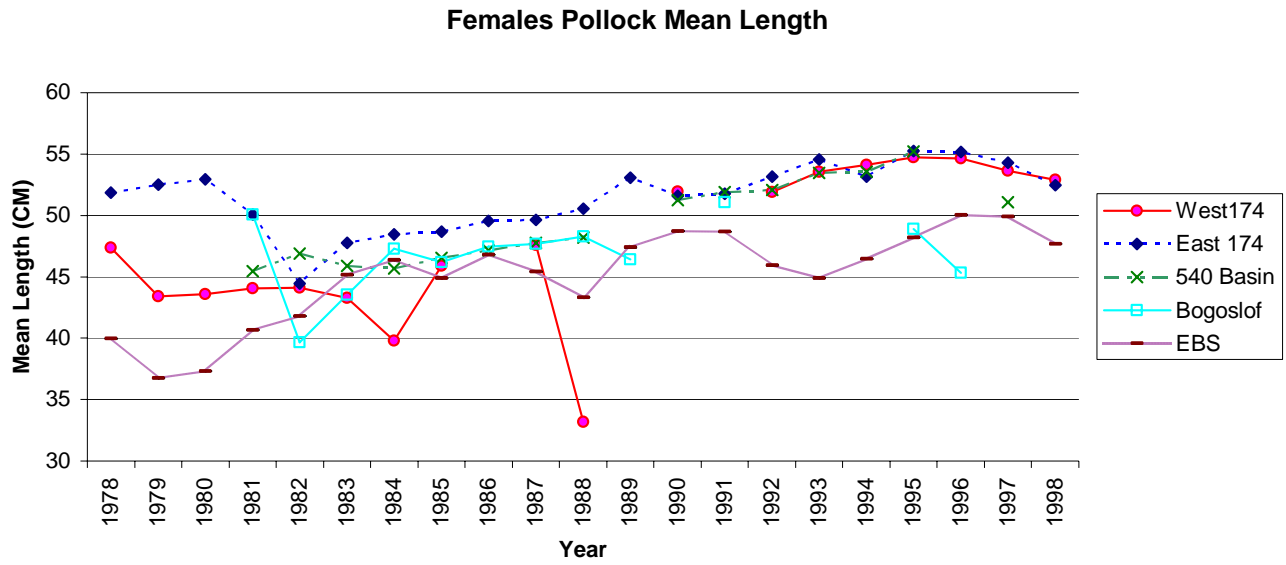


Figure 4. Mean length of female pollock in the catch from various areas based on observer data.

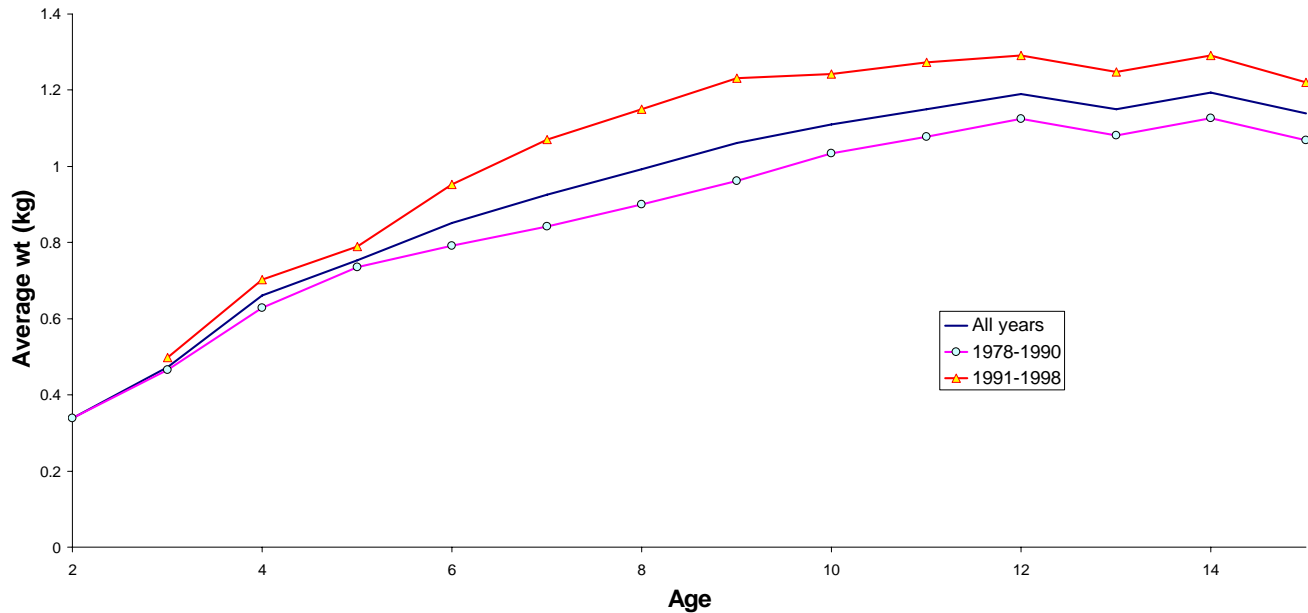


Figure 5. Average weight-at-age for Aleutian Islands pollock for all years combined, 1978-1990, and 1991-1998.

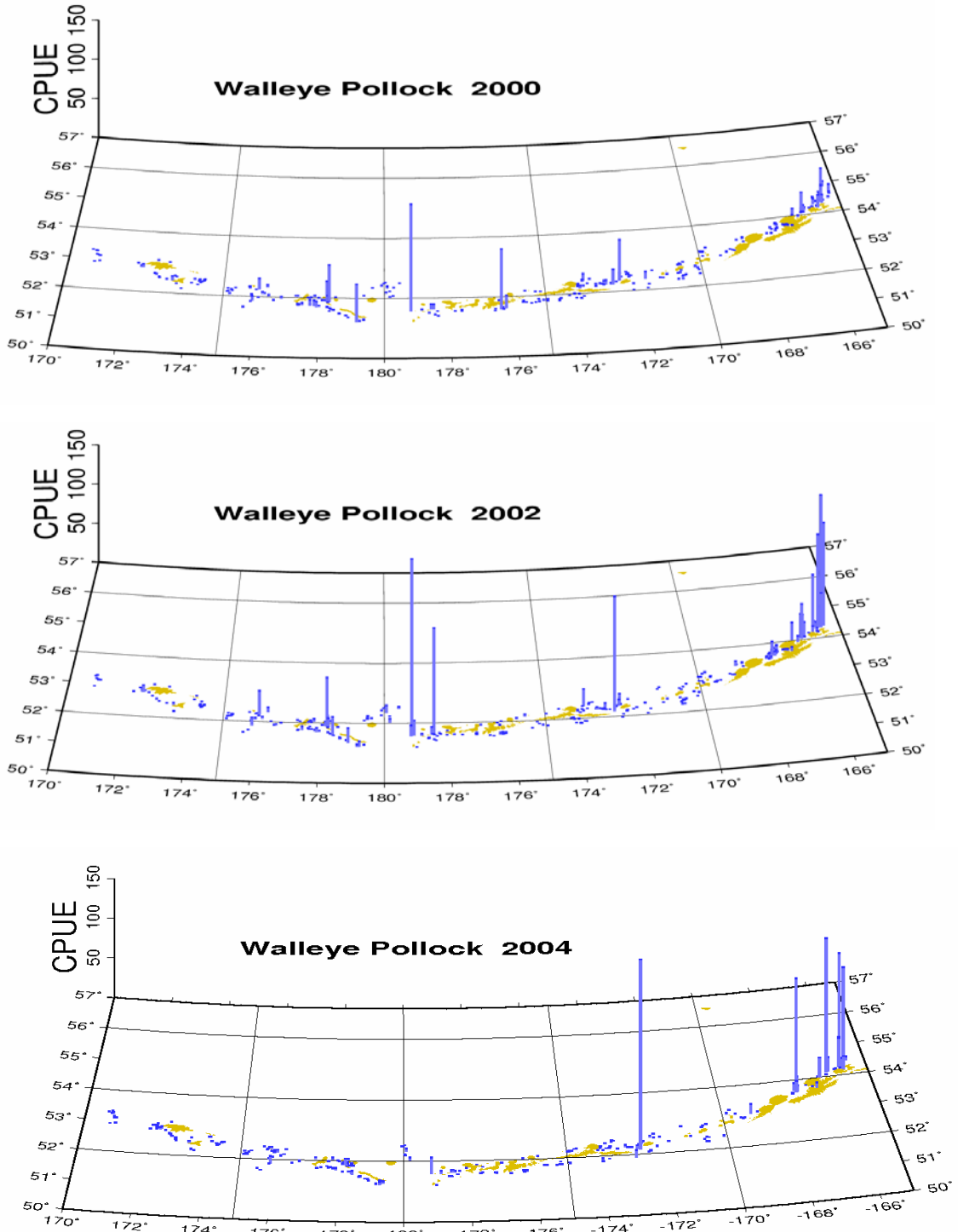


Figure 6. Catch per tow of pollock in the Aleutian Islands Region and east of 170°W during summer months from bottom-trawl surveys, 2000-2004.

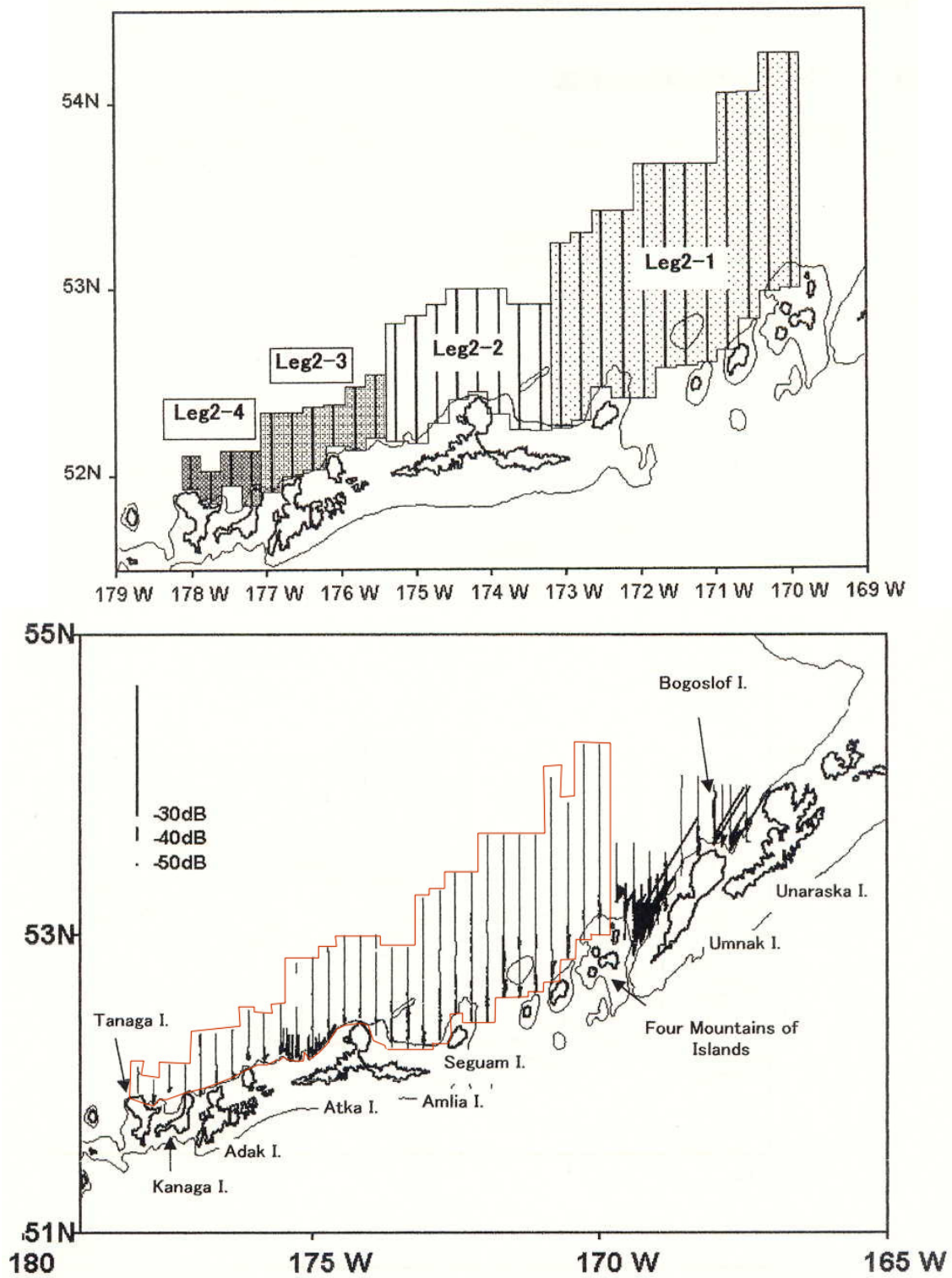


Figure 7. R/V Kaiyo Maru 2002 echo integration-trawl survey (above) strata for leg2 and below observed S_A in both legs. Please note that in the bottom picture the encircled area is leg 2.

Update on the status of Eastern Bering Sea pollock

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The pollock fishery in the EBS is the largest single-species fishery in the US and catches in the past few years have been at the highest levels in recent history, approaching 1.5 million t.

The following is largely extracted from Ianelli et al. (2004). See <http://www.afsc.noaa.gov/refm/docs/2004/EBSpollock.pdf> for further details.

Bottom trawl and echo-integration trawl surveys were conducted in summer 2004 in the eastern Bering Sea. The biomass estimate from the 2004 NMFS summer bottom-trawl survey was 3.75 million tons, a substantial drop from the value of 8.14 million tons estimated in 2003. The biomass estimate from echo-integration trawl survey was 3.31 million tons, down from 3.6 million tons estimated in 2002 but close to the average estimated by this survey since 1982 (3.36 million tons). Stock levels for EBS pollock appear to be lower overall than estimated in 2003 and the projected 2005 biomass is the lowest estimated since 1992. The 2000 year class appears to be above average and the main age group available to the fishery. Subsequent year classes are currently estimated to be below average and will result in further short-term declines in abundance. Projections (based on Tier 3 harvest levels) indicate the ABC could be below 1.1 million t by 2007 (Fig. 1). However, since in the BSAI region there is a cap on the total groundfish TAC of 2 million tons, the catch of pollock is unlikely to exceed 1.5 million t. Hence, projections using alternative constant catch scenarios may be more realistic for projection purposes (e.g., Fig. 2). While current stock levels are quite high, given the expected recruitment and array of year-classes available to this fishery, the stock is expected to decline in the next few years to near or below target levels.

ABC setting process for EBS pollock

The stock assessment for EBS pollock is considered by the NPFMC SSC to have reliable estimates of uncertainty in F_{msy} and SSB and therefore maximum permissible ABC and OFL are derived from Tier 1 of the amended FMP (see WP-7 of this meeting). As with all NPFMC groundfish species, the recommended ABC can be set below the maximum permissible ABC level. In practice, this is done for various conservation reasons including ecosystem concerns, stock status uncertainty, and analyses on risk aversion. The Tier 1 calculations are derived from a risk averse analysis and have the basic property that the greater the uncertainty (in F_{msy} and current stock size), the lower the maximum permissible ABC. For 2005, the maximum permissible ABC was 1.962 million tons, based on the harmonic mean value of F_{msy} . The OFL level was specified at 2.104 million tons corresponding to the arithmetic mean of F_{msy} . The TAC was set to 1.478 million t due to constraints imposed by having the sum of all groundfish TACs be no greater than 2.0 million t.

The 2005 Fishery

Preliminary results for the first half of the 2005 fishery indicate that production rates were similar to recent years (Fig. 3). The distribution of the catch has varied in this period but generally progresses from heavy concentrations of removals north of Unimak Island and extending north and west of this area along the 200 m isobath as the season develops (Fig. 4). A clearer picture emerges on catch-location variability if the spatial aspect of the fishery is plotted each year against some average catch level. This was done for the period 2000-2005 for the first months of the winter fishery (Fig. 5).



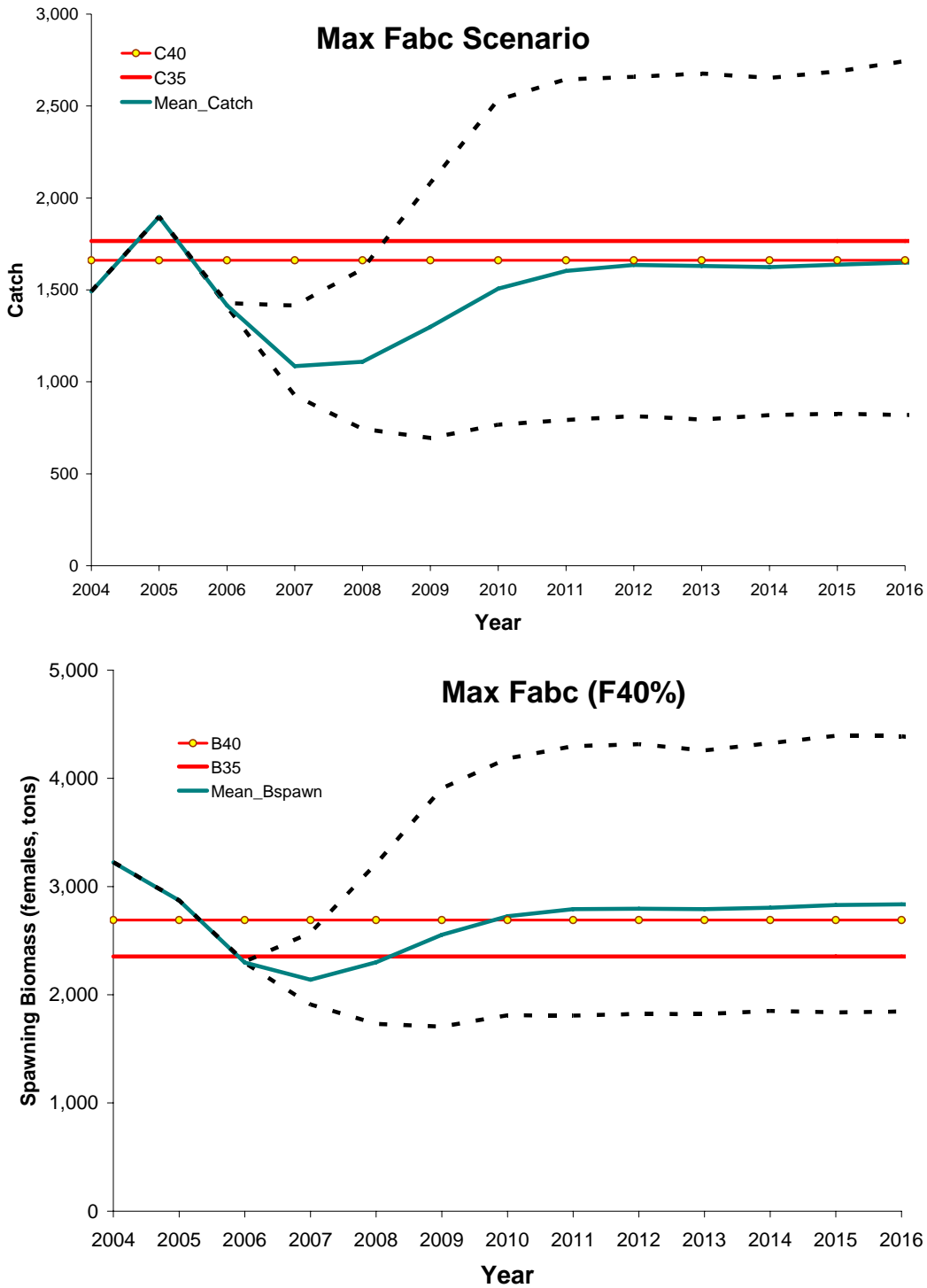


Figure 1. Projected EBS walleye pollock **yield** (top) and **Female spawning biomass** (bottom) relative to the long-term expected values under $F_{35\%}$ and $F_{40\%}$ (horizontal lines) for Model 1. $B_{40\%}$ is computed from average recruitment from 1978-2004. Future harvest rates follow the guidelines specified under Scenario 1, max F_{ABC} assuming $F_{ABC} = F_{40\%}$.

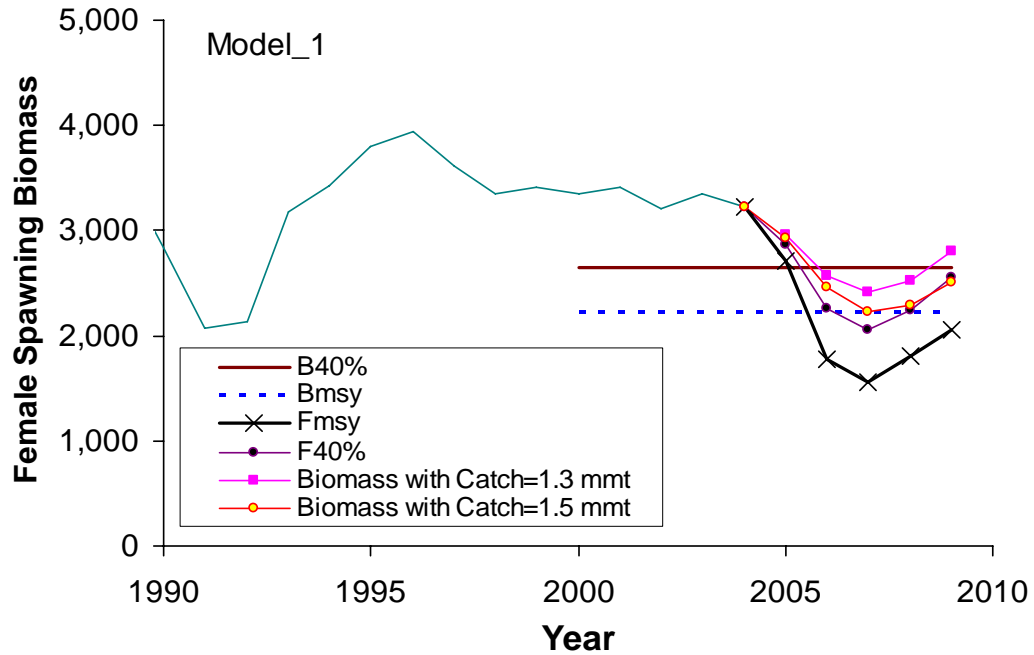


Figure 2. EBS walleye pollock female spawning biomass abundance trends, 1990-2009 as estimated by Ianelli et al., 2004 under different 2005-2009 harvest levels. Note that the F_{msy} and $F_{40\%}$ catch levels are unadjusted arithmetic mean fishing mortality rates. Horizontal solid and dashed lines represent the B_{msy} , and $B_{40\%}$ levels, respectively.

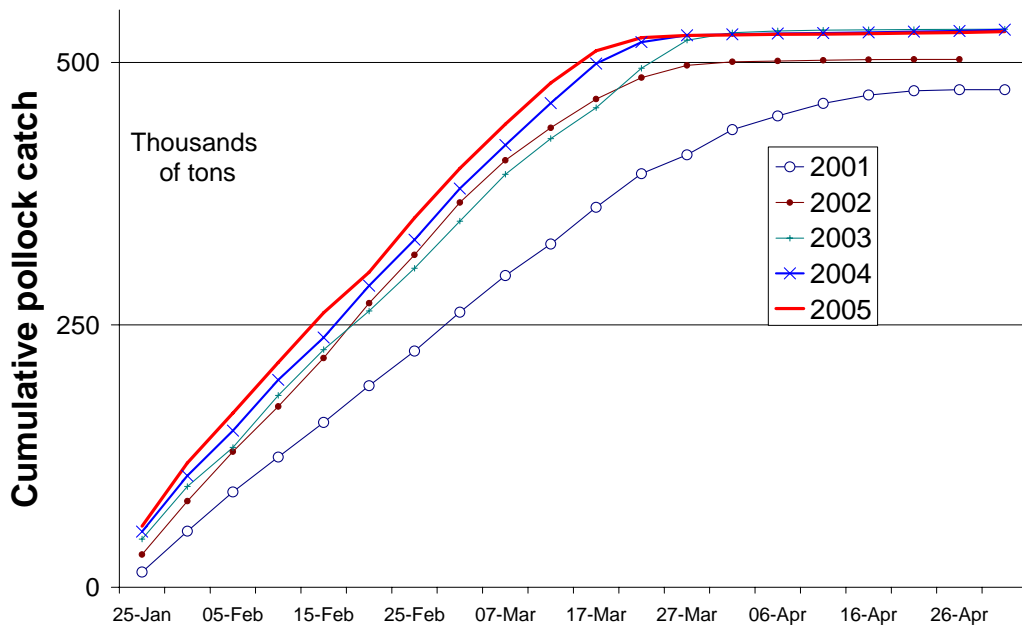


Figure 3. Cumulative catch levels for 2005 compared to recent years for the first season (winter) based on observer data.

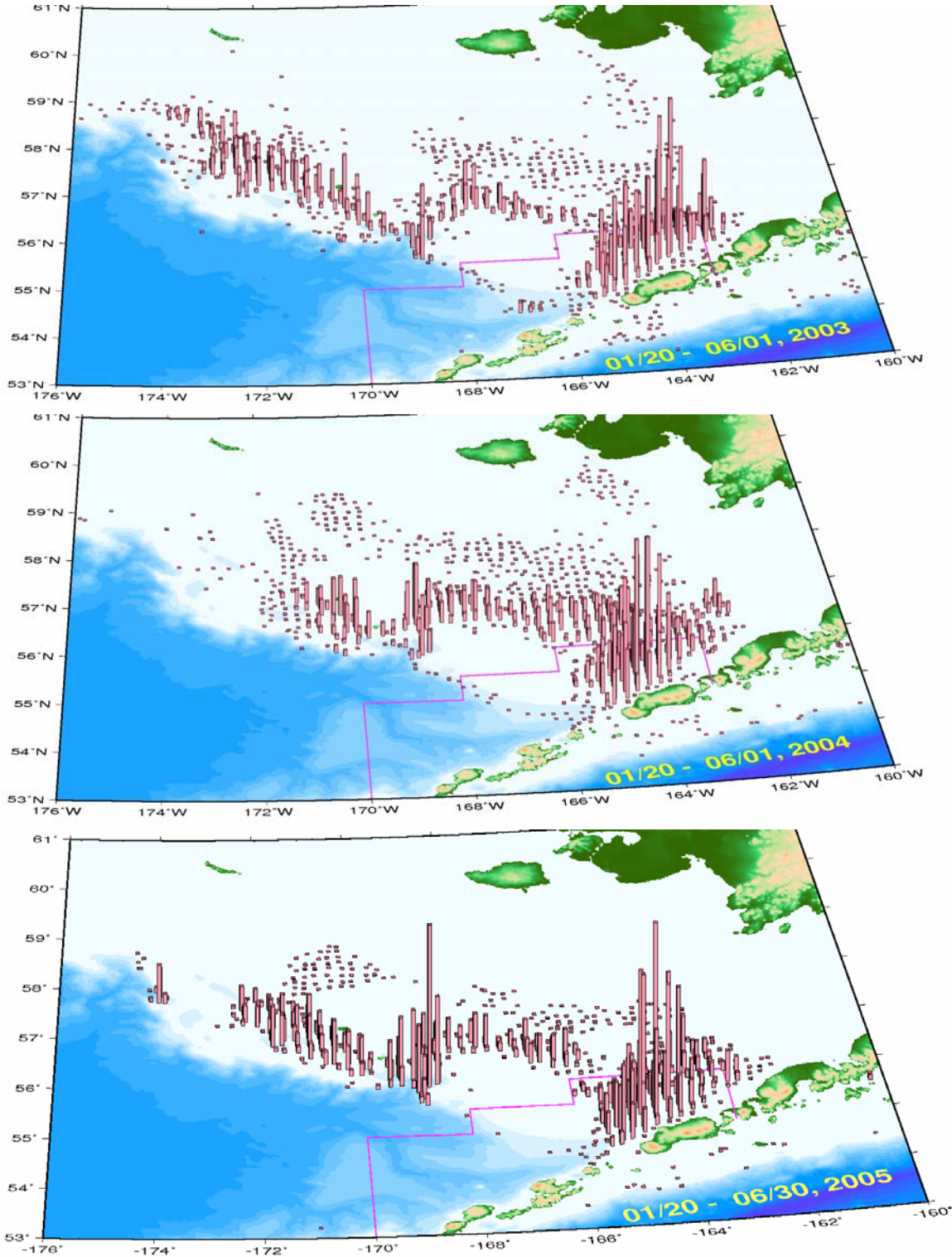


Figure 4. Concentrations of the pollock fishery 2003-2005, January - June on the EBS shelf. Line delineates SCA (sea lion conservation area). The column height represents relative removal on the same scale in all years.

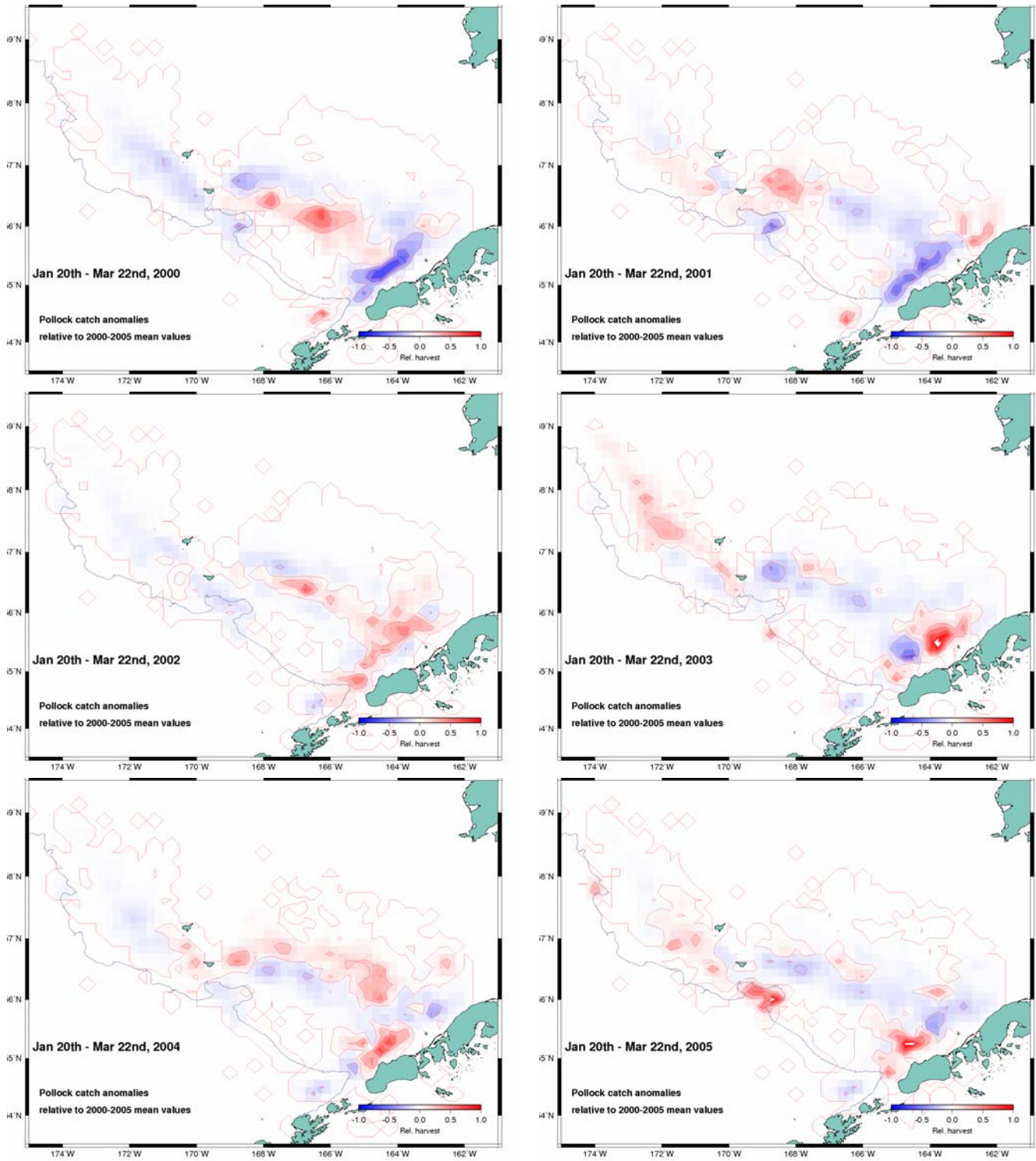


Figure 5. Geographic anomalies of catch for the period Jan 20th – March 22nd by year relative to the average catch over 2000-2005.

Review of the NPFMC approach for setting ABC and OFL levels

Amendment 56 to the GOA Groundfish FMP, approved by the Council in June 1998, defines ABC and OFL for the GOA groundfish fisheries. The definitions are shown below, where the fishing mortality rate is denoted F , stock biomass (or spawning stock biomass, as appropriate) is denoted B , and the F and B levels corresponding to MSY are denoted F_{MSY} and B_{MSY} respectively. The conditions for determining the fishing mortality rate under the amended FMP is shown in Box 1 below.

Acceptable Biological Catch is a preliminary description of the acceptable harvest (or range of harvests) for a given stock or stock complex. Its derivation focuses on the status and dynamics of the stock, environmental conditions, other ecological factors, and prevailing technological characteristics of the fishery. The fishing mortality rate used to calculate ABC is capped as described under “overfishing” below.

Overfishing is defined as any amount of fishing in excess of a prescribed maximum allowable rate. This maximum allowable rate is prescribed through a set of six tiers which are listed below in descending order of preference, corresponding to descending order of information availability. The SSC will have final authority for determining whether a given item of information is reliable for the purpose of this definition, and may use either objective or subjective criteria in making such determinations. For tier (1), a pdf refers to a probability density function. For tiers (1-2), if a reliable pdf of B_{MSY} is available, the preferred point estimate of B_{MSY} is the geometric mean of its pdf. For tiers (1-5), if a reliable pdf of B is available, the preferred point estimate is the geometric mean of its pdf. For tiers (1-3), the coefficient α is set at a default value of 0.05, with the understanding that the SSC may establish a different value for a specific stock or stock complex as merited by the best available scientific information. For tiers (2-4), a designation of the form “ $F_{X\%}$ ” refers to the F associated with an equilibrium level of spawning per recruit (SPR) equal to $X\%$ of the equilibrium level of spawning per recruit in the absence of any fishing. If reliable information sufficient to characterize the entire maturity schedule of a species is not available, the SSC may choose to view SPR calculations based on a knife-edge maturity assumption as reliable. For tier (3), the term $B_{40\%}$ refers to the long-term average biomass that would be expected under average recruitment and $F=F_{40\%}$.

In summary, Figure 1 shows a schematic of how harvest rates are adjusted depending on the current stock size. In this illustration, the MSST represents the minimum stock-size threshold, which for pollock occurs at 50% of the “target” biomass of $B_{40\%}$. Note that due to ecosystem concerns and Steller sea lion prey, the fishing mortalities will be specified to be zero should the stock drop below the MSST. This is further illustrated in a simulation showing catch and fishing mortality for a simple age-structured model result for Bogoslof pollock (Fig. 2). In practice, these harvest control rules have properties that enhance the likelihood that the stock will increase to above the target SSB when it drops below. At the other extremes (when stocks are at high levels), over-arching OY principles (e.g., bycatch constraints, 2 million t cap on all groundfish quotas) play a large role in preventing over-capitalization and thereby relieves some economic pressures when quotas are required to be reduced.



Box 1. Conditions for fishing mortality rates under the current (2004) Tier system used under amendment 56 to the FMP for North Pacific groundfish fisheries.

Tier	<p>1) Information available: <i>Reliable point estimates of B and B_{MSY} and reliable pdf of F_{MSY}.</i></p> <p>1a) Stock status: $B/B_{MSY} > 1$ $F_{OFL} = \mu_A$, the arithmetic mean of the pdf $F_{ABC} \leq \mu_H$, the harmonic mean of the pdf</p> <p>1b) Stock status: $\alpha < B/B_{MSY} \leq 1$ $F_{OFL} = \mu_A \times (B/B_{MSY} - \alpha)/(1 - \alpha)$ $F_{ABC} \leq \mu_H \times (B/B_{MSY} - \alpha)/(1 - \alpha)$</p> <p>1c) Stock status: $B/B_{MSY} \leq \alpha$ $F_{OFL} = 0$ $F_{ABC} = 0$</p> <p>2) Information available: <i>Reliable point estimates of B, B_{MSY}, F_{MSY}, F_{35%}, and F_{40%}.</i></p> <p>2a) Stock status: $B/B_{MSY} > 1$ $F_{OFL} = F_{MSY}$ $F_{ABC} \leq F_{MSY} \times (F_{40\%}/F_{35\%})$</p> <p>2b) Stock status: $\alpha < B/B_{MSY} \leq 1$ $F_{OFL} = F_{MSY} \times (B/B_{MSY} - \alpha)/(1 - \alpha)$ $F_{ABC} \leq F_{MSY} \times (F_{40\%}/F_{35\%}) \times (B/B_{MSY} - \alpha)/(1 - \alpha)$</p> <p>2c) Stock status: $B/B_{MSY} \leq \alpha$ $F_{OFL} = 0$ $F_{ABC} = 0$</p> <p>3) Information available: <i>Reliable point estimates of B, B_{40%}, F_{35%}, and F_{40%}.</i></p> <p>3a) Stock status: $B/B_{40\%} > 1$ $F_{OFL} = F_{35\%}$ $F_{ABC} \leq F_{40\%}$</p> <p>3b) Stock status: $\alpha < B/B_{40\%} \leq 1$ $F_{OFL} = F_{35\%} \times (B/B_{40\%} - \alpha)/(1 - \alpha)$ $F_{ABC} \leq F_{40\%} \times (B/B_{40\%} - \alpha)/(1 - \alpha)$</p> <p>3c) Stock status: $B/B_{40\%} \leq \alpha$ $F_{OFL} = 0$ $F_{ABC} = 0$</p> <p>4) Information available: <i>Reliable point estimates of B, F_{35%}, and F_{40%}.</i> $F_{OFL} = F_{35\%}$ $F_{ABC} \leq F_{40\%}$</p> <p>5) Information available: <i>Reliable point estimates of B and natural mortality rate M.</i> $F_{OFL} = M$ $F_{ABC} \leq 0.75 \times M$</p> <p>6) Information available: <i>Reliable catch history from 1978 through 1995.</i> $OFL =$ the average catch from 1978 through 1995, unless an alternative value is established by the SSC on the basis of the best available scientific information $ABC \leq 0.75 \times OFL$</p>
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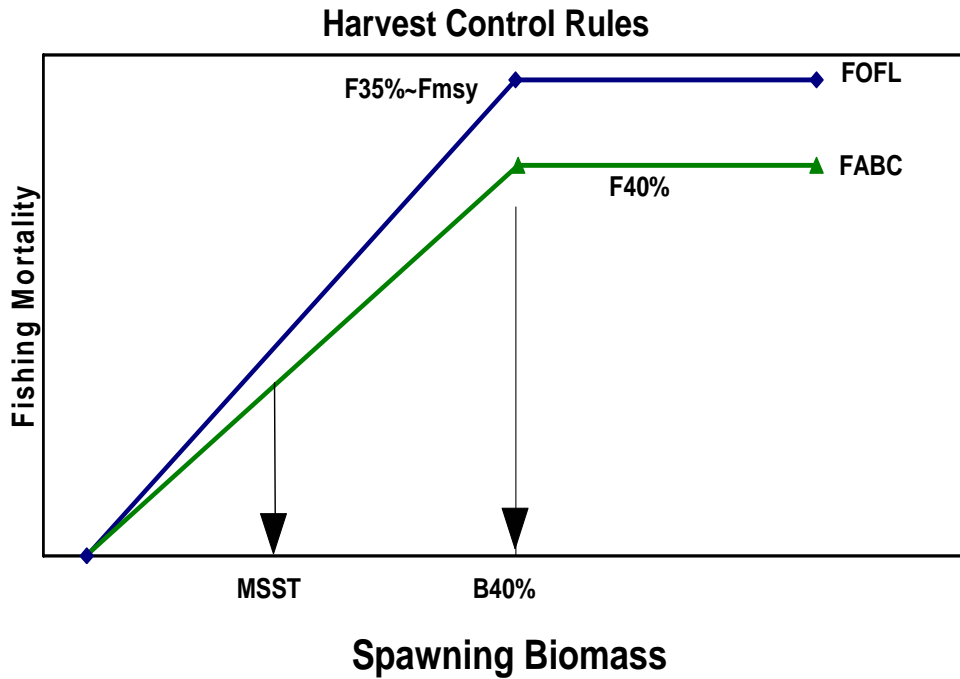


Figure 1. General schematic of harvest control rule used for N. Pacific groundfish stocks.

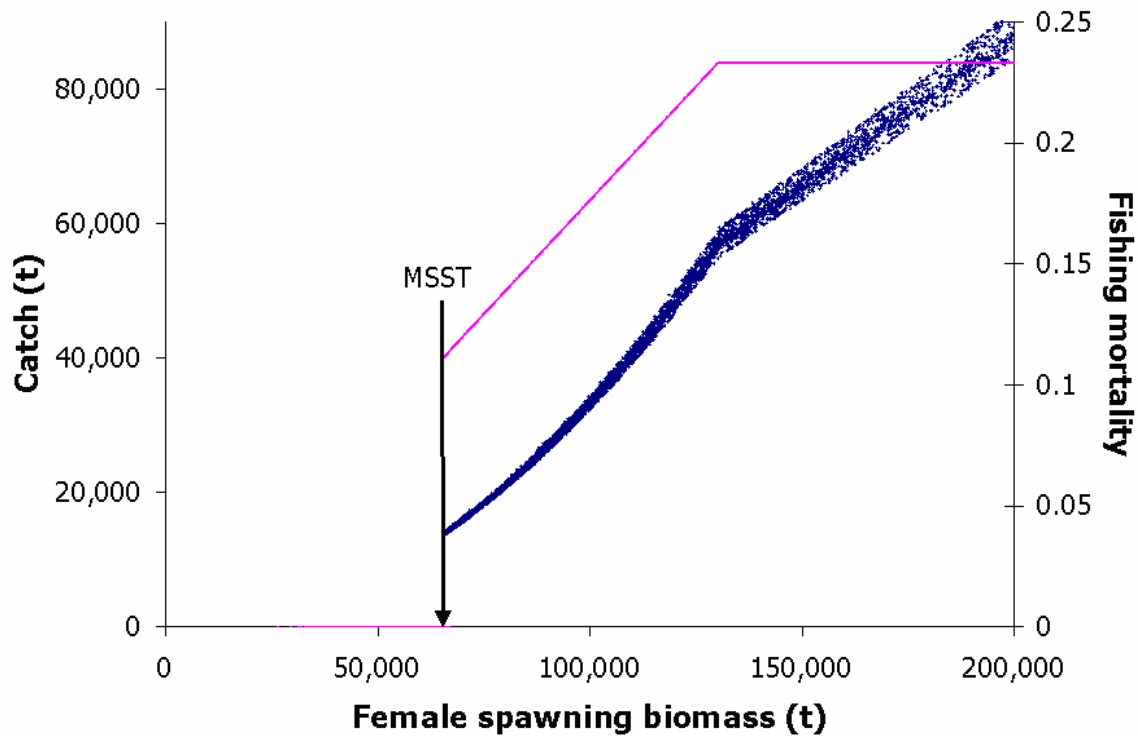


Figure 2. Simulation results showing harvest control rule in effect for Bogoslof pollock where the $B_{40\%}$ level is about 130,000 t of female spawning biomass and the MSST is about 65,000 t. The catch is shown by the band of points and the fishing mortalities by the straight line segments.

ABC, OFL, and TAC levels set for 2005 and 2006

In order to follow the administrative procedures act and follow the guidelines for environmental assessments of actions (including fishing), the NPFMC and NMFS now require estimates of ABC and OFLs (and preliminary TACs) projected for two years. The result of these projections are shown in the table below as published in the Federal Register.

8982 Federal Register / Vol. 70, No. 36 / Thursday, February 24, 2005 / Rules and Regulations

TABLE 1.—2005 AND 2006 OVERFISHING LEVEL (OFL), ACCEPTABLE BIOLOGICAL CATCH (ABC), TOTAL ALLOWABLE CATCH (TAC), INITIAL TAC (ITAC), AND CDQ RESERVE ALLOCATION OF GROUND FISH IN THE BSAI.¹
[Amounts are in metric tons]

Species	Area	2005					2006				
		OFL	ABC	TAC	ITAC ²	CDQ ³	OFL	ABC	TAC	ITAC ²	CDQ ³
Pollock ⁴	BS ²	2,100,000	1,960,000	1,478,500	1,330,650	147,850	1,944,000	1,617,000	1,487,756	1,338,980	148,776
	AI ²	39,100	29,400	19,000	17,100	1,900	39,100	29,400	19,000	17,100	1,900
	Bogoflot	39,600	2,570	10	10		39,600	2,570	10	10	
Pacific cod	BSAI	265,000	206,000	206,000	175,100	15,450	228,000	195,000	195,000	165,750	14,625
Sablefish ⁵	BS	2,950	2,440	2,440	2,013	336	2,690	2,310	2,310	982	87
	AI	3,170	2,620	2,620	2,129	442	2,880	2,480	2,480	527	47
Atka mackerel	BSAI	147,000	124,000	63,000	53,550	4,725	127,000	107,000	63,000	53,550	4,725
	EAI/BS		24,550	7,500	6,375	563		21,190	7,500	6,375	563
	CAI		52,830	35,500	30,175	2,663		45,580	35,500	30,175	2,663
	WAI		46,620	20,000	17,000	1,500		40,230	20,000	17,000	1,500
Yellowfin sole	BSAI	148,000	124,000	90,686	77,083	6,801	133,000	114,000	90,000	76,500	6,750
Rock sole	BSAI	157,000	132,000	41,500	35,275	3,113	145,000	122,000	42,000	35,700	3,150
Greenland turbot	BSAI	19,200	3,930	3,500	2,975	263	11,100	3,600	3,500	2,975	263
	BS		2,720	2,700	2,295	203		2,500	2,500	2,125	188
	AI		1,210	800	680	60		1,100	1,000	850	75
Arrowtooth flounder	BSAI	132,000	108,000	12,000	10,200	900	103,000	88,400	12,000	10,200	900
Flathead sole	BSAI	70,200	58,500	19,500	16,575	1,463	56,100	48,400	20,000	17,000	1,500
Other flatfish ⁶	BSAI	28,500	21,400	3,500	2,975	263	28,500	21,400	3,000	2,550	225
Alaska plaice	BSAI	237,000	189,000	8,000	6,800	600	115,000	109,000	10,000	8,500	750
Pacific ocean perch	BSAI	17,300	14,600	12,600	10,710	945	17,408	14,600	12,600	10,710	945
	BS		2,920	1,400	1,190	105		2,920	1,400	1,190	105
	EAI		3,210	3,080	2,618	231		3,210	3,080	2,618	231
	CAI		3,165	3,035	2,580	228		3,165	3,035	2,580	228
	WAI		5,305	5,085	4,322	381		5,305	5,085	4,322	381
Northern rockfish	BSAI	9,810	8,260	5,000	4,250	375	9,480	8,040	5,000	4,250	375
Shortraker rockfish	BSAI	794	596	596	507	45	794	596	596	507	45
Roughye rockfish	BSAI	298	223	223	190	17	298	223	223	190	17
Other rockfish ⁷	BSAI	1,870	1,400	1,050	883	79	1,870	1,400	1,050	883	79
	BS		810	460	391	35		810	460	391	35
	AI		590	590	502	44		590	590	502	44
Squid	BSAI	2,620	1,970	1,275	1,084		2,620	1,970	1,275	1,084	
Other species ⁸	BSAI	87,920	53,860	29,000	24,650	2,175	87,920	57,870	29,200	24,820	2,190
Total		3,509,332	3,044,769	2,000,000	1,774,719	186,608	3,093,360	2,547,259	2,000,000	1,772,778	187,350

¹These amounts apply to the entire BSAI management area unless otherwise specified. With the exception of pollock, and for the purpose of these harvest specifications, the Bering Sea (BS) subarea includes the Bogoflot District.
²Except for pollock and the portion of the sablefish TAC allocated to hook-and-line and pot gear, 15 percent of each TAC is put into a reserve. The ITAC for each species is the remainder of the TAC after the subtraction of these reserves.
³Except for pollock, squid and the hook-and-line or pot gear allocation of sablefish, one half of the amount of the TACs placed in reserve, or 7.5 percent of the TACs, is designated as a CDQ reserve for use by CDQ participants (see §§679.20(b)(1)(iii) and 679.31).
⁴Under §679.20(a)(5)(i)(A)(1), the annual Bering Sea pollock TAC after subtraction for the CDQ directed fishing allowance—10 percent and the ICA—3.35 percent, is further allocated by sector for a directed pollock fishery as follows: inshore—50 percent; catcher/processor—40 percent; and motherships—10 percent. Under regulations that would be effective with the final rule implementing Amendment 82, the annual AI pollock TAC, after first subtracting for the CDQ directed fishing allowance—10 percent and second the ICA—2,000 mt., would be allocated to the Aleut Corporation for a directed pollock fishery.
⁵Twenty percent of the sablefish TAC allocated to hook-and-line gear or pot gear and 7.5 percent of the sablefish TAC allocated to trawl gear is reserved for use by CDQ participants (see §679.20(b)(1)(iii)).
⁶“Other flatfish” includes all flatfish species, except for halibut (a prohibited species), flathead sole, Greenland turbot, rock sole, yellowfin sole, arrowtooth flounder and Alaska plaice.
⁷“Other rockfish” includes all *Sebastes* and *Sebastolobus* species except for Pacific ocean perch, northern, shortraker, and roughye rockfish.
⁸“Other species” includes sculpins, sharks, skates and octopus. Forage fish, as defined at §679.2, are not included in the “other species” category.

Summary of genetic stock identification studies in the Bering Sea

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Early studies of allozyme variation in walleye pollock (Iwata 1975; Grant and Utter 1980) reported differentiation across broad spatial scales in the Bering Sea. A more recent study using mitochondrial DNA restriction fragment length polymorphism (RFLP) provided some evidence for population substructure at smaller spatial scales in the eastern Bering Sea (Mulligan et al. 1992). However, other studies examining mtDNA (Shields and Gust 1995; Kim et al. 2000), nuclear microsatellite DNA (O'Reilly et al. 2004), or a combination of allozyme and mtDNA variation (Olsen et al. 2002) have failed to resolve stock discretion in the eastern Bering Sea. A study of variation at the pantophysin (Pan I) locus (Canino et al. in press), a gene that appears to be influenced by natural selection (Canino and Bentzen 2004), showed a clear distinction between a sample from the central Bering Sea and the Unimak Pass area (Fig. 1). However, the central Bering Sea sample was taken in September, thus the potential for stock admixture can not be ruled out. Gene frequency distributions at the Pan I locus were correlated with water temperatures (Fig.2) suggesting the effects of temperature-mediated selection over moderate geographic scales. Table 1 summarizes various genetic studies on pollock, the areas covered, methods used, and key results.

Currently, there is no conclusive evidence for genetic discretion of the Donut Hole stock component in the Bering Sea. Results from Mulligan et al. (1992) showed a sample from Adak Island to be distinct from samples in the Donut Hole or from Bogoslof Island but the Donut Hole sample did not show significant differentiation from Bogoslof Island in the eastern Bering Sea. Sample sizes from the two studies that included the Donut hole area (Mulligan et al. 1992, n = 50; Shields and Gust 1995, n = 8) are too small, and mtDNA variation may not be sufficiently polymorphic to resolve expected weak levels of population structuring in walleye pollock. Future efforts should be directed towards collecting larger samples (e.g. 100 - 200 individuals) from spawning aggregates and the use of highly polymorphic markers (e.g. microsatellites).

General conclusions from recent genetic studies

- Evidence for subpopulation structuring within the Bering Sea (Olsen et al. 2002; Canino et al. in press) and between the Bering Sea and the Gulf of Alaska (Olsen et al. 2002; O'Reilly et al 2004;
- No evidence for genetic discretion of the Donut hole stock component

Possible reasons:

- small sample sizes (Mulligan et al. 1992, n = 50; Shields & Gust 1995, n = 8)
- samples taken from non-spawning individuals



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Table 1. Studies of genetic population structure in walleye pollock since 1998

Study	Area	Marker	Results
Kim et al. 2000	Korea -Bogoslov	mtDNA RFLP	<ul style="list-style-type: none"> no significant genetic heterogeneity
Olsen et al. 2002	Western north Pacific, Eastern BS, GOA, PWS	mtDNA RFLP allozyme microsatellites	<ul style="list-style-type: none"> east -west heterogeneity between Asian and N American populations regional heterogeneity among GOA samples (PWS vs SHEL) Discordant results between BS and GOA - significant differentiation observed with allozymes and mtDNA but in different years
O'Reilly et al. 2004	Western north Pacific, North Central BS, Eastern BS, GOA, Puget Sound	microsatellites	<ul style="list-style-type: none"> weak structuring (global $F_{ST} = 0.004$) genetic isolation by distance over moderate scales (~1500 km) sign. genetic differentiation between NCBS and GOA
Canino et al. In press	Western north Pacific, North Central BS, Eastern BS, GOA, Puget Sound	pantophysin (Pan I) locus	<ul style="list-style-type: none"> stronger differentiation than observed with microsatellites (global $F_{ST} = 0.038$) north-south cline in Pan I allele frequencies correlated with water temperature North Central BS sample differentiated from Eastern BS and PWS sample
Grant In review	reanalysis of data from Mulligan et al. 1992 Kim et al. 2000 Olsen et al. 2002	mtDNA	<ul style="list-style-type: none"> nested clade analysis indicated 3 phylogroups within data in Mulligan et al. 1992 and Olsen et al. 2002 studies mosaic patterns in subpopulation diversity over moderate geographic scales but no clear pattern in range-wide diversity patterns best explained by metapopulation dynamics

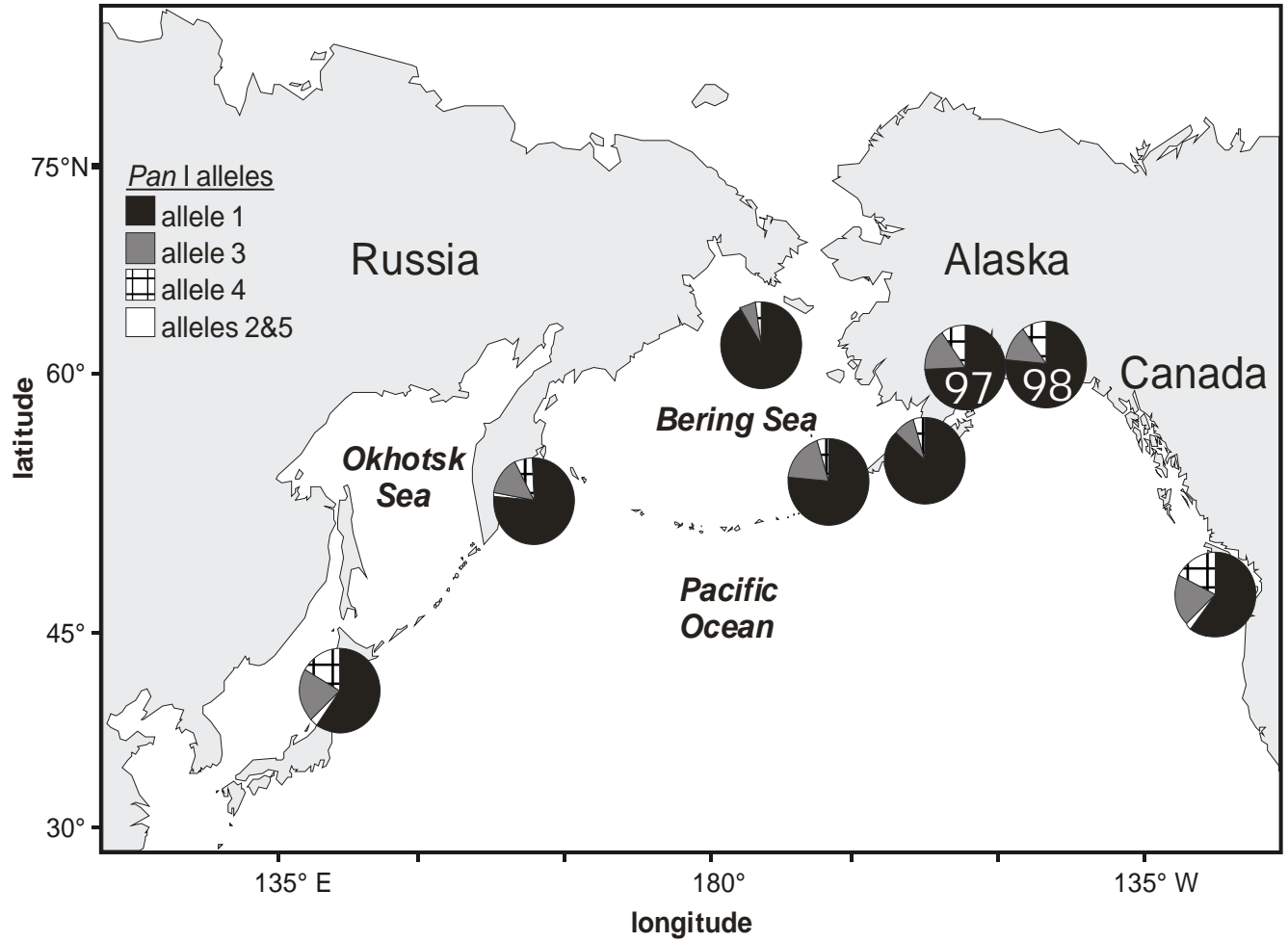


Figure 1. Frequencies of *Pan I* alleles in walleye pollock (*Theragra chalcogramma*). Samples taken in Prince William Sound in 1997 and 1998 are indicated by year. (Canino et al. in press).

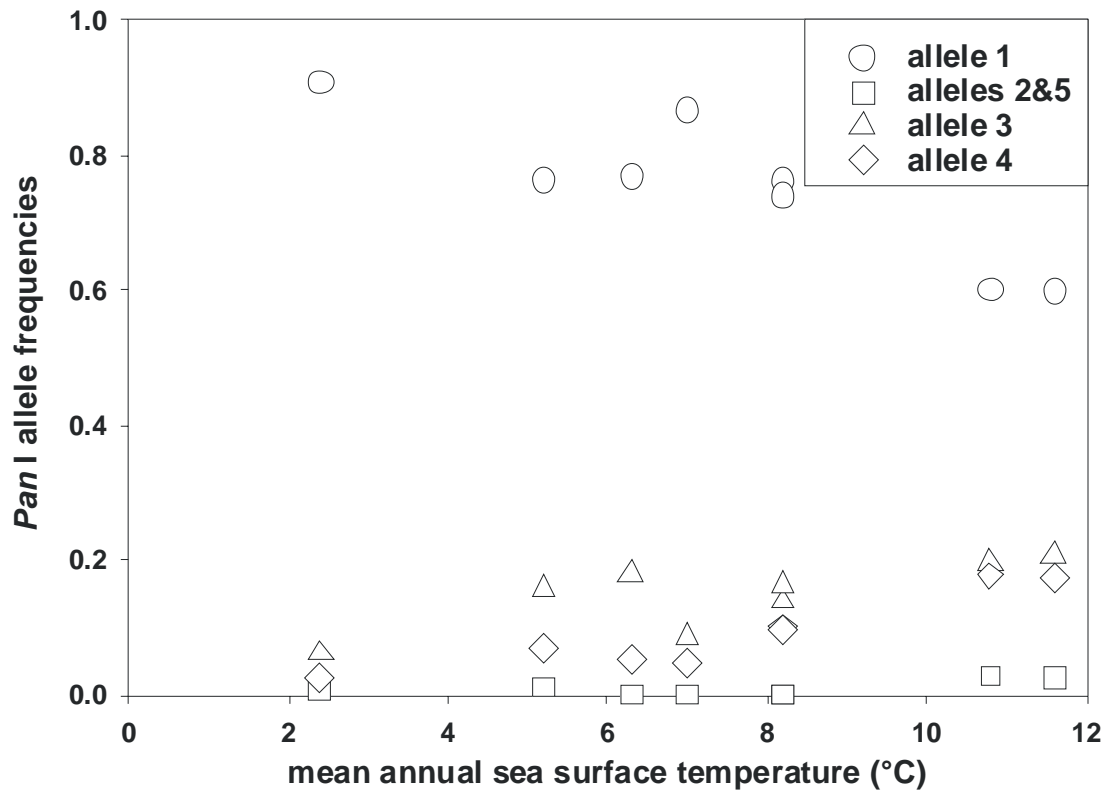


Figure 2. Frequency occurrence of Pan I alleles in walleye pollock (*Theragra chalcogramma*) versus estimated annual mean surface temperature. (Canino et al. in press).

List of Participants

Central Bering Sea Pollock Workshop

June 6-9, 2005

Jimmie Traynor Room, Building 4

NOAA Regional Center

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Microsatellite analysis of the population structure of the Bering Sea pollock

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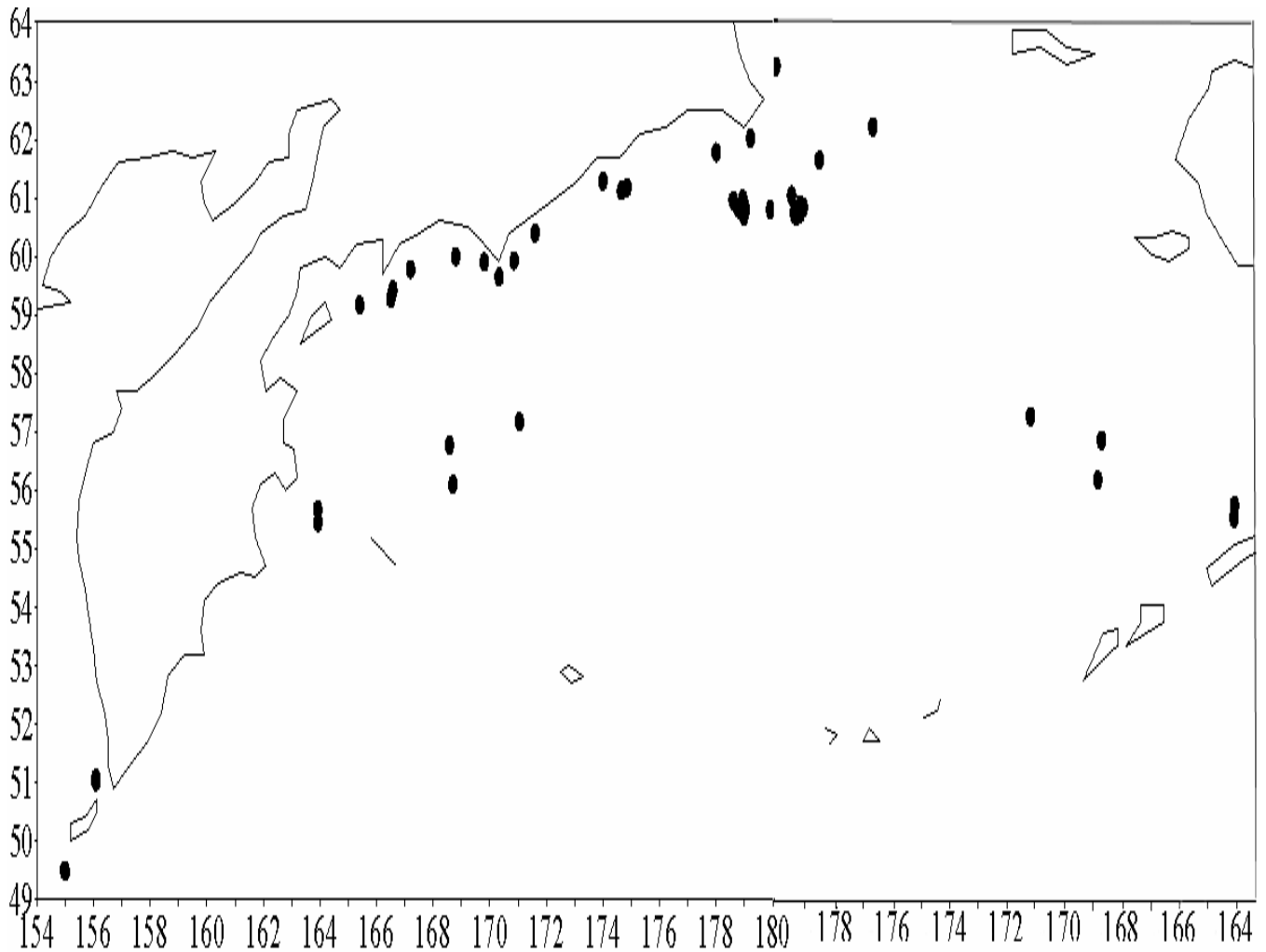
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The study continues a series of effort aimed at genetic certification of the spawning concentrations of the Bering Sea pollock using microsatellite markers. The numerous microsatellite loci are relatively evenly distributed throughout the genomes and, as a rule, are marked by a high allele polymorphism. Such polymorphism emerges thanks to the DNA-polymerase sliding through along one of the chains in the process of replication. The allele variants are inherited according to Mendel laws, and are customarily considered to be selectively neutral. Despite the very low values of differentiation indices caused by the large effective population size and a high level of gene flow, the sea fishes, including pollock, are weakly but significantly genetically structured by neutral loci within a vast spatial scale (Bailey et al., 1999, DeWoody&Avisé, 2000, Bentzen et al., 1996). The Bering Sea pollock was analyzed previously using Karagin, Olutor, Koryak, Navarin and North Kuril concentration samples. It was shown, however, that the genetic distances between the territorially separated spawning concentrations are short, and the dendrograms founded on those distances are not stable. The microsatellite DNA molecular features marked by homoplasies (i.e. differences in the ways of evolution of the same allele variants), and the high probability of reverse mutations slow down the allele frequencies becoming divergent among various spawning concentrations, and entail discrepancies between the results obtained from the samples separated by considerable time intervals (Olsen et al., 2002). The minimum size of sample for the sea fish species of little variance is 70-150 fish depending on the number of allele variants. The number of preparations examined from each sample must not be less than 50. The specimens from territorially distant spawning stocks of an established population status should be introduced into the analysis.

Our study involved the analysis of 306 specimens from six regions of the Bering Sea (Fig. 1): Karagin, Olutor, Shirshov Ridge, Navarin, North Kuril and East Bering Sea. The pollock samples from the East Bering Sea were provided by the courtesy of N. Williamson (Alaska Fisheries Research Center).

N



E

W

Fig. 1. Sites of genetic sampling.

Materials and methods

Nine microsatellite loci identified by O'Reilly (O'Reilly et al., 2000) were selected for analysis: Tch5, Tch10, Tch12, Tch13, Tch14, Tch15, Tch18, Tch19 and Tch22. The sequences of nine microsatellite sites and their primers are given in Figure 2.

Tch5	(GATA) ₁₄ F: gcc tta ata tca cgc aca R: tcg cat tga gcc tag ttt
Tch10	(GGCT) ₆ CTCT (GTCT) ₂ F: gtc tct atg tct gtc ttt cta ttt g R: acg aaa ccc aac cct gat t
Tch12	(GGTT) ₂₂ F: caa ttt gtc agc ctc tgt tac c R: agt aca gct tga ttg ttt ctg gg
Tch13	(GT) ₉ F: ttt ccg atg agg tca tgg R: agt aca gct tga ttg ttt ctg gg
Tch14	(GAAA) ₃₁ F: cat aca ttg gtc act ctt tct tac R: aaa ctg ata tac gcc caa ct
Tch15	(GA) ₃ (CA) ₂ GACA (GA) ₅ CAGATA(GA) ₈ F: aaa ctt cac ctg acc aac R: gca aca caa ctt aat cat ct
Tch18	(GT) ₁₅ F: gga gat ggt gct aac tgg R: aac gca cat gca cat acg.
Tch19	(GTCT) ₁₅ F: tat gct gat tgg tta ggc R: gat cat ttg ttt cag aga gc
Tch22	(GACA) ₆ F: atc ata tct ggc caa gtt c R: ctc tct ctg aat ccc tct g

Fig. 2. The sequences of nine microsatellite sites and their primers (F-forward; R-reverse).

Electrophoretic subdivision of allele variants and genotyping

The PCR products containing microsatellite fragments were divided in a 6% or 8% polyacrylamid gel in TB acetate. Upon the completion of electrophoresis the gels were colored with ethidium bromide and photographed in UV light. Allele variants were typed with KODAK 1D Image analysis software. When data on marker fragment size is introduced this program allowed us to determine the absolute size of microsatellite alleles. An example of stage of typing process is given in the Figure 3.

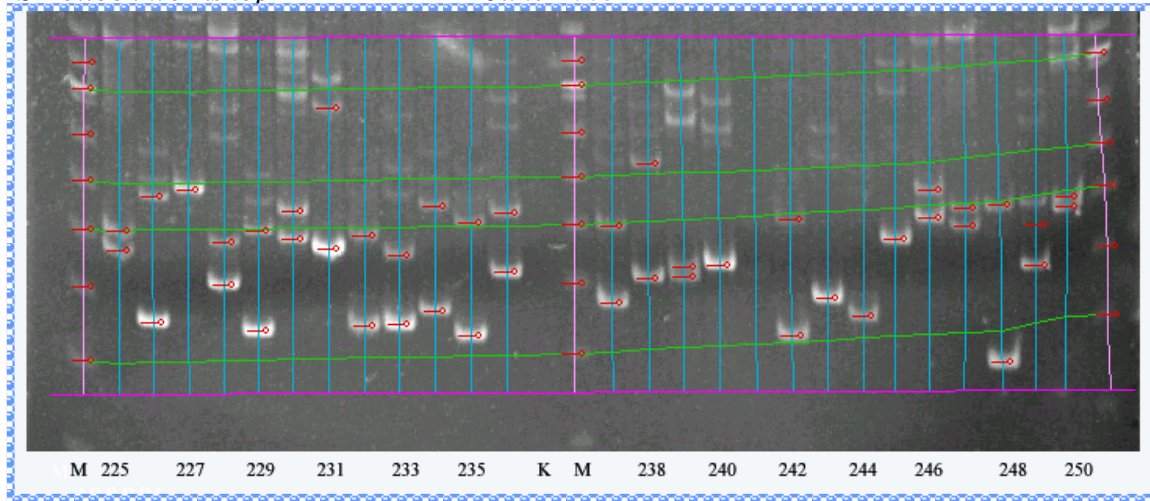


Fig. 3. Locus Tch19 type setting stage.

The products of typing of Tch13, Tch15, Tch18 and Tch22 loci were chemically not stable; that is why those loci were excluded from the analysis.

Tables of allele variants were compiled on the basis of typing.

The genetic parameters of the expected populations examined were determined using TFPGA (Miller, 1997) and GENEPOP 3.1. (Raimond and Rousset, 1995) programs. Hardy-Weinberg equilibrium performance was verified by individual loci of specific populations using criterion χ^2 and Haldane (1954) test, with a 99% significance limit (TFPGA), and Guo-Thompson method for polymial distribution (GENEPOP). The equilibrium of populations in Markov chain algorithms was verified by Haldane (1954), Weir (1990) and Robertson-Hill (1984) summary test and Fisher probability test based on tables of conjugated characteristics for each locus, for the given population, and for all loci and populations in general. The genotype imbalance by conjugation was found by pairs between loci within each population, and for all populations simultaneously. The values of F_{is} , F_{it} and F_{st} . (f , F and Θ in Weir-Cockerham algorithms) was determined for all populations by individual loci and alleles, and for all population pairs. The jackknife procedure applied by the loci totally made it possible to estimate F-statistic variance, while the bootstrap procedure set up confidence limits. In the given case one thousand bootstrap steps were made for the 95% level. The interpopulation genetic distances (Nei, 1972, 1978) were calculated as based on the value of F_{st} ($F_{st} = 2D^2$) and are expressed both as a diagonal matrix, and graphically as an unrooted UPGMA dendrogram (TFPGA, PHYLIP).

The genotype imbalance by linkage was determined by pairs between loci within each population, and by all populations together.

Results and discussion

The results of genotyping of DNA preparations by loci are represented in histograms. The height of tiers corresponds to the absolute values of allele frequencies in the given sample; X-axis shows the allele variants of loci while the Y-axis shows the frequency of their occurrence.

Small differences in histograms from various samples were recorded in locus Tch5 (Fig. 4).

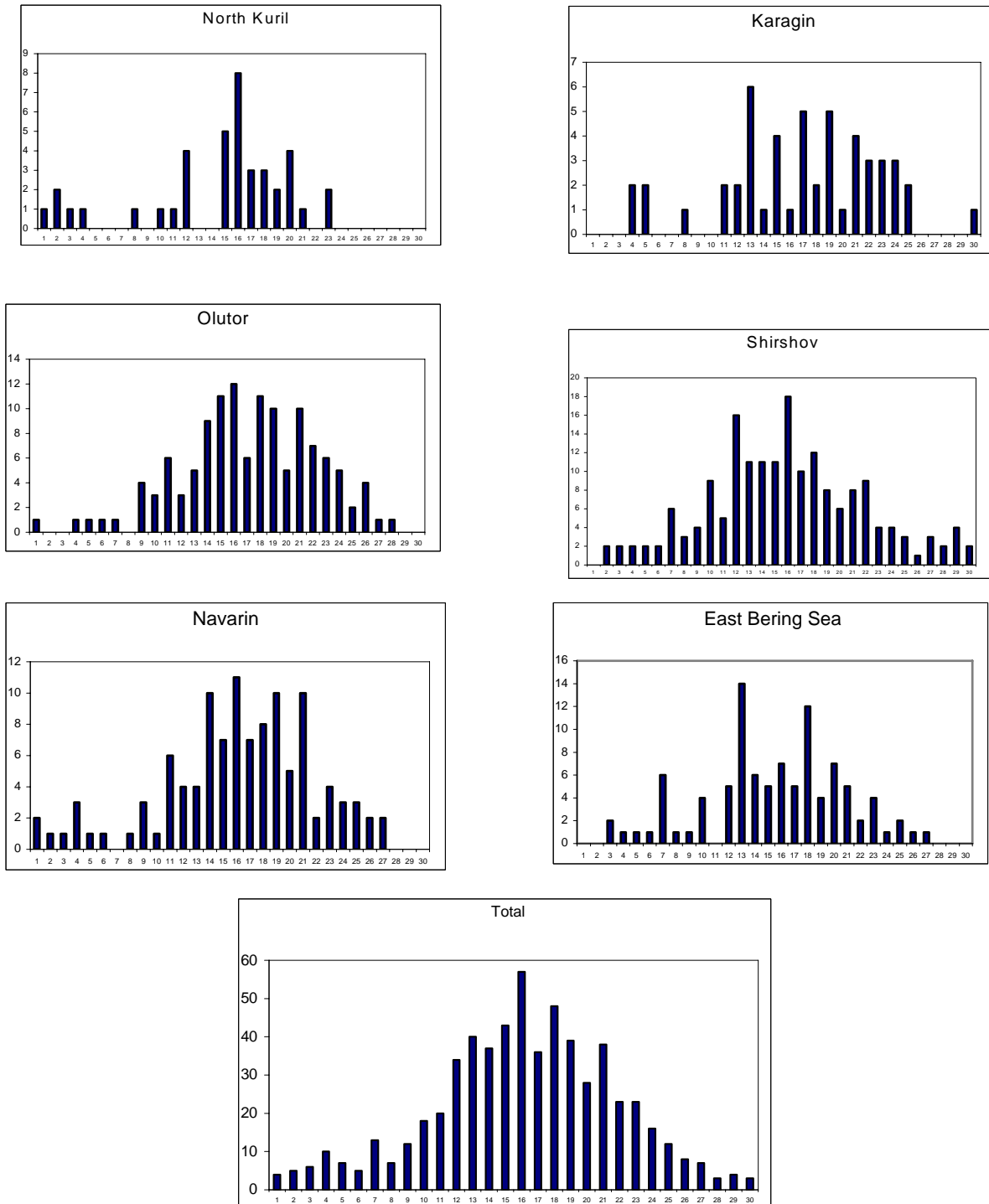


Fig. 4. Distribution of allele frequencies in locus Tch5.

The distribution of allele frequencies in Tch10 varies slightly between the Olutor – Shirshov and East Bering Sea samples. Differences from the small North Kuril sample were observed too. On the whole, however, the profiles were similar (Fig. 5).

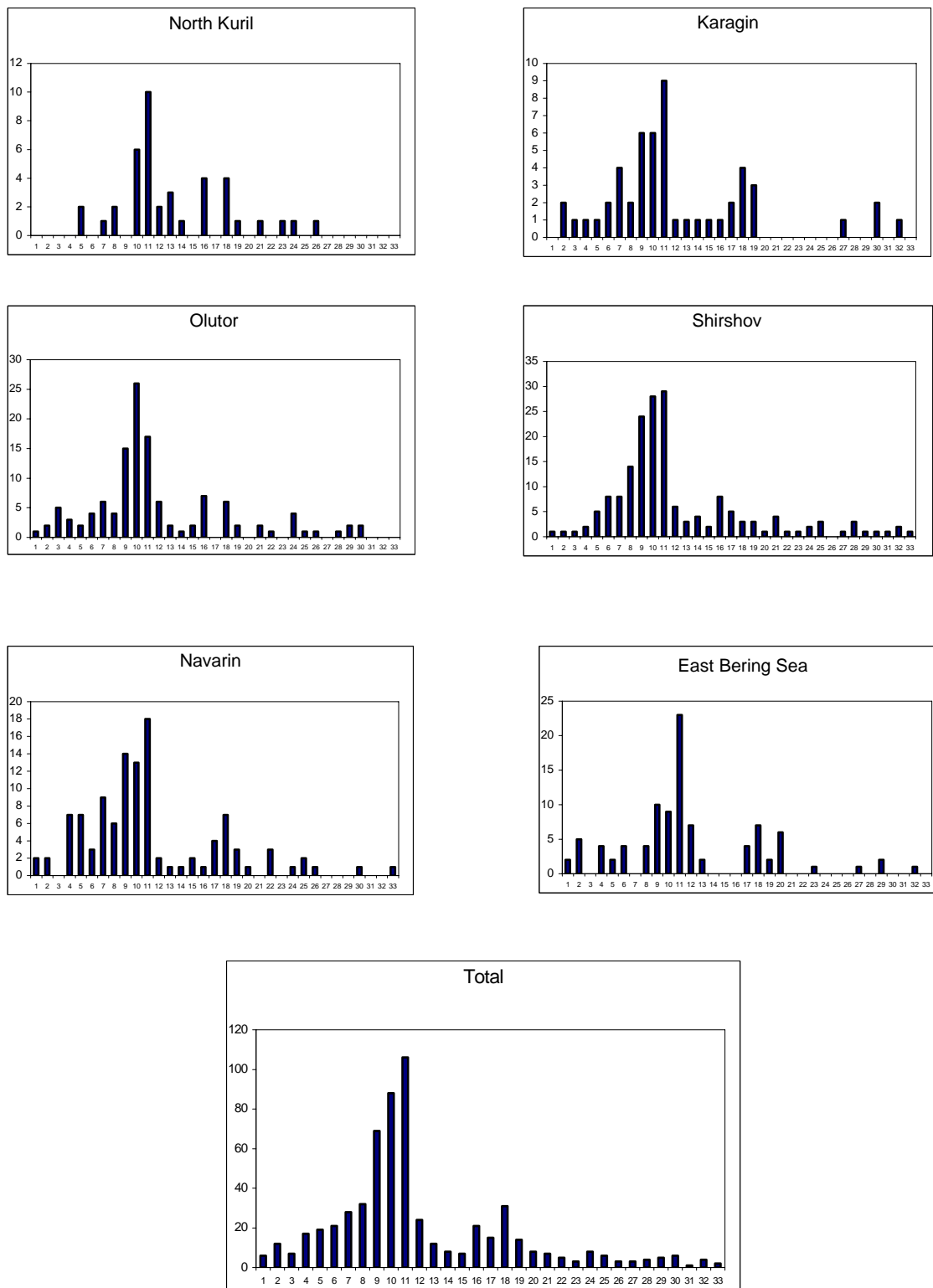


Fig. 5 Distribution of allele frequencies in locus Tch10.

For locus 12 differences were obtained between the North Kuril and Karagin samples only which may result from the insufficient volume of these samples (Fig. 6).

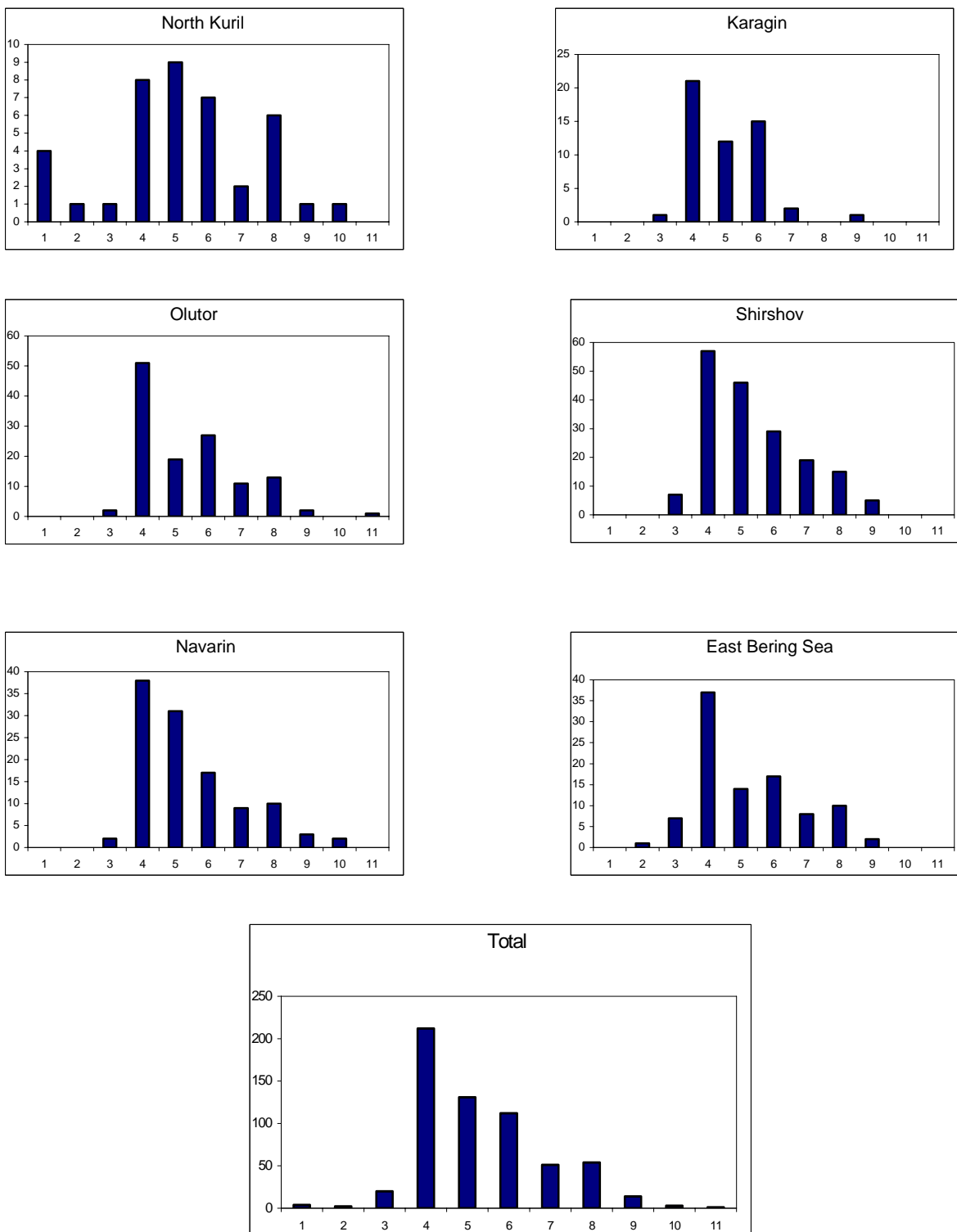


Fig. 6. Distribution of allele frequencies in locus Tch12.

There is some bias in distribution of allele frequencies in the East Bering Sea sample but it occurs smoothly in the series of the Karagin – Olutor – Shirshov– Navarin – East Bering Sea samples (Fig. 7). Totally, the sample’s distribution is close to normal.

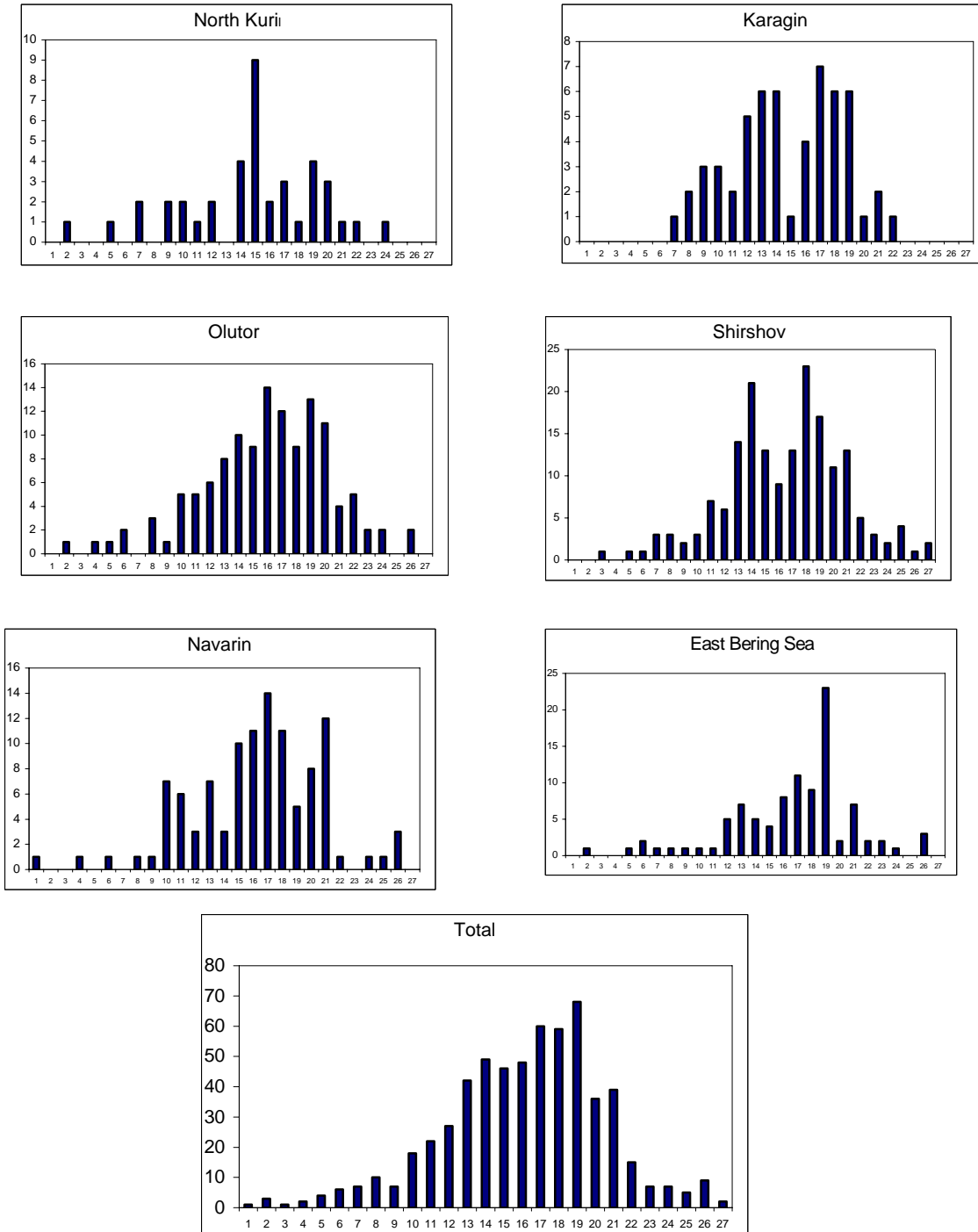


Fig. 7. Distribution of allele frequencies in locus Tch14.

No notable differences were observed in allele frequency distribution in locus Tch19 (Fig. 8).

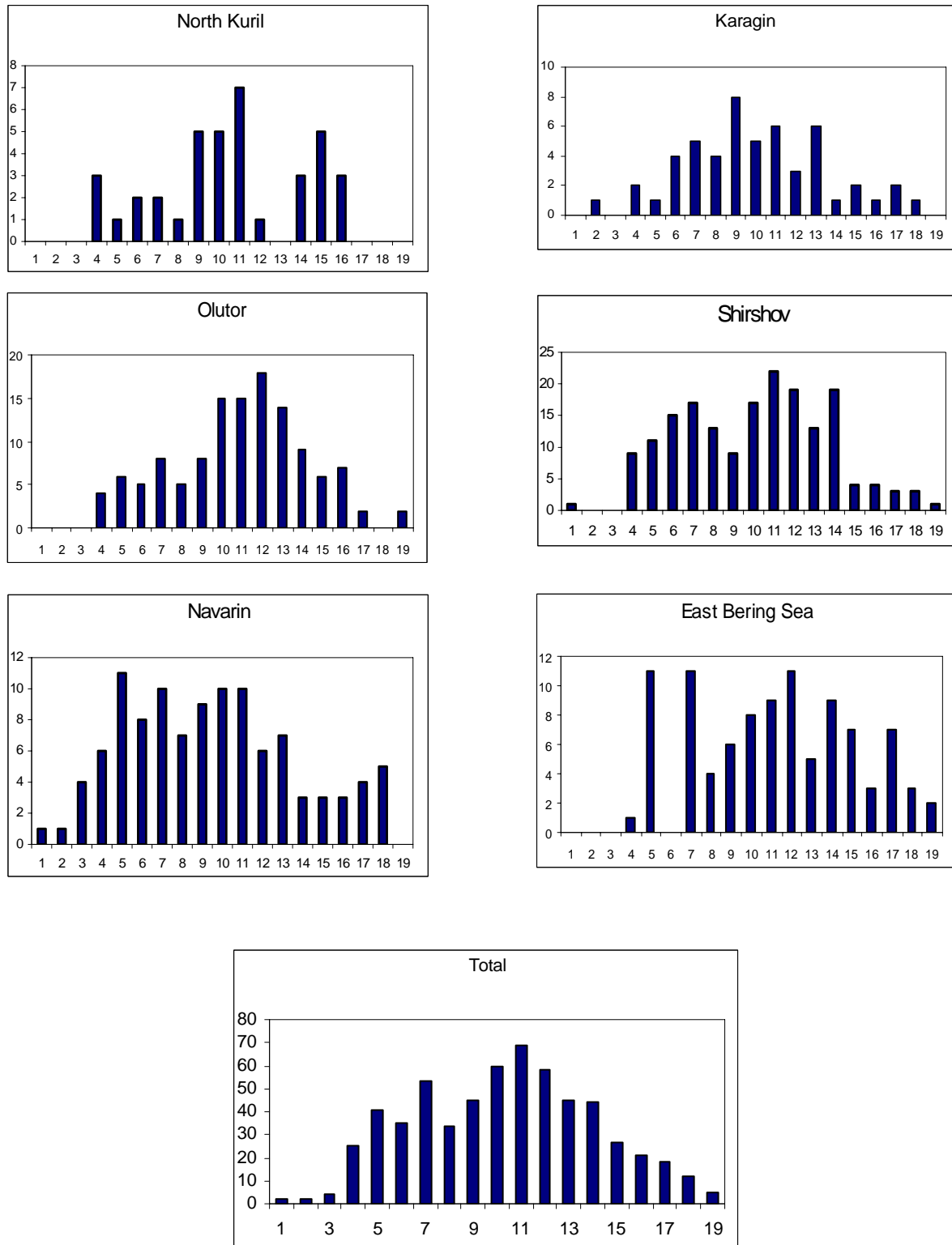


Fig. 8. Distribution of allele frequencies in locus Tch19.

The main genetic indicators of the pollock samples examined and the characteristics of the microsatellite markers used for that are given in Table 1. It includes the volume of the summary samples examined, for each locus, the number of alleles in locus, the allele size pitch in nucleotide pairs, the expected and observed heterozygosity. The most deviant loci are marked with asterisks. The Hardy-Weinberg equilibrium is followed in loci Tch5 and Tch10 only.

Table 1. Characteristics of the main genetic indicators of samples and microsatellite loci. Notation: N – number of specimens examined; Na – number of alleles in locus; R – allele size pitch in nucleotide pairs; He – expected heterozygosity; Ho – heterozygosity observed.

Sample	Loci					
		Tch 5	Tch 10	Tch 12	Tch 14	Tch 19
North Kuril	N	20	20	20	20	19
	Na	16	15	10	13	12
	R	186-274	145-187	118-154	116-212	106-162
	He	0,90	0,88	0,84	0,90	0,88
	Ho	0,90	0,85	0,60*	0,60***	0,74
Karagin	N	25	26	26	25	26
	Na	19	21	7	16	16
	R	198-302	139-209	126-150	144-204	94-162
	He	0,93	0,92	0,70	0,90	0,91
	Ho	0,96	1,00	0,65	0,56***	0,81
Olutor	N	63	63	63	63	62
	Na	25	26	8	22	15
	R	186-294	137-199	126-158	116-220	106-166
	He	0,94	0,91	0,75	0,93	0,91
	Ho	0,83	0,87	0,48***	0,75***	0,66***
Shirshov	N	90	90	89	89	90
	Na	29	33	7	24	17
	R	190-302	137-213	126-150	124-224	90-166
	He	0,95	0,91	0,79	0,93	0,92
	Ho	0,89	0,81	0,61*	0,65***	0,63***
Navarin	N	56	56	56	54	54
	Na	26	25	8	21	18
	R	186-290	139-209	126-154	112-220	90-162
	He	0,94	0,92	0,77	0,92	0,93
	Ho	0,85	0,84*	0,57**	0,70***	0,57***
East Bering Sea	N	49	49	48	49	49
	Na	25	19	8	22	15
	R	194-290	137-209	122-150	119-224	106-166
	He	0,93	0,90	0,78	0,90	0,92
	Ho	0,80**	0,76	0,69	0,71*	0,45***

The analysis of this table shows that heterozygote deficiency of some degree is a feature of all the samples examined. There is no correlation with the size of samples or the number of alleles in polymorphous loci. O'Reilly and others who have developed the set of microsatellite markers used in this paper recognize that in a number of loci (including Tch14 and Tch19) the level of heterozygosity is low (O'Reilly et al., 2004). However, they ascribe that to technical causes, namely to masking in electrophoresis of long alleles by the short ones, and to a greater number of O-alleles (mutations in flanking sequences – Blankenship et al., 2002), and they believe that the “other methods of electrophoresis” and involvement of programs accounting for the probability of deviation from equilibrium make it possible to track down additional alleles which raises the heterozygosity.

The population differences were analyzed by the genotype variants, allele diversity, and gene frequency variance. The North Kuril sample is a significantly differentiated one both in terms of genotypic and allele variants. The second ranking sample showing loci differentiation comes from the East Bering Sea. The concentrations from the Northwest Bering Sea do not show any significant differentiation. The error in summary testing of loci for genotype and allele differentiation is 0.0226 and 0.000 respectively. It is noteworthy that genotype differentiation was found only in loci 5, 10 and 12, for which Hardy-Weinberg law correspondence was shown (Tch12 has a marginal deviation value).

The quantitative measure of the degree of differentiation in a population is a standardized variance of gene frequencies. It is calculated as difference between the variance in an undivided total population and the intrapopulation variance. Table 2 represents the values of variances calculated using two software which apply different algorithms. F_{it} is variance of allele frequencies in the total undivided sample; F_{is} is the intrapopulation variance; F_{st} is the standardized interpopulation variance. The degree of differentiation which we revealed was very low, though the two estimates of this value obtained by using two software agreed almost fully. Locus Tch14 is the only exception where small differences were recorded.

Table 2. F – statistics estimates obtained with GENEPOP and TFPGA software reflecting allele frequency distribution in five microsatellite loci of pollock. * - Locus where differences in variance estimates were recorded.

Software Loci	GENEPOP			TFPGA		
	Estimates F_{IT}	F_{ST}	F_{IS}	F_{IT}	F_{ST}	F_{IS}
Tch5	0,092193	0,001542	0,090791	0,0922	0,0015	0,00908
Tch10*	0,064332	0,002922	0,061589	0,0858	0,0026	0,0834
Tch12	0,244932	0,002893	0,242741	0,2460	0,0031	0,2436
Tch14	0,270590	0,003663	0,267908	0,2706	0,0037	0,2679
Tch19	0,316928	-0,000785	0,317464	0,3313	-0,007	0,3318
average	0,1961	0,0020	0,1945	0,2036	0,0020	0,2020

A precise test for subdivision of samples in general by applying TFPGA program using Markov chains concurrently for each of the five loci showed lack of difference for Tch5 locus only (Raimond and Rousset, 1995).

The multilocus test produced the value of χ^2 as 60.5213, the number of degrees of freedom being equal to the 10% and 100% probability of differentiation.

Table 3. Pairs of genetic Nei distances (original ones above the diagonal; unbiased ones below the diagonal) between various groups of pollock by five microsatellite loci

Concentration	Shirshov	Olutor	North Kuril	Karagin	Navarin	East Bering Sea
Shirshov	***	0,0701	0,2206	0,1128	0,0708	0,1137
Olutor	0,0121	***	0,2375	0,1061	0,0906	0,1148
North Kuril	0,0890	0,0987	***	0,3331	0,2492	0,3042
Karagin	0,0150	0,0011	0,1545	***	0,11185	0,1441
Navarin	0,0045	0,0172	0,1022	0,0053	***	0,1445
East Bering Sea	0,0473	0,0412	0,1570	0,0307	0,0627	***

As is known, Nei distances are functions of the distances expressed in F_{st} units. That is why it is only the unbiased values adjusted by the size of sample that are of interest in Table 3.

The major source of being subdivided in the samples analyzed by genetic distances is the set of the North Kuril samples. The difference between the size of Nei distances for the Bering Sea samples is very small; still, there is some correlation with the sites of samples. At any rate, the East Bering Sea and Navarin samples are genetically somewhat more distant than the Navarin and West Bering Sea ones. The UPGMA cluster based on Nei genetic distances is shown in Figure 9. The bootstrap analysis of the cluster showed that the linkpoint uniting the Shirshov and Olutor samples has a 51% bootstrap coefficient, and is supported by 3 loci; linkpoints 2 and 3 (Navarin and Karagin samples respectively) have bootstrap coefficient of 78% and 66%. Finally, the East Bering Sea and North Kuril samples were 100% supported by all the markers used.

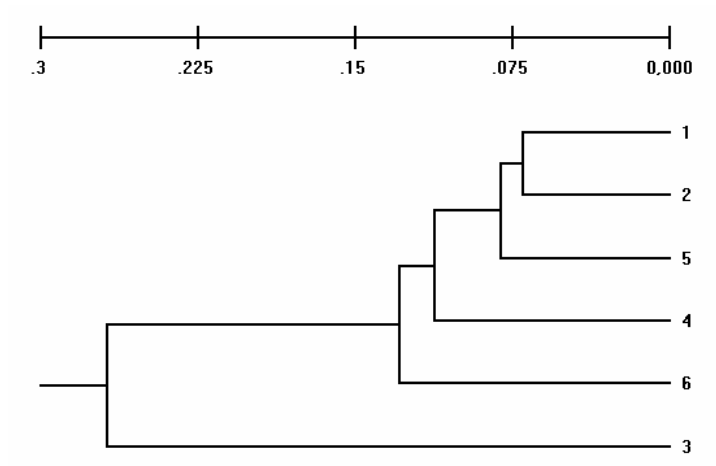
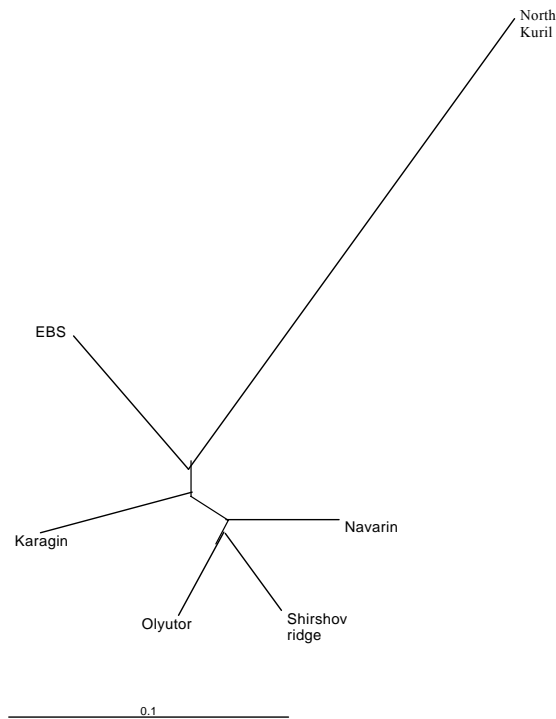


Fig 9. UPGMA dendrogram of pollock concentrations based on Nei genetic distances. Samples; 1. Shirshov; 2. Olutor, 3. North Kuril; 4. Karagin; 5. Navarin; 6 East Bering Sea.

The unrooted dendrogram constructed on the basis of Nei distances shows the degree of genetic distance of pollock groupings from one another which agrees well with the geographic distances between them (Fig. 10).

Fig 10. UPGMA dendrogram of pollock concentrations based on Nei genetic distances (unrooted)



Conclusions

1. Hardy-Weinberg law test confirmed the genetic equilibrium of all the groupings examined.
2. The allele frequency analysis was used as basis for the conclusion regarding the existence of a genetic structure in the sample considered.
3. A quantitative evaluation of the difference showed similarity among the West Bering Sea concentrations, Navarin inclusive. The East Bering Sea samples are very disparate in terms of genetic distances. The North Kuril Grouping stands expressly aside.
4. The genetic distances between the samples on the whole reflect the geographic remoteness of concentrations. The Karagin grouping is an exception. This might result from the insufficiency of the sample.

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Federal Agency of Fisheries Russian Federation
Pacific Research Fisheries Centre (TINRO-centre)

**STATUS OF STOCKS AND REPRODUCTION OF THE EASTERN BERING
SEA POLLOCK (*Theragra chalcogramma*) IN 2003-2005**

(document submitted for Workshop on the Determination of allowable Harvest Levels
and Genetics Research on Pollock Resources in the Central Bering Sea, Seattle)

By

Stepanenko M.A. and A.V. Nikolaev

2005

The trend of Eastern Bering Sea pollock biomass increasing were stable by the end of 1990-s and early 2000-s as result of annual recruitment by average 1995, 1997-1999 and numerous 1996, 2000 year classes. Pollock biomass had increased for 61% in period 1996-2002.

The oceanology condition and pollock spatial distribution were close to average at first part of 1990-s. Some signs of cooling had appears in the Bering Sea by the end of 1997 and it have maximum in 1999. At the same time, cold period in the Bering Sea was short and new warming process began in 2001-2002. The high positive water temperature anomaly observed in the Bering Sea in 2003-2004.

There is direct interrelationship between distribution of pollock and variability of oceanology condition, basically of water temperature, in summer-autumn time. Distribution of pollock in the northwestern Bering Sea have big scale interannual variability depends of changing water temperature. Scale of pollock distribution into northwestern Bering Sea much higher in period warm oceanology condition.

Indicated interrelationships between interannual variability of the Eastern Bering Sea pollock spatial distribution, biomass (5.0 - 9.0 mln.t) and changing oceanology condition were observed in period between middle 1990-s and early 2000-s.

Spatial distribution of the Bering Sea pollock in feeding period depends on it abundance and biomass, age composition and environmental condition. The eastern Bering Sea pollock usually distributed very widely at shelf and deep water Aleutian and Commandor basin in periods of it high abundance (12.0-15.0 mln.t).

The eastern Bering Sea pollock biomass decreased to about 5.5-6.0 mln.t in middle 1990-s but by the end of 1990-s it increased again on behalf of new relatively abundant year classes.

Interannual variation of pollock abundance and biomass in the Navarin area also very significant as indicated by bottom trawl and echointegration survey data (Table 1).

Table 1

Estimated of walleye pollock abundance and biomass in the Navarin area in 1996-2002 (by EI MWT and BT surveys data)

Year	Bottom **			Midwater			Total	
	S (mile ²)	N (mln.fish)	B (ths.t)	S (miles ²)	N (mln. fish)	B (ths.t)	N (mln.fish.)	B (ths.t)
1996	18500	1158	390	17520	769	259	1927	649
1997	24050	1004	333	27036	1323	250	2327	583
1998	15820	962	390	13640	234	71	1196	461
1999	32663	532	250	12688	291	70	823	320
2000	22400	203	64	15420	365	54	568	118
2001	38027	1642	384	22380	218	32	1860	416
2002	42146	938	215	14040	672	58	1610	273

** Estimates of biomass off bottom in 1997-1999, 2001- 2002 by BT surveys (K=1.0), in 2000 by EI MWT survey

As a rule, pollock abundance and biomass have high long term and short term interannual variability everywhere in the North Pacific. By the end of 1980-s and early 1990-s had appeared stable trend decreasing of most pollock populations abundance. Biomass of the eastern Bering Sea pollock decreased to 5.5-6.0 mln.t in middle 1990-s. The Eastern Bering Sea pollock stock is neither overfished and it biomass increased (8.0-9.0 mln. t) by the end of 1990-s and early 2000-s (Table 2).

The AFSC pollock biomass estimate by bottom-trawl (BT) survey for 2003 is very high – 8.51 mln. tons, an increase of 77 % from the 2002 estimate of 4.82 mln. tons. The echo-integration trawl (EIT MWT) survey biomass for 2002 is 3.6 mln. tons. The time series of survey estimates suggest an increasing trend of pollock biomass in the southeastern Bering Sea by the end of 1990-s and early 2000-s.. Interannual variability of biomass estimates is due to the effect of year class variability. (NPFMC Bering Sea/ Aleutian Islands SAFE document, 2003).

The annual catch of pollock in the Bering Sea have varies depends of pollock abundance and biomass and recently have stable trend for increasing (Table 3).

The annual eastern Bering Sea pollock recruitment and spatial distribution of mature and immature fish also variates significantly

Table 2

Biomass of the eastern Bering Sea pollock in 1979-2004, mln.t (according to AFSC data)

<i>Year</i>	<i>Survey data</i>			
	<i>BT,shelf</i>	<i>EI, shelf</i>	<i>EI, Bogoslof</i>	<i>Total</i>
1979	2.00	1.550	-	3.55
1980	0.99	-	-	-
1981	2.27	-	-	-
1982	3.54	4.640	-	8.18
1983	4.81	-	-	-
1984	3.96	-	-	-
1985	4.36	5.450	-	9.82
1986	4.31	-	-	-
1987	5.03	-	-	-
1988	5.94	4.160	2.400	12.50
1989	4.78	-	2.100	-
1990	7.70	-	-	-
1991	5.10	1.400	1.300	7.80
1992	4.30	-	0.980	-
1993	5.50	-	0.680	-
1994	4.98	2.760	0.540	8.28
1995	5.41	-	1.020	-
1996	3.20	2.239	0.682	6.12
1997	3.03	2.590	0.390	6.01
1998	2.21	-	0.490	-
1999	3.57	3.290	0.480	7.34
2000	5.13	3.05	0.301	8.48
2001	4.1	-	0.232	-
2002	4.81	3.60	0.227	8.63
2003	8.5	-	0.198	-
2004	3.75	3.31	-	7.06

Table 3

Catch of the Bering Sea pollock in 1984-2004, ths. m.t. (according to AFSC and TINRO data)

Year	<i>EBS shelf</i>	<i>Bogoslof I.</i>	<i>WBS shelf</i>	<i>Aleutian Basin</i>	<i>Aleutian Islands</i>	<i>Total</i>
1984	1092.05	-	503.0	181.20	81.80	1858.0
1985	1139.67	-	488.0	363.40	58.70	2049.8
1986	1141.99	-	570.0	1039.00	46.60	2797.6
1987	859.41	377.40	463.0	1326.30	28.70	3054.8
1988	1228.72	87.80	852.0	1395.90	30.00	3594.4
1989	1229.60	36.00	684.0	1447.60	15.50	3412.7
1990	1455.19	151.60	232.0	917.40	79.00	2835.2
1991	1217.30	264.70	178.0	293.40	78.60	2037.3
1992	1164.44	0.160	315.0	10.00	48.70	1538.3
1993	1326.60	0.886	389.0	1.95	57.10	1775.4
1994	1363.45	0.566	178.0	-	58.60	1600.6
1995	1262.76	0.264	320.0	-	64.40	1647.4
1996	1192.77	0.387	700.8	-	29.06	1922.2
1997	1124.59	0.168	680.0	-	25.94	1830.6
1998	1101.16	0.080	643.6	-	23.82	1768.7
1999	992.00	0.029	632.7	-	1.00	1625.8
2000	1112.5	0.028	378.0	-	1.24	1490.5
2001	1381.6	0.029	526.1	-	0.80	1908.5
2002	1485.0	0.001	383.4	-	1.04	1869.4
2003	1489.4	0.002	415.6	-	1.64	1906.6
2004	1492.0	-	455.1	-	1.14	1948.2

The annual eastern Bering Sea pollock spatial distribution varies especially significantly in periods of anomalous environmental condition.

In summer, 1999 most of pollock were distributed at shelf placed between Pribilof Isles and 177⁰⁰ W. Relatively intensive northwestern migrations indicated just by the end of August. Distribution pollock in the Bering Sea in 1999 quite different compare the 1994-1997 pattern.

Scale of pollock distribution in the northwestern Bering Sea was less as average also in 2000, especially in first part of summer, because that area was occupied by extremely cold water.

In 2003-2004 water temperature was much higher entire Bering Sea and pollock distribution in the northwestern area had increased.

The some trend of increasing of pollock recruitment in the Bering Sea, including southeastern shelf indicated in 1998 - 2000.

The immature pollock of 2000 year class were really abundant in 2002 both in the northwestern and southeastern Bering Sea.

At the same time, summer 2004 survey data indicated that spatial distribution pollock significantly differs from 2000-2003 data and abundance of 2001-2003 year classes much less as 2000 year class.

In summer 2004 most of immature pollock and fish of numerous 2000 year class were distributed in the northwestern shelf. Older pollock of 1998-1999 year classes predominated in the southeastern Bering Sea (23.8% and 36.6%) and fish of 2000 year class consisted just 16.2% of abundance (Fig. 1). Biomass of pollock in the southeastern Bering Sea estimated in 2.05 mln.t by EI MWT survey data.

The pollock of 2000, 1999 and 2001 year classes predominated in the northwestern Bering Sea in the U.S. EEZ – 31.4%, 21.6% and 19.6% consequently and abundance of 2003 year class pollock very low (Fig. 2). Biomass pollock in the northwestern shelf estimated in 2.93 mln.t.

The pollock biomass in the Bering Sea (0.5 m off bottom-surface, AFSC EI MWT survey data) estimated in 4.98 mln.t in 2004 (in 2002 – 4.63 mln.t, in 2000 - 3.74 mln.t, in 1999 – 4.04 mln.t.) (Table 4). The pollock of 2000 and 1999 year classes predominated in the eastern Bering Sea by numbers – 31.4% and 21.6% consequently (Fig. 3).

Table 4

Biomass and abundance pollock in the Bering Sea in 1996-2004 (by EI MWT survey data).

Год	<i>Biomass, mln.t</i>			<i>Abundance, mln.specimen</i>		
	Surface-3M off bottom	3-0.5M off bottom	Surface-0.5M off bottom	Surface-3M off bottom	3-0.5M off bottom	Surface-0.5M off bottom
1996	2370.7	681.0	2991.7	6525.3	1311.5	7836.7
1997	2631.7	961.9	3593.6	18554.9	2016.4	20571.3
1999	3202.2	842.3	4044.4	8833.7	2046.9	10880.5
2000	3050.3	690.0	3740.3	7629.1	1311.4	8940.6
2002	3707.2	930.4	4637.6	11877.8	1673.7	13551.5
2004*	4115.2	871.6	4986.8	8595.8	1313.7	9909.5
2004	3846.0	814.6	4660.6	7521.7	1149.6	8671.3

* - including biomass estimated in the Navarin area

The 2001 and 2002 year classes abundance much less compare abundance of 2000 year class. Abundance of 1-year old pollock of 2003 year class very low by 2004 EI MWT survey data, in spite of extremely high abundance of pollock juveniles registered both

in the northwestern and southeastern Bering Sea shelf in 2003. It's demonstrates that natural mortality of 0+ year old pollock were very high in winter 2003-2004 but reason of it unknown.

Relative abundance of immature 1-3 years old pollock in the Bering Sea in 2004 much less compare 1999, 2000 and 2002 by EI MWT survey data (Fig. 4).

Aleutian Basin pollock spawning stock in the Bogoslof Island area have been surveyed regular since 1988. The last years surveys data demonstrates low pollock spawning biomass in the area (NPFMC Bering Sea/ Aleutian Islands SAFE document, 2003).

The originally shelf and deep water pollock habits in the eastern Bering Sea shelf before first maturing. Identification of origin immature pollock at shelf unpossibly by present methods. At the same time, there are a lot of observations of distinct differentiation of immature pollock at the Bering Sea shelf by growth rate, length, body morphology as well as it behaviour and distribution.

The survey data of 2000 indicated possibility high abundance Bogoslof I origin of 2000 year class pollock on base of distribution pollock juveniles. A lot number of pollock juveniles were distributed close to shelf edge in area placed from Unimak Pass to eastern side of Pribilof canyon in 2000 and were speculated that the juveniles originally from Bogoslof reproduction area. Another big concentration of pollock juveniles in summer 2000 was found at shelf off eastern side of Pribilof Islands.

The age of first maturing Bogoslof I spawning stock pollock is 4+-5+. Quite possibly that by the end winter and early March some prespawning 4+ - 5+ pollock migrates from outer shelf into adjacent continental slope basically inside the canyons. Most solid concentrations of prespawning fish observed in the Pribylof and Zhemchug canyons in first part of February each year in 1990-2000-s. The recruits of 2005 represent basically pollock of abundant 2000 year class.

Prespawning pollock begin migrate from big canyons area to southeast along direction continental slope, into Bogoslof I spawning ground by the end of February and early March. Big concentrations of prespawning pollock observed in deep water (about 400-500 m) of the Bering canyon, in area placed to north from Akutan I during second part February or early March almost annually.

Interannual data of prespawning pollock maturity dynamics in the Bogoslof I reproduction area (Yanagimoto et al., 2002) indicated that active spawning, especially younger fish, start basically in second part of March (1992-1993, 1995-1996, 1998-1999).

Quite possibly that spawning of abundant 2000 year class recruits in 2005 taken place basically later the regular EI survey time (March 4-11), - in second part of March.

The high density concentrations of mature pollock were observed at shelf and adjacent continental slope off eastern Aleutian Islands (Akun I.- Akutan I. - northern Unalaska I) in summer 2002 and 2004. This pollock differs sharply from fish distributed at shelf by length-age composition and gonads maturity. In 2002 the pollock

of 1995-1996 year classes (42-50 cm) and in 2004 of 1998-1999 year classes (42-48 cm) predominated off eastern Aleutian Islands. Apart from, in 2004 pollock of 1995-1997 year classes also was relatively abundant in that area. The gonads of pollock males have not any remains of sperm and females resorbing eggs of previous generation. It shows that active spawning period of this fish was long time ago and much earlier as spawning of pollock at shelf.

Quite possibly that feeding pollock distributed off eastern Aleutian Islands is a part Bogoslof Island spawning stock and mature fish of 1998-1999 year classes represent a recruits of it spawning stock in 2004.

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Update of Navarin walleye pollock stock assessment

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Navarin pollock stock status was re-estimated using the following data:

- catch-at-age, weight-at-age, maturity-at-age (1984-2004);
- CPUE for 2 fleets (medium and large vessels) – as FSB relative indices;
- age-structured young fish surveys ((1) in summer and (2) in autumn) – as abundance-at-age indices;
- 0-group abundance estimates (from young fish surveys) - as SSB relative index.

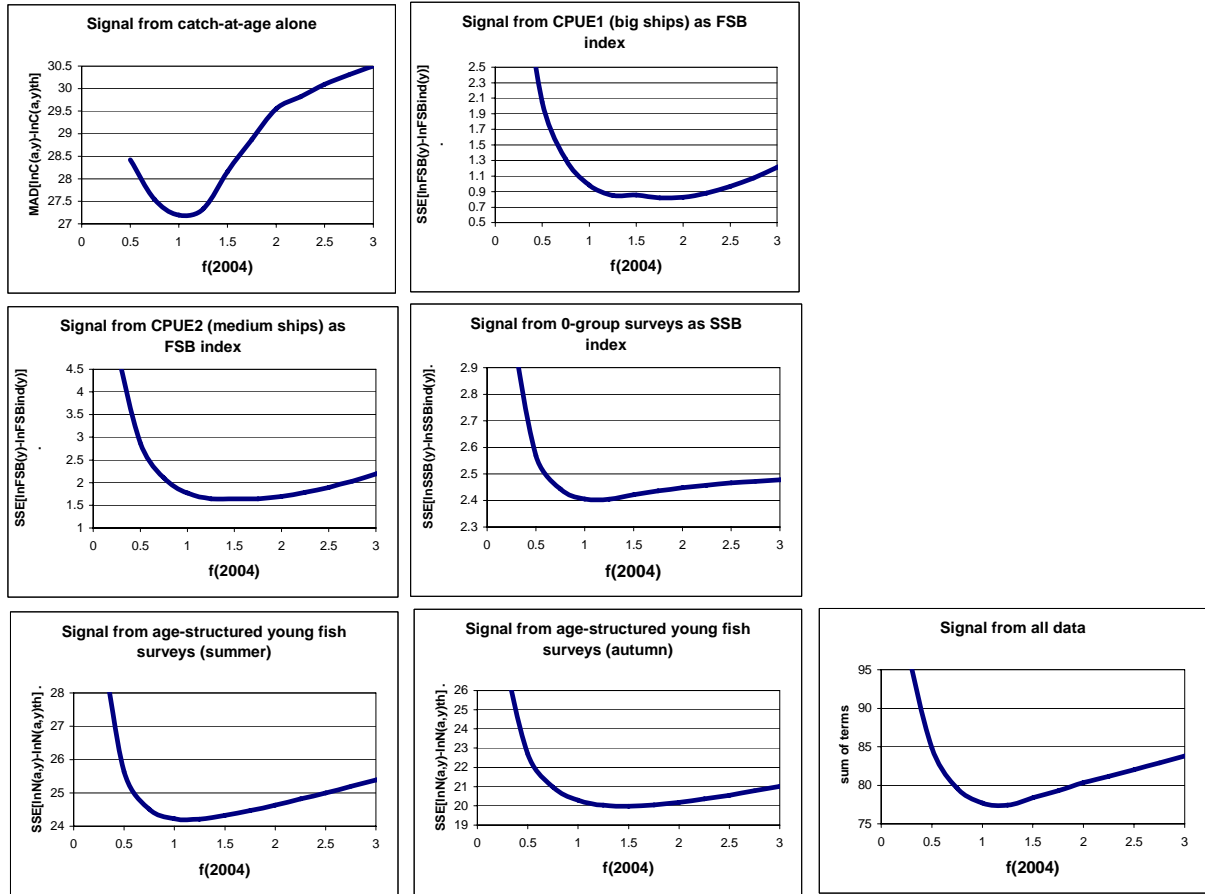
Stock assessment model was so called effort-controlled version of the ISVPA-group of separable cohort models (for details of the model see appendix and references to it). This version of the model attributes residuals in cohort part of the model to errors in catch-at-age data, assuming that selection pattern (patterns) is stable. This version is often more robust for noisy catch-at-age data. Additional robustness of cohort part of the model with respect to outliers in catch-at-age was attained 1) by minimization of median absolute deviation (MAD) of residuals in logarithmic catch-at-age as a measure of closeness of the model fit to catch-at-age data, and 2) condition of unbiased separable representation of fishing mortality coefficients. Change in selection pattern in 2001 was taken into consideration by estimation of two respective selection patterns.

In this assessment for the first time the estimates of abundance from young fish surveys were included. These data were incorporated into the model in two ways: (1) as age-structured abundance index and (2) 0-group abundance was used as relative index of SSB. Other sources of information were catch-at-age of commercial catches and CPUE time series of two fleets (medium and large vessels).

Profiles of components of the model loss function, as well as profile of the total loss function, are presented on figure 1 as a function of the effort factor value in the terminal year. Although level of noise in the survey data was found to be rather high, the results of application of the model revealed rather coherent signals about the stock size from all sources of information, including young fish surveys. It could be concluded that young fish surveys provide reasonable estimates of trends in abundance of young age groups, while survey-derived abundance estimates of age group 0+ may serve as a reasonable index of SSB in frames of age-structured stock assessment models.

Bootstrap-estimated uncertainty levels for model-derived estimates of fishing stock biomass (FSB) and total stock biomass (TSB) for age groups 2 and older (conditional parametric with respect to catch-at-age, non-conditional parametric with respect to auxiliary data; lognormal error distribution in catch-at-age, in FSB and SSB indices, and in age-structured abundance indices was assumed) are presented on figure 2.

Since it was hardly possible to assume any reliable stock-recruitment relationship having existing observations (see figure 3), yield-per-recruit analysis (figure 4) seems to be more reasonable source for biological reference points estimation in current informational situation.



Profiles of components of the ISVPA loss function with respect to effort factor in 2004

Figure.1

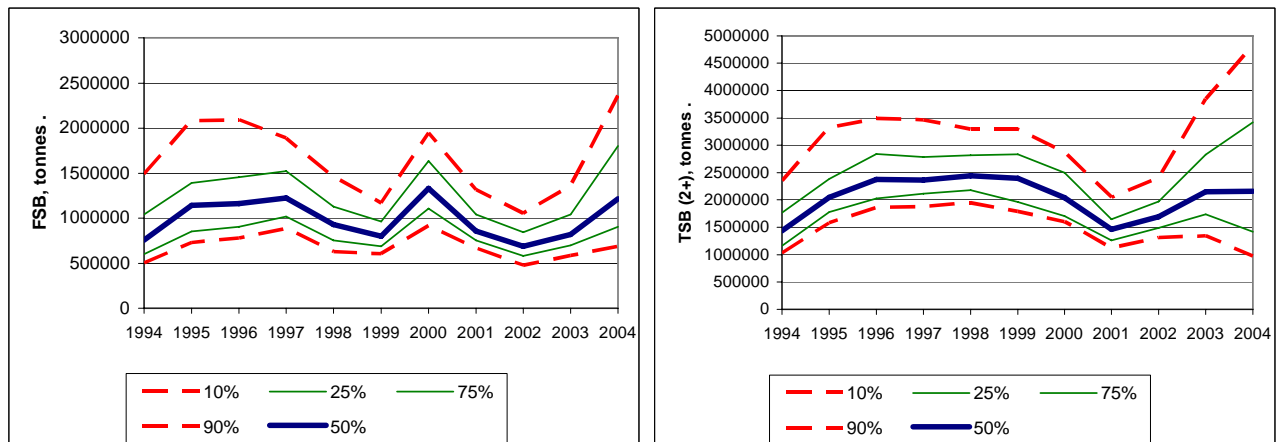


Figure.2. Percentiles of bootstrap distribution for FSB and TSB estimates.

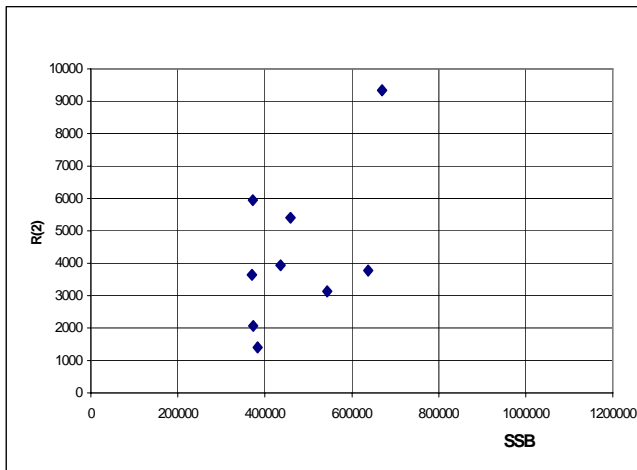
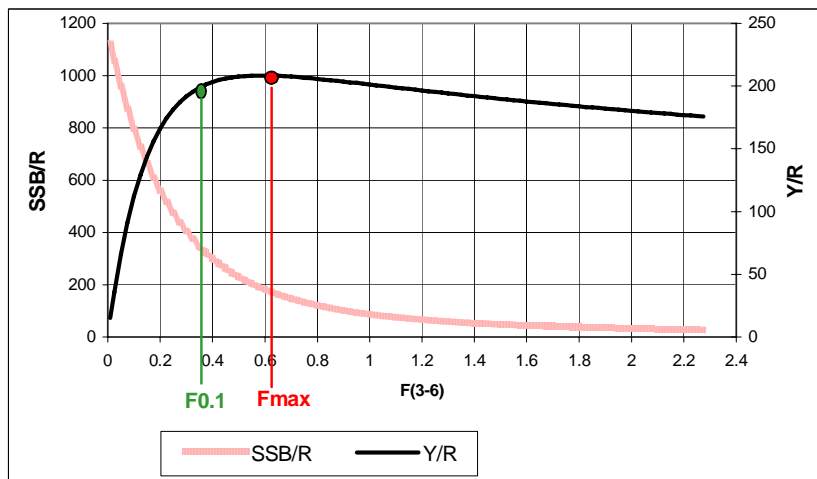


Figure 3. Estimates of recruitment vs. SSB.



YPR analysis

Figure 4.

Appendix

W.D. to ICES WGMHSA, 2004.

DESCRIPTION OF THE ISVPA (version 2004.3)**D.A.Vasilyev** <dvasilyev@vniro.ru>

Brief description of the model is summarized in the table below:

Model	ISVPA
Version	2004.3
Model type	A separable model is applied to one or two periods, determined by the user. The separable model covers the whole assessment period
Selection	The selection at oldest age is equal to that of previous age; selections are normalized by their sum to 1. For the plus group the same mortality as for the oldest true age.
Estimated parameters	
Catchabilities	The catchabilities by ages and fleets can be estimated or assumed equal to 1. Catchabilities are derived analytically as exponents of the average logarithmic residuals between the catch-derived and the survey-derived estimates of abundance.
Plus group	The plus group is not modelled, but the abundance is derived from the catch assuming the same mortality as for the oldest true age.
SSB surveys	Considered as absolute or relative. If considered as relative, coefficient of proportionality is derived analytically as exponent of the average logarithmic residuals between the catch-derived and the survey estimates of SSB.
Surveys in year (terminal + 1)	Can be taken into account (in assumption that fishing pattern in the year (terminal+1) is equal to that of terminal year)
Objective function	<p>The objective function is a weighted sum of terms (weights may be given by user). For the catch-at-age part of the model, the respective term is:</p> <ul style="list-style-type: none"> • sum of squared residuals in logarithmic catches, or • median of distribution of squared residuals in logarithmic catches MDN(M, fn), or • absolute median deviation AMD(M, fn). <p>For SSB surveys it is sum of squared residuals between logarithms of SSB from cohort part and from surveys.</p> <p>For age- structured surveys it is SS, or MDN, or AMD for logarithms of N(a,y) or for logarithms of proportions-at-age, or for logarithms of weighted (by abundance) proportions-at-age.</p>
Variance estimates/ uncertainty	For estimation of uncertainty parametric conditional bootstrap with respect to catch-at-age, (assuming that errors in catch-at-age data are log-normally distributed, standard deviation is estimated in basic run), combined with adding noising to indexes (assuming that errors in indexes are log-normally distributed with specified values of standard deviation) is used.
Other issues	<p>Three error models are available for the catch-at-age part of the model:</p> <ul style="list-style-type: none"> • errors attributed to the catch-at-age data. This is a strictly separable model (“effort-controlled version”) • errors attributed to the separable model of fishing mortality. This is effectively a VPA but uses the separable model to arrive at terminal fishing mortalities (“catch-controlled version”) • errors attributed to both (“mixed version”). For each age and year, F is calculated from the separable model and from the VPA type approach (using Pope’s approximation). The final estimate is an average between the two where the weighting is decided by the user or by the squared residual in that point. <p>Four options are available for constraining the residuals on the catches:</p> <ol style="list-style-type: none"> 1. Each row-sum and column-sum of the deviations between fishing mortalities derived from the separable model and derived from the VPA-type (effort controlled) model are forced to be zero. This is called “unbiased separabilization” 2. As option 1, but applied to logarithmic catch residuals. 3. As option 1, but the deviations are weighted by the selection-at-age. 4. No constraints on column-sums or row-sums of residuals.
Program language	Visual Basic

1. Introduction

Separability assumption is widely used in various cohort models (Pope, 1974; Doubleday, 1976, Pope and Shepherd, 1982; Fournier and Archibald, 1982; Deriso et al. (1985), Kimura (1986), Gudmundsson (1986), Patterson (1995), etc.). A group of separable cohort model, named ISVPA, may serve as an example of comparatively simple stochastic separable cohort models (Kizner and Vasilyev, 1997; Vasilyev 1998, 1998a, 2001). Models of the ISVPA group are similar in many aspects to other separable cohort models and imply the existence of errors in catch-at-age data and in separable representation of fishing mortality coefficients. But their parameter estimation procedures is based on some principles of robust statistics what helps to diminish the influence of error (noise) in catch-at-age data on the results of the assessment. Besides the solution is guaranteed to be unbiased in chosen statistical sense. Special parameterization of the model makes it unnecessary to use any preliminary assumptions about the age of unit selectivity and about the shape of selectivity pattern. This helps to get unique solution in cases when catch-at-age data are noisy and auxiliary information is too controversial or is not available. Otherwise ISVPA may be used in order to outline stock tendencies from catch-at-age data taken alone.

For simplicity any model from the group we will further refer to as ISVPA model, if necessary giving concretization of the version used.

2. Basic relationships

The Instantaneous Separable VPA (or ISVPA) group of models is designed for stock assessment when catch-at-age data are noisy; auxiliary information may be incorporated, or not used at all (if it is not available or considered as unreliable). The word “Instantaneous” means that similarly to Cohort Analysis by Pope (1972) the catch is assumed to be taken “instantaneously”, that is within comparatively short period within a year. The approximation of “instantaneous” catch is absolutely correct for short fishing seasons, but it also can be regarded as being an approximate method for assessment of continuously exploited age-structured populations. It should be noted that the assumption of a constant fishing mortality coefficient during a year, that underlines conventional VPA, is also only a approximation. These two

hypotheses are in fact two opposite marginal simplifications in the frames of cohort models. The acronym ISVPA should not be confused with that of Integrated Stochastic VPA by Lewy (1988).

Let us remind that Pope's Cohort Analysis is based on the observation equation (Baranov's catch equation):

$$C_{a,y} = F_{a,y} / (F_{a,y} + M) * N_{a,y} [1 - e^{-(F_{a,y} + M)}] \quad (1)$$

($a=1, \dots, m; y=1, \dots, n$),

and the dynamic state equation:

$$N_{a,y} = (N_{a+1,y+1} e^{M/2} + C_{a,y}) e^{M/2} \quad (2)$$

($a=1, \dots, m-1; y=1, \dots, n-1$), where a - age index, m - total number of age groups, y - year index, n - total number of years, $N_{a,y}$ - abundance of age group a in year y , $C_{a,y}$ - catch from age group a in year y , M - instantaneous natural mortality coefficient (may be constant or a function of age). For simplicity $a=1$ and $y=1$ correspond to the first age group and first year in the available data respectively.

Equation (1) express the total catch from age group a , accumulated in the y -th year if the dynamics of the group abundance N and the accumulated catch C (at time t) during the year are governed by the well known equations: $dN/dt = -(F+M)N$ and $dC/dt = FN$, where F and M do not depend on t (indices are omitted). Equation (2) is traditionally regarded as a discrete approximation of a continuous process; it becomes an exact one if the catch $C_{a,y}$ is taken instantaneously in the middle of the year y .

However, there are many exploited stocks with such short periods of fishing that the latter may be regarded as momentary. In such a case if the period of fishing falls in the middle of a year, equation (1) may be replaced by

$$C_{a,y} = \varphi_{a,y} N_{a,y} e^{-M/2}, \quad (3)$$

where $\varphi_{a,y}$ plays the role similar to that of $F_{a,y}$ in equation (1) but cannot be called a fishing mortality coefficient. Strictly speaking, it is the fraction of the abundance of the a -th age group, taken as catch in the middle of the year y . The model (2)-(3) may be regarded as "instantaneous" analogue of VPA. The word "separable" shows that the hypothesis of separability (i.e. of age selectivity of the fishery) is accepted.

In terms of ISVPA it means that

$$\varphi_{a,y} = s_a f_y \quad (4)$$

where f_y is proportional to the fishing effort (a year effect), while s_a is the selectivity of the fishery (an age effect). Further we will call them as effort factor and selectivity factor.

Selectivity factors in the model are normalized:

$$\sum_{a=1}^m s_a = 1 \quad (5)$$

It is clear that in reality the fishing season does not necessarily fall within the middle of the calendar year. For the model it means that instead of factors $e^{M/2}$ и $e^{-M/2}$ the Equations (2) and (3) must contain factors $e^{\beta M}$, $e^{(1-\beta)M}$ and $e^{-\beta M}$, where β is a given constant ($0 < \beta < 1$). For simplicity in further explanations we will use $\beta=1/2$.

As can be seen, calculation of abundances in Equation (2) is undertaken directly through catch values. Catch values in this case are treated as true, the same way as in deterministic cohort models. But separabilization of the model makes it possible to look for unique values of $N_{a,y}$. . By this reason the version of the model determined by Equations (2)-(5) may be called ***catch controlled***. In this version of the model the role of separabilization consists only in estimation of terminal populations and this version may be regarded simply as a method of tuning of ordinary cohort analysis, while the loss function of the model (for example - sum of squared residuals between logarithms of real and theoretical catches) may be regarded as a measure of inseparability of the catch-at-age data (in logarithmic form) .

The effort-controlled version of the ISVPA, which do not treat catch-at-age data as true, is based on another dynamic state equation, resulting from substitution of the expression for theoretical catch $\hat{C}_{a,y} = s_a f_y N_{a,y} e^{-M/2}$ instead of real catch $C_{a,y}$ into Equation (2):

$$N_{a,y} = \frac{N_{a+1,y+1} e^M}{1 - s_a f_y} \quad (2')$$

Thus, in estimation of abundance by this version of the model it is implied that separable representation of fishing mortality is true and residuals are attributed to errors in catch-at-age

data. Here the value of loss function may be regarded as a measure of “precision” of catch-at-age data (if to assume that the fishery is fairly separable).

In practice in most cases both assumptions (that catch-at-age data are precise or fishery is well separable) are rather far from reality. If there are some ideas about their relative validity it is possible to use *mixed* version of ISVPA in which the equation of stock dynamics is a mixture (with the coefficient given by user) of equations (2) and (2’). In this version of the ISVPA the same weight (or “level of relative confidence”) of the two assumptions is used for all points.

Since often the user has no preliminary ideas about relative validity of the above mentioned assumptions and since the relative weight of these assumptions may be strongly different for different points (a,y) , the 4-th version of ISVPA named *mixed with weighting by points* is also available. In this version for *every point* (a,y) equations (2) and (2’) are weighted by reciprocal squared residuals between the given catch (a,y) value and its respective “theoretical” value $\hat{C}_{a,y} = s_a f_y N_{a,y} e^{-M/2}$ where $N_{a,y}$ is calculated by equation (2) or (2’). These weights are recalculated on every iteration within the iterative procedure of the model parameters estimation (see below).

Equation (2) or (2’) is treated as an exact one and serves for calculation of the matrix $\|N_{y,a}\|$ through M and $\|C_{y,a}\|$ (in the catch controlled version) or M and the vectors s_a and f_y (in the effort controlled version). Equations (3)-(4), postulating the separability, or age selectivity of fishing, is regarded as approximate ones, and the unknowns M , s_a and f_y are estimated so that to reduce the residual in (3) as much as possible (as a rule, the squared logarithmic error is meant). Equation (5) is a normalizing condition and is treated as an exact one.

Estimated values of $\varphi_{a,y}$ may be recalculated into traditional instantaneous coefficients of fishing mortality $F_{a,y}$ by the formula: $F_{a,y} = -\ln(1-\varphi_{a,y})$, which becomes obvious if to rewrite the equation (2’) as

$$\ln(N_{a,y} / N_{a+1,y+1}) = M - \ln(1-\varphi_{a,y})$$

and to compare it with traditional VPA equation:

$$\ln(N_{a,y} / N_{a+1,y+1}) = F_{a,y} + M.$$

3. Algorithm of the model

In general outline, for each version of the ISVPA the algorithm consists of a 'core', in which all the model parameters are evaluated from the iterative procedure at given natural mortality coefficient, M , and terminal fishing effort, f_n , and an outward 'shell', a loop in which the best M and f_n are fitted.

The 'core' is represented in the program *by 4 iterative procedures*. The three procedures described in details below are designed to ensure "unbiasness" of the solution, each - in its own sense.

The 4-th procedure is intended to produce the best fit to catch-at-age data, but the solution will be free from any restriction on bias. The 4-th procedure is rather time consuming derivative-free procedure, but experiments with very noisy data showed that if parameters are strongly interdependent and minimum is flat it works better (gives better fit) with respect to some of tested algorithms, including Marquardt-Levenberg and Simplex.

Basic iterative procedure (procedure A).

Within any ISVPA iterative procedure the given M and f_n are not changed. The calculations start with setting the initial values of the fishing effort, f_y at $y=1, \dots, n-1$ and selectivity, s_a ; at $a=1, \dots, m$ (the normalizing condition (5) must be kept). Each iteration consists of the following steps.

First, the terminal vectors $\{N_{a,n}\}$ and $\{N_{m,y}\}$ are evaluated from (3), then all other $N_{a,y}$ are determined from (2) or (2'). After that the matrix of fractions $\|\varphi_{a,y}\|$ is evaluated from the Equation

$$\varphi_{a,y} = \frac{C_{a,y}}{N_{a,y}} e^{M/2}, \quad (6)$$

and $\{f_y\}$ and $\{s_a\}$ are determined as

$$f_y = \sum_{a=1}^m \varphi_{a,y} \quad (7)$$

and

$$S_a = \frac{\sum_{y=1}^n \varphi_{a,y}}{\sum_{a=1}^m \sum_{y=1}^n \varphi_{a,y}} \quad (8)$$

To make the convergence better, s_m and s_{m-1} are replaced with their arithmetic mean:

$$S_m = S_{m-1} = \frac{\sum_{y=1}^n (\varphi_{m,y} + \varphi_{m-1,y})}{2 \sum_{a=1}^m \sum_{y=1}^n \varphi_{a,y}} \quad (9)$$

Note that the selectivity values remain normalized since the initial normalization.

Equations (7) and (8) are algebraic consequences of the relationship (4) which represents the hypothesis of separability of the fraction of the a -th age group abundance in the middle of the y -th year taken as catch. Strictly speaking, the symbol $\varphi_{a,y}$ is allotted to the estimate of the fraction given by formula (6) at every iteration IT . To avoid confusion, its separable analog, which also can be evaluated at every iteration, will be designated as $\varphi_{a,y}^{sp} = s_a f_y$.

Assume that the convergence is already achieved, and $\varphi_{a,y}$ and $\varphi_{a,y}^{sp}$ are limits of the corresponding fractions at $IT \rightarrow \infty$. When we deal with the 'pure', completely separable data, convergence means that $\varphi_{y,a} = \varphi_{y,a}^{sp}$. However, in the general case, when the catch-at-age data do not correspond to completely separable fishing (and contain errors), the two fraction estimates, $\varphi_{a,y}$ and $\varphi_{a,y}^{sp}$ must differ. This difference may serve as a measure of non-separability in the data, thus appearing in the role of a random error, $\varepsilon_{a,y}$, in the fraction $\varphi_{a,y}$ with respect to the separable fraction $\varphi_{a,y}^{sp}$:

$$\varphi_{a,y} = s_a f_y + \varepsilon_{a,y} \quad (10)$$

Now let us clear up the question of whether our separable estimates of φ are unbiased or not. Such an analysis requires calculation of the mathematical expectation of the random values

ε . It is reasonable to regard such errors within each age group at $y=1, \dots, n-1$ as being independent and equally distributed. When this is the case, the averaging of ε within the same age group furnishes the required estimation of the bias. At $IT \rightarrow \infty$ relationships (5), (7) and (10) yield:

$$f_y = \sum_{a=1}^m (s_a f_y + \varepsilon_{a,y}) = f_y + \sum_{a=1}^m \varepsilon_{a,y}$$

or

$$\sum_{a=1}^m \varepsilon_{a,y} = 0, \quad (11)$$

for every year y . Similarly, at $IT \rightarrow \infty$, relationships (5), (8), (10) and (11) involve:

$$s_a = \frac{\sum_{y=1}^n (s_a f_y + \varepsilon_{a,y})}{\sum_{a=1}^m \sum_{y=1}^n (s_a f_y + \varepsilon_{a,y})} = s_a + \frac{\sum_{y=1}^n \varepsilon_{a,y}}{\sum_{y=1}^n f_y},$$

or

$$\sum_{y=1}^n \varepsilon_{a,y} = 0 \quad (12)$$

for every age group a (certainly, transformation (9) does not break this result). Relationships (11) and (12) prove that the separable estimates of φ supplied by this iterative procedure are unbiased.

Weighted arithmetical mean procedure (procedure B)

When the selectivity is strongly dependent on age, the errors corresponding to different age groups hardly can be regarded as equally distributed (although, relationship (10) shows that their mean over age also equals zero). In this case, a modified iterative procedure might be appropriate, in which inverse selectivity values serve as weights at the stage of calculating the efforts.

Within this, 'weighted' iterative procedure, relationship (7) is replaced with the following equation for calculating the efforts:

$$f_y = \frac{1}{m} \sum_{a=1}^m \frac{\Phi_{a,y}}{s_a}, \quad (13)$$

(which is also an algebraic consequence of the separability hypothesis), and the efforts are calculated from (13) taking the selectivity values from the previous iteration. Thereupon the current selectivity values are computed from (8).

Analysis of statistical sense of the solution for this procedure is similar to the previous one. At $IT \rightarrow \infty$ relationships (5), (13) and (10) result in:

$$f_y = \sum_{a=1}^m (s_a f_y / s_a + \epsilon_{a,y} / s_a) = f_y + \sum_{a=1}^m (\epsilon_{a,y} / s_a)$$

or

$$\sum_{a=1}^m (\epsilon_{a,y} / s_a) = 0, \quad (11')$$

for every year y . Similarly, at $IT \rightarrow \infty$, relationships (5), (8), (10) and (11') will give:

$$s_a = \frac{\sum_{y=1}^n (s_a f_y / s_a + \epsilon_{a,y} / s_a)}{\sum_{a=1}^m \sum_{y=1}^n (s_a f_y / s_a + \epsilon_{a,y} / s_a)} = s_a + \frac{\sum_{y=1}^n (\epsilon_{a,y} / s_a)}{\sum_{y=1}^n f_y},$$

or

$$\sum_{y=1}^n (\epsilon_{a,y} / s_a) = 0 \quad (12')$$

for every age group a . Relationships (11') and (12') prove that the separable estimates of ϕ weighted by selectivity factor, supplied by this iterative procedure are unbiased.

“Logarithmic” (geometrical mean) procedure (procedure C)

Logarithmic transformation of the relationships (3) and (4) leads to the third iterative algorithm, similar to the basic and the weighed arithmetic mean ones but dealing with logarithms of C , φ , s , f , etc. Within this, logarithmic iterative procedure relationships (6) - (8), that are used at IT -s iteration, must be replaced with:

$$\ln \varphi_{a,y} = \frac{M}{2} \ln \frac{C_{a,y}}{N_{a,y}}, \quad (14)$$

$$\ln f_y = \frac{1}{m} \sum_{a=1}^m \ln \left(\frac{\varphi_{a,y}}{s_a} \right), \quad (15)$$

$$\ln s_a = \frac{1}{n} \sum_{y=1}^n \ln \frac{\varphi_{a,y}}{f_y}, \quad (16)$$

and

$$\ln s_m = \ln s_{m-1} = \frac{1}{2n} \sum_{y=1}^n \left(\ln \frac{\varphi_{m,y}}{f_y} + \ln \frac{\varphi_{m-1,y}}{f_y} \right) \quad (16a)$$

When evaluating f_y from (15), selectivities are taken from the previous iteration. At the end of each iteration, selectivities must be re-normalized so that to satisfy condition (5). This procedure can also be called "weighed geometrical mean procedure", as from (15) and (16) it immediately follows that f_y and s_a equal to the geometrical means of $\varphi_{a,y}$ weighed by s_a and f_y respectively.

In order to understand the statistical meaning of the convergence point of this procedure, it is convenient to use the notion of estimated catch,

$\hat{C}_{a,y} = s_a f_y N_{a,y} e^{-M/2}$, and present $\varphi_{y,a}$ in the form:

$$\varphi_{a,y} = s_a f_y \frac{C_{a,y}}{\hat{C}_{a,y}} \quad (17)$$

As it was noted above, we are considering the convergence of the iterative procedure, i.e., the limits at $IT \rightarrow \infty$ of all the variables participating in the model. Therefore the fractions $\varphi_{a,y}$,

which is determined by equation (14) and figures in (15) and (16), can be replaced with that given by relationship (17), where $\hat{C}_{a,y}$ is substituted by $\hat{C}_{a,y}^*$, the catch estimates supplied by the iterative procedure at $IT \rightarrow \infty$. This substitution implies:

$$\sum_{a=1}^m [\ln C_{a,y} - \ln \hat{C}_{a,y}^*] = 0 \quad (18)$$

and

$$\sum_{y=1}^n [\ln C_{a,y} - \ln \hat{C}_{a,y}^*] = 0. \quad (19)$$

The meaning of (18) and (19) is that the log-transformed estimates of catches are unbiased. It can be simply shown that this procedure provides unbiased estimates of logarithms of $\varphi_{a,y}$, s_a and f_y .

4. Loss functions

In accordance with the assumptions about the error structure in the data the solution of the model may be based on standard minimization of sum of squared residuals or on minimization of more robust loss functions: median of distribution of squared residuals or absolute median deviation of residuals.

Minimization of the median, *MDN*, of squared residuals (that is, the use of the least median or LMSQ principle) instead of their sum (the classical LSQ-principle) sometimes is referred to be more resistant with respect to outliers, those elements of the data set which overstep considerably reasonable confidence limits and, hence, are suspicious of containing extremely high errors (O'Brien, 1997; Hampel et al., 1986).

According to this concept, an alternative ISVPA solution may be looked for as providing estimates of M and f_n , which secure minimum of the median of the distribution of the squared logarithmic residuals,

$$SE_{a,y} = (\ln C_{a,y} - \ln \hat{C}_{a,y}^*)^2$$

($a = 1, \dots, m$; $y = 1, \dots, n$). The corresponding loss function will be denoted as *MDN*(M, f_n).

In practice, the median of a random series is estimated by rearranging its elements in a descending or increasing order and taking the central element of the new series or the mean of two central elements (depending on whether the total number of the elements is odd or even). However, when used within the framework of ISVPA, this estimate sometimes may cause a certain roughness of the surface $MDN(M, f_n)$. In order to make the loss function smoother, the median is estimated here as the mean of a number (for example, 10) central elements of the ordered series of $SE_{a,y}$. So, in this version of ISVPA, the iterative procedures for estimating the vectors f and s remain the same as described above, the only difference being the use of the behavior of the median as an indicator of their convergence. Numerical experiments ascertain workability of the three versions of the ISVPA iterative procedures combined with the LMSQ principle.

As was noted above, in order to smooth the median estimates, averaging over a number of central elements of the ordered series of squared residuals is suggested. Certainly, the number of central elements can vary from one or two to $m-n$, the total length of the series. However, in the latter case, the averaging results in estimation of the mathematical expectation and not the true median of the squared residuals. So, in fact, the suggested approach (when averaging over a number of central squared residuals is applied) can be regarded as a compromise between the true median minimization and the conventional least squares criterion. The advantage of this compromise is that, according to our experience, the use of the least squares approach leads to a sufficiently smooth loss function, while the minima of $MDN(M, f_n)$ are better pronounced.

One of the central issues in fitting a model to real data is the choice of the fitting criterion. Statistically, the use of the LSQ criterion is equivalent to accepting the hypothesis of normality of the distribution of the residuals (in the case when the sum of squared logarithmic residuals is minimized, the errors themselves are supposed to be logarithmically normal). What is the reason for using the median minimization approach? What kind of iterative procedure matches well the LMSQ criterion? To illuminate the nature of combining LMSQ criterion with ISVPA, let us consider the third, weighed logarithmic version of the iterative procedure.

It was shown above that the logarithmically transformed theoretical estimates of catches are unbiased. Strictly speaking, it means only that the mathematical expectation of the corresponding residuals is zero. We, however, believe that in practice, the distributions of the logarithmic residuals often are almost symmetric. This is confirmed by our numerous computer

tests with both simulated and real data. Clearly, if a random value ε is distributed symmetrically the median of its squares, ε^2 , indicates the compactness of the distribution of ε : the higher the median of ε^2 , the greater the variance of ε . Conversely, the lower the median of the distribution of ε^2 , the more compact is the distribution of ε . So, by minimizing the median of the squared logarithms of the catches residuals resulting from estimation of catches by means of the weighed logarithmic iterative procedure, the maximal allowable compactness of the distribution of the errors themselves is reached, thus providing a reasonable fit of the model to the catch-at-age data in the sense of the conventional maximum likelihood concept.

Such a statistical justification cannot be given to the median minimization approach when the first (**A**) or the second (**B**) version of the ISVPA iterative procedure is used, as neither of them impose any reasonable condition on the errors in logarithmically transformed catches. From this point of view for these versions the conventional least squares approach seems to be more appropriate.

From the other side, the approach when the quality of fitting is measured by some “window” in the distribution of residuals which does not include the tails of the distribution, may be considered as a mean to suppress the influence of outliers on the solution (because the residuals which corresponds to outliers, are located near the margin of distribution and will not influence the value of the median). From this point of view minimization of the median seems to be appropriate for procedures **A** and **B** also.

In addition to the two above mentioned ISVPA objective functions, the absolute median deviation $AMD(M, f_n)$ - the median of the absolute deviations of model residuals from their median value, known as one of the most robust measures of scale (Huber, 1981), also may be used. According to the author’s experience in some cases (for example, when distribution of residuals, still having zero mean, has nonzero median) AMD gives more pronounced minimum with respect to $MDN(SE)$ - minimization. But if the data are not informative (for example, if historical changes in catches and in stock are not pronounced) AMD may be not sufficiently sensitive and it may be better to use MDN .

Now let us say a few word about the procedure of estimation of the “best” (in the sense of the loss function chosen) values of (f_n, M) . Its choice in the ISVPA was based on the following considerations:

- algorithmic simplicity, bearing in mind that in the *outer loop* only two (or even one, if M is considered as known) parameters are to be estimated;
- if the loss function surface has more than 1 minimum - possibility to start minimization in the vicinity of the required minimum and to arrive at it even if the surface is very flat (this implies that gradient methods may be ineffective).

As numerous simulation experiments have shown, the method, which was not fastest, but which allowed to precisely reach the minimum even if the error surface was very flat and the minimum was local, was the method of “lowering by coordinates” with successively diminishing steps. The step of the procedure (the increase in the tested parameter value) is fixed by the program and after the minimum is achieved with this step, the step is diminished by a factor of 10. After the minimum is achieved again, the step value is decreased again by the same factor, and so on, till the minimum is reached with the required precision by the tested parameter value.

It is necessary to mention that while minimization of sum of squared errors multiple minima are almost never encountered (here the problem is that for noisy data minimum of SSE is often reached at marginally high or low value of the tasted parameter), for median minimization the surface of the loss function (as a function of f_n and M) may have complex structure. That is why before the final run with precise estimation of the model parameters it is recommended to make preliminary point-by-point scanning of the $(f_n ; M)$ area with sufficiently small step (for example, 0.1 for f_n and 0.01 for M). Program realization of ISVPA gives such a possibility.

5. Suppression of inter-iteration oscillations

When the level of noise in the initial data is high, the estimated effort and selectivity, as well as the sum of squared residuals, SSE , vs. the number of iteration, IT , contain a few visible slowly decaying modes of oscillations superimposed upon a certain rapidly stabilizing trends. These oscillations slow down the convergence of SSE to its limit, SSE^* , or of MDN to MDN^* , or AMD to AMD^* at $IT \rightarrow \infty$, thus becoming significant at the stage of searching for the minimum of $SSE^*(M, f_n)$ or $MDN^*(M, f_n)$, as in practice, at every M and f_n the iterative process is stopped at a finite IT . The most notable in this context are the saw-tooth type oscillations with a 2-year periodicity, i.e., those of the highest frequency. Conventional method for filtering oscillations and extraction of trends from numerical series is moving averaging. We, however, are dealing with an iterative process, where at any iteration IT , the current selectivity, $s_{IT}(a)$, or the effort,

f_{IT} , estimate is calculated after the previous value, $s_{IT-1}(a)$ or $f_{IT-1}(y)$, was found. That is why, by defining the corrected selectivity and effort estimates at IT -th iteration, $s'_{IT}(a)$ and $f'_{IT}(y)$, as

$$s'_{IT}(a) = \alpha s_{IT-1}(a) + (1 - \alpha) s_{IT}(a) \quad (20)$$

$$f'_{IT}(y) = \alpha f_{IT-1}(y) + (1 - \alpha) f_{IT}(y) \quad (21)$$

and by a proper choice of the coefficient $0 < \alpha < 1$, the desired filtration, similar to the moving averaging, can be achieved. According to (20), all the selectivity estimates, which were computed at the previous iterations, participate in the correction for the current, IT -th iteration. The same is valid for the effort (see (21)). So, the size of the averaging interval in this filtration procedure increases with the growth of IT . Nevertheless, as the weights of the last, IT -th, iterations remain constant, while the weights of the early iterations decay, the suggested filtering procedure can be regarded as an analog of a conventional moving averaging. The effective averaging interval is determined by the choice of α : the smaller α , the narrower the effective averaging interval. Experiments showed that the choice of α do not influence the result: there are almost identical for tested diapason of α from 0 to 0.95.

6. Treatment of zero catches.

Existence of zero values in catch-at-age matrix is known to be a rather complicated (and may be logically controversial when dealing with logarithmic residuals) problem and is solved differently in different methods. In ISVPA the following algorithm is applied:

1. If $C_{a,y} = 0$, then the value of $\varphi_{a,y}$ is taken equal to its “theoretical” value, that is

$$\varphi_{a,y} = s_a f_y.$$

2. Residuals for points of zero catches are taken equal zero.

3. Stock abundance is computed as follows:

3.1. If $N_{a+1,y+1} > 0$ and $C_{a,y} = 0$, than $N_{a,y}$ is computed by (2.2).

3.2. If $N_{a+1,y+1} = 0$ and $C_{a,y} = 0$, than $N_{a,y} = 0$.

3.3. If $N_{a+1,y+1} = 0$ and $C_{a,y} > 0$, than $N_{a,y}$ is computed by (2.3) -the same way, as for terminal points.

3.4. If $N_{a+1,y+1} > 0$ and $C_{a,y} > 0$, than $N_{a,y}$ is computed by equation (2.2) or (2.2') or their mixture, according to the version chosen.

7. Some other variants of optimization algorithms

Some other variants of ISVPA parameter estimation procedures were also tested while working at the program. For example, to make faster the parameter estimation procedure an attempt was made to exclude the estimation of natural mortality coefficient from the “outer loop” and to estimate this parameter within the “inner” iterative procedure along with $\varphi_{a,y}$, s_a and f_y . For this purpose on every iteration, after the vectors s_a and f_y , are estimated, new matrix $\varphi_{a,y}=s_a f_y$ is building up and a new parameter X , being the average value of $e^{-M/2}$, is estimated:

$$X_{a,y} = C_{a,y}/(\varphi_{a,y}N_{a,y});$$

$$X = \frac{1}{nm} \sum_{y=1}^n \sum_{a=1}^m X_{a,y}$$

After that a new value of natural mortality coefficient is estimated as $M = -2LnX$. Naturally, an initial guess for M is to be input before the start of the procedure along with initial guess for s_a and f_y . For initial guess it is possible to use any positive values of s_a and f_y , such as $s_a f_y < 1$. For M the initial guess may be taken from the diapason $0 < M < 1$.

Unfortunately experiments showed that this variant of procedure is suitable only for very “clean” data (with very low noise) and for practical purposes this procedure is not effective.

Experiments also proved the importance of organization of ISVPA parameter estimation procedure in form of two concentric loops: attempts to estimate f_n (or both f_n and M) in frames of single loop along with other parameters was not successful: it was needed to use rather precise initial guess for all parameters, what is rarely possible in practice. This is explained by low curvature of loss function for real (that is noisy) data. Consequently, optimization by parameters f_n and M , which are most influenced by values of other parameters, does not work until the “best values” (for the tested values of f_n and M) of other parameters are not estimated (or “almost” not estimated).

8. Estimation of ISVPA parameters without limitation on bias

In order to test experimentally the role of limitation on bias, imposed by the above described ISVPA procedures, an additional, free of such limitations parameter estimation procedure was developed.

For “direct” fitting of multi-parameter models the Marquardt-Levenberg and Gauss-Newton method are traditionally used (Bard, 1974), as it was done, for example, in CAGEAN (Deriso et al., 1985) and ICA (Patterson, 1994). But in our case implementation of these methods is complicated by normalization equation (2.5): parameters are becoming inter-dependent. Attempt to use Simplex-method (Schnute, 1982) was also unsuccessful: for the case of many parameters the procedure is very time-consuming and also requires very qualified initial guess for parameters (the result is extremely sensitive to its choice).

Because of the above mentioned, the procedure of “direct” search for the ISVPA parameters, free of limitations on bias, was finally arranged as follows. The same was, as it was done with “iterative” inner ISVPA procedures, the procedure was designed as two concentric loops. In outer loop optimization by (f_n, M) is made, while the parameters $\{s_a\}$ and $\{f_y\}$ (except f_n) are estimated in the inner loop.

The inner loop is arranged as follows. Each parameter is optimized in succession, while the order of optimization appeared to be important. Starting from a set of initial guesses for all parameters s_1, \dots, s_m и f_1, \dots, f_{n-1} , optimization begins from f_{n-1} ; after that the value of f_{n-2} is optimized, and so on till f_1 . After that, the best value (from point of view of the loss function) of s_1 is estimated, the other values of s_a being changed by means of normalization equation (5). The found value of s_1 is then “frozen up” and the “best” value of s_2 is searched for (here the normalization equation (5) is applied to the rest of selectivity factors: s_3, \dots, s_m ,). Then the next, s_3 , selectivity factor is estimated, and so on till s_{m-2} . The rest of selectivities, $s_m = s_{m-1}$, appears to be already estimated by the normalization equation. After that the procedure again returns to estimation of f_1 , and the sequence of calculations is repeated till convergence.

The above described procedure gives the solution free from restrictions on bias. For “clean” catch-at-age data (simulated data without noise) the procedure gives absolutely correct estimates of all parameters (as well as “iterative” procedures **A**, **B** and **C**). For noisy simulated data and for real data the solution based on this “unrestricted” fitting procedure as a rule is much worse, while the final value of loss function may be lower than for “unbiased” solutions.

It is necessary to mention that implementation of the above described procedure of “parameter-by-parameter” optimization for *median* minimization may be problematic if one (or a group) of parameters s_1, \dots, s_m and f_1, \dots, f_{n-1} occasionally influences only those values of

residuals which are located on tails of distribution of residuals and, hence, do not influence the median value.

9. Dealing with auxiliary information

There is possibility to include up to 3 SSB indexes and up to 7 age structured stock abundance indexes into the model. In such a case ISVPA loss function will include additional components representing measures of discrepancy:

- for each SSB index : between logarithms of SSB from cohort part and from surveys;
- for each age-structured index: between logarithms of abundance (a,y) from cohort part of the model and from surveys (corrected to estimated age-dependent "fleet catchabilities" or not).

It is also possible to fit the model not only on survey abundance-at-age data, but on survey age proportions and “weighted” survey age proportions. In fact, age-structured abundance indexes, when being used for tuning of cohort models, sometimes give unclear or controversial signals about stock size, more precisely - about the value of terminal fishing mortality coefficient (F_{term}). In some cases the minimum of corresponding component of loss function of a model may be completely deteriorated, that is, the best fit is found for extremely low or high F_{term} . This indicates that abundance-at-age index data from surveys (or in cpue of a fishing fleet) are so far from the values calculated in cohort part of a model from catch-at-age data (theoretical values), that the best fit corresponds to almost zero (or extremely high) stock size in terminal year. It is not always clear why we have such a discrepancy. At least there could be two possible explanations: 1) age structure of abundance-at-age index from surveys (or for a fleet, used for tuning) is unrepresentative with respect to the whole stock (data are very noisy), and 2) there is a trend in catchability of surveys. Naturally, both the above mentioned factors may act simultaneously.

Considering the second reason (year-dependent factor in survey catchability), it is theoretically possible to make an attempt to estimate time trend in catchability, but this requires additional data and may make the model to be too flexible. That is why in some cases it is preferred to substitute fitting of the model to abundance-at-age index data by fitting on age composition (in proportion) of survey data (that is, by minimization of residuals between age composition of surveys and age composition of abundance derived from a model). Usually in such a case multinomial (Fournier et al., 1998) or, as it is done in COLERANE (Hilborn et al., 2000), robust-normal error model is used.

Influence of the first above mentioned reason (high level of noise in the survey data) may be diminished by robustization of the model, for example, by application of robust loss functions, such as the median of distribution of squared residuals instead of their sum.

In some cases survey data may have different quality in different years. For example, representativity of the data may correlate with stock abundance. In such a case a specific weights may be needed for specific years.

Let us assume lognormal error model. Then the residuals between “theoretical” (derived from a model) abundance-at-age $N_{a,y}^{(th)}$ and index abundance-at-age $N_{a,y}^{(Ind)}$ may be represented as:

$$res_{a,y} = Ln\left(\frac{N_{a,y}^{(th)}}{N_{a,y}^{(Ind)}}\right) = Ln\left(\frac{P_{a,y}^{(th)} \sum_{a=a \min}^{a \max} N_{a,y}^{(th)}}{P_{a,y}^{(Ind)} \sum_{a=a \min}^{a \max} N_{a,y}^{(Ind)}}\right) = Ln\left(\frac{P_{a,y}^{(th)}}{P_{a,y}^{(Ind)}}\right) + Ln\left(\frac{\sum_{a=a \min}^{a \max} N_{a,y}^{(th)}}{\sum_{a=a \min}^{a \max} N_{a,y}^{(Ind)}}\right) \quad (22)$$

where $P_{a,y}^{(th)}$ and $P_{a,y}^{(Ind)}$ are proportions of age group a in the “theoretical” and “index” stock abundance in year y . From expression (22) it is clearly seen that, when dealing with minimization of residuals between abundances, in fact for each point (a,y) we are simultaneously minimizing residuals between age compositions and between total abundances. It is also seen that the ratio of total abundances may be considered as a “weighting factor” for ratio of proportions.

As it was mentioned above, for minimization of residuals in age compositions (proportions) it is more traditional to assume multinomial or robust-normal error model. Nevertheless in the ISVPA we use logarithmic residuals, because experiments shows that in some cases lognormal error model seems to be at least not less appropriate (e.g. see Vasilyev 2003). To be comparable, age proportions in each year are calculated only for those age groups, which are simultaneously present both in stock and in index data.

Another option, which was also added to the model, consisted in possibility of tuning by minimization of residuals between logarithms of models-derived abundance $LnN_{a,y}^{(th)}$ and index age structure $LnP_{a,y}^{(Ind)}$. In such a case model-derived estimates of total abundance serves as weighting factors for age proportion ratios (see expression (22)). This option could be helpful for stocks with strongly variable abundance, if representativity of survey data is strongly dependent

on stock size. As well as for catch-at-age and for tuning on index abundance-at-age data, minimization for age structures (or for abundance and index age structures) can be undertaken in the model by minimization of the sum of squared logarithmic residuals (SSE), or by minimization of more robust statistics: the median of distribution of squared logarithmic residuals (MDN). Possibility for minimization of absolute median deviations (AMD) – the median of distribution of absolute deviations between logarithmic residuals and their median value is also reserved.

Thus, for each age-structured index the discrepancy may be measured as traditional sum of squared residuals, or by MDN, or AMD. The measure may be stated independently for each of "fleet".

For SSB indexes the only available measure in the model is the sum of squared residuals (because, as a rule, available number of years of SSB surveys is rather low).

10. The program

Current realization of ISVPA is made in Visual Basic and can be run from any Windows environment. If Visual Basic is installed on your computer it will be enough to copy only exe – file. If not – use ISVPA set up package.

Input files are blank-separated text files and include:

- "necessary" files: catch-at-age by years, weight-at-age by years in the stock and maturity-at-age by years;
- "optional" files (may be not given): natural mortality by ages, up to 3 files with SSB estimates by years and up to 7 files with age-structured abundance indexes by years.

All input files must be positioned into **C:\vbisvpa** directory or its subdirectories.

Output files include: the file with records of minimization (minim.out), the file of results (its name is given by user) of initial ("basic") run, as well as bootstrap output files:

- 1) bootf.out - includes effort factor estimates by years and bootstrap runs;
- 2) bootm.out - includes natural mortality estimates by ages and bootstrap runs (if it was considered as unknown parameter);
- 3) boots1.out and boots2.out - include the estimates of selectivities (for first and second time intervals) by ages and bootstrap runs (the program gives possibility to fit 2 different selectivity patterns for 2 different successive time intervals);

- 4) bootssb.out - includes the SSB estimates by years and runs;
- 5) boottsb.out - includes the estimates of total stock biomass by years and runs;
- 6) bootntrm.out - includes terminal year abundance estimates by ages and runs.

The procedure of working with the program is the following.

1. First what is needed to be done while running the program is to enter the names of catch-at-age and weight-at-age files. If they are located directly in C:\vbisvpa directory - simply print their names (with extension). If they stand in some sub-directory of C:\vbisvpa - print the name of the file with the name of this subdirectory.
2. After that you will be asked about the **situation with natural mortality**: 1) to find M as age-independent value; 2) to find it as a simple quadratic function of age; 3) to use known values of $M(a)$. If option 2 is chosen, you will be asked to enter the age of minimum M (as a rule it may be taken equal to the age of 'mass' maturity). If option 3 is chosen, you will be asked to enter the name of file with known $M(a)$ values.
3. Next you have to choose the method for parameter estimation. 4 options are available. Option 1 will produce solution with "unbiased separabilization"; option 3 - with "unbiased weighted separabilization"; option 2 will ensure "unbiased" estimates of logarithms of all parameters; option 4 will produce solution corresponding to best fit to logarithmic catches, not restricted by any condition on bias. While using option 4 be patient - it takes time. In most cases option 2 is recommended. It is strongly recommended **not to use option 4** when you minimize the median - error surface may be too "broken".
4. The next choice is what to minimize. It is possible to minimize sum of squared residuals in logarithmic catches, or median of distribution of squared residuals in logarithmic catches $MDN(M, f_n)$, or absolute median deviation $AMD(M, f_n)$. For noisy data minimization of MDN or AMD is recommended.
5. Selection of first and last year of analysis and the last year of first selectivity pattern (**the program gives possibility to fit 2 different selectivity patterns for 2 different successive time intervals**). After that it is needed to input the first and the last age groups. Naturally, they should be within the limits of the input data. After that you will be asked: is the oldest age in the data a "normal" age group, or it is +-group ?
6. Next question is about the "version" of the program (1. Catch-controlled, 2. Effort-controlled, 3. Mixed, 4. Mixed, weighted by points). Version 1 is preferable if fishery is known to be extremely non-separable. It also may be useful as a part of "mixed" versions 3 and 4. Version 2 is preferable if M is considered as unknown parameter and/or the data are very noisy.
7. If version 3 is chosen you will have to input relative weight of catch-controlled routine.
8. You may 1) scan the error surface or 2) look for precise solution. If scanning is chosen, you will be asked about minimum and maximum values of the parameter (f_{term} or (M and f_{term})) and of "step". It is recommended to make scanning first - there could be several local minima of the loss function. Option 2 allows to find precise solution. If several local minima

exist, you may look for the solution corresponding to the required minimum - by proper choice of initial guess for the parameter and sufficiently small initial step. Please note that if “scan” mode was chosen, the output file will contain the result at **rough** minimum of the loss function. To get the result at precise minimum you have to start the program again and to choose the option “precise solution”. If “precise solution” is looked for - you have to input the value of initial guess for f_{term} or (M and f_{term}) and of initial step for searching procedure.

9. Next you will have to set the value of “inter-iteration smoother”. In most cases any value within 0.5-0.9 will be OK. For very noisy data to suppress possible oscillations you may take the higher value - up to 0.9. Don’t worry about “precise” value of this parameter: if procedure converges - it is OK. Experiments proved that final result will be the same even for 0.95.
10. If you have chosen the median minimization, you will have to input the number of central elements of the ordered series of squared residuals (or residuals) to use as its measure. In most cases 10 points is OK. If error surface contain too many local minima it may be useful to increase the number of central elements; if minimum is too flat - you may diminish the number of central elements. Please note that this setting will be used for MDN or AMD measures everywhere (for indexes also, if one of these measures will be used for some of them).
11. Enter the portion of the year for peak of catches (since the model is based on Pope’s approximation of “instantaneous” catch). If fishing goes on uniformly all over the year - enter classic 0.5.
12. Enter the name of output file. It will be in C:\vbisvpa directory.
13. You have possibility to make output of currents results on screen. Output on screen makes the calculations slower, but it is comfortable to see what’s happening.
14. Input maturity-at-age file name.
15. You will be asked to include SSB surveys or not. If “yes”, you will have to input names of files with SSB surveys by years (up to 3).
16. If you have age-structured abundance indexes, you may use up to 7 different indexes. If “yes”, input their names.
17. If any auxiliary information is used, you will be asked to input weight for catch-at-age-derived component in the overall loss function (any value is allowable, including 0).
18. If SSB surveys are included - for each of them input weights for components of the overall loss function, representing measures of their closeness to cohort part -derived estimates of SSB (for SSB indexes only one kind of measure is available - sum of squared residuals between their logarithmic values).
19. Input portion from start of the year before the moment when surveys are made (the same for all SSB indexes).
20. If SSB surveys are included – for each of them input the values of standard deviation of lognormal distribution, which will be used in stochastic runs.

21. If SSB surveys are included - state how to treat each of them: as absolute or relative index.
22. If age-structured indexes are included - input portion from start of the year before the moment when age-structured survey is made (for each kind of survey).
23. If age-structured indexes are included - state index of what they are (mature part, whole stock, or immature part).
24. If age-structured indexes are included - for each of them input weights for components of the overall loss function, representing measures of their closeness to cohort part- derived estimates of abundance.
25. If age-structured indexes are included - for each of them answer the question: to estimate age-dependent catchabilities or not (if “not” is chosen then it will be assumed that $q(a)=1$).
26. If age-structured indexes are included - choose for each of them what measure of closeness of fit will be used: MDN, SSE, or AMD.
27. If age-structured indexes are included – choose what you want to compare in tuning : 1) logarithmic abundances(a,y) from cohort part of the model and logarithmic abundances(a,y) in survey; 2) logarithmic abundance(a,y) (from cohort part of the model) and logarithmic age structure(a,y) of surveys; 3) logarithmic age structure of the stock(a,y) (from cohort part) and logarithmic age structure(a,y) of surveys.
28. If age-structured indexes are included –for each of them input the values of standard deviation of lognormal distribution, which will be used in stochastic runs.
29. When calculations are finished, you may make stochastic runs. Current version of the program gives possibility to run parametric conditional bootstrap with respect to catch-at-age, (assuming that errors in catch-at-age data are log-normally distributed, standard deviation is estimated in basic run), combined with adding noise to indexes (assuming that errors in indexes are log-normally distributed with specified values of standard deviation).

If something goes wrong or in unwanted direction, it is always possible to **stop the program** by clicking the button “stop”. The program will return to initial (input) screen and you may run it again. The only what is necessary to remember when using stop by user is that if option of “direct search” of inner parameters is used, you have to let the program to finish at least one inner cycle (that is to finish calculation of inner parameters for at least one f_{term}) and to stop it after that (if not – interrupt will cause error and abortion of the program).

Note: current version gives possibility to use surveys for terminal+1 year (that is for year without known catch-at-age) Fishing pattern in this year is assumed equal to that of “true” terminal year. In such a case all input files should be entailed to include data for this year (it is becoming terminal one); catch-at-age file should include zero values of catch-at-age for this year.

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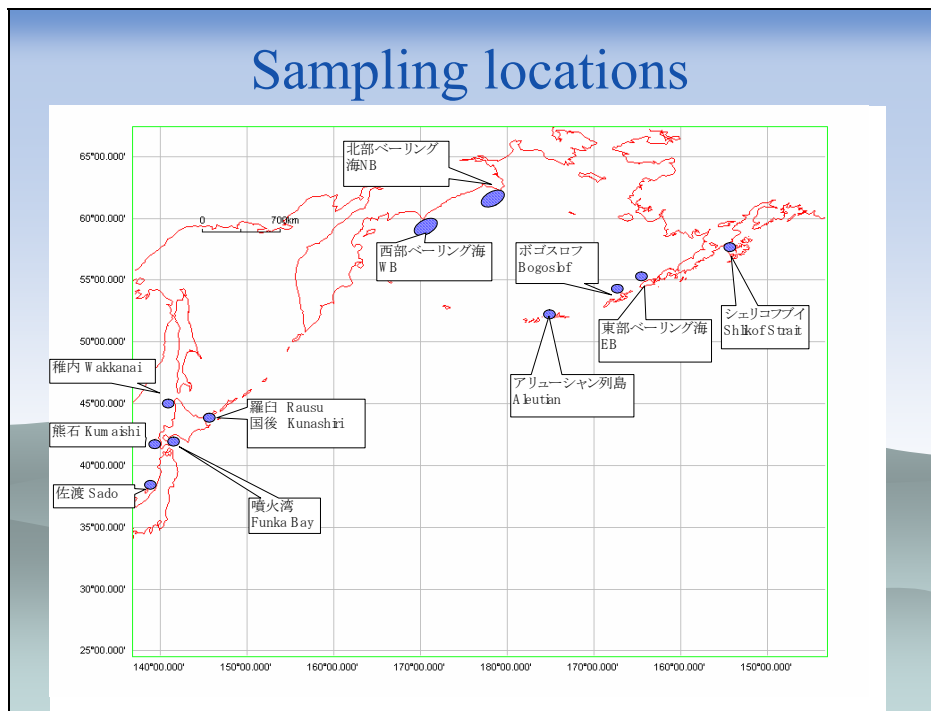
Summary of DNA analysis of walleye pollock by Japanese Scientists (2005)

- ◆ Takashi Yanagimoto (FRA, HNF)
- ◆ Toru Kitamura (Japan NUS co. jp)
- ◆ Takanori Kobayashi (FRA, NRIFS)
- ◆ Ichiro Nakayama (FRA, NRIFS)

DNA analysis

- ◆ Total mtDNA Sequenced
- ◆ mtDNA PCR-RFLP analysis
- ◆ mtDNA control region sequenced
- ◆ Nuclear DNA analysis (RAPD, TREP, SNP analysis of Calmodulin gene)

Sampling locations

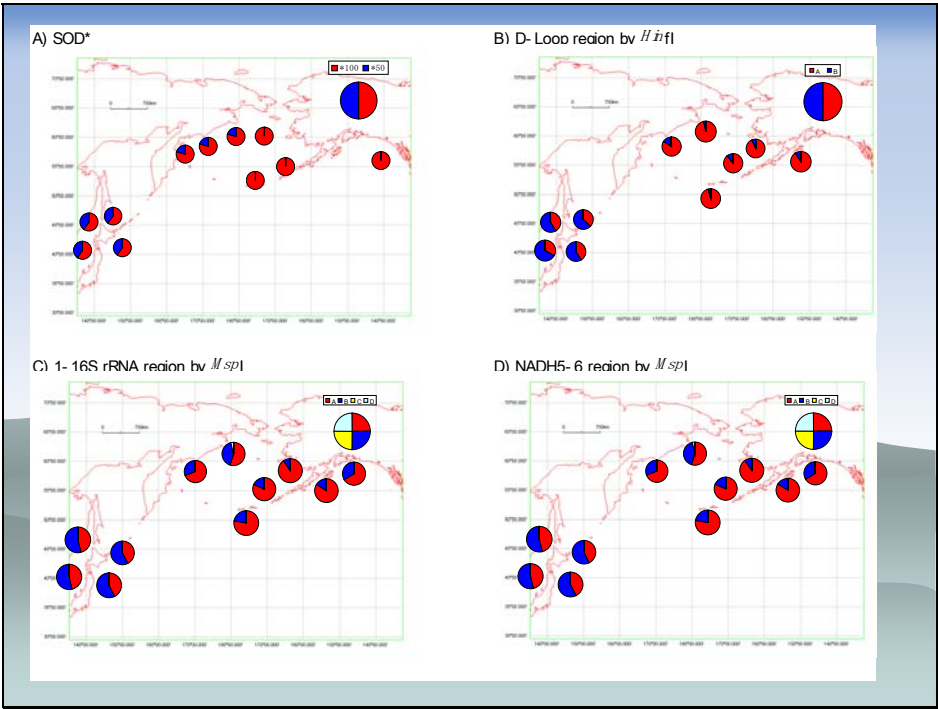
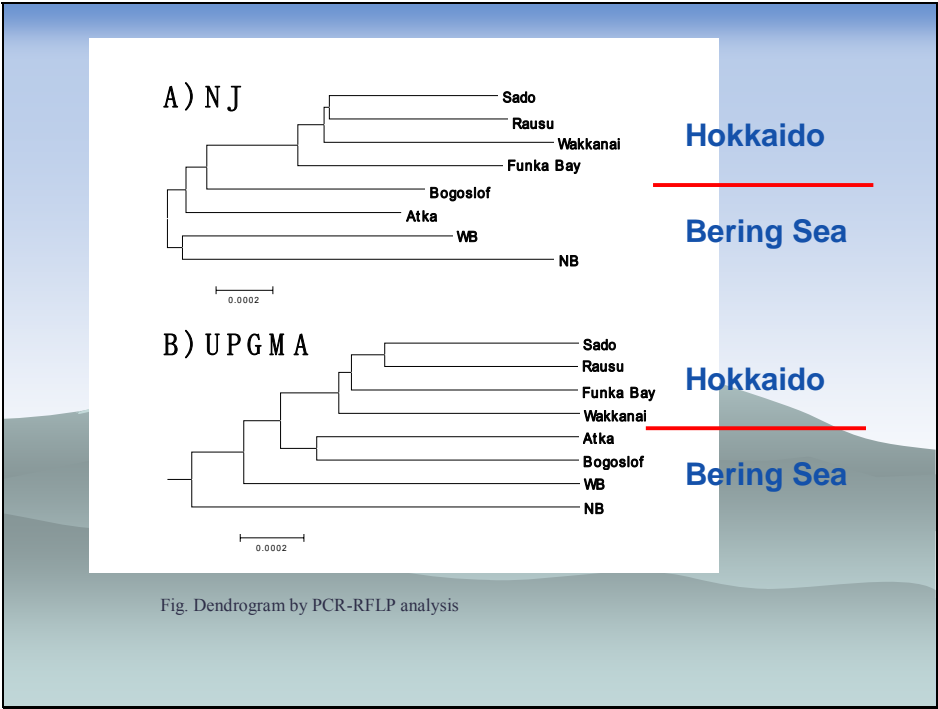


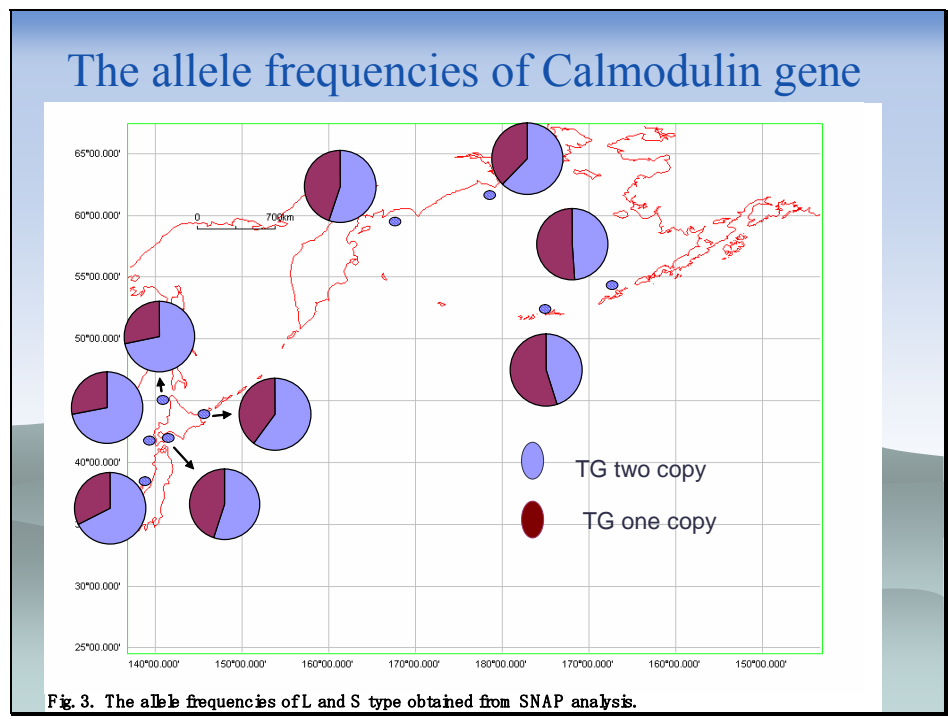
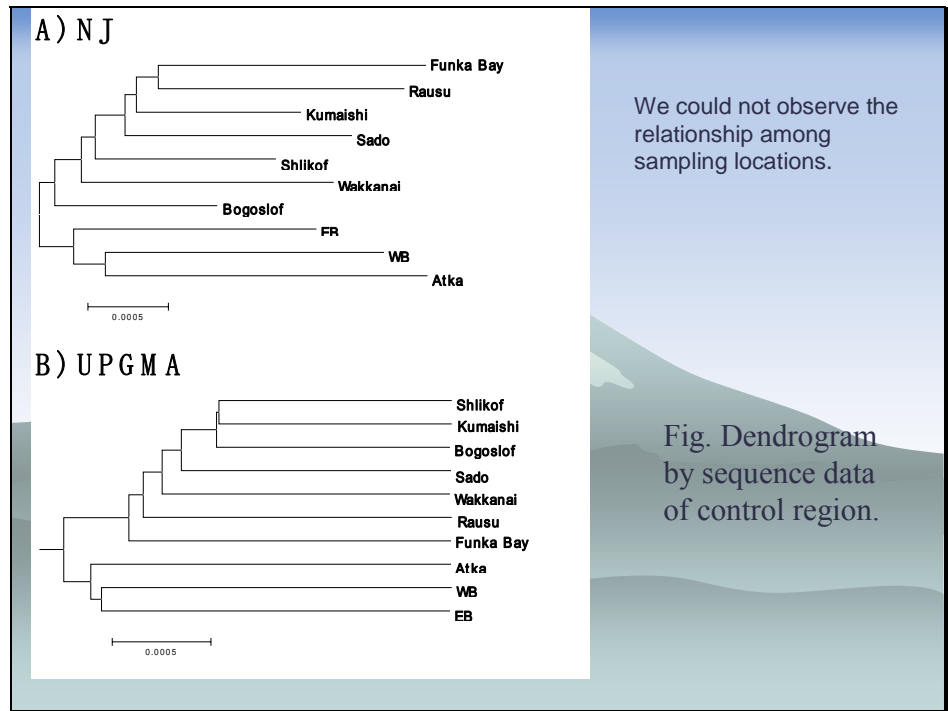
Number of nucleotide substitutions and average nucleotide substitution rate of mtDNA from walleye pollock in the Japan Sea and the Bering Sea.

Table 5. Number of nucleotide substitutions and average nucleotide substitution rate of mtDNA from walleye pollock in the Japan Sea and the Bering Sea.

Region	Size (bp)	Number of nucleotide substitutions	Average nucleotide substitution rate (%)
12S rRNA	953	6	0.20
16S rRNA	1665	4	0.05
ND1	975	21	0.61
ND2	1047	16	0.42
CO I	1551	13	0.23
CO II	699	2	0.10
ATPase8	168	2	0.45
ATPase6	684	11	0.45
CO3	786	10	0.29
ND3	351	6	0.55
ND4L	297	1	0.07
ND4	1386	17	0.34
ND5	1839	35	0.54
ND6	522	6	0.26
Cytb	1161	17	0.40
Control Region	873	12	0.50

AB094061, AB182300-AB182308





Dendrogram of relationships among sampling areas using SNAP data

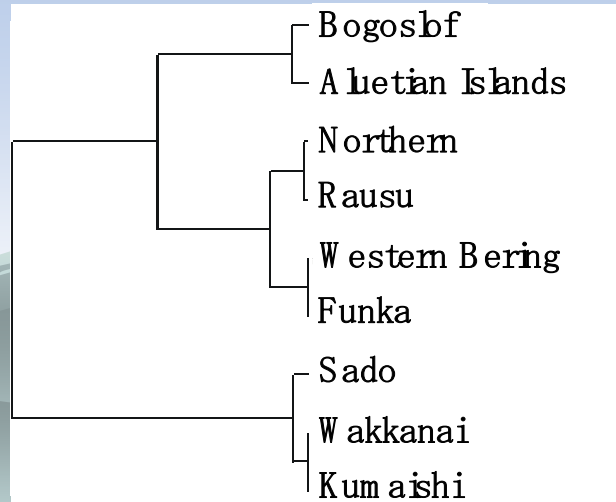


Fig. 4. UPGMA dendrogram of relationships among sampling area of walleye pollock.

Population structure

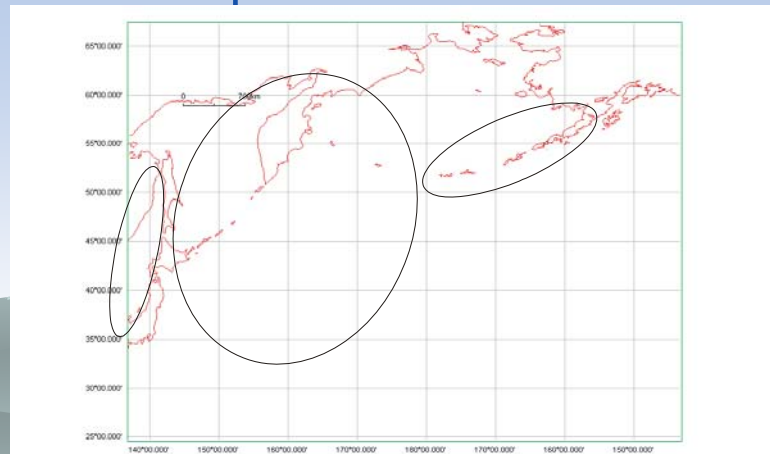


Fig. 5. Population structure of walleye pollock from this study.

Summary

- ◆ There were no area-specific nucleotide variations among sequences of mtDNA control region.
- ◆ In NJ tree, groups were formed without relations of the sampling locations by sequences data.
- ◆ In RFLP analyses, there were no area-specific fragment patterns. But the distribution of fragment patterns from three regions showed differences among sample sites.
- ◆ Composite mtDNA haploptype frequencies were different between Western Pacific and Bering Sea.
- ◆ Based upon SNAP analysis of Calmoduline region, these results are similar to past results (Allozyme).